

**Supplementary Table 1. Genes detected in guard cells.**

Affy probe <sup>a</sup>	Description	AGI number <sup>b</sup>	Experiment 1		Experiment 2		Experiment 3	
			Signal Value <sup>c</sup>	p-value <sup>d</sup>	Signal Value	p-value	Signal Value	p-value
11986_at	CaLB protein	At3g61050	2996.9	0.284715	2359.5	0.009985	1952.3	0.035163
11992_at	unknown protein	At1g24160	4651.8	0.081337	4537.1	0.003585	6165.4	0.002228
12008_at	unknown protein	At1g03140	4475.6	0.189687	4637	0.02786	3621.5	0.017001
12029_at	putative phosphatidylinositol synthase	At4g38570	5824.6	0.11716	8205.5	0.011447	7198.1	0.002617
12030_at	ES43 like protein	At4g39100	3396.8	0.284747	3324.6	0.02786	3190.7	0.005643
12035_at	unknown protein	At1g79130	3653.7	0.32083	6552.1	0.05447	2268.8	0.039365
12036_at	30S ribosomal protein S31	At2g38140	8042	0.002617	10848	0.001602	18822.5	0.000388
12053_at	no hits		3540.3	0.006524	4656.8	0.043968	4332.3	0.001141
12065_at	unknown protein	At5g26800	2693.1	0.189687	2862.5	0.011447	1647.6	0.024711
12078_at	glycolate oxidase	At3g14415	6914.8	0.006532	8485.4	0.013092	6418.8	0.007543
12098_at	unknown protein	At1g16320	10248.4	0.02786	8830.3	0.019304	4739.5	0.035163
12100_at	myb family transcription factor	At2g21650	9272	0.014937	7529.3	0.05447	3975.8	0.014937
12107_i_at	unknown protein	At4g04200	2158.2	0.468736	8181.9	0.058332	4360.8	0.009301
12109_g_at	putative uracil phosphoribosyl transferase	At4g26510	640.9	0.438361	3421.6	0.035163	2351.2	0.031336
12117_at	unknown protein	At4g27520	7571.2	0.302517	21283.7	0.05447	16463.8	0.001354
12125_at	unknown protein	At4g16450	17377.4	0.005643	17878	0.002228	30597.9	0.000322
12131_at	unknown protein	At2g30000	6041.1	0.011447	3628.4	0.014937	4843.3	0.004863
12150_at	unknown protein	At2g44080	6158.8	0.035163	2534.5	0.418069	1529	0.039365
12151_at	putative extensin	At2g43150	3453.4	0.138765	3769.4	0.031336	1640.9	0.017001
12156_at	unknown protein	At2g29020	12375.6	0.005643	12383.6	0.006532	16428.3	0.000805
12159_at	postsynaptic protein CRIPT	At1g61780	5580.1	0.035163	4509.3	0.001602	4335.1	0.001602
12163_at	unknown protein	At2g42780	5623	0.081337	2014.6	0.031336	1964.5	0.009985
12167_at	unknown protein	At3g51670	8815.9	0.000673	9530	0.02786	8893.2	0.002228
12171_at	unknown protein	At3g52500	6679.6	0.017001	6930.7	0.07383	7689.1	0.011447
12175_at	unknown protein	At2g02180	4891.1	0.138765	4515.5	0.004863	2269.4	0.024711
12177_at	unknown protein	At1g67350	7241	0.043968	3475.4	0.218983	14280.3	0.000388
12178_s_at	cysteine synthase (cpACS1)	At2g43750	6512.9	0.060419	7884.6	0.003585	7677.9	0.000673
12180_at	unknown protein	At5g44720	8599.5	0.007543	5691.1	0.002228	2162.7	0.00418
12187_at	unknown protein	At1g10410	2548.5	0.284747	4909.2	0.039365	2357.9	0.004863
12188_at	unknown protein	At2g28870	9621.9	0.007543	9206.2	0.002228	11113.5	0.001354
12192_at	unknown protein	At2g01620	4063.4	0.107301	3829.4	0.019304	2128.7	0.007543
12196_at	unknown protein	At2g28410	20983.1	0.000322	27821.4	0.000388	91172.8	0.001354
12222_s_at	unknown protein	At2g20990	6336.9	0.014937	3251.4	0.008689	8023	0.000388
12233_at	succinyl-CoA-ligase alpha subunit	At5g08300	1668.6	0.5	4766.2	0.043968	3313.1	0.003585
12234_at	putative ribosomal protein S16	At4g34620	10210.1	0.001141	5654.7	0.021866	13882.8	0.000266
12237_at	unknown protein	At3g50810	3635	0.098054	3006	0.008689	827.3	0.039365
12245_s_at	DNA-directed RNA polymerase (EC 2.7.7.6) II	At4g35800	9375.5	0.05447	15654.2	0.048995	6448.5	0.00418
12261_at	receptor kinase	At1g11340	7162.6	0.05447	8749.3	0.000673	7999.6	0.001354
12275_s_at	calcium-dependent protein kinase	At3g51850	3342.4	0.267463	3194.8	0.048995	3804.7	0.003585
12284_at	somatic embryogenesis receptor-like kinase	At1g34210	6944.6	0.002228	7655.4	0.00418	10004	0.000673
12322_at	heterogeneous nuclear ribonucleoprotein(hnRNP)	At2g33410	3394.4	0.162935	2708.3	0.048995	1873.3	0.05447
12338_at	putative pectin methylesterase	At3g14310	12326.2	0.008689	20163.5	0.008689	15391.3	0.002228
12345_at	no hits		3443.3	0.013092	1577.9	0.418069	1325	0.02786
12359_s_at	G-box-binding factor 1	At4g36730	410.3	0.956032	3511.4	0.000468	2333.4	0.001141
12374_i_at	myb DNA-binding protein (AtMYB73)	At4g37260	2611.8	0.149658	4560.2	0.010742	2309.1	0.00293
12381_at	no hits		6654.4	0.014937	8735	0.009985	12549.7	0.000219
12409_at	small nuclear ribonucleoprotein U1A	At2g47580	27686.9	0.000562	17550.7	0.000673	52702.5	0.000673
12410_g_at	small nuclear ribonucleoprotein U1A	At2g47580	10175.1	0.019304	9626.5	0.000673	14628.2	0.000959
12448_at	putative acyl-CoA synthetase	At2g47240	8554.7	0.017001	9843.7	0.008689	5568.6	0.001892
12454_at	putative ferredoxin	At2g27510	2187.9	0.378184	2813	0.021866	3622.5	0.005643
12492_at	no hits		20509.3	0.017001	14931.2	0.001141	20620.4	0.000468
12493_g_at	CLC-c chloride channel protein	At5g49890	3850.8	0.043968	7039	0.006532	4685.2	0.008689
12499_at	putative phosphatidylinositol phosphatidylcholine 4-epoxide hydrolase	At2g16380	6782.1	0.039365	7601.3	0.021866	3274.4	0.039365
12505_s_at	CONSTANS B-box zinc finger family protein	At2g47890	6668.5	0.019304	10287	0.060419	4510.2	0.008689
12510_at	no hits		225.5	0.975289	3029.5	0.048967	933.3	0.039365
12535_at	Dof zinc finger protein	At4g38000	1086	0.732537	4085.7	0.048967	5150.6	0.002617
12552_at	no hits		314.1	0.52062	3047.2	0.021866	1811.5	0.035163
12576_at	dynein light chain like protein	At4g15930	14486.7	0.001141	17028.5	0.000468	15748.9	0.000266
12579_at	unknown protein	At4g22750	5259.5	0.013092	2822.1	0.048995	2914.7	0.001892
12581_s_at	chaperonin	At1g14980	6114.8	0.02786	6607.1	0.162935	17896.9	0.000388
12592_at	HMG delta protein	At4g35570	9182.7	0.003585	7067.9	0.004863	4533.9	0.000673
12602_at	ATP-dependent RNA helicase	At3g26560	3040	0.302547	4215.2	0.02786	6677.2	0.000266
12604_at	dynein light chain like protein	At4g15930	11507.9	0.007543	12729.1	0.014937	19894.3	0.000673
12605_at	high mobility group protein 2-like	At3g51880	9157	0.039365	9175.6	0.004863	8724.5	0.002228
12606_at	putative fibrillin	At4g04020	4762.8	0.267463	4912.5	0.035163	2078.3	0.039365
12614_at	unknown protein	At4g02790	2207.6	0.267463	3703.4	0.003067	1535.1	0.019304
12616_i_at	phosphoribosyl pyrophosphate synthetase	At2g35390	1545.3	0.652557	3068.3	0.02493	5121.9	0.001109

12622_at	chaperonin	At1g23100	5644.2	0.11716	3545.4	0.017001	2679.9	0.00418
12645_at	fibrillin precursor	At4g22240	5549.4	0.035163	1716.5	0.397994	2345	0.003585
12648_at	putative lysine histidine-specific permease	At1g24400	8671.4	0.031336	8936.6	0.002228	10050.4	0.000673
12666_at	arginine serine-rich splicing factor, atRSp31	At3g61860	5282.8	0.048995	5668.2	0.107301	3057.4	0.003067
12674_at	putative oxidoreductase	At2g37540	13202.5	0.000805	7184.6	0.014937	16483	0.003585
12682_at	putative zinc finger protein	At4g02670	4259.2	0.150527	6628.2	0.014923	2359.2	0.011447
12686_at	calcium sensor homolog	At5g24270	804.7	0.458816	4514.6	0.043968	2069.2	0.048995
12739_s_at	photosystem II type I chlorophyll a b binding p	At2g34420	15883.5	0.000266	188720.5	0.000266	393379.5	0.000219
12742_at	enolase (2-phospho-D-glycerate hydrolyase)	At2g36530	49369	0.000322	55767.2	0.000388	98651.6	0.000219
12744_at	putative lectin	At3g16470	7099.1	0.004863	5083	0.127645	8963.1	0.000562
12749_at	similar to cold acclimation protein WCOR413	At2g15970	9067.4	0.162935	10122.2	0.048995	21279.5	0.00418
12753_at	putative nonspecific lipid-transfer protein	At2g38540	13612.9	0.003067	21596.1	0.000388	55381.8	0.000219
12757_at	cathepsin B-like cysteine protease	At1g02300	3153.1	0.204022	2723.7	0.017001	1962.9	0.013092
12762_r_at	putative glycine-rich protein	At2g05520	13965	0.019304	15214.1	0.000959	8452.9	0.005643
12767_at	unknown protein	At2g23120	120148.2	0.000266	118267	0.000266	212831.2	0.000219
12768_at	unknown protein	At2g15890	21404.7	0.002228	19957.7	0.004863	6322.5	0.004863
12773_at	putative membrane channel protein	At2g28900	223196.7	0.000219	189894.7	0.000219	177885.6	0.000219
12774_at	unknown protein	At1g09310	7360	0.019304	3773.7	0.017001	6196.4	0.014937
12775_s_at	ATPase 70 kDa subunit	At1g78900	8972.1	0.008689	7549.3	0.011447	9999.9	0.002617
12776_at	no hits		6778.6	0.11716	7539.2	0.043968	3569	0.001354
12780_s_at	unknown protein	At4g10840	5142.5	0.03934	6363.4	0.009985	3332.8	0.001141
12781_at	unknown protein	At1g13930	9132.4	0.02786	6006.9	0.009985	102917.8	0.000266
12783_s_at	no hits		7987.9	0.066865	10904.3	0.024711	15006.5	0.002617
12788_at	unknown protein	At1g23130	107913.7	0.000219	112029.9	0.000388	36522.2	0.000219
12791_r_at	unknown protein	At2g45180	10482.8	0.006575	5982.3	0.181343	16901.8	0.000491
12795_at	cytochrome p450 family	At1g13090	6737.3	0.006532	6365.1	0.017001	2684	0.013092
12796_s_at	beta-ketoacyl-CoA synthase	At2g26250	18070.9	0.000388	20115.7	0.001602	24685.1	0.000673
12797_s_at	S-adenosylmethionine synthase 2	At4g01850	8378.7	0.005643	6087.4	0.019304	3729.1	0.008689
12800_at	glycine hydroxymethyltransferase like protein	At4g37930	9284.1	0.107301	8900.7	0.013092	15089.5	0.000562
12803_s_at	protein induced upon wounding	At4g24220	5294.6	0.017001	827.4	0.175989	3545.8	0.021866
12808_at	40S ribosomal protein S26	At2g40510	10408.1	0.008689	15211.4	0.048995	24380.9	0.000266
12818_at	E2, ubiquitin-conjugating enzyme	At2g36060	11292.5	0.003585	9212.9	0.000805	10325.3	0.001892
12819_at	lectin like protein	At4g19840	12122.5	0.021866	25766.5	0.001354	4303.1	0.089405
12830_f_at	polyubiquitin	At5g20620	8427.8	0.019287	8155.6	0.001141	7134.8	0.000959
12842_s_at	no hits		20687.1	0.000266	19092.1	0.009985	31768.9	0.000322
12843_s_at	unknown protein	At2g16590	11927.4	0.003585	12123.2	0.001602	16926	0.000219
12844_s_at	unknown protein	At2g16590	10542.9	0.008689	9951.4	0.000805	2178.1	0.001892
12846_s_at	no hits		46654.7	0.000219	31791.2	0.000266	26770.6	0.000219
12847_at	no hits		39992.5	0.000388	33434.7	0.000266	60101.3	0.000219
12857_at	putative thioredoxin	At1g08570	7946.1	0.014937	7347.6	0.000673	19308.6	0.000266
12858_at	no hits		2000.2	0.35869	7447	0.000219	26484.4	0.000219
12860_s_at	thioredoxin h	At1g11530	5783.6	0.02786	7795.4	0.001892	5020	0.014937
12861_s_at	thioredoxin	At5g06690	7072.2	0.081337	7376.2	0.005643	2590.5	0.014937
12876_at	MADS-box protein	At5g60910	1042.4	0.849473	2664.1	0.017001	4089.3	0.00418
12877_at	leaf development protein Argonaute	At1g48410	9835.6	0.013092	7214.8	0.000322	13002.9	0.000388
12878_at	bZIP transcription factor, HBP-1b homolog	At5g06950	1674.9	0.561639	3400.4	0.024711	1407	0.043968
12881_s_at	no hits		27326.1	0.000388	22173.3	0.000219	16010.5	0.000219
12885_s_at	ascorbate peroxidase, putative (APX)	At4g35000	21285.5	0.000219	22867.8	0.000219	49020.6	0.000219
12893_at	alcohol dehydrogenase	At5g43940	34334.9	0.006532	36349.5	0.003585	52661.2	0.003585
12894_g_at	alcohol dehydrogenase	At5g43940	11643.6	0.014937	9608.6	0.001354	18901	0.000562
12900_r_at	no hits		4528.5	0.057926	3192.1	0.324822	2805.5	0.0232
12914_s_at	COP1 regulatory protein	At2g32950	13286.6	0.005643	11793.6	0.004863	15088.4	0.001141
12920_at	no hits		12451.9	0.003585	13980.7	0.000562	39276.3	0.000219
12934_at	PRL1 protein	At4g15900	1833.6	0.561639	7938.4	0.000673	10392.2	0.000322
12936_s_at	no hits		126032.1	0.000219	141867.5	0.000219	184929	0.000219
12940_at	thioredoxin	At1g19730	6891.7	0.138765	8976.2	0.048995	8049.3	0.001141
12941_g_at	thioredoxin	At1g19730	6638.9	0.039365	485	0.824011	4980.5	0.000562
12959_at	putative serine threonine protein kinase	At2g32850	7252.2	0.004863	13533.6	0.003067	10207.4	0.000562
13007_at	putative ferredoxin-thioredoxin reductase	At2g04700	22770.6	0.003585	36929.6	0.001602	27548	0.000468
13042_at	no hits		9809.1	0.017001	3132.3	0.458816	3166.1	0.006532
13044_at	unknown protein	At2g39670	2664.6	0.339558	4848.5	0.039365	2852.3	0.019304
13062_at	unknown protein	At2g14910	7134.7	0.00418	4268.6	0.043968	3316.4	0.003585
13069_at	putative ADP-ribosylation factor	At1g23490	10268	0.001141	4842.8	0.007534	9224.8	0.000673
13070_at	putative pyruvate kinase	At2g36580	13158.4	0.009985	9336.5	0.007543	11973.3	0.011447
13073_s_at	ribosomal protein L11	At4g18730	9813.5	0.02786	6106	0.000959	14665.6	0.006532
13074_at	putative ribosomal protein S4	At2g17360	2184.9	0.47938	5372.9	0.024711	4855.9	0.017001
13075_i_at	putative putative 60S ribosomal protein L17	At1g04480	7571.8	0.04974	6242.8	0.035595	7079.8	0.02987
13076_r_at	putative putative 60S ribosomal protein L17	At1g04480	15764.4	0.00418	10916.3	0.005643	14265.1	0.000468
13077_f_at	putative putative 60S ribosomal protein L17	At1g04480	17574.2	0.009985	17541.8	0.009985	22457.3	0.003067
13078_at	putative dTDP-glucose 4-6-dehydratase	At2g47650	9169.3	0.002228	9253.7	0.005643	8977.1	0.000219
13080_at	40S ribosomal protein S25	At2g21580	17630.5	0.008689	14502.1	0.001141	36349	0.000219
13088_at	ubiquinol-cytochrome c reductase - like protein	At4g32470	16990.6	0.002617	15075.7	0.014937	31382.8	0.000388
13089_at	putative dTDP-glucose 4-6-dehydratase	At2g27860	12987.7	0.066865	13334.3	0.019304	44339.2	0.000266

13091_r_at	putative transport protein SEC61 beta-subunit	At2g45070	25645.2	0.046875	17867.7	0.296875	209889.4	0.001953
13093_at	B12D-like protein	At3g48140	33004.6	0.000266	31724.4	0.000219	104283.6	0.000219
13095_at	putative signal sequence receptor, alpha subunit	At2g21160	25158.9	0.000266	29415.1	0.000562	44604.5	0.000219
13096_g_at	putative signal sequence receptor, alpha subunit	At2g21160	7760.8	0.000805	6039.1	0.00418	6708	0.003067
13101_at	unknown protein	At4g28470	746.6	0.234557	8507.7	0.031314	3889.2	0.003067
13102_at	putative protein transport protein SEC61 alpha subunit	At2g34250	8753.8	0.011447	5818.3	0.006524	8390.7	0.000673
13104_s_at	20S proteasome beta subunit E1	At1g13060	4672.6	0.016986	5150.2	0.175989	10948	0.001892
13105_at	60S ribosomal protein L23	At2g33370	5503.6	0.066865	4766.2	0.007543	11534.2	0.000805
13106_at	E2, ubiquitin-conjugating enzyme	At1g78870	2038.6	0.284747	6765.3	0.02786	5822.6	0.001892
13107_s_at	40S ribosomal protein S17	At2g04390	7039.8	0.024711	3652.2	0.098054	5606.8	0.001141
13108_at	40S ribosomal protein S26	At2g40590	595	0.749276	5525.2	0.013092	1793.5	0.02786
13109_at	protein translation factor Sui1 homolog	At1g54290	7770.8	0.019304	9047.2	0.035163	6324.6	0.001892
13110_at	putative symbiosis-related protein	At4g04620	3760.7	0.011447	4333.5	0.011447	2148.4	0.014937
13116_at	unknown protein	At2g20760	6708.2	0.003067	3629.5	0.32083	4579.8	0.017001
13117_at	unknown protein	At1g65220	11310.3	0.039365	7679.8	0.014937	7420.5	0.008689
13121_at	chloroplast chaperonin 10	At2g44650	5724	0.043968	4769.7	0.006532	3885.9	0.008689
13122_at	unknown protein	At4g20150	16899.4	0.000673	16711.1	0.000805	31820.7	0.000219
13124_at	phosphoenolpyruvate carboxylase	At2g42600	13720.2	0.05447	9922.3	0.066865	28431.1	0.000266
13125_at	ubiquitin activating enzyme 1 (UBA1) E1	At2g30110	17691.7	0.007543	26171.8	0.002617	33938.9	0.000219
13128_at	protein phosphatase 2C (PP2C)	At4g31860	5993	0.035163	6075	0.000959	7184.9	0.000322
13129_f_at	ubiquitin extension protein 1 (UBQ1)	At3g52590	39850	0.000562	46010.4	0.002617	67132.5	0.000219
13132_at	putative ribosomal protein L7	At2g01250	15345.1	0.001602	12773	0.004863	22669.1	0.000266
13134_s_at	putative galactinol synthase	At2g47180	4117.8	0.009985	4760.6	0.048995	9906.2	0.000219
13139_at	unknown protein	At1g78620	4348.1	0.05447	1525.7	0.5	4411.7	0.001602
13140_at	putative RING zinc finger ankyrin protein	At2g28840	3044.4	0.35869	6953	0.02786	4310.4	0.001354
13142_at	unknown protein	At4g34190	8349.3	0.02786	10313.3	0.002617	9866.2	0.000805
13148_at	unknown protein	At1g64750	17809.3	0.003585	15427	0.003585	44252.1	0.000322
13150_at	putative rubisco subunit binding-protein alpha subunit	At2g28000	30245.7	0.000219	31696.1	0.000219	100764.8	0.000219
13162_at	unknown protein	At4g34030	2885.3	0.267463	3765.3	0.007543	1404.9	0.031336
13166_at	60S ribosomal protein L39	At2g25210	14788.9	0.003067	17478.3	0.013092	39227.5	0.000322
13167_at	unknown protein	At1g60170	4048.7	0.009985	6180.5	0.150527	2494.8	0.039365
13169_r_at	no hits		24983.8	0.039365	28493.2	0.127645	25408.5	0.021866
13177_at	growth factor like protein	At4g12720	1517	0.715253	5792.6	0.006532	2138.2	0.000219
13179_at	putative SF16 protein	At2g43680	4234.6	0.035163	6626.9	0.001892	2519	0.013092
13180_s_at	putative inorganic pyrophosphatase	At2g18230	10917.5	0.014937	10803.1	0.043968	6565.6	0.003585
13182_i_at	thioredoxin	At5g42980	486845.9	0.001109	625736.3	0.001109	542678.9	0.001109
13183_r_at	thioredoxin	At5g42980	415257.8	0.000219	397327.9	0.000266	389776.9	0.000266
13184_s_at	thioredoxin	At5g42980	197709.3	0.000219	232276.7	0.000219	250637.3	0.000219
13185_at	thioredoxin	At5g39950	77756.4	0.000388	77524.4	0.000266	180907.6	0.000219
13186_g_at	no hits		14501.2	0.011447	14982.3	0.021866	31354.7	0.000673
13187_i_at	thioredoxin	At1g45145	65886.1	0.000327	39815.2	0.000327	117220.5	0.000327
13188_r_at	thioredoxin	At1g45145	10606.1	0.006532	7939.1	0.006532	15213.5	0.000388
13189_s_at	thioredoxin	At1g45145	43802	0.000322	41996.4	0.000219	62415.6	0.000219
13190_s_at	putative thioredoxin reductase	At2g17420	6914.9	0.019287	3259.2	0.218983	4739.7	0.000959
13205_at	putative transitional endoplasmic reticulum ATPase	At3g09840	8947.9	0.031336	7541.1	0.284747	12461.7	0.001354
13208_s_at	RUB-activating enzyme AXR1	At1g05180	5991.2	0.014937	6197.4	0.017001	5725.6	0.002228
13213_s_at	light-harvesting chlorophyll a b binding protein	At3g54890	42335.5	0.000959	47183.7	0.000562	81763.2	0.000388
13214_at	light-harvesting chlorophyll a b binding protein	At3g47470	322406.5	0.000673	304876.2	0.000805	83395.2	0.000562
13232_s_at	plastid protein	At2g33430	12631.6	0.002228	7949.7	0.005643	16140.2	0.000388
13233_at	unknown protein	At2g35240	840.2	0.88284	3860.8	0.008689	5228.8	0.000805
13234_s_at	plastocyanin	At1g20340	7753.8	0.009975	1578.2	0.048995	14684.2	0.000562
13236_at	2-dehydro-3-deoxyphosphoheptonate aldolase	At4g39980	15315.3	0.001892	13992.3	0.107301	36678.3	0.000388
13237_at	2-dehydro-3-deoxyphosphoheptonate aldolase	At4g33510	16769	0.000805	15539.1	0.000673	30187.8	0.000468
13242_at	no hits		10846.6	0.000805	10626.5	0.000562	15726.6	0.000219
13250_s_at	Flowering time control protein (FCA)	At4g16280	6819.9	0.081337	11979.1	0.014937	18969.1	0.000266
13254_at	farnesyl pyrophosphate synthetase 2 (FPS2)	At4g17190	29518.6	0.000219	25650.1	0.000388	101218.3	0.000322
13257_s_at	geranylgeranyl pyrophosphate synthase (GGP)	At1g49530	4466.9	0.007543	4089.5	0.007543	1402.7	0.117121
13259_s_at	glutathione peroxidase	At2g31570	49182.7	0.008689	63139	0.000959	140773.5	0.000219
13261_at	glutathione reductase	At3g24170	3608.3	0.267463	5702.5	0.048995	10414.1	0.013092
13264_s_at	glutathione transferase	At2g30860	9140.7	0.048995	11625.7	0.007543	6263.9	0.013092
13267_at	glutathione transferase	At1g78380	7840.2	0.006532	7551.5	0.000673	11777.4	0.001892
13270_at	no hits		1435.4	0.732537	2380.9	0.021866	13103.6	0.000388
13283_at	mitochondrial chaperonin hsp60	At3g23990	2726	0.250724	2704.2	0.035163	3279.1	0.013092
13287_at	putative heat-shock protein	At1g79930	8613.7	0.005643	5869.6	0.043968	4234.1	0.006532
13305_at	putative protein kinase	At2g35050	11294.6	0.014937	12059	0.00418	10078.6	0.000805
13314_at	unknown protein	At2g04090	7310.9	0.048995	11798.9	0.048995	8401.6	0.007543
13334_at	putative sugar transporter protein	At1g05030	2142	0.697453	4806.8	0.043968	3761.9	0.007543
13347_at	thymidylate kinase	At5g59440	2863.7	0.162935	6294.5	0.009985	1883.8	0.011447
13366_s_at	no hits		5586	0.175989	11391.2	0.014937	5348.5	0.007543
13374_at	unknown protein	At1g23570	6174.5	0.000805	3103.8	0.127645	1781.6	0.048995
13383_at	putative DNA-directed RNA polymerase II subunit	At2g04630	4726.4	0.066865	4897.1	0.008689	4780.1	0.004863
13471_g_at	unknown protein	At2g43105	6492	0.11716	8396.5	0.02786	5436.2	0.021866
13482_at	nodulin - like protein	At2g37450	9009.6	0.007543	5812.7	0.02786	1779.8	0.001141

13484_at	putative membrane transporter	At2g13100	3528.8	0.089405	3062.1	0.00418	1578.7	0.02786
13534_at	nodulin - like protein	At5g25940	4959	0.005643	3454.3	0.267463	4875.7	0.007543
13544_at	unknown protein	At4g26850	5671.3	0.031336	3011.9	0.048995	14199.9	0.000322
13547_at	3-isopropylmalate dehydratase, small subunit	At2g43100	9370.7	0.035163	9179.5	0.004863	2388.3	0.043968
13551_at	putative MAP kinase	At2g42880	2407.5	0.11716	4321	0.031336	3653.2	0.008689
13553_at	disease resistance protein (CC-NBS-LRR class)	At1g61190	3564.6	0.089405	3372.8	0.048995	3339.5	0.019304
13554_at	putative beta-ketoacyl-CoA synthase	At2g16280	9241.7	0.004863	10923	0.002228	21806.6	0.001141
13560_at	putative Ser Thr protein kinase	At1g16270	6947.1	0.003067	8726.2	0.011447	14875	0.000562
13561_at	no hits		5740.7	0.175989	6039.7	0.039365	8705.6	0.001141
13562_at	carbonic anhydrase	At1g70410	4272.2	0.32083	6474.9	0.024711	3872.2	0.05447
13563_at	CONSTANS B-box zinc finger family protein	At2g24790	5961.1	0.031336	5733.1	0.019304	7438	0.001892
13569_at	FAD-linked oxidoreductase family	At4g20840	3802.2	0.039365	2026.7	0.127645	1240.5	0.043968
13570_at	Calmodulin-binding protein	At2g18750	4806.8	0.048995	5026.1	0.07383	2531.6	0.043968
13572_s_at	no hits		22042.2	0.002228	15531.7	0.000219	26438.3	0.000219
13573_at	formamidase	At4g37550	9231.8	0.043968	8616	0.05447	20009.7	0.000562
13574_at	putative vacuolar ATPase	At4g02620	18080.2	0.000266	11936.9	0.002228	16919	0.000266
13577_s_at	CER2	At4g24510	36481.1	0.001892	40054.4	0.000673	91193.4	0.000219
13578_at	ribosomal protein L14	At4g27090	36528.7	0.000468	42890.3	0.000219	59711.9	0.000219
13585_at	unknown protein	At2g34170	5750.5	0.127645	7055.5	0.001354	12390.1	0.000388
13590_at	unknown protein	At2g12140	4792.4	0.031336	2810.2	0.418069	9056.3	0.001892
13594_at	unknown protein	At2g23090	16366.7	0.000562	15229.4	0.001141	21234.7	0.000388
13606_at	26S proteasome subunit 4	At2g20140	7101.3	0.021866	4148.2	0.066865	3649.6	0.006532
13612_at	E2, ubiquitin-conjugating enzyme	At2g16740	8792.7	0.019304	4355.9	0.043968	1138.5	0.107301
13616_s_at	60S ribosomal protein L23A	At2g39460	5466.2	0.107301	11076	0.017001	19614.4	0.000959
13630_at	putative WD-40 repeat protein	At2g19540	4664.2	0.089369	3947.5	0.005643	4535.8	0.001354
13637_at	AX110P -like protein	At4g09670	351.8	0.849473	1840.5	0.039365	1260.1	0.039365
13644_at	unknown protein	At2g45990	4952.2	0.098054	2912.2	0.035163	1899.1	0.048995
13645_at	unknown protein	At1g05340	9443.6	0.006532	7185.7	0.043968	11698.2	0.000388
13646_at	unknown protein	At2g34690	13006	0.003585	9936.3	0.000805	6575.4	0.008689
13652_at	unknown protein	At2g47710	20024.4	0.001892	37244.6	0.001354	40121.9	0.000322
13655_at	putative esterase D	At2g41530	9389.7	0.007543	8761.7	0.003585	7390.3	0.007543
13657_at	unknown protein	At1g49410	12651.1	0.003585	8836.3	0.000805	32992.3	0.000219
13663_s_at	auxin-regulated protein (IAA8)	At2g22670	14564.7	0.00418	16524.5	0.000959	39917.5	0.000805
13664_s_at	auxin-induced protein IAA9	At5g65670	11859.8	0.000468	18538.4	0.009985	16043.1	0.000388
13667_s_at	isopentenyl pyrophosphate:dimethylallyl pyrophosphate transferase	At5g16440	3672.3	0.02786	5165.8	0.011447	9971.2	0.000673
13669_at	kinase associated protein phosphatase	At5g19280	9372.6	0.017001	6033.8	0.014937	20242.6	0.000562
13670_s_at	putative K+ channel, beta subunit	At1g04690	8664.6	0.013092	10938.6	0.035163	11718.3	0.000805
13672_at	no hits		7607.8	0.005643	6965.4	0.001141	2807.7	0.002228
13678_at	light-harvesting chlorophyll a b binding protein	At1g19150	7546.9	0.107301	10020.3	0.048995	27516.1	0.000562
13680_at	lipoxygenase	At1g55020	8958.3	0.150527	8332.6	0.024711	10295.9	0.00418
13681_s_at	zinc-finger protein Lsd1	At4g20380	11311.9	0.00418	9396.2	0.019304	12868.8	0.000562
13698_at	putative shikimate kinase	At3g26900	7032.4	0.019304	5529.9	0.02786	5739.4	0.024711
13700_at	unknown protein	At3g04550	4140.9	0.11716	3995.9	0.013092	4762.1	0.014937
13785_s_at	cold-regulated protein cor15b precursor	At2g42530	16778.9	0.003585	10311.3	0.001602	11925.1	0.003067
13829_at	unknown protein	At4g33680	4776.2	0.07383	4029.4	0.008689	5532.5	0.000805
13858_at	putative PHD-type zinc finger protein	At2g36720	3233.7	0.127645	3682.1	0.021866	1489.3	0.035163
13870_at	steroid 22-alpha-hydroxylase (DWF4)	At3g50660	5841.5	0.05447	2768.9	0.089405	4828.1	0.013092
13883_at	DNA binding protein GT-1	At1g13450	4971.6	0.150527	6629.7	0.009985	2542.9	0.001141
13895_at	putative phospholipase	At2g39420	1565.5	0.52062	2828	0.02786	1298.5	0.035163
13902_at	unknown protein	At5g18620	2869.4	0.32083	2646.3	0.039365	2383.7	0.014937
13904_s_at	chloroplast FtsH protease	At1g50250	6746.7	0.035163	5676.3	0.024711	4392.6	0.008689
13907_at	putative small nuclear ribonucleoprotein E	At2g23930	2569.8	0.189687	2404.4	0.05447	2397.5	0.019287
13916_at	unknown protein	At2g19800	18914.2	0.001892	14299.6	0.039365	5222.8	0.001141
13917_at	unknown protein	At1g03330	2058.9	0.397994	4509	0.001892	7307.6	0.000562
13919_at	unknown protein	At1g78780	4212.9	0.32083	4902.2	0.048995	3898.5	0.003585
13940_at	putative acidic ribosomal protein	At4g25890	16719.8	0.003067	13689.8	0.009985	26964.8	0.000673
13950_at	unknown protein	At4g17550	2838.6	0.47938	3180.2	0.048995	1889.8	0.043968
13953_at	unknown protein	At2g33255	11546.1	0.003585	8889.7	0.001141	35078.7	0.000219
13957_at	putative calmodulin	At2g03150	2700.7	0.089405	1668.5	0.039365	2125.9	0.019304
13981_s_at	unknown protein	At2g45720	258.5	0.438361	3469.8	0.039365	4134.7	0.00418
13997_at	MADS-box protein	At5g26950	4398.2	0.043941	3460	0.189687	2590	0.014937
14020_i_at	starch branching enzyme II	At2g36390	19102.4	0.008057	14163.9	0.000244	70469.4	0.000244
14021_r_at	starch branching enzyme II	At2g36390	9473.6	0.031336	6949	0.005643	24063.2	0.000562
14022_s_at	starch branching enzyme II	At2g36390	10986.3	0.007543	9960.2	0.007543	9953.9	0.00418
14048_at	putative protein kinase	At2g18890	18390.1	0.024711	11383.1	0.024711	15202.9	0.000388
14065_at	unknown protein	At2g22900	6397.1	0.107301	8084.5	0.021866	12927.4	0.00418
14067_at	putative small heat shock protein	At2g19310	9894	0.060419	7355.5	0.048995	8394.6	0.002617
14073_at	water stress-induced protein	At1g54410	865759.3	0.000219	750957.8	0.000219	756295.6	0.000219
14078_at	unknown protein	At2g25110	2795.9	0.5	9520.7	0.02786	8345.6	0.000805
14088_at	unknown protein	At1g51160	8721.2	0.009985	5879.2	0.000562	10669	0.001141
14090_i_at	unknown protein	At2g15830	34205.1	0.000893	25958.9	0.000494	142212.3	0.000893
14091_r_at	unknown protein	At2g15830	12573.7	0.006532	11383.3	0.035163	13151.4	0.001354
14099_at	auxin-regulated protein	At2g20820	28104.2	0.006532	35303	0.02786	53282.5	0.000322

14101_at	unknown protein	At4g33640	420	0.837065	3462	0.05447	1797.6	0.039365
14103_at	unknown protein	At2g46390	14431.5	0.003067	23873	0.008689	23686.1	0.001141
14108_at	unknown protein	At4g30010	283702.8	0.000388	119112.8	0.000388	455582.7	0.000266
14116_at	hexose transporter	At5g26340	17363.5	0.001892	14369	0.000959	16231.2	0.000266
14117_at	cytochrome p450 family	At4g37410	4279.9	0.05447	10260.1	0.017001	2386	0.048995
14118_i_at	similar to cytochrome p450 family	At3g48280	11201.6	0.04343	5520.5	0.057926	10767.5	0.016523
14123_at	MADS-box protein (AGL20)	At2g45660	2528.7	0.066865	5177	0.017001	2294.5	0.048995
14239_s_at	transcription factor inhibitor I kappa B	At1g64280	7029.2	0.043968	4528.6	0.07383	5965.8	0.009985
14245_at	no hits		64738.3	0.000266	80080.9	0.000219	144870.5	0.000219
14391_at	RING-H2 finger protein RHF1a	At4g14220	7625.2	0.05447	1982.5	0.52062	5494.9	0.005643
14397_at	unknown protein	At4g28440	3601.1	0.302547	8121.3	0.043968	7047.6	0.001141
14400_at	unknown protein	At4g25260	6000.8	0.107301	6079.7	0.013092	6734.4	0.008689
14418_at	nodulin - like protein	At2g37460	5832.1	0.035163	5641.5	0.002228	1670.7	0.004863
14460_at	unknown protein	At2g18090	5048.3	0.021866	3051.5	0.098054	2746.8	0.001892
14463_at	unknown protein	At2g37200	4186.8	0.021866	4841	0.009985	5560	0.003067
14472_at	monooxygenase 2 (MO2)	At5g05320	4660	0.043968	136.3	0.849473	1201.2	0.024711
14477_at	unknown protein	At4g32760	5186	0.043968	4501.4	0.218983	2343.2	0.021866
14479_at	EF-Hand containing protein	At4g38810	4545.3	0.043968	3805.6	0.150527	11630.9	0.001141
14481_at	unknown protein	At4g10140	11196.8	0.003585	6942.8	0.02786	9076.7	0.000959
14483_at	unknown protein	At1g07960	10114.6	0.009985	7202.8	0.039365	2538.7	0.011447
14486_at	unknown protein	At4g15770	10494.3	0.008689	4376.5	0.162935	13009.1	0.000805
14490_at	unknown protein	At2g06530	7029	0.035163	4015.5	0.011447	2475.2	0.003585
14491_at	putative trypsin inhibitor	At2g43530	13900.5	0.000805	8698.1	0.000805	21603.2	0.000266
14492_s_at	histone H1 like protein	At2g30620	17038.1	0.000805	13384.3	0.000266	37696.1	0.000219
14495_at	unknown protein	At2g26660	6028	0.031336	4197.7	0.035163	3022.9	0.039365
14498_at	unknown protein	At2g41160	3803.5	0.204022	5010.3	0.009985	4525.8	0.013092
14511_at	putative protein with C-terminal RING finger	At2g37150	7707.1	0.006532	1473.6	0.837065	2570.1	0.02786
14513_s_at	putative lipase	At2g42690	425.8	0.561639	2961.5	0.039365	1912.9	0.035163
14516_at	unknown protein	At2g35110	9676.2	0.175989	17206.8	0.05447	19168.5	0.009985
14527_at	unknown protein	At2g30500	6675.7	0.007543	11498.9	0.000388	9828.1	0.000805
14536_s_at	no hits		6290.9	0.002228	4635.6	0.005643	9598.1	0.000388
14543_r_at	no hits		6863	0.04974	32748.7	0.091169	6169.5	0.003825
14555_at	unknown protein	At2g36400	11412.1	0.007543	2352.1	0.175989	2566.2	0.031336
14556_at	unknown protein	At4g35920	4155.9	0.175989	4763.7	0.014937	2489.8	0.001141
14563_at	unknown protein	At2g34860	3426.2	0.009985	6535	0.005643	4043.8	0.004863
14564_at	unknown protein	At2g38710	4756.5	0.11716	4616.2	0.019304	5769.5	0.002617
14565_at	putative steroid binding protein	At2g24940	65232.5	0.000673	57176.1	0.000266	81976.3	0.000266
14580_at	unknown protein	At2g28370	13116.9	0.021866	12576.4	0.000959	17669	0.000388
14581_s_at	unknown protein	At2g04900	11262.6	0.035163	15336.8	0.001892	11361.2	0.000266
14582_at	Calmodulin-binding protein	At2g38800	10133.9	0.007543	10044.4	0.001892	8701.1	0.000672
14584_at	unknown protein	At2g40110	6761	0.000805	6436.1	0.001602	6201.8	0.000388
14586_at	unknown protein	At4g34600	8021.8	0.039365	4793.8	0.267463	5760	0.024711
14596_at	rhodanese-like domain protein	At4g27700	389.4	0.933135	3773.9	0.009985	1885.2	0.024711
14598_at	2-hydroxy-6-oxohepta-2,4-dienoate hydrolase	At4g12230	2782.1	0.378184	4578.1	0.031336	2353.7	0.014937
14601_at	unknown protein	At1g15270	26064.8	0.000673	21799.3	0.011447	21896.5	0.000468
14602_at	unknown protein	At1g15370	3776.7	0.267463	3136.9	0.019304	4159.9	0.000562
14610_at	glycosyl hydrolase family 1	At1g60260	5771.1	0.031336	2230.9	0.098054	2961.3	0.011447
14622_at	putative phytochrome A	At1g09570	14004.7	0.000468	16905.9	0.000266	30168.2	0.000219
14625_g_at	phytochrome B	At2g18790	1092	0.732537	5829.8	0.043968	2541.2	0.003585
14628_r_at	no hits		10204	0.031336	19934.2	0.004863	8503.7	0.001892
14641_at	ATP dependent copper transporter	At5g44790	21297.7	0.000673	20229.3	0.001141	28380.7	0.000266
14658_s_at	cysteine proteinase RD19A	At4g39090	24024.1	0.002228	22577.7	0.001892	15961.6	0.001602
14663_s_at	glycosyl hydrolase family 37 (trehalase)	At4g24040	9951.8	0.008689	17055.3	0.001354	11928.3	0.008689
14664_i_at	trehalose-6-phosphate synthase	At1g78580	41510.8	0.000936	39345.3	0.011565	89871.4	0.000737
14665_r_at	trehalose-6-phosphate synthase	At1g78580	37079.5	0.005859	45432.1	0.001953	80153.8	0.005859
14667_at	tryptophan synthase beta chain 1 precursor	At5g54810	26155.7	0.000959	16622.6	0.000322	24256.9	0.001141
14670_at	putative thioredoxin M	At2g15570	8532.3	0.031336	9104.9	0.043968	7655.1	0.066865
14684_s_at	unknown protein	At4g01150	16846.4	0.007543	42283.6	0.002617	43015.7	0.000468
14688_at	unknown protein	At2g37490	9961.9	0.00418	17973.4	0.003585	15962.3	0.000266
14689_at	unknown protein	At5g67490	17474.4	0.003067	11850.9	0.021866	20720.9	0.000673
14691_at	no hits		3263	0.5	6606.4	0.043968	2886.9	0.009985
14697_g_at	auxin-regulated protein	At2g21620	5135.8	0.005643	8541.8	0.189687	3203.5	0.003067
14703_at	unknown protein	At1g47420	10674.2	0.001892	16839.3	0.000266	22928.6	0.000468
14712_s_at	PINHEAD	At5g43810	6194	0.035163	2891.9	0.02786	4891.2	0.002228
14713_s_at	plasma membrane proton ATPase (PMA)	At2g18960	25401.6	0.000959	31014.6	0.000673	109506.1	0.001602
14714_s_at	gamma tonoplast intrinsic protein	At2g26520	7912.1	0.048995	10080.1	0.007543	22400.4	0.002228
14717_s_at	CLC-a chloride channel protein	At5g40890	68596.1	0.000322	49786	0.000388	403318.9	0.000219
14719_s_at	3-ketoacyl-CoA thiolase	At2g33150	202006.7	0.000219	149411.9	0.000219	309354.1	0.000219
14721_s_at	S-adenosylmethionine decarboxylase	At3g02470	9167.8	0.013092	17488.9	0.004863	12959.6	0.00418
14722_s_at	14-3-3 protein GF14 lambda	At3g10450	44315.4	0.000468	43050	0.000805	65051.5	0.000266
14723_f_at	AP2 domain protein RAP2.3	At3g16770	8979.8	0.05447	10067.5	0.250724	11226.4	0.008689
14724_f_at	reversibly glycosylated polypeptide-3	At5g15650	5038.8	0.250724	5274.7	0.017001	5413.2	0.002228
14726_s_at	germin-like protein	At1g72610	12007.4	0.035163	3157.6	0.127606	37599.9	0.000673

14727_s_at	ankyrin repeat-containing protein 2	At4g35450	20906.4	0.001892	16999.4	0.000468	53239.7	0.000219
14728_s_at	no hits		5922.5	0.039365	4523.6	0.204022	1945.3	0.035163
14729_s_at	glyceraldehyde 3-phosphate dehydrogenase A	At3g26650	42442.2	0.000805	30664	0.001141	32643.8	0.017001
14730_s_at	glutamate decarboxylase 2 (GAD 2)	At1g65960	16009.8	0.000805	13428.4	0.05447	8975.3	0.013092
14731_s_at	glutathione S-conjugate ABC transporter (AtMR)	At2g34660	3189.1	0.060419	4788	0.004863	3533.6	0.005643
14733_s_at	delta-1-pyrroline 5-carboxylase synthetase (P5C)	At2g39800	36088.3	0.000388	41322.8	0.000219	123912.6	0.000266
14734_s_at	14-3-3 protein GF14 psi	At5g38480	4813	0.066865	14885.4	0.043968	38173.4	0.000562
14736_s_at	E3 ubiquitin ligase SCF complex subunit, SKP1	At1g75950	12987.4	0.024711	18680.9	0.001602	35658	0.000562
14737_s_at	alanine-glyoxylate aminotransferase	At2g13360	13250.3	0.039365	18915.8	0.02786	34552.3	0.001141
14843_at	unknown protein	At1g04620	3480.7	0.250724	5936.9	0.05447	1608	0.009985
14870_at	auxilin-like protein	At1g21660	7378.3	0.043968	4700.6	0.043968	4578.3	0.008689
14907_at	unknown protein	At1g10030	9265.5	0.035163	3634.9	0.138765	3987.1	0.002617
14917_at	unknown protein	At2g35760	4556.5	0.02786	4276	0.127645	3119.6	0.004863
14920_g_at	unknown protein	At2g27350	6374.8	0.378184	3652.4	0.005643	6444.7	0.001354
14946_at	unknown protein	At4g21620	37341.9	0.000468	46395.5	0.001892	49837	0.000388
14954_i_at	unknown protein	At4g29850	20683.7	0.023926	39418.5	0.018555	23868.7	0.01416
14956_at	unknown protein	At2g18440	26942.7	0.001141	24610.2	0.000673	24754.6	0.000322
14974_at	unknown protein	At1g27530	8928.2	0.021866	6171.1	0.127645	3496.9	0.009985
14982_at	nodulin - like protein	At2g34350	1642.4	0.602006	3596.2	0.039365	1756	0.02786
14990_at	putative tetracycline transporter protein	At2g16990	9320.8	0.019304	8718.3	0.009975	6121.6	0.002617
15003_at	putative clathrin assembly protein	At2g19790	14385.8	0.000959	12583.2	0.000322	29923.3	0.000322
15004_at	putative microtubule-associated protein	At2g05630	8149.5	0.003067	6687.4	0.004863	5914.2	0.000322
15006_at	unknown protein	At2g32480	5726.1	0.035163	2853.6	0.11716	3954.2	0.003585
15009_at	putative ribophorin I	At2g01720	10623.5	0.007543	7071.3	0.031336	5787.1	0.001354
15020_at	Mago Nashi-like protein	At1g02140	5347.9	0.031336	3996.6	0.031336	7462.2	0.001139
15034_at	unknown protein	At2g39340	7794.2	0.019304	4417	0.043968	2667.5	0.003067
15048_at	unknown protein	At2g17990	4107.4	0.162935	3813.9	0.05447	2389.5	0.014937
15058_s_at	cinnamyl-alcohol dehydrogenase ELI3-1	At4g37980	11831.6	0.05447	7000.6	0.060419	13282.6	0.003067
15079_at	unknown protein	At2g24020	1146.1	0.458816	5138.6	0.043968	7009.4	0.000673
15081_at	unknown protein	At2g03390	6851.8	0.189687	4660.9	0.009985	3464	0.006532
15087_at	glyoxalase I	At1g11840	5227.9	0.013079	4328.6	0.11716	2740.2	0.005643
15089_at	unknown protein	At2g44870	3335	0.397994	4606.4	0.014937	2114.4	0.017001
15091_at	unknown protein	At2g38360	18878.6	0.011447	16542.2	0.006532	28252.4	0.001892
15096_at	unknown protein	At2g48030	4895.9	0.138765	4407.6	0.013092	4073.4	0.008689
15097_at	chlorophyll binding protein	At1g15820	8231.6	0.048995	8660.2	0.021866	19154.5	0.000388
15102_s_at	light-harvesting chlorophyll a b binding protein	At4g10340	12640.3	0.002228	8148.4	0.004863	27419.5	0.000266
15103_s_at	unknown protein	At1g20450	75336.7	0.000219	71776.8	0.000219	220533.1	0.000219
15104_s_at	ERD15 protein	At2g41430	106371.4	0.000219	854043.3	0.000219	664315.3	0.000219
15105_s_at	glycine-rich RNA binding protein AtGRP7	At2g21660	14204.4	0.000673	12208.7	0.001354	27972	0.000266
15108_s_at	no hits		16398.6	0.017001	22938.3	0.035163	80982.6	0.000388
15109_s_at	putative NPK1-related protein kinase 2	At1g12110	3268	0.189687	2955.7	0.043968	13378.5	0.000388
15110_s_at	dehydrin	At1g76180	3893.7	0.05447	8935.3	0.043968	15683.4	0.000388
15112_s_at	putative cryptochrome 2 apoprotein	At1g04400	12083.6	0.011447	14809	0.013092	13629.2	0.000805
15113_s_at	GDP dissociation inhibitor	At2g44100	39690.2	0.003067	54320.2	0.000673	101544.3	0.000266
15114_s_at	glycosyl hydrolase family 9 (endo-1,4-beta-glucanase)	At5g49720	35177.7	0.000266	43157.5	0.000219	71974.1	0.000219
15115_f_at	unknown protein	At2g05380	6168.1	0.003585	7548.7	0.00418	4683.2	0.003585
15118_s_at	glutathione transferase	At4g02520	9478.5	0.000673	6785.8	0.001354	8076.4	0.000468
15119_s_at	protein phosphatase 2A (PP2A)	At2g42500	32419.6	0.000959	20353.4	0.008689	35130.8	0.000219
15126_s_at	delta 9 desaturase	At2g31360	7003.4	0.039365	7385.2	0.002617	14868.1	0.001354
15127_s_at	putative response regulator 3	At1g10470	7608.9	0.031336	17348.6	0.00418	12389.7	0.019304
15128_s_at	cysteine synthase CysC1	At3g61440	8139.4	0.007543	9432.1	0.011447	2288.5	0.019304
15129_at	NOI protein, nitrate-induced	At5g55850	5699.3	0.07383	8397.3	0.003067	4421.3	0.000388
15130_s_at	20S proteasome alpha subunit A2	At2g05840	14470.6	0.007543	9329.9	0.001354	27375.5	0.001141
15131_s_at	dormancy-associated protein	At1g28330	136707.8	0.000219	114598.2	0.000219	67590.8	0.000468
15133_at	light-harvesting chlorophyll a b binding protein	At3g61470	5925.9	0.019304	4526.6	0.039365	15115.8	0.001141
15134_s_at	omega-6 fatty acid desaturase, endoplasmic reticulum	At3g12120	14830.4	0.001354	11618.1	0.00418	20052.5	0.000388
15136_s_at	dnaJ protein homolog atj3	At3g44110	21249.8	0.002228	18077.8	0.000322	44051.8	0.000322
15139_s_at	no hits		9649.3	0.02786	7734.1	0.007543	9180.4	0.004863
15140_s_at	ER-type Ca2+-pump protein	At1g07810	18506.4	0.00418	18278.5	0.089405	30307.5	0.000805
15147_s_at	probable plasma membrane intrinsic protein 1c	At4g00430	14372.4	0.008689	18359.1	0.000219	56372.2	0.000219
15149_s_at	mitochondrial F1-ATPase, gamma subunit (ATP6)	At2g33040	10225.5	0.004863	17166.9	0.000805	18369.4	0.000266
15150_s_at	GTP-binding protein atran3	At5g55190	17878.4	0.000388	24531.4	0.006532	33977.8	0.000219
15151_f_at	20S proteasome beta subunit B	At5g40580	3255.3	0.204022	5143.8	0.003585	2125.2	0.009985
15152_s_at	importin alpha	At3g06720	11836	0.003585	10411.5	0.006532	55055.2	0.000219
15155_s_at	ribosomal protein	At1g43170	3974.2	0.098054	5846.4	0.019304	10903	0.000388
15163_s_at	14-3-3 protein GF14 mu	At2g42590	55131.1	0.000219	45647.2	0.000219	63170.3	0.000219
15164_s_at	acyl-coA dehydrogenase	At3g51840	22744.5	0.001892	29376	0.001354	46246	0.000322
15165_s_at	nucleoside-diphosphate kinase	At4g09320	25767.3	0.00418	14968.1	0.001354	46284.5	0.000219
15166_s_at	auxin response transcription factor (ARF7)	At5g20730	11287.4	0.000959	8651.4	0.014937	30650.4	0.000388
15167_s_at	no hits		736.3	0.795978	5696.6	0.008689	11216.1	0.000266
15170_s_at	light-harvesting chlorophyll a b binding protein	At5g54270	4359.3	0.127645	7102.6	0.031336	31976.3	0.000388
15171_s_at	phosphoprotein phosphatase-type 1 catalytic subunit	At2g29400	7477.8	0.002228	13926.1	0.000562	14607.6	0.000562
15173_f_at	calmodulin 1 (CAM1)	At5g37780	32941.9	0.000322	43578.9	0.000388	29329.1	0.000562

15174_f_at	E2, ubiquitin-conjugating enzyme 9 (UBC9)	At4g27960	7250.4	0.011447	6271.4	0.003585	12852.8	0.000562
15176_s_at	calcium-dependent protein kinase-like protein	At5g12480	4734.8	0.024711	1950.3	0.150527	1549.7	0.005643
15177_s_at	eukaryotic translation initiation factor 3 delta subunit	At2g46290	4795.2	0.009985	5741.3	0.031336	6040	0.002617
15179_s_at	putative cystathionine gamma-synthase	At3g01120	12837.5	0.02786	7796.7	0.011447	10869	0.00418
15180_s_at	SAR1 GTP-binding secretory factor	At4g02080	15958.9	0.001354	15782.2	0.001602	7284.7	0.000673
15182_at	hydroxypyruvate reductase (HPR)	At1g68010	9245.7	0.003585	5251.5	0.066865	12624.4	0.000562
15187_s_at	fimbrin 2	At5g48460	6918.4	0.019304	6835.5	0.004863	4015.6	0.005643
15190_s_at	no hits		10961.6	0.00418	6529	0.001602	5066.4	0.008689
15191_at	vacuolar H+-transporting ATPase 16K chain	At4g34720	207353.6	0.000322	179961.9	0.000219	292855.9	0.000266
15192_at	ATP-dependent Clp protease ATP-binding subunit	At5g51070	5280.4	0.019304	6389	0.007543	5148.5	0.003067
15193_s_at	glutathione transferase	At2g30870	7705.6	0.05447	10411.3	0.003067	15924.6	0.000322
15194_s_at	GASA4	At5g15230	119462	0.000219	120006.8	0.000219	284358.8	0.000219
15197_s_at	arginine decarboxylase	At2g16500	19142	0.007543	14519.4	0.000219	49421	0.000219
15200_s_at	AtRer1B	At2g21600	13834.2	0.002228	30903.1	0.000219	78692.7	0.000219
15201_f_at	ATHP2	At3g29350	8205.6	0.017001	6384.8	0.007543	6666	0.013092
15202_s_at	His-Asp Phosphotransfer Signal Transducer A	At5g39340	10352.2	0.014937	9524.3	0.000562	7581.5	0.000322
15205_at	ethylene-insensitive 3 (EIN3)	At3g20770	97605.8	0.000266	88365.5	0.000219	163339.6	0.000219
15206_s_at	putative K+ channel, beta subunit	At1g04690	32799.3	0.000562	32992.3	0.000266	59670.5	0.000219
15209_s_at	Lil3 protein	At4g17600	4338.9	0.081337	4355.3	0.001602	4898.8	0.000959
15210_s_at	putative pyruvate dehydrogenase E1 beta subunit	At2g34590	9777.9	0.013092	5243	0.089405	6774.9	0.004863
15211_s_at	glutathione synthetase (GSH2)	At5g27380	4805.2	0.048995	4864.8	0.019304	1376.5	0.024711
15212_s_at	glycine decarboxylase complex H-protein	At2g35370	9452.4	0.007543	9287.7	0.02786	9853.9	0.002617
15213_s_at	ornithine carbamoyltransferase precursor	At1g75330	30244.6	0.001602	29583.7	0.000805	68369.7	0.000219
15215_s_at	auxin-induced protein	At3g04730	12775.4	0.004863	8888.6	0.001141	5528.1	0.001141
15216_at	germin-like protein	At1g09560	648.1	0.418069	6133.3	0.004863	23752.7	0.000219
15220_at	unknown protein	At1g05550	1000.5	0.697453	5408.5	0.003067	2790.9	0.021866
15251_at	unknown protein	At3g01100	4641.1	0.035163	3585.8	0.000805	3986.6	0.000322
15270_at	no hits		4683.8	0.081337	6802.1	0.019304	4446.4	0.02786
15271_at	unknown protein	At2g34510	3916.1	0.098054	1777.4	0.05447	2077.3	0.013092
15296_at	putative translation initiation factor eIF-1A	At2g04520	13507.7	0.001141	9858.9	0.000219	17421.9	0.000266
15368_at	unknown protein	At4g14830	7049.7	0.014937	7117.6	0.035163	4178.1	0.002617
15370_at	no hits		9982.4	0.060419	7857.6	0.035163	3284.4	0.048995
15371_at	unknown protein	At2g47690	5938.9	0.002228	6759.8	0.014937	4710.6	0.001354
15372_at	no hits		22198.3	0.001141	15302.1	0.000219	23872.2	0.000266
15373_g_at	plastocyanin	At1g76100	26746.8	0.000959	25113.1	0.000562	29049.7	0.000219
15384_at	unknown protein	At2g39530	4770.5	0.47938	19586.4	0.017001	7094.6	0.031336
15386_at	unknown protein	At1g60210	6445.6	0.066865	15203.1	0.011447	6821.3	0.009985
15387_at	unknown protein	At2g26240	3806.9	0.024711	4449.7	0.089405	2810.2	0.013092
15389_at	unknown protein	At2g22860	5681.3	0.006532	8440.4	0.035163	2845.4	0.017001
15401_at	unknown protein	At2g28430	4324.1	0.175989	3553.4	0.007543	3734.9	0.000673
15412_at	unknown protein	At2g31440	13226.2	0.005643	9961.1	0.005643	13482.8	0.003067
15422_at	unknown protein	At4g04330	7373.9	0.009985	2582.1	0.017001	2052.7	0.035163
15448_at	copper transport protein	At3g46900	5553.2	0.060419	7533.2	0.002228	4496.3	0.004863
15453_at	unknown protein	At4g14020	20688.5	0.000805	12264.9	0.019304	10727.9	0.000562
15461_at	unknown protein	At2g36470	1743	0.52062	4169.9	0.019304	2385.4	0.05447
15469_at	unknown protein	At1g04000	6372.7	0.07383	10444.6	0.021866	3722.2	0.021866
15472_at	unknown protein	At2g22550	5981.1	0.014937	3025.2	0.043968	2647.8	0.011447
15491_at	unknown protein	At4g12360	4496.6	0.089405	10797.9	0.039365	5547.3	0.043968
15510_r_at	no hits		13375.4	0.002617	22946	0.001602	15896.3	0.000219
15521_at	unknown protein	At4g22890	9831.1	0.02786	15907.9	0.000805	18071.2	0.000673
15523_s_at	unknown protein	At4g24360	16922.3	0.02786	13710	0.031336	15576.8	0.002617
15528_at	putative electron transfer flavoprotein ubiquinol	At2g43400	4453	0.035163	4309.7	0.021866	2089	0.035163
15534_f_at	histone H4	At2g28740	10126.4	0.002228	10594.8	0.003067	27935.5	0.000266
15540_at	unknown protein	At2g24860	15385.8	0.000805	8012.7	0.001141	12159.9	0.000388
15548_at	glycosyl hydrolase family 17	At1g11820	10975.9	0.000959	9829.6	0.009985	26290.8	0.000266
15550_at	unknown protein	At1g15200	3705.1	0.039365	3067	0.014937	1538	0.035163
15570_i_at	unknown protein	At2g47960	14102.3	0.023438	3288.6	0.111328	14025.9	0.001953
15571_s_at	unknown protein	At2g47960	7735.6	0.009985	5376.5	0.013092	5809.7	0.004863
15576_s_at	putative CCCH-type zinc finger protein	At2g25900	16202	0.000673	18481.7	0.000219	21392.7	0.000219
15579_s_at	developmentally regulated GTP-binding protein	At1g17470	914	0.581931	2804.3	0.05447	2868.1	0.035163
15580_at	acyl-CoA oxidase	At5g65110	4079.2	0.039365	3840.7	0.11716	2758.7	0.00418
15581_s_at	copper zinc superoxide dismutase (CSD2)	At2g28190	32189.7	0.000219	31724.2	0.000266	28564.8	0.000266
15582_s_at	alternative oxidase 1a precursor	At3g22370	7739.4	0.02786	5477.8	0.024711	37379.7	0.000219
15584_s_at	vacuolar H+-ATPase proteolipid (16 kDa) subunit	At1g19910	41480.8	0.000805	76905.2	0.001354	205034.9	0.000219
15585_s_at	dynammin-like protein	At5g42080	8452.8	0.005643	12356.1	0.001602	12016	0.001354
15586_s_at	protein phosphatase ABI1	At4g26080	21503.9	0.001354	26766.1	0.000388	68841.4	0.000219
15591_s_at	glutamate dehydrogenase (EC 1.4.1.-)	At5g18170	11338.6	0.004863	11336.6	0.003585	18903.1	0.000388
15592_s_at	Rac-like GTP-binding protein (ARAC1)	At2g17800	17593.2	0.002228	19314	0.001141	51386.7	0.000266
15593_s_at	26S proteasome regulatory subunit	At2g39990	16996.1	0.000468	9302.7	0.000562	26190.6	0.000673
15596_s_at	homeodomain containing protein 1	At4g32040	6347.3	0.060419	4745.7	0.035163	8872.4	0.000959
15602_f_at	cellulose synthase catalytic subunit (Ath-A)	At4g39350	8176.3	0.031336	6469.6	0.039365	9847	0.001354
15603_at	cellulose synthase catalytic subunit	At5g05170	21325.9	0.008689	24265.5	0.003067	40106.9	0.000219
15607_s_at	cyclic nucleotide-regulated ion channel (CNGC	At5g15410	11255.5	0.031336	10077.3	0.021866	17320.2	0.000805

15608_at	nitrate transporter (NTL1)	At1g69850	10782.2	0.011447	10437.3	0.000959	8180.4	0.001602
15617_s_at	no hits		22980.8	0.000959	17025.1	0.000388	70957.7	0.000266
15618_s_at	aspartate aminotransferase	At1g62800	1241.8	0.561639	3146.9	0.035163	1354.8	0.004863
15620_s_at	4-coumarate:CoA ligase 1	At1g51680	7618.5	0.013092	5979.9	0.005643	3241.5	0.021866
15624_s_at	ADPG pyrophosphorylase small subunit	At5g48300	43223.1	0.000266	51825.8	0.000266	81113.9	0.000219
15625_at	glyoxalase II	At1g53580	8228.1	0.014937	15856.6	0.001602	12871.1	0.000468
15626_s_at	Spot 3 protein and vacuolar sorting receptor hc	At3g52850	30390.5	0.001602	30538.1	0.000266	57557.6	0.000388
15632_s_at	two-component phosphorelay mediator	At3g21510	3347.6	0.175989	3325.6	0.02786	2214	0.05447
15634_s_at	nucleotide diphosphate kinase Ia	At5g63310	3776.8	0.003067	4604.7	0.05447	7571.4	0.006532
15640_at	ribosomal protein S27	At3g61110	11434.6	0.019304	9091.4	0.017001	8146.9	0.003585
15642_at	very-long-chain fatty acid condensing enzyme	At1g68530	55883.3	0.000219	66764.1	0.000219	93068	0.000219
15643_s_at	putative purine-rich single-stranded DNA-bindin	At2g32080	10362.3	0.007543	18238	0.000562	33612.2	0.000266
15647_s_at	ATP-sulfurylase	At4g14680	6248.4	0.013092	5612.5	0.039365	2453.6	0.00418
15650_s_at	putative pattern formation protein EMB30	At1g13980	1865.1	0.47938	3983.7	0.043968	2656.9	0.039365
15655_s_at	putative prohibitin 2	At1g03860	26219.3	0.000959	24663.5	0.009985	34927.7	0.000219
15659_at	light-harvesting chlorophyll a b binding protein	At1g61520	179607.5	0.000219	136241.6	0.000219	513129.8	0.000219
15660_s_at	glutathione peroxidase	At4g11600	13806.5	0.000322	15269.6	0.000219	11763	0.000219
15668_s_at	nucleoside diphosphate kinase 3 (ndpk3)	At4g11010	27654.1	0.000322	25731.9	0.000219	42594.7	0.000219
15670_s_at	branched-chain alpha-keto acid decarboxylase	At1g55510	3637.7	0.250724	4734.3	0.000468	4914.6	0.001892
15671_s_at	rac-like GTP-binding protein	At4g35950	2925.9	0.150527	3212.9	0.004863	3928.8	0.000388
15676_at	zinc finger protein 1 (zfn1)	At3g02830	3291.6	0.267463	3862.4	0.021866	10762.9	0.000673
15677_s_at	no hits		46384.6	0.001354	35748.3	0.001602	84051.5	0.000266
15681_s_at	farnesyl-diphosphate farnesyltransferase	At4g34640	3107.6	0.138765	3174.4	0.048995	6809.2	0.014937
15690_f_at	cytosolic cyclophilin (ROC3)	At2g16600	11439.6	0.003067	14750.5	0.000322	22082.8	0.000219
15691_s_at	profilin 1	At2g19760	3581.6	0.11716	5350.6	0.021866	3482	0.007543
15695_s_at	histone H1	At2g18050	45332.1	0.000322	51211.6	0.000219	43714.1	0.000266
15703_i_at	putative trypsin inhibitor	At2g43520	52810.8	0.000737	52899.5	0.000737	73337.9	0.000737
15709_at	protein kinase	At1g62400	9289.9	0.003067	10138.5	0.003585	15106.2	0.000322
15774_at	unknown protein	At4g11800	6254.7	0.008689	7009.2	0.021866	4722.8	0.024711
15781_at	unknown protein	At4g36910	7320.8	0.060419	3472	0.014937	3655.1	0.001354
15825_at	unknown protein	At2g33390	1082.1	0.458816	3131.1	0.02786	1615.5	0.02786
15833_at	copia-like retroelement pol polyprotein	At2g19680	4722.4	0.024692	4060.4	0.021866	2753.5	0.007543
15835_at	NAM (no apical meristem)-like protein	At2g02450	9730	0.014937	6377.4	0.011447	4913.7	0.001892
15837_at	putative thiamin biosynthesis protein	At2g29630	6716.4	0.003067	3953.2	0.081337	3591.6	0.007543
15849_at	unknown protein	At2g32090	4970.3	0.031336	5569.3	0.007543	11527.8	0.001141
15855_at	unknown protein	At2g22640	3878.5	0.107301	5174.2	0.000388	2841.1	0.000959
15857_at	unknown protein	At2g46540	14611.9	0.000266	27873.3	0.000805	14807.3	0.000805
15861_at	unknown protein	At2g35850	9193.7	0.024711	11055.9	0.11716	12116.6	0.004863
15868_at	En Spm-like transposon protein	At2g22080	13152.2	0.000805	13381.5	0.004863	41478.9	0.000266
15874_at	probable calcium-dependent protein kinase	At4g26470	4980.3	0.089369	4433.2	0.003585	2536.3	0.035163
15890_at	60S ribosomal protein L27A	At1g70600	12200.2	0.006532	10016.1	0.009985	10455.9	0.000805
15896_at	unknown protein	At1g11850	5619.6	0.089405	4241	0.039365	7750.3	0.000805
15900_at	unknown protein	At2g31090	9787.2	0.066865	9993.6	0.000468	7472.7	0.001354
15909_at	unknown protein	At1g64850	6696	0.011447	3722.4	0.014937	7391.9	0.000322
15910_at	putative glycine-rich protein	At2g05540	535496.2	0.000219	497761.5	0.000219	471363	0.000219
15937_at	unknown protein	At4g17840	19015.2	0.014937	10849.2	0.035163	18715.2	0.00418
15939_at	unknown protein	At4g33140	5583.8	0.00418	6423.8	0.081337	3405.7	0.043968
15949_s_at	auxin-regulated protein	At2g39730	30016.6	0.000562	38749.9	0.000219	121978.5	0.000219
15952_i_at	dnaK-type molecular chaperone hsc70.1	At5g02500	26176.9	0.011455	18305.8	0.002371	58085.5	0.001437
15959_at	no hits		5936	0.043968	3880.2	0.043968	2198	0.05447
15960_at	heat-shock protein (At-hsc70-3)	At3g09440	7522.1	0.021866	10167.7	0.003067	38830.4	0.000388
15962_at	putative aquaporin	At2g36830	12819	0.001602	21938.3	0.002228	45442.9	0.000266
15963_at	adenylate translocator	At3g08580	30009.8	0.000388	45018.9	0.001892	26492	0.000673
15972_at	cysteine proteinase	At4g16190	14198.6	0.009985	12276.4	0.000219	7894.7	0.000805
15973_at	cysteine proteinase RD21A	At1g47128	1699.2	0.32083	2123.6	0.048995	2290.4	0.024711
15977_s_at	aquaporin	At2g45960	32252.7	0.009985	65849.6	0.000266	158054.5	0.000219
15982_s_at	peroxidase, putative (ATP2a)	At2g37130	7420.4	0.017001	12637.3	0.011447	3359.4	0.000959
15986_s_at	oxygen-evolving complex protein 16, chloropla	At4g21280	8136.1	0.003067	9353.4	0.048995	7521.9	0.001892
15988_at	tubulin beta-4 chain	At5g44340	7302.7	0.019304	11983.2	0.005643	9272.1	0.011447
15989_at	plasma membrane intrinsic protein 2a	At3g53420	2142.2	0.175989	3382.8	0.043968	29082.2	0.000562
15997_s_at	unknown protein	At1g20440	57003.5	0.000219	47742.4	0.000959	34493.9	0.000219
15999_s_at	60S ribosomal protein L10A	At2g27530	4250.4	0.017001	4246	0.007543	3783	0.002228
16004_s_at	light-harvesting chlorophyll a b binding protein	At3g54890	36503	0.005643	33967.5	0.002228	37194.5	0.001602
16008_i_at	glutathione transferase	At2g47730	33973.6	0.003815	46675.2	0.002607	68791	0.000944
16009_s_at	glutathione transferase	At2g47730	6386.5	0.02786	7282	0.107301	12938.4	0.000803
16010_s_at	metallothionein-like protein	At3g09390	299006.6	0.000266	420010.5	0.000219	125344.5	0.000219
16011_s_at	metallothionein-like protein	At3g09390	536609.3	0.000219	453353	0.000219	265787.3	0.000219
16014_at	unknown protein	At1g75750	259472.2	0.000388	203101.2	0.000219	326368.2	0.000219
16015_at	geranylgeranyl reductase	At1g74470	10107.2	0.006532	11723.7	0.001141	20462.6	0.001354
16017_at	putative APG protein	At3g16370	13714.6	0.024711	11951	0.07383	15624.2	0.000219
16019_at	unknown protein	At4g15545	4154.9	0.039365	945.4	0.541184	2865.7	0.035163
16022_at	putative ATP synthase	At2g21870	12090.1	0.000219	6979	0.02786	16776.4	0.000805
16023_at	similar to late embryogenesis abundant protein	At2g44060	6129.8	0.048995	3706.6	0.019304	6643.2	0.001602



16024_at	unknown protein	At2g06520	29155.1	0.000562	28465.8	0.001354	89438.3	0.000266
16026_at	eukaryotic translation initiation factor 4A-1 (eIF4A1)	At3g13920	22370.8	0.000388	21394.9	0.000959	40759.7	0.000219
16027_s_at	eukaryotic translation initiation factor 4A-2 (eIF4A2)	At1g54270	26250	0.002617	19285.6	0.002228	39279.9	0.000266
16030_s_at	plasma membrane intrinsic protein 1c	At1g01620	12198.3	0.000959	12233.2	0.000805	20244	0.000219
16031_at	ferritin 1 precursor	At5g01600	8848.6	0.002617	5446	0.019304	7432.7	0.008689
16032_s_at	thioredoxin	At5g42980	309083.2	0.000219	219750.7	0.000219	265706.6	0.000219
16035_at	metallothionein 2b	At5g02380	977476.8	0.000219	737972.1	0.000219	954901.1	0.000219
16036_i_at	no hits		334770.3	0.000327	274026.5	0.000327	445206.4	0.000327
16037_s_at	unknown protein	At1g20696	1870.2	0.47938	6819.2	0.014937	5840.1	0.001354
16038_s_at	dehydrin RAB18-like protein	At5g66400	23777.1	0.001354	18155.3	0.000468	54228.1	0.000219
16039_s_at	plant defensin protein	At2g02100	20125.1	0.006532	21879.2	0.000562	27881	0.000388
16042_s_at	cytochrome p450 family	At5g05690	12114.9	0.013092	19522.4	0.000959	20549.6	0.000322
16044_s_at	photosystem I subunit V precursor	At1g55670	60112	0.000468	78324	0.001602	112892.8	0.000468
16046_s_at	light regulated protein	At3g26740	384728.8	0.000266	342864.1	0.000219	241817.3	0.000219
16047_at	unknown protein	At2g25510	5869.2	0.021866	3306.5	0.162935	4563.4	0.031336
16050_at	putative fructose bisphosphate aldolase	At2g36460	6056.8	0.031336	3886	0.150527	3829.2	0.000322
16051_at	tubulin beta-9 chain	At4g20890	30257.9	0.000388	32144.1	0.013092	26865.1	0.000673
16056_s_at	spot 3 protein and vacuolar sorting receptor homolog	At2g14720	14265.3	0.00418	13443.7	0.000219	24545.1	0.000266
16057_s_at	acetyl-CoA carboxylase	At5g35360	10963.8	0.001141	12228.4	0.000562	12134.1	0.001354
16058_s_at	glutathione peroxidase	At2g31570	57194.9	0.001892	67811.3	0.000388	173755.8	0.000266
16060_at	zinc finger protein ATZF1	At1g08930	4184.8	0.438361	7407.2	0.048995	3746.2	0.031336
16068_s_at	Rho1Ps homolog Rac-like protein	At4g35020	12156.2	0.05447	17377.9	0.066865	14810.9	0.008689
16069_s_at	splicing factor SRZ_21 9G8-like serine arginine	At1g23860	4428.8	0.234557	5629.4	0.05447	2392.1	0.003067
16075_f_at	calcineurin B-like protein 3	At4g26570	5141.5	0.05447	4367.3	0.001892	2530.2	0.035163
16079_s_at	putative C2H2-type zinc finger protein	At2g24500	10414.9	0.017001	12238.9	0.162935	9932	0.006532
16080_f_at	60S ribosomal protein L10	At1g66580	24499.5	0.001354	21839	0.013092	60747.7	0.000562
16083_at	putative progesterone-binding protein homolog	At3g48890	3594	0.019304	1860.6	0.378184	3764.1	0.001602
16087_s_at	putative ribosomal-protein S6 kinase (ATPK6)	At3g08730	8427.8	0.05447	19546.8	0.162935	80437.6	0.000322
16092_s_at	potassium channel protein KAT1	At4g36240	7644.5	0.021866	7495.9	0.001602	15818.7	0.000322
16093_s_at	phosphoprotein phosphatase 1, PP1	At3g46820	7677.7	0.017001	861.4	0.872355	6715.1	0.000673
16098_s_at	phosphoprotein phosphatase 2A	At1g25490	29666.9	0.000219	25780.9	0.000388	49493.3	0.000219
16106_at	G-protein beta family	At1g18080	2619.4	0.267463	5871.2	0.031336	4475.6	0.00868
16108_s_at	cytochrome p450 family	At2g24180	2142	0.250724	5572.5	0.02786	7633.2	0.003067
16110_s_at	sigma factor SigC	At3g53920	7684.2	0.008689	9288.4	0.039365	29334.8	0.000219
16118_s_at	putative WD-40 repeat protein, MSI4	At2g19520	14239.9	0.003067	18309.7	0.009985	26171	0.000219
16120_at	nonphototropic hypocotyl 1	At3g45780	6385.4	0.081337	10728.8	0.008689	11646.6	0.000673
16125_s_at	nucleotide diphosphate kinase la	At5g63310	2209.8	0.438361	4581.4	0.021866	3650.6	0.014937
16132_s_at	auxin transporter splice variant b	At1g73590	10971.5	0.019304	18156.8	0.011447	8877.1	0.021866
16133_at	ARG1 protein (Altered Response to Gravity)	At1g68370	7936.6	0.014937	8094.9	0.005643	11325.1	0.000219
16135_at	thioredoxin f1	At3g02730	32662.1	0.003585	20040.8	0.019304	214285.2	0.004863
16136_at	thioredoxin f2	At5g16400	10766.8	0.024711	6116.9	0.001141	26459.9	0.000219
16138_at	small zinc finger-like protein	At5g50810	5572.4	0.013092	2438.9	0.009985	7174.4	0.000562
16141_s_at	amino acid permease I	At1g58360	6496.8	0.031336	12524.8	0.000266	5190	0.000219
16142_at	GTP-binding protein ara-3	At3g46060	2926.2	0.150487	4146.8	0.024711	4082.5	0.002617
16145_at	vacuolar ATP synthase	At1g75630	61672.4	0.001602	54125.7	0.000468	81039	0.000388
16146_at	CASEIN KINASE II, ALPHA CHAIN 2 (CK II)	At3g50000	5371.5	0.107301	9530.5	0.039365	12201.8	0.000562
16147_s_at	recombination signal sequence recognition protein	At3g28730	8632.3	0.002617	5451.7	0.07383	6936.9	0.019304
16148_s_at	kinesin-like protein C (katC)	At5g54670	5623.7	0.014937	5624.2	0.011447	4719	0.003067
16152_s_at	S-like ribonuclease RNS2	At2g39780	12014.6	0.001141	12241.9	0.000673	10450.5	0.003585
16154_s_at	casein kinase II beta chain CKB2	At4g17640	4204.1	0.008689	3299.2	0.267463	4190.6	0.008689
16160_f_at	phosphoglycerate kinase	At1g56190	5876.1	0.11716	8786.5	0.031336	6179.5	0.003585
16161_s_at	glycine-rich protein (AtGRP2)	At2g21060	10249	0.00358	7314.6	0.002228	10099.4	0.000805
16168_s_at	proline iminopeptidase	At2g14260	6350.7	0.019304	3694.4	0.024711	4581	0.008689
16169_s_at	peptidylprolyl isomerase (pasticcino 1)	At3g54010	8841.4	0.009985	10731.2	0.003585	10355.7	0.000266
16245_at	unknown protein	At2g47210	3607	0.031336	4903.3	0.048995	1055.2	0.07383
16313_at	unknown protein	At4g12990	8676.3	0.048995	8035.3	0.00418	3579.1	0.00418
16321_at	unknown protein	At3g48195	4112.2	0.05447	354.1	0.837065	2167.1	0.048995
16343_at	myosin	At5g43900	2727.3	0.267463	4817.1	0.035163	2653.2	0.043968
16403_at	putative ADP-glucose pyrophosphorylase large subunit	At2g21590	5054.4	0.031336	5266.7	0.021866	1873.1	0.009985
16414_at	photosystem II oxygen-evolving complex 23 (OEC23)	At1g06680	1896.8	0.162935	6331	0.002228	5797.6	0.003067
16416_at	plant defensin protein	At2g02130	16580.2	0.001354	22709.8	0.000219	4743.4	0.002617
16418_s_at	photosystem II polypeptide	At1g79040	47615.4	0.000219	28824.3	0.000959	131985.8	0.000219
16422_at	auxin-regulated protein	At2g33830	144749.3	0.000805	166402.3	0.000388	86774.8	0.000388
16424_g_at	photosystem II reaction center 6.1KD protein	At2g30570	38171.9	0.007543	46281.7	0.001602	143217.1	0.000266
16427_at	amino acid transport protein AAP2	At5g09220	22232.3	0.000562	13726.7	0.000562	12231.3	0.000219
16428_at	carbonic anhydrase, chloroplast precursor	At3g01500	8156.6	0.006532	9832	0.00418	10032	0.000266
16430_at	glutathione transferase	At2g30860	48254.4	0.000388	77686.8	0.000219	56123.3	0.000219
16433_at	40S ribosomal protein S12	At2g32060	8104.1	0.011447	3825.5	0.02786	3672.1	0.007543
16435_at	RNA binding protein 45 (RBP45)	At1g11650	4842.4	0.07383	3257.4	0.013092	1768.9	0.048995
16436_at	unknown protein	At3g15353	978496.9	0.000219	933532.6	0.000219	651214.9	0.000219
16437_s_at	S-adenosylmethionine decarboxylase	At3g02470	7265	0.008689	1034.4	0.52062	1943.8	0.000322
16443_at	elongation factor Tu, chloroplast precursor (EF-Tu)	At4g20360	12293.2	0.000266	7599.8	0.031336	9877.2	0.007543
16446_at	plasma membrane intrinsic protein 1a	At3g61430	12013.7	0.004863	8566.7	0.024711	8959.8	0.002617

16447_at	HSP90-like protein	At4g24190	4615	0.150527	6929	0.000219	8976.9	0.000219
16448_g_at	HSP90-like protein	At4g24190	3832.5	0.07383	5914.7	0.02786	3953.2	0.014937
16451_at	ketol-acid reductoisomerase	At3g58610	5715.7	0.005643	8780.9	0.000219	10416.6	0.000219
16453_s_at	histone H1 like protein	At1g06760	18377	0.001354	18226.8	0.003585	17259	0.000673
16454_s_at	unknown protein	At2g42680	16544.7	0.002617	29938.4	0.001602	33797.8	0.001892
16456_at	unknown protein	At1g56280	62102.9	0.008689	52579.4	0.006532	56039.5	0.000959
16458_s_at	no hits		16676.9	0.002228	25666.6	0.000562	19950.8	0.000266
16464_g_at	elongation factor 1-beta, putative	At1g30230	15604.3	0.024711	32155.7	0.00418	23288.8	0.002228
16466_s_at	heat-shock protein (At-hsc70-3)	At3g09440	5490.1	0.024711	2367.3	0.107301	5962.6	0.001602
16469_at	no hits		14968.5	0.011447	16113.7	0.001141	13779.5	0.001602
16476_at	actin 2	At3g18780	29015	0.000388	28583.4	0.001892	115956.7	0.000266
16477_at	arabinogalactan-protein (AGP9)	At2g14890	12332.8	0.009985	13147.3	0.066865	28142.3	0.000388
16480_at	tubulin beta-6 chain	At5g12250	18281.5	0.011447	16823.2	0.024711	14793.7	0.003585
16482_s_at	gamma-VPE (vacuolar processing enzyme)	At4g32940	10517.1	0.021866	7740.5	0.000562	5788	0.000468
16486_at	putative serine carboxypeptidase precursor	At3g10410	17360.3	0.001602	10953.5	0.005643	8729.5	0.001602
16487_at	putative dioxygenase	At2g25450	23793.3	0.014937	18206	0.001354	9279.7	0.000468
16488_at	glucose transporter	At1g11260	91983.3	0.000322	132403.9	0.000805	110571	0.000266
16491_at	sterol-C-methyltransferase	At1g20330	6001.5	0.02786	8012.4	0.081337	9837.1	0.000959
16497_at	unknown protein	At3g21055	15101.7	0.011447	10883.8	0.007543	14950.6	0.001354
16500_at	unknown protein	At2g16590	9981	0.00418	6771.1	0.043968	15465.7	0.000562
16503_at	glutamate-ammonia ligase (EC 6.3.1.2) precursor	At5g35630	8329.4	0.00418	5870.3	0.021866	11535.2	0.00418
16506_at	40S ribosomal protein S6	At5g10360	7598.3	0.05447	4669	0.05447	11415.1	0.001892
16507_at	40S ribosomal protein S2	At2g41840	4553.9	0.07383	5592.7	0.048995	11872.2	0.007543
16508_at	adenine nucleotide translocase	At1g15500	10570.4	0.081337	6566.8	0.014937	8459.4	0.002228
16515_at	unknown protein	At4g34700	12235.1	0.000562	30897	0.002228	52677.4	0.000266
16516_at	unknown protein	At2g02510	13230.4	0.001141	15506.9	0.000959	18986	0.001141
16517_at	cobalamin biosynthesis protein	At5g13630	6991	0.031336	7216	0.011447	16090.9	0.000805
16518_at	putative shaggy-like protein kinase dzeta	At2g30980	5143.5	0.07383	4371	0.035163	4748.5	0.000322
16522_at	amino acid transporter AAP4 (pir)[S51169]	At5g63850	3258.3	0.127645	5778.4	0.008689	2855.2	0.007543
16523_s_at	copper zinc superoxidase dismutase (CSD1)	At1g08830	74597.8	0.000673	77672.2	0.001602	106620.6	0.000266
16525_at	60S ribosomal protein L7A	At2g47610	3251.7	0.060419	4695.6	0.043968	5413.5	0.017001
16526_at	adenine nucleotide translocase	At1g80300	5661.7	0.021866	6076.5	0.32083	13274.5	0.000468
16527_at	60S acidic ribosomal protein P2	At2g27720	15732.7	0.005643	20751.5	0.001602	56879.6	0.000562
16529_at	putative RGA1	At2g01570	3867	0.081337	3627.3	0.006532	4487.4	0.000468
16530_at	arginine serine-rich splicing factor RSp41	At5g52040	9402	0.002617	8496.1	0.02786	11119.1	0.004863
16531_s_at	putative 60S ribosomal protein L21	At1g09690	17824.8	0.000219	16476.9	0.001141	25189.2	0.000562
16540_s_at	heme oxygenase 1 (HO1)	At2g26670	19464	0.000468	16030	0.000322	25552	0.000266
16544_s_at	60S ribosomal protein L23A	At2g39460	9003.2	0.001354	8830.8	0.009985	16458.4	0.003585
16546_s_at	20S proteasome alpha subunit G	At2g27020	15066.2	0.003067	17491.8	0.000219	28248	0.000219
16548_at	one helix protein (OHP)	At5g02120	6601.9	0.019304	1001.7	0.438361	16873.3	0.001892
16552_at	polypyrimidine tract-binding protein	At3g01150	7110.6	0.003585	107.8	0.732572	2777.8	0.014937
16567_s_at	putative putative sister-chromatide cohesion protein	At2g47980	8368	0.001602	14218.8	0.001892	6552.1	0.000959
16571_s_at	calcium-dependent protein kinase	At1g35670	8686.9	0.00418	4419.7	0.189687	8033.7	0.000266
16574_s_at	acyl carrier protein	At2g44620	67861	0.000219	56727.8	0.000219	309582.4	0.000219
16583_s_at	no hits		2843.5	0.250724	5469.9	0.000322	6292.5	0.001892
16591_s_at	26S proteasome regulatory subunit S5A	At4g38630	4637.4	0.019304	8624.3	0.031336	1185.9	0.043968
16596_at	sterol delta7 reductase	At1g50430	8658	0.031336	7553	0.001141	8259.1	0.000468
16604_s_at	putative fumarase	At2g47510	10151.8	0.003067	5886.4	0.014937	8208.3	0.003067
16605_s_at	flavonol synthase (FLS)	At5g08640	4930.5	0.05447	3019.6	0.066865	10118.5	0.000322
16606_at	auxin response transcription factor	At5g62010	5413.2	0.002617	743.9	0.397994	2426.1	0.02786
16607_s_at	sulfate transporter	At5g10180	4978	0.048995	3863.8	0.017001	1223.7	0.081337
16620_s_at	xyloglucan endotransglycosylase (TCH4)	At5g57560	16630.4	0.00418	17497.2	0.001141	33887.2	0.000219
16622_s_at	putative GTP-binding protein (extra large)	At2g23460	492	0.67917	3811.8	0.004863	2130.1	0.004863
16624_s_at	myb family transcription factor	At1g08810	12662.6	0.043968	17358.3	0.001141	17940.8	0.000219
16627_s_at	GDP-mannose pyrophosphorylase	At2g39770	3190.6	0.35869	5180	0.039365	10539.4	0.000266
16628_at	26S proteasome AAA-ATPase subunit RPT5a	At3g05530	4669.6	0.150527	5419.5	0.021866	4556.2	0.007543
16631_s_at	putative urease accessory protein	At2g34470	3830.4	0.060419	2443.3	0.019304	1751	0.035163
16636_at	ABC transporter family protein	At5g44110	6706.1	0.043968	3870.7	0.089405	5048.4	0.000468
16640_s_at	no hits		5684	0.009985	8438.2	0.003067	9078.2	0.000219
16647_s_at	omega-3 fatty acid desaturase, endoplasmic reticulum	At2g29980	7230	0.11716	9513.2	0.024711	21925.8	0.000805
16652_s_at	protein kinase (AME2 AFC1)	At3g53570	15856.1	0.001141	14112.3	0.000388	25030.5	0.000219
16673_at	photosystem II stability assembly factor HCF13	At5g23120	3002	0.250724	6978.5	0.014937	6753	0.0016
16674_at	putative sugar transporter	At2g48020	4958.9	0.162935	6409.7	0.013092	2492.6	0.002617
16732_at	unknown protein	At1g65170	3724.7	0.081337	3344.8	0.005643	1291.6	0.008689
16807_at	putative protein kinase	At2g34650	2790.1	0.697453	4470.6	0.00418	1638.1	0.017001
16863_at	protein phosphatase 2A regulatory subunit	At1g13320	4568.2	0.234557	5052.4	0.007543	4773.2	0.000468
16897_i_at	unknown protein	At5g15350	128512.8	0.000488	119501.6	0.000488	361184.4	0.000488
16898_s_at	unknown protein	At5g15350	14291.3	0.000468	11321.2	0.001602	18826.4	0.000219
16899_at	photosystem II 5 KD protein	At1g51400	20560.7	0.000468	27976.7	0.006532	21117.6	0.000468
16901_at	unknown protein	At2g28910	16934.9	0.003067	14884	0.000562	41029.6	0.000388
16908_at	pyruvate dehydrogenase E1 alpha subunit	At1g24180	7352.5	0.039365	7732.9	0.013092	3084.9	0.073796
16912_at	delta-1-pyrroline-5-carboxylate synthetase	At3g55610	4337.6	0.02786	4340.9	0.014937	3222.5	0.003585
16913_s_at	ubiquitin extension protein (UBQ2)	At2g36170	7128.1	0.039365	4589.8	0.011447	10555.9	0.000219

16917_at	E2, ubiquitin-conjugating enzyme 2 (UBC2)	At2g02760	68049.8	0.003067	40280.4	0.001141	78648.6	0.000673
16918_s_at	no hits		87407.1	0.000219	103725.1	0.000219	229949.2	0.000219
16921_at	histone H2B like protein	At5g22880	1347.6	0.602006	5318.6	0.021866	4277.9	0.003585
16922_i_at	Putative S-phase-specific ribosomal protein	At4g34670	61441.9	0.000613	52685.6	0.000491	78811.3	0.000491
16923_s_at	Putative S-phase-specific ribosomal protein	At4g34670	8817.4	0.035163	14205.6	0.001354	8566.7	0.00418
16926_at	60S ribosomal protein L15 homolog	At4g17390	7629.2	0.011447	6935.7	0.039365	9501.3	0.003067
16930_at	ribosomal protein	At4g14320	11297	0.000959	7550.7	0.001141	13974.8	0.000468
16931_s_at	ribosomal protein S27	At3g61110	30882	0.000322	33951.4	0.001892	79149.1	0.000219
16933_at	40S ribosomal protein S3	At2g31610	4541.3	0.014937	9664.8	0.089405	3768.7	0.001141
16935_s_at	H+-transporting ATPase chain E, vacuolar	At4g11150	6421.8	0.024711	5182.2	0.014937	10427.7	0.000673
16938_at	60s ribosomal protein L34	At1g26880	5276.9	0.048995	3929.2	0.204022	8404.4	0.004863
16940_g_at	no hits		114853.7	0.000322	79429.9	0.000266	333543.6	0.000219
16948_at	F-box protein family, AtFBL6	At2g25490	7754.8	0.127645	5713.3	0.05447	12007.9	0.000673
16956_at	unknown protein	At4g01000	3503.5	0.11716	2851.9	0.043968	2644.8	0.035163
16957_at	putative thioredoxin-m	At1g03675	20106.8	0.031336	26433.4	0.021866	17790.1	0.006532
16960_at	putative triosephosphate isomerase	At2g21170	13368.9	0.000673	11937.9	0.002617	22814.4	0.000266
16961_at	unknown protein	At2g02960	4215.3	0.127645	6154	0.05447	4239.2	0.043968
16967_s_at	H+-transporting ATPase 16K chain P2, vacuolar	At4g38920	7830.9	0.013092	13185.5	0.001602	22067.7	0.000266
16969_i_at	putative vacuolar proton-ATPase 16 kDa protein	At2g16510	12896.7	0.059082	17589	0.011719	16653.3	0.001465
16975_at	histone H2B	At3g45980	15753.2	0.000673	20149.7	0.005643	15066.9	0.000805
16979_at	small GTP-binding protein	At1g49300	4643.6	0.024711	3454.9	0.234557	2171.2	0.008689
16981_s_at	thioredoxin	At1g45145	84583.3	0.000219	43684.1	0.000219	52104.7	0.000219
16982_at	tumor suppressor	At1g14320	12953.2	0.011447	11450.6	0.002228	21721	0.000562
16983_at	ferredoxin precursor isolog	At1g10960	12103.3	0.008689	14032.1	0.006532	39968.6	0.000322
16984_at	ribosomal protein S18	At1g34030	4713.6	0.081337	3340.5	0.02786	9330.9	0.000322
16985_s_at	cytosolic ribosomal protein S11	At3g48930	55286.6	0.000219	39204.2	0.000266	87090.5	0.000266
16988_at	transcription factor L2	At3g55770	10357.2	0.02786	10405	0.002228	26028.9	0.000673
16992_at	putative protein kinase	At2g24360	7474.8	0.002228	8386.1	0.001141	6894.8	0.002617
16998_at	dTDP-glucose 4-6-dehydratase homolog D18	At3g62830	17236.6	0.000673	19758.2	0.000388	36000.8	0.000266
16999_at	putative nucleosome assembly protein	At2g19480	7675	0.005643	5399.4	0.02786	6235.9	0.001354
17000_at	50S ribosomal protein L24, chloroplast precursor	At5g54600	1328.8	0.5	3371.2	0.007543	1750.6	0.043968
17004_s_at	60S ribosomal protein L18A	At2g34480	7378.2	0.007543	8428.2	0.021866	10094.8	0.000673
17005_at	putative ribosomal protein	At4g26230	62738.2	0.000388	49265.5	0.000959	125835.1	0.000959
17006_at	selenium-binding protein like	At4g14030	5461.6	0.011447	7680.7	0.05447	21110.1	0.000468
17017_s_at	aspartate aminotransferase (AAT1)	At2g30970	12811.7	0.001354	16791.4	0.001354	28999	0.000562
17025_s_at	prohibitin-like protein	At4g28510	26163.9	0.001141	17669.8	0.000388	45084.6	0.000468
17029_s_at	Terminal flower1 (TFL1)	At5g03840	5318.7	0.001141	2465.6	0.008689	1401.7	0.060419
17030_at	unknown protein	At5g51400	15707.4	0.000959	15073.6	0.001354	50612.8	0.000673
17032_s_at	MADS-box protein (AGL3)	At2g03710	9498.1	0.021866	5393	0.000959	4332.5	0.001602
17033_at	unknown protein	At5g39410	8796.5	0.001892	12903.5	0.003067	5021.8	0.002228
17040_s_at	cytochrome p450 family	At1g13080	5755.3	0.060419	7923.7	0.000959	5218.6	0.001602
17044_at	ethylene responsive element binding factor 3 (ERF3)	At1g50640	5178.5	0.107301	4403.8	0.035163	7397.6	0.011447
17046_s_at	putative zinc transporter	At2g46800	5961.8	0.021866	4226	0.089405	5327.6	0.003067
17048_s_at	plastid division protein (FtsZ)	At2g36250	51297.1	0.000219	56905.2	0.000219	84781.3	0.000219
17056_s_at	unknown protein	At2g29530	13297.4	0.001602	18262.8	0.000388	35025.3	0.000266
17063_s_at	Ras-related GTP-binding protein (ARA-4)	At2g43130	11029.4	0.009985	9064.5	0.002617	23789.5	0.000266
17075_s_at	Nitrilase 4	At5g22300	11479	0.000805	15313.3	0.000673	28254.1	0.000219
17084_s_at	biotin carboxyl carrier protein 1 (BCCP1)	At5g16390	5604.6	0.048967	3531.5	0.024711	9818.3	0.000805
17087_at	photosystem I reaction center subunit PSI-N protein	At5g64040	8186.1	0.00418	8180.3	0.005643	14489	0.000322
17089_s_at	ferulate-5-hydroxylase (FAH1)	At4g36220	12099.8	0.002617	8551.3	0.089369	34073.7	0.000562
17094_s_at	no hits		5729.5	0.089405	6512.6	0.004863	20540.2	0.001141
17095_s_at	high affinity Ca2+ antiporter	At2g38170	40431.8	0.00418	35743.2	0.000388	41936.4	0.000219
17101_f_at	clathrin assembly protein AP19, small subunit	At2g17380	3038.3	0.007543	4158.4	0.02786	5895.5	0.003067
17103_s_at	xyloglucan endotransglycosylase (EXGT-A3)	At2g01850	8308.7	0.014937	9410.6	0.019304	8537.6	0.001141
17104_s_at	phosphoserine aminotransferase	At4g35630	5850.4	0.004863	4836.8	0.008689	8030	0.000673
17109_s_at	glycosyl hydrolase family 1	At3g03640	7990.1	0.081337	6188.1	0.008689	10327.7	0.000673
17112_s_at	geranylgeranyl pyrophosphate synthase (GGP)	At4g36810	6435.4	0.048995	5995.2	0.006532	6945.7	0.017001
17117_s_at	kinesin-like calmodulin-binding protein	At5g65930	1886.1	0.397994	2708.5	0.002617	2520	0.005643
17118_at	Rad51-like protein	At5g20850	7720.5	0.098054	14315.3	0.043968	10808.2	0.017001
17119_s_at	no hits		5056	0.098054	6627	0.006532	4322.7	0.003067
17126_at	WD-40 repeat protein MSI1	At5g58230	11428.4	0.014937	9987.1	0.000388	17105.8	0.000219
17129_at	transcription factor IIB (TFIIB)	At2g41630	10322.8	0.001141	6269.3	0.060419	34048.1	0.000805
17143_s_at	unknown protein	At2g38300	15494.8	0.039365	12072.9	0.000322	17155.4	0.000388
17215_at	putative trypsin inhibitor	At2g43550	6228.7	0.060419	6471.7	0.021866	3772.3	0.005643
17373_at	putative auxin-responsive protein	At2g46370	4007.2	0.013092	3406.7	0.081337	2967.7	0.006532
17375_at	putative poly(A) binding protein	At2g15500	2822.9	0.284747	4013.7	0.05447	1623.8	0.048995
17380_at	unknown protein	At4g34180	2815.7	0.302547	4646.7	0.003585	2605.2	0.02786
17383_at	unknown protein	At4g28770	3328.9	0.204022	6349.6	0.000959	7374.8	0.002617
17384_at	unknown protein	At4g23630	14830.8	0.001892	13586.7	0.00418	26895.4	0.000322
17386_at	proline-rich protein	At2g21140	56616.6	0.000266	42065.6	0.001602	74084.7	0.000219
17388_at	unknown protein	At2g36120	20693.4	0.003067	29768.4	0.001354	11203.5	0.001354
17389_at	unknown protein	At4g37830	53352.8	0.000388	51260	0.003585	176503.4	0.000266
17390_at	no hits		6986.3	0.002617	7150.5	0.009985	8139.9	0.000805

17393_at	Rubisco subunit binding-protein beta subunit	At1g55490	8206.4	0.006532	8231.5	0.001141	10004.3	0.000322
17398_at	putative protein disulfide-isomerase	At2g47470	3528	0.284747	3671.6	0.019304	3771.9	0.007543
17399_at	DEAD DEAH box RNA helicase	At2g45810	5489.7	0.060419	5751.4	0.001141	3023.4	0.014937
17409_at	unknown protein	At1g09200	7342.4	0.048995	7340.7	0.162935	7928.5	0.002228
17414_at	E2, ubiquitin-conjugating enzyme 8 (UBC8)	At5g41700	13819.1	0.005643	20192.2	0.006532	16431.8	0.002617
17416_at	ankyrin-like protein	At1g04430	1881.1	0.250688	3372.6	0.005636	2144.5	0.011447
17418_s_at	unknown protein	At2g46505	3952.7	0.189648	1859.8	0.05447	5850.8	0.000468
17421_s_at	E2, ubiquitin-conjugating enzyme 6 (UBC6)	At2g46030	22095.2	0.000219	20431.3	0.000388	29257.2	0.000219
17423_s_at	purple acid phosphatase precursor	At2g27190	6066.4	0.011447	6988.5	0.003585	8486.4	0.000673
17426_at	AP2 domain protein RAP2.4	At1g78080	5447.7	0.043968	6763.6	0.218983	17651.2	0.003067
17427_at	E2, ubiquitin-conjugating enzyme 4 (UBC4)	At5g41340	4804.6	0.05447	5605.8	0.009985	4914.4	0.000468
17428_at	phosphoenolpyruvate carboxykinase (ATP)	At4g37870	18521.9	0.001141	17138.4	0.001141	21347.1	0.000219
17429_at	translation initiation factor	At4g27130	9403.6	0.05447	10101.7	0.005643	8414.2	0.000805
17430_s_at	ubiquitin-like protein	At4g26840	5513	0.031314	4469.1	0.081337	15826.6	0.000673
17431_at	putative VAMP-associated protein	At2g45140	5933.2	0.048995	1934.7	0.47938	4649.6	0.00418
17433_at	uridine diphosphate glucose epimerase	At1g12780	9047.4	0.019304	14111	0.005643	17865.1	0.000562
17435_at	putative PRP19-like spliceosomal protein	At2g33340	14445.5	0.019304	17054.1	0.000673	28904.8	0.000266
17438_at	spermidine synthase	At1g70310	72830.4	0.000266	57902.6	0.000219	175351.7	0.000266
17443_at	protein phosphatase 2C (PP2C)	At2g20630	288.5	0.64131	5260.2	0.014937	3094.3	0.002228
17457_at	unknown protein	At4g13010	4345.1	0.098054	9572.3	0.05447	8961.8	0.001141
17458_at	unknown protein	At2g37110	6691.6	0.006532	6415.1	0.019304	5768.1	0.001602
17463_at	glyceraldehyde-3-phosphate dehydrogenase	At1g79530	3061.5	0.5	4534.4	0.024711	4290.5	0.003067
17467_at	shaggy related protein kinase	At3g05840	6572.9	0.024711	8455.9	0.000219	13795.7	0.000266
17468_at	cellulose synthase catalytic subunit	At5g64740	10374.2	0.024711	10215	0.008689	12646.3	0.000388
17470_at	eukaryotic translation initiation factor 4A (eIF-4	At3g19760	8424.9	0.009985	8505.6	0.001141	7260.3	0.001354
17471_at	stearyl-ACP desaturase	At2g43710	9150.5	0.162935	10114.3	0.004863	25233.3	0.000266
17473_at	calnexin - like protein	At5g61790	3367.5	0.218983	4294.6	0.007543	4731.5	0.001354
17474_at	signal recognition particle 54 kDa protein 2	At1g48900	2829.2	0.204022	5906.7	0.014937	1988.1	0.021866
17475_at	serine threonine-specific protein kinase ATPK6	At5g55910	7161.9	0.048995	4068.2	0.267463	3830.6	0.011447
17482_at	ras-related small GTP-binding protein RAB1c	At4g17530	9544.6	0.001602	10793	0.000673	10358	0.000562
17483_at	casein kinase I	At5g43320	8617.8	0.00418	6372.5	0.0016	2099.4	0.035163
17488_at	putative aquaporin	At2g25810	4504.3	0.05447	5946.9	0.035163	1496.1	0.267463
17495_s_at	cycloartenol synthase [(S)-2,3-epoxysqualene	At2g07050	5841.5	0.043968	6760.8	0.000388	10273.9	0.000266
17505_s_at	P II nitrogen sensing protein GLB I	At4g01900	7212.5	0.013092	3192.5	0.5	9215	0.000805
17508_at	leucine-rich repeat transmembrane protein kin	At1g29750	3865.1	0.039365	5317.6	0.000959	2227.9	0.060419
17510_at	no hits		3802.4	0.150527	4363	0.043968	22083.1	0.000805
17518_s_at	transcriptional regulator (FUSCA3)	At3g26790	20298	0.002613	12647.4	0.005643	13381	0.002228
17520_s_at	DRE binding protein (DREB1A)	At4g25480	3999.8	0.089405	4158.2	0.009985	1883.2	0.05447
17523_s_at	Ras-related GTP-binding protein	At3g53610	5368.6	0.048995	1848.4	0.204022	1295.2	0.008689
17532_at	TATC-like protein	At2g01110	5861	0.098054	7681.2	0.024711	3077.4	0.005643
17536_at	lycopene epsilon cyclase	At5g57030	5207.2	0.017001	4824.2	0.008689	2270.9	0.054441
17537_s_at	3-phosphoserine phosphatase	At1g18640	626.1	0.765443	3285	0.05447	2281.1	0.031336
17539_at	nuclear cap binding protein CBP20	At5g44200	5960.9	0.007543	4816.1	0.024711	2732	0.006532
17542_s_at	putative DNA-binding protein	At1g09770	4377.3	0.07383	4826.6	0.017001	6516.6	0.001141
17552_s_at	E3 ubiquitin ligase, RMA1 E3	At4g03510	10756	0.013092	5312.4	0.32083	23807.8	0.000266
17562_at	unknown protein	At2g29700	7989.2	0.008689	7788.3	0.008689	13684	0.000219
17563_g_at	unknown protein	At2g29700	8394.7	0.007543	6829.6	0.005643	11711.2	0.000673
17564_s_at	mercaptopyruvate sulfurtransferase (Mst1 Rdh	At1g79230	9481.9	0.11716	10315.1	0.000219	8510	0.002228
17565_s_at	mercaptopyruvate sulfurtransferase (Mst2 Rdh	At1g16460	16915.1	0.000562	17472.9	0.000266	33851.8	0.000388
17567_at	unknown protein	At5g03540	6684.8	0.008689	8012.9	0.021866	2119.5	0.035163
17569_at	unknown protein	At3g52200	12381.6	0.006532	7194	0.000322	9619.4	0.002617
17580_at	putative gigantea protein	At1g22770	36117.1	0.000562	27076.7	0.000322	26990.3	0.000673
17593_r_at	unknown protein	At4g39660	5023.1	0.024711	6845.3	0.00418	3405.4	0.000959
17631_at	unknown protein	At5g26820	3024.7	0.32083	5439.9	0.043968	2511.5	0.024711
17660_at	putative protein kinase	At1g80640	7277	0.039365	5819.7	0.089405	3853.4	0.006532
17684_at	unknown protein	At2g39690	4505.6	0.039365	3021.3	0.089369	3401.3	0.001354
17701_at	unknown protein	At2g25830	4578.7	0.039365	1148.2	0.418069	1363.7	0.031336
17730_at	no hits		10320.2	0.024711	10597.3	0.150527	8240.8	0.009985
17752_at	putative protein kinase	At2g32800	4207.7	0.127645	5429.7	0.004863	6503.6	0.000673
17769_s_at	trehalose-6-phosphate synthase	At1g78580	4879.6	0.107301	5117.4	0.035163	6095.8	0.002617
17850_s_at	no hits		2987.6	0.602006	7562.4	0.006532	2729.1	0.021866
17851_at	E2, ubiquitin-conjugating enzyme 14 (UBC14)	At3g55380	6013	0.021866	4428.9	0.019304	4028.8	0.007543
17852_g_at	E2, ubiquitin-conjugating enzyme 14 (UBC14)	At3g55380	9531.9	0.017001	1107.1	0.795978	6252.4	0.003067
17857_at	cytoplasmic aconitate hydratase	At2g05710	2398.6	0.218983	13553.3	0.011447	8056.5	0.000322
17858_at	AP2 domain protein RAP2.12	At1g53910	5937.2	0.189687	11109.1	0.013092	21155.5	0.000468
17865_at	isoflavone reductase homolog P3	At1g75280	8288.5	0.013092	6765	0.089405	4266.2	0.002228
17870_at	60S ribosomal protein L31	At2g19740	8277.6	0.089405	4728.4	0.043968	7531.9	0.001892
17878_at	pectinacetylesterase	At4g19410	15521.2	0.014937	15327.9	0.000673	20151.7	0.000959
17881_at	WRKY family transcription factor	At2g23320	6796.3	0.066865	5597	0.035163	4074.6	0.013092
17882_at	PROTEIN TRANSPORT PROTEIN SEC61 GA	At4g24920	26228	0.000562	22692.8	0.000673	61986	0.000266
17892_at	OXA1 protein (OXA1p)	At5g62050	7071.3	0.039365	3225.6	0.035163	3087.4	0.005643
17902_s_at	unknown protein	At2g35330	6792.4	0.035163	4895.3	0.035163	8108.1	0.001892
17908_at	unknown protein	At2g27730	7965	0.016986	5891.1	0.035163	5710.7	0.000219

17910_at	60S acidic ribosomal protein P2	At2g27710	5504.5	0.043968	8839.1	0.007543	15137.1	0.000266
17913_at	unknown protein	At4g37300	16910.8	0.004863	16056.9	0.001892	54084.1	0.000562
17918_at	putative phosphoglucomutase	At1g23190	12013.8	0.048995	9118.7	0.098054	17899	0.003067
17924_at	no hits		6537.9	0.017001	7193.3	0.001354	3277.5	0.004863
17926_s_at	unknown protein	At1g15310	22769.2	0.098054	23907.2	0.048995	19320.2	0.019304
17935_at	putative protein kinase	At2g30740	4065.3	0.204022	8043.4	0.002617	5249	0.000959
17938_at	histone H3	At5g65360	6781.7	0.098054	3641.2	0.02786	4072.8	0.003585
17943_at	putative histone H2B	At2g28720	5608	0.05447	6754.9	0.009985	5120	0.007543
17944_at	histone H2A	At4g27230	9950.4	0.014937	3287.1	0.32083	7478.1	0.007543
17949_s_at	GTP-binding protein (At-RAB2)	At4g17170	11953.3	0.002617	13187.7	0.002617	17191.7	0.000468
17952_at	no hits		12662	0.021866	8775.4	0.002228	5335.7	0.004857
17955_at	GTP-binding protein	At4g19640	5764.2	0.001602	5985.4	0.00358	3498.3	0.000219
17957_at	putative acetone-cyanohydrin lyase	At2g23600	5488.8	0.035163	8845.2	0.048995	4925	0.000673
17962_at	putative citrate synthase	At2g42790	4164.4	0.11716	2114.6	0.02786	1521	0.00418
17964_at	putative phosphatidylinositol phosphatidylcholine	At2g21520	5654.4	0.024711	3882.3	0.035163	2519.2	0.005643
17966_at	cytochrome p450 family	At4g00360	6499.6	0.066865	4986.3	0.013092	4314.2	0.005643
17986_s_at	unknown protein	At4g20410	4798.7	0.11716	4482.9	0.031336	7214.1	0.003585
17987_at	calmodulin 7	At3g43810	13605.7	0.002617	11457.3	0.005643	8314.9	0.001354
17990_at	putative calmodulin	At3g51920	8478	0.009985	3353	0.127645	5992.3	0.043968
17991_g_at	putative calmodulin	At3g51920	1271.3	0.520633	3513.8	0.014937	7639.3	0.000322
17993_at	metal ion transporter	At1g80830	8478.7	0.005643	4881.7	0.003585	1831.2	0.039365
17994_r_at	no hits		11029	0.039365	9909.2	0.003067	12541.5	0.002617
17995_s_at	vacuolar membrane ATPase subunit G (AVMA)	At3g01390	2472.4	0.218983	3084	0.02786	1796.1	0.05447
17996_at	methylene-tetrahydrofolate reductase MTHFR1	At3g59970	5303.3	0.081337	3815	0.013092	5260.2	0.004863
18000_s_at	putative protein translocase	At2g37410	5095.1	0.107301	9226	0.004863	8097.2	0.000266
18002_at	fibrillarin 1 AtFib1 SKIP7	At5g52470	9846.6	0.001892	3965.8	0.043968	8206.8	0.001141
18004_at	fructose-2,6-bisphosphatase	At1g07110	4662.2	0.07383	7760.9	0.009985	7766.6	0.007543
18011_s_at	Rab GDP dissociation inhibitor	At3g59920	102771.6	0.000266	72826.9	0.000219	270408.9	0.000219
18018_s_at	cysteine synthase AtcysC1	At3g61440	7290.5	0.048995	6550.8	0.013092	3318	0.048995
18019_s_at	chloroplast Cpn21 protein	At5g20720	7892.6	0.024711	8148	0.005643	6177.9	0.001602
18021_at	glucose-6-phosphate 1-dehydrogenase	At3g27300	6014	0.009985	5054.7	0.05447	7826	0.000673
18022_at	glucose-6-phosphate dehydrogenase	At5g40760	9400.4	0.006532	4765.1	0.098054	6016.5	0.001602
18025_at	putative cysteine synthase	At3g04940	7489.2	0.03934	6137.7	0.000266	3987.4	0.009985
18032_i_at	no hits		32851.3	0.000977	26839.8	0.000977	92551.4	0.000977
18033_r_at	no hits		22236.6	0.001354	13932.7	0.000562	37357.8	0.000468
18036_s_at	putative squamosa-promoter binding protein	At2g33810	25157.1	0.008689	17390.7	0.019304	13816.3	0.013092
18038_i_at	putative squamosa-promoter binding protein 2	At1g27370	4073.5	0.056641	6602.3	0.113281	3539.8	0.042969
18046_s_at	nucleotide diphosphate kinase la	At5g63310	2675.8	0.52062	4714.9	0.019304	6395.9	0.003585
18047_at	mitochondrial NAD-dependent malate dehydrogenase	At1g53240	6124.5	0.150487	7485.8	0.031336	9120.2	0.009985
18052_s_at	photosystem II oxygen-evolving complex 33 (C)	At3g50820	3306.8	0.250724	5185.4	0.035163	2722.5	0.021849
18053_s_at	F12A21.13 putative photosystem II Core Complex	At1g67740	15014.7	0.002228	16991.3	0.035163	27460.6	0.000805
18062_at	no hits		19814.5	0.001892	6089.1	0.066865	7790.3	0.006532
18063_i_at	no hits		13247.8	0.011565	18015.6	0.016523	18364	0.002325
18072_at	putative component of cytochrome B6-F complex	At4g03280	92986.1	0.000266	71620.8	0.000219	225568.7	0.000219
18073_g_at	putative component of cytochrome B6-F complex	At4g03280	14057.2	0.019304	25014.4	0.001602	22412.6	0.000468
18075_r_at	H+-transporting ATP synthase chain 9	At4g32260	58413.8	0.003585	48063	0.001141	103358.2	0.000673
18077_at	photosystem I subunit III precursor, putative	At1g31330	14490.1	0.004863	17079.5	0.001602	41449	0.000388
18078_at	photosystem I subunit V precursor	At1g55670	48132.6	0.000388	53428.8	0.000387	137347.8	0.000266
18079_g_at	photosystem I subunit V precursor	At1g55670	72181.1	0.000266	84754	0.001892	187518	0.000266
18080_at	photosystem I subunit VI precursor	At3g16140	20413.8	0.004863	33456	0.000805	45149.8	0.001141
18082_at	photosystem I subunit X precursor	At1g30380	43990.2	0.000805	39538.3	0.000219	79205.8	0.000266
18083_r_at	probable photosystem I chain XI precursor	At4g12800	13609.2	0.001892	11677.6	0.000219	17095.9	0.000266
18085_r_at	putative photosystem I reaction center subunit	At4g02770	41967.1	0.00418	75391.5	0.000266	68979.6	0.000562
18086_s_at	putative photosystem I reaction center subunit	At4g02770	12356.2	0.001141	18296.6	0.000562	20550.5	0.000218
18088_i_at	photosystem I subunit PSI-E - like protein	At4g28750	41609.6	0.000762	43162.7	0.010972	157076.4	0.000944
18089_r_at	photosystem I subunit PSI-E - like protein	At4g28750	3790.4	0.05447	12068	0.002617	7222.9	0.002228
18135_at	putative chromosome associated protein	At2g27170	5737.6	0.019287	2498.8	0.397994	2375.3	0.013092
18175_at	CHP-rich zinc finger protein	At4g26380	4825.5	0.024711	3870.2	0.031336	1204.6	0.107301
18218_at	26S proteasome regulatory subunit	At2g32730	4558	0.048995	3725.3	0.060419	4351.1	0.011447
18219_at	salt-tolerance protein	At1g06040	7830.5	0.07383	5494.2	0.039365	33087.8	0.000468
18221_at	40S ribosomal protein S30	At2g19750	8622.9	0.001354	8669.4	0.060419	11004.3	0.001354
18223_at	unknown protein	At2g24420	16634.9	0.003067	8189.9	0.127645	9897.1	0.001141
18225_at	60S ribosomal protein L14	At2g20450	1654.3	0.418069	2780.7	0.048995	2991.8	0.035163
18227_at	unknown protein	At2g25430	7608.3	0.035163	6779.1	0.035163	12730.1	0.000562
18230_at	symbiosis-related like protein	At4g16520	33641.3	0.001892	29376.7	0.001602	28681	0.001354
18238_at	unknown protein	At1g22750	10284.3	0.008689	8274.4	0.004863	16780.2	0.000388
18239_g_at	unknown protein	At1g22750	7184.2	0.07383	10944.8	0.004863	18000.6	0.000468
18240_s_at	putative PHD-type zinc finger protein	At2g02470	3302.6	0.175989	2721.4	0.02786	2600	0.000673
18243_at	peptide methionine sulfoxide reductase (msr)	At5g07470	12029.8	0.008689	12736.7	0.003067	20862.4	0.000468
18245_s_at	unknown protein	At3g26580	2009.6	0.267463	5228.4	0.031336	3769.6	0.009985
18252_at	unknown protein	At4g11220	5218.1	0.024711	10323.1	0.039365	11685.2	0.000805
18256_at	unknown protein	At2g40060	4127.1	0.11716	6488.2	0.013092	1121.3	0.039365
18257_at	phosphatidylinositol synthase (PIS1)	At1g68000	8758	0.021866	3881.7	0.150527	2812.2	0.007543

18262_at	unknown protein	At2g43170	7044.8	0.07383	5997.6	0.000959	5440.4	0.000562
18264_at	unknown protein	At2g26500	8141	0.031336	11186	0.001892	19115	0.000805
18272_at	unknown protein	At2g40080	10382.9	0.02786	9769.4	0.000805	2676.1	0.002617
18274_s_at	50S ribosomal protein L15	At3g25920	7894.1	0.004863	4967.2	0.048995	6564.4	0.003067
18276_at	photosystem II protein family	At1g03600	5327.6	0.07383	5953.2	0.017001	9461.4	0.000805
18278_at	FtsH protease	At2g26140	6992.8	0.117121	5352.3	0.031336	6928.2	0.009985
18280_at	unknown protein	At1g21000	2783.8	0.039365	3420.5	0.043968	589.8	0.175989
18284_at	unknown protein	At4g34150	2655.6	0.11716	4683.2	0.019304	1348.4	0.02786
18285_at	unknown protein	At4g33250	4642.8	0.11716	3577.8	0.002617	5499.7	0.004863
18286_at	unknown protein	At3g47810	6824.8	0.05447	4073.4	0.001602	4350.5	0.019304
18287_at	unknown protein	At2g37940	5079.5	0.006532	3517.4	0.02786	2353.4	0.001602
18300_at	CALMODULIN-RELATED PROTEIN 2	At5g37770	4050.8	0.11716	3763.2	0.004857	4692.5	0.000959
18304_s_at	MAP kinase (ATMPK6)	At2g43790	6737.3	0.043968	4585.1	0.014937	2628.1	0.004863
18305_at	dynamain-like protein	At2g14120	3260.2	0.162935	8517.9	0.000468	7575.2	0.000266
18308_i_at	protein phosphatase 2C (PP2C)	At2g25070	4306.1	0.324748	3175.4	0.039146	4372.7	0.000735
18314_i_at	glycosyl hydrolase family 1 beta-glucosidase	At4g27830	6909.2	0.015454	3826	0.013378	4028.3	0.001305
18315_s_at	glycosyl hydrolase family 1 beta-glucosidase	At4g27830	17577.1	0.000266	19072.9	0.005643	31871	0.000219
18316_at	protein serine threonine kinase	At1g01540	6034.4	0.003585	4890.5	0.048995	7380.3	0.000388
18318_at	no hits		3447.4	0.162935	5204.1	0.000266	22515.2	0.000219
18319_g_at	WRKY family transcription factor (ZAP1)	At2g04880	7847.1	0.005643	6204.4	0.009985	12622.1	0.000959
18327_at	spot 3 protein and vacuolar sorting receptor homolog	At2g14740	6016	0.039365	7108.7	0.014937	11447.3	0.000562
18328_at	monosaccharide transport protein, STP4	At3g19930	10711.1	0.001354	15162.9	0.000673	15262.9	0.000322
18329_at	pectinesterase family	At2g43050	571.9	0.660442	5680.4	0.031336	2227.4	0.043968
18330_at	acyl-CoA synthetase	At4g23850	7299.7	0.003067	4907.4	0.302547	7272.1	0.001892
18365_s_at	auxin-binding protein 1 precursor	At4g02980	6780.4	0.150527	9254.9	0.02786	8850.6	0.00418
18478_at	receptor protein kinase	At1g78530	5524.3	0.048995	4479.3	0.002617	6673.6	0.000388
18487_at	farnesyltransferase beta subunit (ERA1)	At5g40280	14691.6	0.002617	7069.7	0.021866	19565.8	0.000322
18500_at	indole-3-acetate beta-glucosyltransferase like protein	At4g15500	839.6	0.964837	6030.7	0.035163	1678.6	0.05447
18522_at	kinase like protein	At4g14480	5288.3	0.007543	3075.6	0.003585	2587.6	0.000388
18549_s_at	potential calcium-transporting ATPase 7	At2g22950	1127.8	0.541212	5081	0.00418	2035.6	0.021866
18550_at	E2, ubiquitin-conjugating enzyme 7 (UBC7)	At5g59300	6227.4	0.039365	3465.3	0.014937	6624.3	0.000562
18556_at	cyclophilin (CYP2)	At2g21130	27983.1	0.001602	18371.2	0.000219	33036.7	0.000219
18561_at	cystatin	At5g12140	9401.2	0.000468	5549.6	0.003585	11105.8	0.003585
18565_i_at	flavin-type blue-light photoreceptor	At4g08920	8803.4	0.00293	23860.7	0.000977	30688.8	0.000977
18566_s_at	flavin-type blue-light photoreceptor	At4g08920	5742	0.011447	5667.9	0.189687	5433.7	0.005643
18573_at	acidic ribosomal protein p1	At4g00810	9641.9	0.004863	8402.6	0.07383	21122.4	0.000805
18575_at	E3 ubiquitin ligase SCF complex subunit SKP1	At2g03170	4519.7	0.302547	7048.4	0.024711	1921.9	0.043968
18594_at	unknown protein	At1g01470	85087.6	0.001141	72904.4	0.000219	67148.4	0.000219
18595_at	60S ribosomal protein L38	At2g43460	1028.4	0.250724	7097.6	0.003585	10164.3	0.002617
18601_s_at	putative microtubule-associated protein	At2g45170	123379.1	0.001141	85442.7	0.000219	23171.2	0.000219
18605_s_at	similar to zinc finger - like protein	At4g22820	6827.6	0.035163	5461	0.066865	9328.5	0.001354
18611_at	unknown protein	At5g26570	10686.9	0.004863	9999.8	0.043968	1112.4	0.234557
18612_s_at	no hits		2310.7	0.162935	4943.6	0.001892	4504	0.003067
18613_s_at	protein-methionine-S-oxide reductase	At4g25130	8485.1	0.031336	5203.1	0.07383	1881.5	0.05447
18614_at	no hits		10233.8	0.000959	15034.2	0.001141	8826.2	0.000562
18621_at	V-ATPase subunit G	At4g23710	3691.7	0.138765	3646.2	0.048995	4971	0.001141
18622_g_at	V-ATPase subunit G	At4g23710	9135	0.002228	14041.8	0.000219	13257.6	0.000219
18625_at	unknown protein	At1g03290	5628.1	0.035163	3657	0.011447	4011.8	0.017001
18627_s_at	G-protein beta family	At2g30050	963.1	0.64131	5069.4	0.02786	3586.3	0.024711
18629_s_at	remorin	At2g45820	22502.2	0.000266	45183.3	0.000562	53770.2	0.000388
18644_at	unknown protein	At2g35260	13778.7	0.021866	12834.9	0.204022	15223	0.000266
18650_s_at	stress-induced protein OZI1 precursor	At4g00860	38642.4	0.000322	38615.7	0.000266	50167.9	0.000219
18651_at	stress-induced protein OZI1 precursor	At4g00860	76905.7	0.000322	52156	0.000266	89583.4	0.000322
18653_s_at	succinyl-CoA ligase beta subunit	At2g20420	7910.2	0.013092	11295.1	0.000673	11831	0.000322
18655_at	unknown protein	At2g42210	5386.8	0.009985	5928.5	0.004863	10488	0.007543
18657_at	NADC homolog	At2g01350	5613.8	0.098054	4661.7	0.009985	4204.4	0.011447
18659_at	unknown protein	At5g45350	17140.4	0.001141	36679.5	0.000219	19546.5	0.000388
18661_at	unknown protein	At4g26710	30374.2	0.000219	29365.3	0.000322	54389.6	0.000266
18663_s_at	unknown protein	At4g24130	9044.5	0.021866	8730.2	0.000673	25037.2	0.000266
18673_at	no hits		18888.4	0.000562	22252.7	0.000322	21116.3	0.000388
18678_at	peptidylprolyl isomerase ROC4	At3g62030	17627.1	0.001354	13671.2	0.000959	27250.1	0.000388
18679_s_at	metallothionein-like protein	At1g07600	2114763	0.000219	1578109	0.000219	1742094	0.000219
18682_s_at	GTP-binding protein	At2g44610	4131.2	0.039365	4348.5	0.017001	7692.1	0.001141
18683_s_at	omega-3 fatty acid desaturase, chloroplast precursor	At5g05580	7245.5	0.013092	5359.1	0.003067	12072.2	0.000266
18685_at	chloroplast omega-6 fatty acid desaturase (fadL)	At4g30950	6578.8	0.048995	4963.4	0.002617	4897.8	0.003067
18687_at	pyruvate dehydrogenase E1 alpha subunit	At1g59900	84970.2	0.000219	90661.2	0.000219	188129.1	0.000219
18688_at	no hits		15811.2	0.007543	15824.1	0.000266	12322.3	0.000468
18691_at	GTP-binding protein	At5g05000	2545.4	0.732537	3466.1	0.031336	1836.7	0.05447
18694_s_at	chloroplast membrane protein	At2g28800	5790.3	0.035163	12467.8	0.000219	11278.4	0.000388
18695_s_at	glyoxalase II (hydroxyacylglutathione hydrolase)	At2g43430	6610.4	0.081337	6054	0.000959	25597.3	0.000219
18699_i_at	cold-regulated protein COR6.6 (KIN2)	At5g15970	410579.7	0.000244	345222.3	0.000244	1035837	0.000244
18700_r_at	cold-regulated protein COR6.6 (KIN2)	At5g15970	761297.4	0.000219	627808.3	0.000219	980368.9	0.000219
18701_s_at	cold and ABA inducible protein kin1	At5g15960	286450.3	0.000388	354147.3	0.000266	783385.3	0.000219

18702_at	Macrophage migration inhibitory factor (MIF) fa	At5g01650	9252.6	0.000468	5709.8	0.002617	15284.2	0.000266
18703_at	no hits		2942	0.250724	2217.7	0.048995	5352.4	0.000468
18705_at	myosin	At3g19960	4642.2	0.320802	4055.1	0.005643	1473.5	0.05447
18706_s_at	putative adenosine phosphosulfate kinase	At2g14750	4592.6	0.066865	6296.8	0.017001	2278.8	0.031336
18708_at	ripening-related protein	At5g62350	52544.4	0.000388	61577.6	0.000322	60618.8	0.000388
18709_at	no hits		3672.2	0.35869	7188.5	0.009985	9548.2	0.000266
18710_at	NADH dehydrogenase	At5g11770	15553.1	0.002617	18278	0.002228	37603.5	0.000266
18711_at	NADH dehydrogenase	At1g79010	6727.5	0.007543	8355.5	0.000219	23525.8	0.000266
18712_g_at	NADH dehydrogenase	At1g79010	10567.5	0.031336	14904.3	0.007543	13786.9	0.003067
18713_at	mitochondrial elongation factor Tu	At4g02930	3871.1	0.284747	5011.7	0.035163	2678.5	0.001352
18722_s_at	chloroplast FtsH protease	At1g50250	8442.2	0.017001	3233.5	0.07383	4126.2	0.005643
18725_s_at	no hits		460.8	0.933135	2089	0.014937	1749.6	0.019304
18726_s_at	putative signal peptidase I	At2g30440	6428.7	0.017001	5140.9	0.009985	1869.9	0.043968
18729_at	unknown protein	At1g20693	208828	0.000219	148599.1	0.000219	107642.1	0.000219
18730_at	calmodulin-4	At1g66410	94757.9	0.000219	93330.5	0.000219	171377	0.000219
18731_at	calmodulin 7	At3g43810	52763.1	0.001141	41042.1	0.000388	109311.1	0.000388
18732_i_at	ribosomal protein precursor	At5g14320	78349.3	0.000977	41407.4	0.000977	138318.1	0.000977
18733_r_at	ribosomal protein precursor	At5g14320	18961.3	0.004863	9469.3	0.000468	16067.3	0.000388
18735_s_at	gamma-glutamylcysteine synthetase	At4g23100	6368.6	0.019287	6132.4	0.024711	6793.4	0.002228
18736_at	50S ribosomal protein L21 chloroplast precursor	At1g35680	11069.2	0.000388	9243.7	0.001602	12002.9	0.001141
18761_at	CHP-rich zinc finger protein	At4g02540	4540.8	0.00418	8927.2	0.02786	5224.3	0.003067
18762_at	unknown protein	At4g02490	4778.1	0.162935	15807.8	0.006532	7997.4	0.00418
18806_at	naringenin 3-dioxygenase like protein	At4g16330	6741.2	0.089405	5605.1	0.043968	3545.3	0.035163
18824_at	Rab family GTP-binding protein (Ara6)	At3g54840	3230.9	0.234557	4592.9	0.048995	3326	0.003585
18832_s_at	similar to axi 1 protein	At2g03280	3293.1	0.284747	3094.6	0.024711	1464.6	0.031336
18874_at	unknown protein	At1g27290	13415.6	0.024711	10152.8	0.05447	8744.3	0.00418
18880_at	putative 3-isopropylmalate dehydrogenase	At1g80560	4295.9	0.07383	4406.6	0.043968	2995.9	0.014937
18882_at	no hits		49999.7	0.000322	87848.6	0.000562	75060.1	0.000219
18883_g_at	3-isopropylmalate dehydratase, small subunit	At2g43090	3203.4	0.250724	3667.5	0.02786	1568.4	0.05447
18892_at	unknown protein	At4g39300	9962.3	0.024711	7885.8	0.035163	7332.6	0.005643
18897_at	putative tyrosine decarboxylase	At2g20340	2903.1	0.621816	8103.7	0.019304	2785.2	0.05447
18907_s_at	flavanone 3-hydroxylase (FH3)	At3g51240	1671.3	0.52062	5483.6	0.031336	17701.5	0.000388
18918_at	no hits		10192.6	0.000468	9571.9	0.001602	11923.7	0.000266
18929_s_at	chalcone synthase	At5g13930	15707.4	0.017001	12030.5	0.060419	34369	0.000959
18933_at	putative ferritin	At2g40300	21506.2	0.001602	19259.8	0.000219	81706.7	0.000219
18934_g_at	putative ferritin	At2g40300	5002.9	0.021866	1794.7	0.11716	2587.1	0.000468
18937_at	casein kinase I	At4g14340	15176.9	0.005643	12686.4	0.009985	32058.2	0.001892
18940_at	GTP-binding protein, ara-5	At1g02130	23160.5	0.000322	22101.6	0.024711	50336.4	0.000219
18947_i_at	E2, ubiquitin-conjugating enzyme 11 (UBC11)	At3g08690	4428.5	0.119658	5058.1	0.009301	12696.2	0.02493
18953_at	branched-chain alpha keto-acid dehydrogenase	At1g21400	3044.1	0.05447	7592.8	0.002228	3728.7	0.000959
18954_at	putative cysteine proteinase inhibitor B	At2g40880	16289	0.00418	17403.4	0.000388	19121.7	0.000959
18956_at	ethylene response sensor (ERS)	At2g40940	35540.8	0.000219	42886.2	0.000219	34631.9	0.000219
18962_s_at	putative uricase subunit	At2g26230	12495	0.001602	9008.9	0.001602	8992.6	0.000562
18967_s_at	putative calmodulin	At3g51920	2275.3	0.47938	3151.7	0.00418	8141.8	0.000388
18974_at	protein kinase 6	At4g35780	12094.9	0.024711	6536	0.267463	7852.9	0.006532
18975_g_at	protein kinase 6	At4g35780	12520.6	0.005643	9738.5	0.019304	9217.8	0.000562
18977_at	glutathione transferase	At1g10360	3194.9	0.039365	2464.9	0.397994	2434.8	0.039365
18978_at	DEAD DEAH box RNA helicase	At5g11170	3388.3	0.060419	2890	0.002228	1003.5	0.05447
18985_g_at	unknown protein	At2g34680	9060.3	0.043968	4247.7	0.32083	3431.7	0.039365
18987_g_at	putative CCAAT-binding transcription factor subunit	At2g38880	7200.9	0.021866	3089.5	0.284715	3744.2	0.039365
18989_s_at	dnaJ protein homolog atj3	At3g44110	5136.1	0.035163	3161	0.006532	4403.2	0.000805
19008_s_at	glycosyl hydrolase family 35 (beta-galactosidase)	At2g28470	12485.5	0.001141	14054.6	0.007543	20933	0.000266
19039_at	putative sugar transport protein, ERD6	At1g08900	5282.8	0.048995	4363.3	0.048995	3195	0.00418
19115_at	no hits		4495.6	0.71497	2246.2	0.055848	2403.5	0.008529
19130_at	unknown protein	At1g77180	6918.9	0.048995	4573.5	0.011447	3447.5	0.000468
19132_at	putative NADPH quinone oxidoreductase	At4g21580	4505.4	0.035163	6839.4	0.024692	2745.3	0.009985
19133_at	H+-transporting ATPase	At4g32530	15356.1	0.000959	15336.2	0.002228	15795.6	0.000219
19139_at	RUB1-conjugating enzyme RCE1	At4g36800	9597.9	0.017001	11549.5	0.009985	14439.1	0.000388
19147_at	unknown protein	At5g65910	4589.1	0.043968	3895.9	0.098054	5412.4	0.00418
19155_s_at	cyclic nucleotide-regulated ion channel (CNGC)	At2g23980	1613.8	0.660442	2555.9	0.03934	2036.8	0.011447
19161_at	putative acyl-CoA binding protein	At4g27780	3952.6	0.043968	3073.8	0.418069	801.9	0.039365
19169_g_at	transcription factor IIA large subunit	At1g07480	5363.7	0.081337	5917.6	0.011447	2937.3	0.003067
19171_at	putative trypsin inhibitor	At2g43510	5423.8	0.127645	6161	0.001354	8400.5	0.000266
19172_at	scarecrow-like protein	At1g50600	4791.1	0.009985	10011.6	0.003067	1654.4	0.014937
19181_s_at	unknown protein	At4g02380	6375.4	0.043968	4188.8	0.066865	11694.8	0.000266
19183_at	unknown protein	At4g25210	8830.9	0.00418	3593.5	0.162935	4833.1	0.006532
19186_s_at	dehydrin Xero2	At3g50970	13111.1	0.000219	14737	0.000468	3629.5	0.001892
19206_at	unknown protein	At2g38980	5214.7	0.004863	5027	0.05447	3997.8	0.000958
19224_at	phytochelatin synthetase	At5g60920	4138.4	0.039365	4895.9	0.008689	4028.1	0.001892
19302_at	putative prohibitin	At2g20530	6168.1	0.043968	4108.5	0.043968	3381.2	0.002617
19314_at	unknown protein	At2g26890	3496.8	0.127645	3982.7	0.006532	2453.6	0.009985
19321_at	pentacyclic triterpenoid synthase cyclase family	At1g78480	2249.3	0.378184	2726	0.043968	1508.5	0.009985
19365_s_at	cinnamyl-alcohol dehydrogenase CAD1	At4g39330	4488.9	0.054441	2519.2	0.039365	6281.6	0.004863

19382_at	unknown protein	At2g46225	5424	0.011447	1927.4	0.218983	5743.6	0.003585
19401_at	unknown protein	At2g02050	16497.2	0.008689	13005.9	0.002617	22792.2	0.000562
19402_at	unknown protein	At2g04690	7197.3	0.039365	5061.1	0.107301	4521.7	0.001892
19403_at	unknown protein	At2g31490	19703.4	0.001141	24826.1	0.001141	33235	0.000266
19407_at	similar to putative adenylate kinase	At2g39270	10795.8	0.017001	6314.8	0.081337	9427.3	0.007543
19412_at	F-box protein family	At1g21760	3149.1	0.043968	2978.3	0.204022	1493	0.048995
19413_at	unknown protein	At3g51610	3147.6	0.024711	2379.2	0.043968	1506.9	0.02786
19422_at	putative heat shock protein	At2g04030	9953.5	0.002617	5341.4	0.007543	9350.2	0.005643
19431_s_at	multidrug resistance P-glycoprotein	At4g25960	5007.4	0.098054	3118.8	0.017001	4104.5	0.004863
19439_at	aldehyde dehydrogenase like protein	At4g36250	7329.5	0.05447	15540	0.002617	13016.7	0.000673
19446_i_at	mannose 6-phosphate reductase (NADPH-dep	At2g21250	6835.7	0.004591	4848.6	0.020663	5816.4	0.000613
19448_s_at	glycosyl hydrolase family 9 (endo-1,4-beta-gluc	At1g70710	5641.9	0.05447	3316.4	0.060419	3579.4	0.011447
19453_at	putative serine carboxypeptidase I	At2g22980	3073.9	0.05447	2195	0.007534	341.6	0.660468
19464_at	putative MAP kinase	At2g01450	5927.4	0.031336	3307.6	0.02786	1260.9	0.003585
19512_at	unknown protein	At1g61980	3205.8	0.284747	4485	0.017001	4240.5	0.00418
19599_at	acyl carrier protein 1 precursor (ACP)	At3g05020	2222.6	0.175989	2556.1	0.043968	2682.2	0.009985
19607_at	putative casein kinase II catalytic (alpha) subu	At2g23080	5421.3	0.039365	6468.8	0.000562	4701.9	0.001602
19611_s_at	myb family transcription factor	At4g34990	1842.8	0.541184	4574.1	0.005643	8735.5	0.000562
19616_s_at	putative phospholipid cytidylyltransferase	At2g32260	7776.5	0.039365	3623	0.098054	10520.9	0.000388
19617_at	14-3-3 protein GF14 omicron	At1g34760	8586.9	0.019287	10400.8	0.000959	14121	0.000388
19623_at	putative cytochrome C	At1g22840	24663.3	0.002228	24981.2	0.004863	57364	0.000266
19627_s_at	putative serine carboxypeptidase II	At4g35780	4066.5	0.150527	5924.3	0.02786	3476.7	0.006532
19642_at	putative cullin-like 1 protein	At4g02570	6384.2	0.011447	3808.9	0.021866	4597	0.013092
19650_at	coatomer alpha subunit	At2g21390	8323.1	0.081337	3996.4	0.048995	5587.5	0.009985
19651_s_at	20S proteasome alpha subunit B	At1g16470	4935.3	0.127645	4250.2	0.008689	4294.1	0.00418
19663_at	putative tropinone reductase	At2g29360	3516.6	0.127645	3132.3	0.031336	2233.8	0.019304
19665_at	defender against cell death protein	At1g32210	3368.6	0.175989	5069.8	0.007534	7174.4	0.000388
19667_at	glycolate oxidase	At4g18360	4153.2	0.048995	3531.1	0.039365	1453.6	0.089405
19674_s_at	disease resistance protein (CC-NBS-LRR class	At5g43470	5824.3	0.039365	1125	0.267463	1975.5	0.000959
19681_at	unknown protein	At4g24805	2493.8	0.581931	4031.8	0.031336	4285.9	0.000805
19686_at	putative HMG protein	At2g17560	5497.2	0.11716	7978.8	0.002617	12729.7	0.000322
19687_g_at	putative HMG protein	At2g17560	7837.3	0.031336	3614.6	0.000266	3791.6	0.001354
19690_s_at	eukaryotic peptide chain release factor subunit	At1g12920	4792.9	0.098054	4232	0.00418	9307.6	0.000266
19700_s_at	unknown protein	At4g23420	3580.3	0.541184	6197.8	0.02786	6985.1	0.008689
19708_at	unknown protein	At2g23420	4532.4	0.039365	1621.3	0.715253	3616.6	0.003067
19720_at	putative gibberellin-regulated protein	At1g22690	737790.4	0.000219	654949.7	0.000219	1207819	0.000219
19734_at	unknown protein	At3g26630	427.7	0.795978	8428.1	0.001892	3112	0.008689
19753_at	putative helicase	At2g14300	3882.8	0.250724	3363.7	0.02786	1589.4	0.006532
19759_at	putative superoxide-generating NADPH oxidase	At1g23020	5307.7	0.043968	3275.9	0.098054	2383.1	0.039365
19838_i_at	putative ARP2 3 protein complex subunit p41	At2g30910	7685	0.02832	3641.6	0.011719	50335.4	0.001465
19848_s_at	Calmodulin-binding protein	At2g41100	28104.1	0.000388	26634.7	0.000562	34546.2	0.000388
19852_s_at	cytoplasmatic aconitase hydratase (citrate hydr	At4g35830	13757.6	0.017001	12321.9	0.019304	12951	0.001141
19854_at	putative amine oxidase	At2g43020	6782.3	0.019304	4973.9	0.039365	3434.5	0.035163
19858_s_at	unknown protein	At4g39660	6377.7	0.019304	3193	0.175989	3248.1	0.043968
19866_at	DNA-binding protein	At1g01060	1947.6	0.5	3848	0.031336	21908.8	0.000388
19887_s_at	leucine zipper-containing protein AT103	At3g56940	9249.7	0.014937	2632.2	0.11716	3717.4	0.003585
19889_at	unknown protein	At2g32870	9480.3	0.013092	21048.4	0.005643	2166.4	0.081337
19894_at	succinate dehydrogenase flavoprotein alpha su	At5g66760	9506.9	0.006532	9932.8	0.000562	11604.4	0.000673
19896_s_at	putative squamosa-promoter binding protein	At2g33810	24953	0.011447	16343.8	0.003067	23326.6	0.003585
19897_s_at	outward rectifying potassium channel KCO	At5g55630	552.7	0.781017	9224.4	0.035163	6166.1	0.02786
19898_at	GATA zinc finger protein	At3g60530	7237.4	0.00418	6438	0.234557	7181.2	0.005643
19900_at	9-cis-epoxycarotenoid dioxygenase	At3g63520	5172.6	0.066865	6927.6	0.003585	8805.5	0.001892
19904_at	MAP kinase	At3g51630	5025.2	0.127645	4283.8	0.021866	4476	0.001354
19919_i_at	unknown protein	At1g14910	23572.7	0.000488	28082.7	0.126953	29536.3	0.000488
19925_at	unknown protein	At2g43940	5760.8	0.048995	5475.9	0.098054	4280	0.001354
19927_at	unknown protein	At2g41470	2871	0.204022	6732.2	0.039365	2987.4	0.039365
19932_at	protein phosphatase homolog (PPH1)	At4g27800	113036.4	0.000266	106277.1	0.000219	181092.6	0.000219
19933_g_at	protein phosphatase homolog (PPH1)	At4g27800	6956.3	0.004863	4852.5	0.009985	3497.6	0.004863
19940_at	endomembrane protein 70	At2g01970	4293.9	0.150527	7301.9	0.021866	3998.5	0.002228
19946_at	unknown protein	At2g23810	5448.3	0.127645	5577.9	0.006532	7933.8	0.000562
19948_at	unknown protein	At2g31580	6231.7	0.017001	6270.8	0.009985	6302.1	0.001354
19949_at	senescence-associated protein	At4g28050	4993.8	0.035163	1870.1	0.302547	1915	0.013092
19955_at	unknown protein	At2g32580	4623.8	0.039365	2734.5	0.11716	1999.5	0.014937
19963_at	unknown protein	At1g07320	34965.8	0.000805	25401.8	0.000468	78448.5	0.000219
19964_g_at	unknown protein	At1g07320	7679.5	0.008689	6600.8	0.05447	6523.9	0.0016
19968_at	putative chloroplast initiation factor 3	At2g4060	5345.6	0.089405	3002.2	0.043968	1642.1	0.039365
19977_at	unknown protein	At3g48360	2523.4	0.117121	3499.8	0.007543	2639.7	0.007543
19984_at	unknown protein	At1g61900	2688.9	0.234557	3472.8	0.048995	2262.1	0.00418
19999_s_at	unknown protein	At2g46490	19540.7	0.05447	12351.7	0.418069	26431	0.007543
20001_at	unknown protein	At2g33220	7663.6	0.024711	7514.5	0.189687	12495.2	0.000805
20012_g_at	unknown protein	At1g24240	6297.7	0.021866	5574.2	0.009985	4582.2	0.001892
20013_at	unknown protein	At2g45640	3678.6	0.162935	3328.5	0.008689	3351.1	0.003585
20014_at	unknown protein	At2g44140	5056.6	0.013092	4750.2	0.204022	2727	0.031336



20016_at	no hits		7805.4	0.019287	3330.1	0.05447	2918.4	0.035163
20032_at	unknown protein	At1g27350	7026	0.003585	9355.1	0.003585	12286.7	0.000388
20049_at	unknown protein	At2g34160	7250.4	0.007543	3745.5	0.138765	2559.6	0.001892
20050_at	unknown protein	At2g37660	3285.3	0.017001	5100.5	0.043968	3744.9	0.004863
20064_at	unknown protein	At1g09330	5952	0.089405	4541.2	0.004863	3330.5	0.001892
20066_at	unknown protein	At2g35840	2430.3	0.234557	4711.8	0.013092	5214	0.019304
20067_at	unknown protein	At2g04280	6568.8	0.02786	5539.5	0.048995	4649	0.014937
20081_at	unknown protein	At1g30590	4698.5	0.267463	6165.7	0.039365	2643.1	0.02786
20121_at	no hits		5217.5	0.150487	8738.8	0.005643	6434.8	0.001141
20129_at	putative pyrophosphate--fructose-6-phosphate	At2g22480	6381.8	0.017001	6306.8	0.00418	4427.6	0.007543
20133_i_at	unknown protein	At2g04100	5791.6	0.04977	3903.4	0.055884	2786.6	0.007298
20166_at	unknown protein	At2g33470	11801.8	0.066865	6350.7	0.035163	8074.3	0.011447
20167_i_at	5-enolpyruvylshikimate-3-phosphate (EPSP) sy	At2g45300	387.2	0.694336	4096.9	0.032227	7208.8	0.00293
20171_s_at	unknown protein	At2g29700	6263.7	0.003585	5764.2	0.07383	4634.1	0.000322
20172_at	unknown protein	At1g61620	4922.9	0.013092	5092.8	0.378184	2421	0.02786
20175_at	unknown protein	At2g28420	3619.1	0.204022	9130.8	0.006532	6583	0.00418
20180_at	arabinogalactan-protein (AGP13)	At4g26320	9868.8	0.048995	17901.3	0.081337	24797.5	0.002617
20191_at	putative thioredoxin M	At2g15570	7931	0.011447	4883	0.098054	4241.1	0.001141
20197_at	unknown protein	At3g52180	2639.8	0.098054	3911.5	0.002617	2415.4	0.007534
20200_at	unknown protein	At4g25690	4123.5	0.204022	4067.6	0.008689	4007.9	0.000805
20213_at	leucine-rich repeat transmembrane protein kin	At2g01950	3133	0.048967	3932.8	0.039365	1153.1	0.218983
20244_at	aminopeptidase- like protein	At4g33090	902.8	0.32083	4518.3	0.039365	3347.4	0.031314
20261_at	protein phosphatase 2A 65 kDa regulatory sub	At3g25800	15248.4	0.001354	11252.1	0.009985	13289.9	0.000562
20282_at	putative protein kinase	At2g28930	67186.3	0.002617	55510	0.000959	180054.9	0.000468
20317_at	leucine-rich repeat transmembrane protein kin	At1g48480	350.8	0.88284	5044.7	0.009985	2670.3	0.017001
20330_at	Ras-related GTP-binding protein (Rab7)	At1g22740	4692.6	0.014937	2177.3	0.204022	2214.2	0.011447
20337_at	E2, ubiquitin-conjugating enzyme 3 (UBC3)	At5g62540	3905.9	0.098054	8358.3	0.001892	7881.6	0.000805
20350_s_at	cyclophilin	At2g29960	2786.4	0.267463	4485.4	0.031336	2020.4	0.004863
20353_at	no hits		3258.2	0.267463	5287.3	0.048995	7332.7	0.000322
20369_s_at	ammonium transport protein (AMT1)	At4g13510	4370.9	0.019304	6816.8	0.014923	3622.4	0.002617
20378_g_at	ADP-ribosylation factor 3	At2g24765	13580.9	0.011447	14122.5	0.000388	12859.8	0.000468
20382_s_at	WRKY family transcription factor	At2g30250	3622.1	0.127645	3450.9	0.039365	2710.9	0.019304
20405_at	no hits		5430	0.043968	1293.9	0.150527	2603.1	0.048995
20412_at	oleosin	At4g25140	5585	0.001141	6592.2	0.009985	2065.8	0.081337
20459_i_at	no hits		67060.5	0.000488	71838.8	0.000488	117466.3	0.000488
20461_at	pumilio-like protein	At4g25880	4215.4	0.024692	962.2	0.47938	1974.4	0.00418
20463_s_at	no hits		5279.5	0.098054	4883.2	0.035163	9647.2	0.001141
20464_at	40S ribosomal protein S15A	At2g19720	445.5	0.795978	2165.6	0.013079	2298.3	0.031336
20467_at	unknown protein	At4g04340	7174.9	0.107301	7420.3	0.013092	6305.9	0.013092
20510_at	putative ubiquitin fusion-degradation protein	At2g21270	3963.6	0.302547	17123.6	0.048995	5137.7	0.011447
20518_at	unknown protein	At1g10060	20095.5	0.004863	28800	0.00418	29361.3	0.000322
20529_at	cysteine proteinase inhibitor	At4g16500	7039.4	0.043968	4578.3	0.07383	4289.9	0.003585
20537_at	extensin-like protein	At4g13340	15224	0.02786	17349.7	0.006532	9882.2	0.001602
20559_at	light induced protein homolog	At4g22310	34624.4	0.000468	32938.6	0.000322	57349.3	0.000219
20568_i_at	G2484-1 protein	At4g17330	6353.9	0.02987	3042.7	0.173261	4624	0.002371
20570_at	putative trehalose-6-phosphate phosphatase (A	At4g12430	7367.3	0.019304	6089.5	0.003067	9558.9	0.000219
20574_at	unknown protein	At4g01290	5137.2	0.024711	6312.2	0.021866	3325.3	0.02786
20576_at	unknown protein	At4g31820	1662.5	0.378184	5030.5	0.007543	1450.5	0.05447
20585_at	putative glutaredoxin	At2g47880	14071	0.048995	5142.7	0.47938	9042.1	0.019304
20612_s_at	AUX1-like amino acid permease	At2g21050	5917.4	0.013092	1643.1	0.284747	2030.5	0.05447
20629_at	unknown protein	At2g04410	6146.2	0.048995	5894.8	0.035163	13274.4	0.000322
20631_s_at	TCP1-chaperonin cofactor A isolog	At2g30410	9568.4	0.039365	8790.3	0.021866	10730.8	0.009985
20636_at	unknown protein	At4g17870	8166.7	0.05447	3509.8	0.418069	13090	0.000388
20644_at	putative phospholipid cytidyltransferase	At2g38670	4342.1	0.127645	10080.7	0.05447	2320.4	0.009985
20647_at	bHLH protein	At2g42280	2676.4	0.150527	3470.8	0.017001	1626.6	0.001892
20661_at	no hits		4385.1	0.048995	5408.2	0.02786	4034.4	0.002617
20662_g_at	alanine--tRNA ligase	At1g50200	7299.2	0.017001	8937.4	0.001141	7130.3	0.000805
20670_at	thioredoxin	At2g35010	6603.3	0.005643	8892.4	0.021866	5463.4	0.003585
20672_at	unknown protein	At2g11260	3980.6	0.013092	1641.4	0.284747	1946.3	0.009985
20689_at	putative calcium binding protein	At2g43290	3721.8	0.127645	2181	0.021866	5866.3	0.001141
20694_s_at	no hits		7569.2	0.05447	3056.6	0.11716	4002.3	0.006532
20700_i_at	no hits		4221.7	0.056152	11292.7	0.018555	1694.4	0.334473
20701_s_at	unknown protein	At4g10970	4763.1	0.107301	5902.6	0.043968	2980	0.035163
20704_at	unknown protein	At4g24750	5042.7	0.043968	3285.1	0.089405	2541.6	0.001354
20709_s_at	putative 3-oxoacyl [acyl-carrier protein] reducta	At1g24360	101924.5	0.000468	108839.4	0.003585	319573.9	0.000219
20713_at	unknown protein	At1g21630	6248.9	0.054441	11453.4	0.039365	5732	0.001354

<sup>a</sup>Describes names of probe set on Affymetrix chip.

<sup>b</sup>Arabidopsis Genome Initiative locus numbers.

<sup>c</sup>Signal value which assigns a relative measure of abundance of transcript of each gene

<sup>d</sup>Detection P-value which indicates whether a transcript is reliably detected.

This table contains genes which have a detection P-value  $\leq 0.06$  in at least two experiments (Present or Marginal in Affymetrix nomenclature).