Cluster 1. 314 genes					
Probe	ID	Sample 1	Sample 2	Sample 3	Sample 4
CNGC10	AT1G01340	1.1235391	0.82403594	1.6654401	1.5698885
BXL2	AT1G02640	3.9587743	3.779866	4.143905	4.26304
AT1G02660	AT1G02660	2.3853707	2.1693103	2.595884	2.7480652
ATPCS2	AT1G03980	-1.3185683	-1.5101261	-0.48549724	-0.1490158
AT1G04990	AT1G04990	2.9209232	2.9477901	3.3592904	3.4818819
ZIP5	AT1G05300	0.63450634	0.22828014	1.4479922	1.226447
AT1G05805	AT1G05805	2.9971066	3.0627563	3.3685284	3.601634
ORA59	AT1G06160	1.0111014	0.8589948	1.5482154	1.6680164
ATMYB13	AT1G06180	2.4597604	2.1242201	2.7157717	2.7211263
AT1G07360	AT1G07360	4.2622967	4.12786	4.5276647	4.594372
ATECA4	AT1G07670	4.4595876	4.333609	4.734613	4.7924705
AT1G09300	AT1G09300	2.5755978	2.313814	3.045962	2.876351
AT1G10140	AT1G10140	2.2304637	2.2664013	2.7951365	2.9379673
AT1G10310	AT1G10310	2.9953191	2.9896898	3.4091175	3.488515
AT1G10900	AT1G10900	3.9035892	3.5968304	4.296495	4.214391
AT1G11070	AT1G11070	-3.8899834	-5.0270414	-2.3667824	-2.0543365
AT1G11180	AT1G11180	1.6922054	1.670578	2.2155404	2.3275614
AT1G11200	AT1G11200	2.5238695	2.4712546	3.0115843	3.0600154
AT1G11362	AT1G11362	-4.217343	-4.309707	-1.9125925	-1.6320744
AT1G11950	AT1G11950	2.150304	1.6849937	2.527688	2.53511
AT1G12700	AT1G12700	-5.0293904E-4	-0.28745323	0.85474205	1.0476209
RSH2	AT1G12950	0.5445505	0.7171486	1.1333557	1.6281519
AT1G13790	AT1G13790	1.3857579	1.0918801	1.8799428	1.8944597
AT1G15125	AT1G15125	2.6836965	2.9386733	3.1201992	3.8968546
AtRLP3	AT1G17250	-0.4015464	-1.4790894	0.6209526	0.42909995
AT1G17640	AT1G17640	0.5745917	0.4491221	1.2904669	1.2532768
AT1G20380	AT1G20380	2.6596973	2.198351	3.1525393	2.831576
EMB1968	AT1G21690	3.5349967	3.4621992	3.8953083	3.918913
AT1G23050	AT1G23050	-1.3360575	-1.6506138	-0.16328345	-0.045034423
AT1G23720	AT1G23720	4.792722	4.568189	5.1164513	5.21857
AT1G26660	AT1G26660	1.6934896	1.6575745	2.1686382	2.323101
AT1G29560	AT1G29560	1.2512412	0.9707527	1.9516376	1.7207537
RKF1	AT1G29750	3.1355553	2.961436	3.481183	3.4819334
AT1G29820	AT1G29820	3.0732582	2.8689172	3.2710984	3.3538835
ARF6	AT1G30330	4.928846	4.869064	5.2412615	5.362352
ECS1	AT1G31580	-4.6579857	-5.128377	-3.10758	-1.8912768
XLG3	AT1G31930	3.5176804	3.3379714	3.7430441	3.856309
ATDAD1	AT1G32210	4.17636	4.21482	4.5610356	4.6530585
AOX1D	AT1G32350	-5.0419865	-5.128377	-3.1211274	-2.0112422
AT1G32920	AT1G32920	2.354914	2.3589694	2.8985155	2.9737072
AT1G33910	AT1G33910	-5.0419865	-5.128377	-3.491581	-2.9011927
ATUPF3	AT1G33980	3.8705368	3.7725894	4.2336016	4.2035995
AT1G43650	AT1G43650	0.18928559	-0.05682735	0.94014335	0.9441128
AT1G45231	AT1G45231	1.6711607	1.3703893	2.1110249	2.0339377
AT1G48460	AT1G48460	3.5636408	3.366853	3.967481	3.9324524
AT1G49790	AT1G49790	-5.0419865	-5.128377	-2.5928066	-2.3445756
AT1G50460	AT1G50460	2.423588	2.2962952	2.9486942	2.8986206
TRZ3	AT1G52160	2.8808277	2.715934	3.3394833	3.263137
AT1G52200	AT1G52200	3.8212092	3.89861	4.5955634	4.7238564
AT1G53440	AT1G53440	4.767445	4.5320864	5.0815167	5.0019264
AT1G53600	AT1G53600	-1.0057018	-1.3172807	-0.09197318	0.14749007
AT1G53790	AT1G53790	-0.033048738	-0.74521154	0.4254142	0.6110861
AT1G54000	AT1G54000	5.700113	5.1630034	5.991995	5.8979897
AT1G54310	AT1G54310	2.6783836	2.4383464	3.0505416	3.028986
AT1G55430	AT1G55430	-0.61738914	-1.2382675	-0.23099303	-0.0037861466
AT1G55450	AT1G55450	3.591657	3.901748	4.107649	4.353865

AT1G58025	AT1G58025	3.2181408	3.1271245	3.5747032	3.5851526
AT1G59710	AT1G59710	2.3479807	2.5330937	2.8101242	3.0282147
AT1G60095	AT1G60095	-0.37790117	-0.3579546	0.5045536	1.004388
AT1G61470	AT1G61470	-4.991319	-5.077709	-2.7235792	-2.1360407
AT1G61660	AT1G61660	2.9603336	2.6878242	3.4497893	3.2578487
AT1G62000	AT1G62000	-5.0419865	-5.128377	-2.9692345	-2.2803605
AT1G62970	AT1G62970	1.9768553	1.7100549	2.3730042	2.482607
AT1G63100	AT1G63100	2.842007	2.6327178	3.1675441	3.1867788
AT1G63480	AT1G63480	2.207823	2.283619	2.6979768	2.9220746
AT1G63810	AT1G63810	4.252671	3.8766692	4.5931344	4.388389
ATCHX16	AT1G64170	2.4595919	1.9984051	2.7249477	2.7627976
AT1G64910	AT1G64910	-3.3616629	-4.448053	-1.5186758	-1.5247649
AT1G67120	AT1G67120	5.000012	4.318508	5.3424454	5.033135
POLA2	AT1G67630	2.761936	2.6182053	3.120969	3.191969
AT1G68500	AT1G68500	-0.25793585	-0.41911983	0.68572646	0.7620178
DVL5	AT1G68825	-1.3307437	-2.428422	-1.4719499	-0.7823641
AT1G70880	AT1G70880	-0.27341738	0.054834057	0.32037318	1.0358838
AT1G70990	AT1G70990	0.24824484	0.3434004	0.6581064	1.1829934
AT1G71100	AT1G71100	2.6725676	2.6678994	3.1627998	3.1993992
AT1G71528	AT1G71528	2.0061119	1.4124943	2.3298388	2.1630793
SOL1	AT1G71696	2.8930876	2.7880118	3.2198353	3.2584054
HISN6B	AT1G71920	-4.078997	-5.128377	-1.4719499	-2.0543365
AT1G72040	AT1G72040	4.913055	4.6095138	5.2523026	5.104693
AT1G72416	AT1G72416	1.4281121	1.6175755	2.2784784	2.5053337
AT1G75340	AT1G75340	3.1529891	2.9092486	3.418616	3.4320679
ATEXT4	AT1G76930	6.9955173	7.0214615	7.417319	7.601856
ADH1	AT1G77120	2.5429294	2.2258384	3.2579787	3.1657171
MEI1	AT1G77320	2.3357992	2.1318629	2.8584836	2.8685925
AT1G77330	AT1G77330	4.37547	4.428821	4.670999	4.8850245
ATTPPB	AT1G78090	2.4912932	2.4866383	2.5207498	2.983414
DRS1	AT1G80710	0.722251	0.650919	1.422739	1.4793243
AT2G02160	AT2G02160	5.296057	5.116771	5.624943	5.5832963
AT2G04050	AT2G04050	-1.3542067	-1.3914114	-0.51928955	0.084478796
AT2G04170	AT2G04170	3.641318	3.7133682	4.1154113	4.2553587
AT2G06040	AT2G06040	1.5784703	1.2000165	2.020786	1.9288441
AT2G13460	AT2G13460	-5.0419865	-5.128377	-2.9692345	-2.5063841
AT2G14247	AT2G14247	3.2540882	3.1618545	3.7596543	3.7303925
ATPRB1	AT2G14580	1.8132356	1.7414618	2.4065554	2.5203245
AT2G17080	AT2G17080	-0.5418522	-0.85317475	-0.13736589	0.34112096
NTRA	AT2G17420	4.5958366	4.591287	4.875044	5.040222
AT2G17570	AT2G17570	0.39256468	0.59090877	1.1208643	1.3562082
AT2G18193	AT2G18193	1.6866254	1.3410454	2.3687625	2.3382657
SDH1-2	AT2G18450	-0.9025925	-1.2270647	0.08865807	0.19394152
HMA4	AT2G19110	4.330194	4.1133695	4.621323	4.576774
FRK1	AT2G19190	-0.2513571	0.06725687	1.2585768	1.1411206
AT2G19270	AT2G19270	3.1210206	3.065121	3.5119426	3.618882
CDA1	AT2G19570	3.533122	3.6824028	3.9608185	4.337384
AT2G20060	AT2G20060	4.3276567	4.2542696	4.684414	4.6756034
AT2G23680	AT2G23680	1.2852615	1.2222248	1.7952323	2.036288
AT2G25730	AT2G25730	4.899634	4.511978	5.194456	5.0683208
SE	AT2G27100	4.860065	4.772575	5.1678715	5.180004
ATC	AT2G27550	2.3702118	2.692794	2.6650746	3.2891703
AT2G27660	AT2G27660	1.4609122	1.1631051	1.7846075	1.8454894
AT2G28940	AT2G28940	1.8777189	1.6051322	2.327077	2.5241811
SAG13	AT2G29350	-2.4541743	-1.8905779	-0.36464062	0.5716699
AtIPCS3	AT2G29525	1.0227138	0.8290164	1.323697	1.594461
CYP71A13	AT2G30770	-2.2543533	-1.8766378	-1.7176051	-0.35105953
PARP2	AT2G31320	2.6349437	2.3496282	2.9363081	2.8976974
GUN1	AT2G31400	7.0264916	6.84868	7.33065	7.285086

AT2G32870	AT2G32870	2.6954792	2.5275753	3.2014036	3.2545054
RALFL18	AT2G33130	-3.5000086	-2.2666128	-1.5137936	-0.56107634
AT2G33830	AT2G33830	5.594044	5.756373	6.2236695	6.331932
AT2G35075	AT2G35075	-0.89010096	-1.8259702	0.060361814	-0.028731242
AtGRF3	AT2G36400	3.7957983	3.6629667	4.2187996	4.1603293
AT2G36970	AT2G36970	2.0249794	1.7567328	2.5811584	2.3536234
AT2G37362	AT2G37362	1.3923994	1.0998803	1.6329182	1.7901465
WRKY33	AT2G38470	3.1337821	3.1373532	3.428901	3.6410484
AT2G38550	AT2G38550	4.6269608	4.4963017	4.947333	4.907947
WRKY54	AT2G40750	-2.1160076	-2.1964238	-0.9159438	-0.2803604
AT2G41670	AT2G41670	1.7774128	1.5948261	2.3571627	2.2453234
CYP76C2	AT2G45570	-1.2308903	-0.9324215	-0.31397292	0.4562594
AT2G47550	AT2G47550	0.15781085	0.42163467	1.0556747	1.2492892
RPA32B	AT3G02920	1.4455389	1.4067577	2.053944	2.109497
CYP89A9	AT3G03470	3.0873468	3.189602	3.552242	3.6708114
PTAC3	AT3G04260	5.10712	4.8750224	5.447779	5.347809
PPCK2	AT3G04530	0.4581478	0.8523616	1.2302135	1.6333624
AT3G06530	AT3G06530	5.3281775	4.8092537	5.7282166	5.3846455
ATSIK	AT3G08760	2.9603546	2.9655526	3.2729824	3.4643688
AT3G09010	AT3G09010	-0.09902853	-0.24427561	0.4638351	0.74226713
DML2	AT3G10010	3.2192795	2.755849	3.4109068	3.244669
AT3G10180	AT3G10180	1.5712599	1.3790312	2.1181362	2.050556
GYRA	AT3G10690	5.2756915	5.053381	5.6225	5.495258
AT3G11385	AT3G11385	-5.0419865	-5.0270414	-2.9632604	-1.7902536
AT3G12040	AT3G12040	-0.8918658	-0.9999544	0.09946525	0.38324395
TET6	AT3G12090	1.6042653	1.5577527	1.990353	2.2201138
ARP5	AT3G12380	2.7359955	2.628723	3.1095533	3.194537
PSF2	AT3G12530	1.0662905	1.0102066	1.6629685	1.8465614
AT3G12770	AT3G12770	0.78116757	0.39401147	1.290296	1.3643814
AT3G13130	AT3G13130	-4.324652	-4.7443757	-2.6162698	-1.7852181
AT3G13225	AT3G13225	3.503547	3.3695056	3.8986027	3.8813007
RAP2.2	AT3G14230	6.3964543	6.2655663	6.7414813	6.693936
AT3G16660	AT3G16660	4.6356564	4.368451	4.863849	5.016964
AT3G16670	AT3G16670	4.71532	4.5821733	5.019642	5.21253
AT3G17950	AT3G17950	0.9498338	0.68787986	1.4013752	1.503746
AT3G18510	AT3G18510	0.95564467	0.53502494	1.508758	1.584395
RAD54	AT3G19210	1.6868538	1.5100393	2.0940278	2.2749662
CYO1	AT3G19220	2.3706138	2.2014434	2.756263	2.7456205
ATM1	AT3G19960	4.2518535	4.0094914	4.5573745	4.541296
ATHXK4	AT3G20040	1.2842206	0.9779153	1.621737	1.7729301
AT3G20160	AT3G20160	-1.7260326	-3.11472	-1.1063293	-0.9888706
POLGAMMA1	AT3G20540	3.9042456	3.517516	4.188869	4.010271
AT3G21160	AT3G21160	3.07518	3.0519574	3.4938605	3.613232
AT3G21480	AT3G21480	2.3587637	2.0305145	2.7332304	2.6320083
AOX1A	AT3G22370	2.8940532	2.9940689	3.4537442	3.4880075
AtRLP41	AT3G25010	-5.0419865	-5.077709	-3.1075802	-2.260729
AT3G25930	AT3G25930	2.463969	2.7085183	3.0034716	3.3767612
AT3G26540	AT3G26540	0.5934529	0.41594353	1.3718438	1.4669474
MIR169K	AT3G26815	-4.607318	-4.693708	-2.1494236	-2.0158439
PAD3	AT3G26830	0.9547486	1.4335375	1.5233517	2.2348206
AT3G26922	AT3G26922	-2.3616629	-3.1147196	-0.7942783	-0.8202788
PGP16	AT3G28360	-3.8840096	-5.077709	-1.9768077	-1.0754571
AT3G28750	AT3G28750	-4.9406514	-4.693708	-2.4719498	-2.0975482
AT3G44260	AT3G44260	1.1335404	1.2363626	1.7916021	1.9812561
AT3G44420	AT3G44420	-5.0419865	-5.128377	-2.861925	-2.451885
AT3G46280	AT3G46280	3.7165596	3.7567837	4.163749	4.299961
AT3G47200	AT3G47200	-1.4516002	-1.4136238	-0.17855132	0.07857813
AT3G47460	AT3G47460	2.4094892	2.05838	2.830869	2.7174375
AT3G48410	AT3G48410	1.9224488	1.8025341	2.2803555	2.4483552

CYP94B3	AT3G48520	-1.8258859	-2.7813864	-0.7209563	-0.7372415
AT3G49710	AT3G49710	0.58590746	0.45015088	1.3035973	1.2776104
UGT72E1	AT3G50740	4.471735	4.494454	4.7427793	4.952537
AT3G51050	AT3G51050	4.366779	4.2773366	4.6703925	4.748401
AT3G52210	AT3G52210	2.2913392	2.0961344	2.5800486	2.660354
AT3G53960	AT3G53960	1.3658925	1.1441342	1.9640914	1.8739952
ATJRG21	AT3G55970	2.3875673	2.1851053	2.9595711	3.0034838
AT3G56360	AT3G56360	5.175023	5.054281	5.433703	5.522122
AT3G57400	AT3G57400	3.0044582	2.9219697	3.4673195	3.4433222
AT3G57450	AT3G57450	2.9973326	2.9360154	3.3640585	3.4421568
AT3G58520	AT3G58520	1.68657	1.3803506	2.1654303	2.0676997
AT3G60180	AT3G60180	1.0157032	0.87609404	1.6579629	1.6122128
AT3G61280	AT3G61280	-4.991319	-3.9197323	-2.949603	-1.4087905
ADF8	AT4G00680	0.8084752	0.9608221	1.5534177	1.9096256
AT4G04130	AT4G04130	-4.462998	-5.077709	-3.4409134	-2.313539
AT4G04223	AT4G04223	-4.0283294	-3.7813864	-1.6804848	-1.4497427
AT4G08290	AT4G08290	2.4742846	2.092103	2.9451447	2.8916092
AT4G08790	AT4G08790	1.5161347	1.344501	2.1095774	1.988977
ATISA3	AT4G09020	3.5496738	3.340964	3.9605553	3.8544362
AT4G11610	AT4G11610	0.3809762	0.5941818	0.9598455	1.492299
BAT5	AT4G12030	3.1579916	3.1207516	3.6066828	3.5743916
AT4G12670	AT4G12670	1.5170053	1.2690802	1.8939825	2.036306
CAM8	AT4G14640	-2.4677212	-1.8812399	-0.62110287	-0.044574033
AT4G14820	AT4G14820	0.32105273	-0.015875122	1.0196761	0.94009876
AT4G14850	AT4G14850	1.0699573	0.6592563	1.4975977	1.556429
AT4G17140	AT4G17140	5.1764765	4.7330627	5.5540786	5.455788
AT4G17616	AT4G17616	1.3311261	1.2044996	1.9459664	1.9683657
ATPUP7	AT4G18197	1.8963251	1.9896898	2.4233458	2.6581223
ATSS4	AT4G18240	4.8449636	4.6242104	5.1874733	5.114388
WAVE5	AT4G18600	3.0828342	2.8736095	3.460749	3.4179938
AT-HSFA4A	AT4G18880	1.6307478	1.4517728	2.1756995	2.2368114
AT4G19185	AT4G19185	2.1297681	2.120661	2.6188323	2.726864
AT4G19470	AT4G19470	-3.782674	-4.6430407	-1.628445	-1.6555372
IRT2	AT4G19680	0.25749156	0.25736785	1.128334	1.3844241
AT4G20030	AT4G20030	1.6102749	1.4191846	2.130847	2.21007
AT4G20350	AT4G20350	0.34025225	0.25274217	1.0181566	1.1086745
AT4G21910	AT4G21910	3.8669167	3.492881	4.3163095	4.0925756
CRK10	AT4G23180	2.644461	2.7926376	3.1265724	3.3318536
AT4G23540	AT4G23540	3.51861	3.2436879	3.889658	3.795576
AT4G26055	AT4G26055	-2.9210198	-3.1457565	-1.1419678	-0.76558685
BGAL12	AT4G26140	1.3333322	1.2218243	1.8186661	1.9786912
PFK3	AT4G26270	1.3098227	1.139719	1.8442446	1.9660994
AT4G27010	AT4G27010	3.6489055	3.1043835	3.9841595	3.7193203
AT4G27340	AT4G27340	3.5419176	3.3520443	3.9497213	3.8607416
AT4G27640	AT4G27640	5.3060937	5.044014	5.634928	5.512769
CRF4	AT4G27950	1.2759658	1.1481863	1.8910221	1.8385258
ATPHB1	AT4G28510	4.282406	4.1183414	4.652304	4.5926723
AT4G28970	AT4G28970	-5.0419865	-5.128377	-2.750784	-1.7655869
AT4G30150	AT4G30150	3.6041925	3.1724834	3.8567216	3.767027
AT4G31810	AT4G31810	3.8612988	3.759695	4.255226	4.232836
PC-MYB1	AT4G32730	3.886238	3.7405863	4.1410556	4.178905
AT4G32920	AT4G32920	3.9299653	3.5537207	4.204986	4.0424857
AT4G33180	AT4G33180	2.6881037	2.4483433	3.1182988	3.0983093
CDC20.1	AT4G33270	3.3764222	3.2095356	3.7446918	3.7136166
AT4G36648	AT4G36648	5.2804923	5.2466187	5.7048435	5.7105637
AT4G37380	AT4G37380	0.8235199	0.78558034	1.4175581	1.6323534
AT4G37530	AT4G37530	2.6040652	2.6210756	2.981252	3.2393377
AT4G38780	AT4G38780	0.47801122	0.1265717	1.1427679	1.0690217
AT4G39240	AT4G39240	3.3055232	3.2067974	3.5135033	3.6496744

AT4G39420	AT4G39420	4.5726905	4.254557	4.962324	4.8428864
AT4G40042	AT4G40042	1.6690477	1.786035	2.1331136	2.382061
LAC8	AT5G01040	3.7341874	3.9131355	4.1568074	4.5476255
LSN	AT5G02030	1.590953	1.3626565	2.129862	2.212347
NAK	AT5G02290	2.7833385	2.6442928	3.1888158	3.1405337
AT5G02350	AT5G02350	-5.0419865	-5.128377	-3.0002708	-1.7520396
AT5G03360	AT5G03360	0.30701518	0.4889213	0.9493745	1.3597573
AT5G04360	AT5G04360	3.206356	3.08634	3.5700028	3.5885181
AT5G05600	AT5G05600	3.8520355	3.7378862	4.650732	4.5141163
AT5G05790	AT5G05790	0.9940133	0.934885	1.6677195	1.7278175
AT5G05840	AT5G05840	-2.6519015	-2.428422	-0.97395366	-0.5940625
AT5G05890	AT5G05890	2.333436	2.388235	2.846035	2.9260724
AT5G08565	AT5G08565	0.13998501	0.02919986	0.8838117	0.98204255
GTE2	AT5G10550	4.82838	4.7137666	5.0340962	5.147432
AT5G11250	AT5G11250	1.9253964	1.5904032	2.4244442	2.4263856
AT5G11470	AT5G11470	0.68297213	0.3726958	1.2922196	1.2259556
AT5G11610	AT5G11610	1.0420613	1.0957484	1.758557	1.8456268
ZIFL1	AT5G13750	3.080376	2.604986	3.5273807	3.211665
AtCXE17	AT5G16080	-0.08385697	-0.24314976	0.81624967	1.2185243
AT5G17110	AT5G17110	-5.0419865	-5.128377	-3.830888	-2.4753478
AT5G19070	AT5G19070	1.5985571	1.5539168	2.1566722	2.1786735
AT5G19520	AT5G19520	2.664193	2.2727573	2.8727543	2.8931484
AT5G22860	AT5G22860	1.1112183	1.0225683	1.4928912	1.7429461
AT5G24200	AT5G24200	-2.5876865	-2.8690643	-0.86192495	-0.36608884
AT5G24610	AT5G24610	3.773537	3.575044	4.1196256	4.058248
BIN4	AT5G24630	2.1673985	2.0802026	2.5465214	2.6334562
AT5G25250	AT5G25250	0.21274872	0.470521	1.1281103	1.5256828
AT5G26230	AT5G26230	0.6984105	0.8811831	1.4383807	1.7368264
ACP5	AT5G27200	-1.3145776	-1.3664662	-0.084952645	0.24651808
AT5G27220	AT5G27220	0.76790065	0.088083215	1.5346147	1.4157201
RECQSIM	AT5G27680	1.9370517	1.7575588	2.4706328	2.376042
AT5G34800	AT5G34800	-2.6519015	-3.0074103	-1.0224832	-0.72155124
AT5G36002	AT5G36002	-0.7300568	-1.2374586	0.3399016	0.5371906
HCF109	AT5G36170	4.578122	4.3869033	4.930804	4.8186874
AT5G38730	AT5G38730	-0.40027258	-0.80373544	0.53090113	0.3636209
AT5G38750	AT5G38750	-4.991319	-5.128377	-3.0569124	-2.2568972
AT5G38890	AT5G38890	2.7307541	2.551444	3.1332595	3.0835469
AT5G39070	AT5G39070	-4.462998	-4.693708	-2.333604	-1.8270618
AT5G39471	AT5G39471	-4.462998	-5.077709	-2.2829363	-2.06191
AtHB23	AT5G39760	2.8229654	2.943453	3.3070548	3.505994
AT5G42680	AT5G42680	1.63349	1.9134701	2.1344283	2.562105
AT5G43450	AT5G43450	3.0192254	3.2685373	4.1280856	4.120276
FLA13	AT5G44130	4.9061728	5.09379	5.511027	5.7755833
MAP18	AT5G44610	2.6154325	2.8778543	3.1101637	3.383339
AT5G45520	AT5G45520	-0.33250844	-0.94910175	0.4438326	0.36244616
AT5G46040	AT5G46040	-3.2543535	-3.919732	-1.6616236	-1.4187063
MCM3	AT5G46280	3.8411314	3.801512	4.2480497	4.29566
AT5G46460	AT5G46460	0.060599487	-1.3430033	0.5625182	-0.0017295679
TET1	AT5G46700	2.6404083	2.6538773	3.0865848	3.2106383
AT5G47920	AT5G47920	-0.37984812	-0.3793535	0.51112026	0.74994165
AT5G48120	AT5G48120	3.7803364	3.5148895	4.064383	3.9480116
AT5G49060	AT5G49060	1.3115196	1.2362424	1.8514189	1.9737641
SUS2	AT5G49190	-0.59272236	-0.89264506	0.27003875	0.30560294
AAP6	AT5G49630	2.042414	2.1272597	2.5952091	2.6897533
AT5G49780	AT5G49780	0.10309864	-0.047039043	0.934798	0.9365571
QS	AT5G50210	3.7071934	3.6231089	4.005281	4.0840087
AT5G51540	AT5G51540	2.4060295	1.9635029	2.826702	2.5982983
AT5G51670	AT5G51670	2.051792	2.1445324	2.373311	2.8542042
AT5G52760	AT5G52760	-3.6715329	-2.8124228	-1.1992826	-0.74458367

AT5G54260	AT5G54260	2.023303	2.0283782	2.5068312	2.5776522
AT5G56350	AT5G56350	5.1319537	5.2017536	5.5817733	5.6568646
AT5G57080	AT5G57080	-0.10624508	-0.42244783	0.555801	0.64242285
EIR1	AT5G57090	3.170987	2.993695	3.3737657	3.618946
AHA3	AT5G57350	5.2318935	4.9725165	5.584514	5.503015
ENODL10	AT5G57920	-4.4123306	-5.077709	-2.7235792	-2.2568972
AT5G60530	AT5G60530	2.8735154	2.7309208	3.2496226	3.505708
COBL5	AT5G60950	1.4662942	1.3680719	1.6934586	2.046416
AT5G61520	AT5G61520	3.4541264	3.0971909	3.9101937	3.6954765
AT5G61660	AT5G61660	1.7165599	1.7329222	2.2581975	2.4165986
AT5G62190	AT5G62190	6.5279765	6.2379527	6.8799148	6.697779
AT5G64150	AT5G64150	2.2238805	2.0413797	2.6289594	2.6045773
AT5G64550	AT5G64550	1.9108872	1.4724985	2.4131253	2.3232806
AT5G64552	AT5G64552	1.9108872	1.4724985	2.4131253	2.3232806
WRKY51	AT5G64810	-2.2308903	-1.3144265	-0.63246936	-0.04090652
AT5G65160	AT5G65160	0.40473995	0.09718633	0.7753555	1.0471853
AT5G66750	AT5G66750	3.0598013	2.9227774	3.3930283	3.4337559
AT5G66910	AT5G66910	2.5950081	2.3810184	2.921271	2.9060047
AT5G67090	AT5G67090	-2.3926992	-3.9763737	-1.8052832	-1.2372662
ATP6-1	ATMG00410	-1.3517469	-4.11472	-2.949603	-1.3927053
COX3	ATMG00730	-0.4612272	-1.659279	-1.3842716	-0.13576235
PSAI	ATCG00510	0.5439438	-1.4471148	-1.1975178	-0.05480628