Cluster 2. 480 genes					
Probe	ID	Sample 1	Sample 2	Sample 3	Sample 4
PDH-E1 ALPHA	AT1G01090	6.6259856	6.6702094	6.3869843	6.5063934
AN	AT1G01510	4.144768	4.082392	3.8592546	3.8827522
AT1G01640	AT1G01640	1.1966343	0.9854455	0.2933999	0.5507024
KEA1	AT1G01790	4.922983	4.824333	4.571487	4.545973
GL22	AT1G02335	2.3003745	2.1032045	1.716206	1.826461
AT1G02470	AT1G02470	0.670507	0.08261018	-0.34500933	-0.5815432
AT1G02700	AT1G02700	-1.3827834	-2.919732	-3.8815563	-4.0543365
SPI	AT1G03060	5.048992	4.6274815	4.7504478	4.713618
AT1G03940	AT1G03940	-0.9532602	-4.4987206	-4.302567	-5.0679936
AT1G04030	AT1G04030	1.6200706	1.622551	1.0224762	1.3628902
ERS2	AT1G04310	3.1174088	3.1249087	2.7908127	3.1458473
AT1G04560	AT1G04560	-1.8643783	-3.0912564	-4.9828916	-4.633325
AT1G05510	AT1G05510	-2.1160076	-5.0270414	-4.9828916	-5.0679936
AT1G07400	AT1G07400	0.7792883	0.42565894	-0.007844116	-0.016313875
AT1G07450	AT1G07450	-1.0302116	-1.824598	-3.3025675	-3.9159906
AT1G07870	AT1G07870	1.9020243	1.7705736	1.2853081	1.4791018
ADT6	AT1G08250	2.1728213	2.2825248	1.7610159	2.0669773
ACHT4	AT1G08570	4.5541186	4.4702396	4.31288	4.255257
AT1G09600	AT1G09600	0.40250835	0.21849616	-0.6177749	-0.69008404
AT1G10910	AT1G10910	4.292244	4.081731	4.037543	3.925235
SS3	AT1G11720	4.272562	4.009372	4.022789	3.8101428
GLX1	AT1G11840	6.80981	6.7004476	6.545601	6.5356197
PEPKR1	AT1G12580	3.9134486	3.8715162	3.616957	3.7071056
CYP78A5	AT1G13710	1.8253077	2.1199877	1.2467912	2.222228
THH1	AT1G14530	0.8782523	0.86004764	0.13405077	0.29029086
AT1G14890	AT1G14890	2.4339924	2.125715	2.028323	1.9042546
AT1G15060	AT1G15060	3.7047398	3.8059254	3.4403584	3.6135833
AT1G15290	AT1G15290	5.9539466	5.5419426	5.6583195	5.363964
AT1G15830	AT1G15830	0.8045096	0.5558738	-0.1569971	-0.097548194
CCR1	AT1G15950	5.0347795	5.044397	4.8146567	4.8163314
REV7	AT1G16590	1.7539848	1.933745	1.1827698	1.453817
AT1G17360	AT1G17360	3.70784	3.4988973	3.385018	3.2563002
AT1G17710	AT1G17710	-1.2727338	-2.2099712	-3.8308885	-1.8903853
HDG12	AT1G17920	1.9379164	1.8721972	1.4418974	1.7861971
LAC1	AT1G18140	0.6305551	0.010157655	-0.38510743	-0.21380293
AT1G18420	AT1G18420	-0.2422955	-0.33743635	-1.3978192	-0.89756316
IBS1	AT1G18670	2.9631717	2.7507803	2.5062132	2.394438
AT1G18880	AT1G18880	3.1729205	2.9967754	2.5038412	2.7217093
AT1G19330	AT1G19330	1.8075428	1.8526446	1.2660846	1.8345436
AT1G19690	AT1G19690	2.93103	2.8057737	2.5596535	2.6322732
AT1G19740	AT1G19740	4.868263	4.9595857	4.65519	4.769797
ATSBT5.2	AT1G20160	3.390585	2.8848047	2.6534164	2.5552504
AT1G21945	AT1G21945	-1.3468647	-2.812423	-3.3025675	-2.613694
AT1G22510	AT1G22510	1.6954266	1.662649	0.93836814	1.2611428
AT1G22650	AT1G22650	2.595114	2.4754524	1.9054642	2.2109451
ATTPS9	AT1G23870	4.8248005	4.5777736	4.610187	4.7062874
AT1G24430	AT1G24430	0.7001173	0.3973627	-0.15376961	-0.22841702
AT1G25400	AT1G25400	0.42692915	0.44571137	-0.6434743	0.07434425
AT1G25530	AT1G25530	3.1471703	3.075637	2.566026	2.7941844
AT1G26920	AT1G26920	4.3424644	4.5920386	4.0232577	4.3708057
AT1G26930	AT1G26930	2.7408273	2.3167684	2.033557	2.2580397
AT1G27921	AT1G27921	2.0364287	1.5846654	1.3439435	1.3525068
GH3.17	AT1G28130	3.2636635	3.0895932	2.958018	2.8415318
AT1G28260	AT1G28260	2.441896	2.2683413	2.0232222	1.908007
AGP31	AT1G28290	6.5186934	6.4460654	6.03614	6.284391
AT1G28650	AT1G28650	-1.1941626	-1.5607938	-3.8308885	-2.4753478

AT1G29090	AT1G29090	2.7518892	2.50129	2.2197874	2.0706336
AT1G29720	AT1G29720	-0.048592135	-0.9659217	-1.4212823	-1.4829211
PHV	AT1G30490	4.1223836	3.9255412	3.7980776	3.690729
RECQL2	AT1G31360	2.2672482	2.0345294	1.810881	1.7672215
AT1G33080	AT1G33080	1.287793	0.9765697	0.5192029	0.45405495
AT1G34315	AT1G34315	1.1721576	0.9431033	0.4559789	0.38961354
CYCB1;5	AT1G34460	-1.906222	-2.7247448	-4.932224	-5.0173264
MLP165	AT1G35260	2.2438693	2.4174216	1.7872995	2.1417596
ACC1	AT1G36160	6.299949	5.993242	5.9438515	5.874756
NIA2	AT1G37130	9.045643	8.802936	8.742312	8.557335
VIP1	AT1G43700	3.9479725	3.8146448	3.5904796	3.590578
AT1G45170	AT1G45170	2.6050289	2.4536889	2.145346	2.1440618
WOX4	AT1G46480	0.5578838	0.6335337	-0.2485071	0.16128314
AT1G47340	AT1G47340	1.7363528	1.7361833	1.1947168	1.3051862
AT1G47655	AT1G47655	0.029563008	-0.35627016	-1.0879489	-0.93004817
AT1G47980	AT1G47980	-1.2085189	-3.3097074	-4.8308883	-5.0173264
CIPK17	AT1G48260	0.66519314	0.5982508	-0.118985385	0.033811104
AT1G48750	AT1G48750	5.6181054	5.6095853	5.157484	5.3739433
ATUSPL1	AT1G49320	1.3917403	1.1410141	0.62673324	1.0982271
PUB26	AT1G49780	1.6886563	1.6863619	1.0512017	1.3526516
AT1G50900	AT1G50900	5.8130856	5.8461933	5.6090984	5.6305757
AT1G51840	AT1G51840	-0.13707916	-0.3717802	-1.7742468	-0.96540755
AT1G52070	AT1G52070	4.681065	4.6350746	4.0468907	4.306772
ALDH7B4	AT1G54100	5.672008	5.496094	5.369999	5.2905197
AT1G54870	AT1G54870	-2.0283294	-4.0270414	-4.9828916	-5.0679936
VIM5	AT1G57800	-2.0283291	-3.1964238	-4.9828916	-5.0679936
AT1G58602	AT1G58602	1.4437441	1.0366706	0.6564312	0.50323075
AT1G60200	AT1G60200	5.45421	5.20292	5.2469287	5.131666
AT1G61210	AT1G61210	3.69491	3.4101098	3.2355156	3.2488406
AT1G62310	AT1G62310	2.8427265	2.5742674	2.5044603	2.5727355
STM	AT1G62360	0.06274153	-0.22058325	-1.2262946	-1.4583689
AT1G63290	AT1G63290	4.1350465	4.1323366	3.9251175	4.025377
APO1	AT1G64810	3.031435	2.9666917	2.6911867	2.649031
AT1G65010	AT1G65010	5.2070007	4.9717774	4.940685	4.925437
GTB1	AT1G65440	5.769579	5.3553557	5.4984016	5.449959
MYB20	AT1G66230	1.0310699	1.04588	0.20082808	0.39097977
AT1G66840	AT1G66840	2.5126503	2.128965	2.0383317	1.8125142
LBD40	AT1G67100	-1.3225926	-4.2530656	-4.598891	-4.683993
AT1G67680	AT1G67680	5.3877387	5.34252	5.125443	5.182741
AT1G67790	AT1G67790	-1.2665286	-1.1789347	-4.158248	-2.7520397
AT1G68810	AT1G68810	2.46549	2.2041461	1.9261383	1.8321291
AT1G69520	AT1G69520	1.3828939	1.1196805	0.6703868	0.5928425
AT1G69526	AT1G69526	1.485161	1.4804736	0.88546896	1.2462877
SNL4	AT1G70060	4.2685046	4.091898	4.0532384	4.0135713
ATTPS8	AT1G70290	4.7036366	4.418157	4.4671226	4.4266396
WEI8	AT1G70560	4.1466265	4.0249476	3.7276661	3.8545809
AT1G70985	AT1G70985	1.7016636	1.6587914	1.1439562	1.2335536
AT1G71180	AT1G71180	2.8806906	2.6674461	2.4335866	2.6292164
AtRLP12	AT1G71400	1.9880918	1.8029408	1.5207592	1.4047338
AT1G71870	AT1G71870	0.82772857	0.5659094	-0.069521405	0.44144276
ABCG25	AT1G71960	2.9154975	2.9083803	2.5869434	2.779199
AT1G72100	AT1G72100	-2.0184135	-3.1653874	-4.9828916	-5.0679936
PIN1	AT1G73590	3.198858	3.1309865	2.730428	2.8166065
AT1G73660	AT1G73660	4.8342	4.6581397	4.4475007	4.4314227
AT1G75180	AT1G75180	3.8189437	3.8115904	3.5711482	3.624388
AT1G75490	AT1G75490	0.87727714	0.41511202	-0.49439558	-0.30066392
AVA-P4	AT1G75630	4.949301	4.901178	4.7207503	4.776274
AT1G75730	AT1G75730	2.8744898	2.3927934	2.5150702	2.176079
AT1G76470	AT1G76470	-0.54688776	-0.8434593	-1.9768076	-1.9470271

SOB3	AT1G76500	1.5970064	1.6528744	0.9967142	1.5309652
LAX3	AT1G77690	4.351621	4.173022	4.0891194	4.0666146
NIA1	AT1G77760	8.050406	7.87538	7.761564	7.659652
AT1G78120	AT1G78120	2.2646646	1.7964531	1.7909561	1.5511956
AT1G78780	AT1G78780	0.38007307	0.50881016	-0.98547274	-0.27773762
AVP2	AT1G78920	5.34113	5.1132464	5.1280265	5.155552
ATNADP-ME4	AT1G79750	7.0955806	6.986019	6.8472385	6.832355
AT1G80240	AT1G80240	3.05279	3.3582017	2.617983	3.0948637
NIP6;1	AT1G80760	2.2237148	2.1654003	1.5181813	1.7216549
AT2G01010	AT2G01010	0.0714066	-0.7716239	-2.0644858	-1.2583307
AT2G01020	AT2G01020	1.8550647	0.7287491	0.953218	1.6038166
AT2G01021	AT2G01021	5.9594	5.231131	4.893917	6.1441784
TOM3	AT2G02180	4.0139003	3.878814	3.7430437	3.722585
ATPI4K GAMMA	AT2G03890	5.191229	4.9828973	4.902591	4.782455
AT2G05920	AT2G05920	6.2719765	6.2450466	6.0421042	6.1027236
AT2G07080	AT2G07080	2.2306645	0.8331504	-0.091872185	0.43402982
AT2G07674	AT2G07674	-0.7781868	-3.040589	-3.245926	-2.4968615
AT2G07687	AT2G07687	-0.73360586	-3.1789348	-3.3025675	-0.89598376
AT2G07708	AT2G07708	0.67494744	-0.60263735	-1.1386164	-0.31256714
AT2G07715	AT2G07715	1.404889	1.0240039	0.27108458	0.57997704
AT2G12470	AT2G12470	0.7970417	0.40378952	-0.5566318	-0.13687623
AT2G12646	AT2G12646	0.8541755	0.5303507	0.051335275	0.4297726
AT2G13610	AT2G13610	2.8930702	2.656456	2.5069294	2.3022745
ATTPS11	AT2G18700	3.9685125	3.8046153	3.6197407	3.5753796
AT2G21300	AT2G21300	4.47133	4.3600225	4.222292	4.2256594
AT2G21340	AT2G21340	4.0522666	3.8941104	3.8088493	3.6965857
AT2G21630	AT2G21630	2.6667187	2.5933006	2.3190453	2.3624942
AT2G22080	AT2G22080	4.378893	4.4942174	4.1363044	4.3513484
CYP79B3	AT2G22330	4.799393	4.7341704	4.5439343	4.612743
AT2G24090	AT2G24090	6.788955	6.8519588	6.6190467	6.6089096
AT2G25800	AT2G25800	4.3846755	4.4065404	4.145473	4.382478
AT2G25890	AT2G25890	-0.89186573	-2.8690643	-4.932224	-4.966658
ALPHA-VPE	AT2G25940	0.07394437	-0.24100769	-1.6616236	-1.1037534
PYL2	AT2G26040	0.2814234	-0.2535354	-0.76679087	-1.0975482
AtGLDP2	AT2G26080	7.129954	6.9983277	6.873343	6.80222
BAS1	AT2G26710	0.8611512	0.062475104	0.019360444	-0.35444424
AGL46	AT2G28700	-2.4493408	-3.340744	-4.9828916	-5.0173264
AT2G29300	AT2G29300	2.055528	1.9421333	1.3914694	1.6153988
AT2G30100	AT2G30100	2.4200943	2.185305	2.006846	1.9202299
TCP10	AT2G31070	3.0927346	3.0220754	2.6236293	2.76325
AT2G31670	AT2G31670	5.095637	5.0225997	4.8111963	4.919063
AtCYS2	AT2G31980	0.96534795	0.023508692	-0.17125873	-0.5952663
AT2G33450	AT2G33450	6.8619766	6.8844466	6.633167	6.669661
AT2G34560	AT2G34560	4.668484	4.717879	4.450147	4.52233
EXL1	AT2G35150	0.2600336	-0.014983699	-0.7667908	-0.53742087
DOT1	AT2G36120	6.3167953	6.177344	6.1096325	6.199852
AT2G36810	AT2G36810	4.410807	4.2198405	4.034271	3.973615
RD28	AT2G37180	4.3514714	4.304972	3.953022	4.0524387
ASP1	AT2G30970	4.8348927	4.8005786	4.625877	4.7164407
IRX12	AT2G38080	2.9100964	2.868758	2.571232	2.7008536
CXIP2	AT2G38270	4.977742	4.910583	4.7585416	4.7360053
AT2G38370	AT2G38370	2.1666996	2.043712	1.6608539	1.6747808
AT2G38430	AT2G38430	-1.1160074	-1.1147197	-3.5617702	-2.2062294
AT2G38820	AT2G38820	2.2145345	2.1182632	1.797218	1.7287688
RHC2A	AT2G39720	3.9749553	4.0379696	3.7488604	3.9917717
ISA1	AT2G39930	4.779054	4.587769	4.4663563	4.3998837
ATEM6	AT2G40170	-1.7902474	-4.6430407	-4.9828916	-5.0679936
AT2G41130	AT2G41130	1.5768734	1.1056255	0.63200825	0.76359195
PGAZAT	AT2G41850	1.3580972	0.39780772	0.24733417	0.65842086

AT2G42560	AT2G42560	-2.4062464	-4.360375	-4.9828916	-5.0679936
MAX2	AT2G42620	3.7673962	3.7571566	3.5131454	3.7158253
PDF1	AT2G42840	6.7630086	6.948424	6.5603046	6.793461
AT2G43590	AT2G43590	3.0626688	3.2582982	1.8373915	2.7675374
AT2G44830	AT2G44830	3.0252705	2.698624	2.6430855	2.4466896
AT2G45910	AT2G45910	3.6355102	3.2066097	3.1269372	3.0948896
CHR2	AT2G46020	5.44124	5.111526	5.223062	5.2145953
GBF3	AT2G46270	2.8014317	2.9304473	2.3582408	2.7331314
SPA1	AT2G46340	4.9450507	4.833986	4.6114173	4.628325
IAA20	AT2G46990	-1.2583776	-2.284102	-3.5617702	-2.2803605
AtGolS1	AT2G47180	2.9719048	3.1837265	2.5848987	2.9269044
CP12-1	AT2G47400	7.4855766	7.5252495	7.272047	7.324557
RFI2	AT2G47700	4.0477443	4.0851455	3.775861	3.972641
ATTSPO	AT2G47770	-1.1654245	-2.8124228	-3.9692342	-4.438338
AtSS2	AT3G01180	3.9488325	3.6805906	3.6801507	3.627657
CPuORF33	AT3G01472	6.2955203	6.46755	6.0950103	6.3311477
ATHB-1	AT3G01470	6.2955203	6.46755	6.0950103	6.3311477
CYP38	AT3G01480	6.355625	6.378081	6.1385922	6.1175714
AT3G01820	AT3G01820	3.6251423	3.481624	3.2922852	3.1727865
AT3G01840	AT3G01840	-2.4433668	-3.2530653	-4.932224	-2.5260155
AT3G02720	AT3G02720	4.027403	4.0493913	3.7984467	3.9356756
AT3G02750	AT3G02750	4.576952	4.5249124	4.367146	4.3288007
AT3G03341	AT3G03341	-1.4925526	-2.0891144	-4.598891	-4.1926823
AT3G03680	AT3G03680	3.1508648	3.0562646	2.8138351	2.8283322
SWP	AT3G04740	4.306747	4.1100903	4.086058	4.1333747
DRT102	AT3G04880	4.1617627	4.201529	3.8006828	3.9764073
RBK2	AT3G05140	1.5002426	1.5900593	0.8805335	1.1851091
ALY2	AT3G05380	3.8570325	3.5954425	3.462591	3.5053532
AT3G05950	AT3G05950	-2.7368395	-3.3407438	-4.9828916	-5.0173264
AT3G06780	AT3G06780	1.9528509	1.9961748	1.408734	1.5458301
AT3G09030	AT3G09030	2.4590437	2.457071	2.0354393	2.2033455
AT3G09070	AT3G09070	3.0946312	2.7475262	2.7549222	2.7177172
AT3G09162	AT3G09162	0.8882589	0.91669446	-0.037040845	0.33193693
AT3G10080	AT3G10080	2.7481935	2.7595546	2.3585348	2.5195732
NHL2	AT3G11650	1.7531027	1.8013796	1.0485147	1.3960227
AT3G14130	AT3G14130	2.4472432	2.1997652	1.9547447	1.8064817
WSIP2	AT3G15880	4.846944	4.7116756	4.625541	4.67198
AT3G16175	AT3G16175	-0.0042107305	-0.0362145	-1.0784259	-0.5642298
PDR1	AT3G16340	3.7833939	3.5223866	3.484473	3.4306052
ARR1	AT3G16857	4.514525	4.4695735	4.170065	4.3748403
ATGSKB6	AT3G17820	5.3741784	5.485588	5.195391	5.3565726
AT3G17850	AT3G17850	5.4322343	5.1695676	5.233911	5.1522403
AT3G18280	AT3G18280	4.1355624	3.9703119	3.90345	3.74922
SYTF	AT3G18370	3.7304428	3.7842808	3.4591064	3.587744
ATPRP40B	AT3G19670	3.7436962	3.525315	3.3697746	3.3452444
AtOCT4	AT3G20660	2.3193142	1.8485988	1.721187	1.8034669
AT3G21360	AT3G21360	1.5133834	1.4641515	0.962948	0.8845914
AT3G21380	AT3G21380	0.9938895	-0.27856806	-4.2655573	-4.1556716
ABI3	AT3G24650	-1.833342	-4.360375	-4.9828916	-5.0679936
AT3G24880	AT3G24880	2.999175	2.701246	2.354294	2.387557
AT3G25030	AT3G25030	1.2066624	1.2135978	0.2535797	0.77264977
AT3G25290	AT3G25290	1.5957752	1.292648	0.8752089	0.88111305
AT3G26100	AT3G26100	4.6222854	4.609722	4.4114575	4.4781246
AT3G26350	AT3G26350	-0.9843771	-1.2581013	-3.3025677	-3.451885
AT3G27040	AT3G27040	-2.3926992	-3.2530658	-4.9828916	-4.9666586
GHS1	AT3G27160	7.0014825	7.0027657	6.8245964	6.8076463
GC6	AT3G27530	4.280679	4.303287	4.0165935	4.098017
AT3G28170	AT3G28170	-1.6134094	-2.9615757	-4.9828916	-5.0679936
AT3G29075	AT3G29075	3.3216267	3.2410352	2.8436358	2.9765854

AT3G29110	AT3G29110	-2.6519015	-3.1147196	-4.9828916	-5.0679936
AT3G30320	AT3G30320	-1.9716877	-2.8456013	-4.9828916	-5.0679936
AT3G32047	AT3G32047	-2.3185682	-3.2023976	-4.9828916	-5.0679936
AT3G41768	AT3G41768	10.168572	9.327357	9.06523	10.034282
HIRA	AT3G44530	3.3461654	3.0807714	2.9553883	2.8989894
AT3G44610	AT3G44610	1.3786397	1.2898382	0.730918	0.67218333
AT3G45530	AT3G45530	-2.2308903	-3.4480531	-4.9828916	-5.0679936
CDF3	AT3G47500	2.4600499	2.6072834	2.0373828	2.1278312
CSR1	AT3G48560	7.262202	7.0696545	6.9387717	6.882235
PGL2	AT3G49360	2.4922535	2.2856839	2.0351593	1.9398612
AT3G50370	AT3G50370	6.1445746	5.788189	5.7771106	5.76672
AT3G50380	AT3G50380	4.539107	4.1630783	4.2663455	4.0354238
F3H	AT3G51240	3.728433	3.3869216	3.3936665	3.3318264
AT3G53040	AT3G53040	-0.77642196	-2.7813864	-4.403903	-3.2803605
AT3G53540	AT3G53540	3.52328	3.4332821	3.244178	3.2473419
HAT1	AT3G54610	2.9355946	2.7822168	2.5253813	2.546058
AT3G54680	AT3G54680	2.4732444	2.440457	1.9785839	2.2413964
AT3G54920	AT3G54920	5.087102	4.9579635	4.8835545	4.9446363
AT3G55080	AT3G55080	2.5361106	2.484709	2.1341374	2.160505
AT3G55430	AT3G55430	4.3560576	4.475414	4.090245	4.382994
ATEXPA16	AT3G55500	0.8100284	0.5879765	-0.15130593	-0.11808205
AT3G56750	AT3G56750	3.658109	3.5570505	3.4059503	3.453767
AT3G56810	AT3G56810	2.085141	2.1008375	1.6220869	1.704311
UBA2A	AT3G56860	5.206528	5.0676155	4.9682155	4.951533
AT3G57860	AT3G57860	1.6862612	1.6845617	1.1227102	1.2625762
AT3G58450	AT3G58450	-2.1012096	-3.9197323	-4.9828916	-5.0679936
AT3G60290	AT3G60290	2.1076949	1.5304831	1.5846916	1.2133822
TTN1	AT3G60740	3.994529	3.7695873	3.7656946	3.6776905
AT3G60900	AT3G60900	1.980137	1.8488125	1.3004203	1.6444119
AT3G61520	AT3G61520	1.2756343	0.85458297	0.19596744	0.36007968
ARF18	AT3G61830	2.3071315	2.2014837	1.8134733	1.8284494
AT3G62540	AT3G62540	-1.1867067	-1.4021047	-4.881556	-3.1926823
ATMRP10	AT3G62700	5.6431737	5.3190303	5.415767	5.217423
PLP9	AT3G63200	4.827661	4.645668	4.557728	4.497435
AT3G63490	AT3G63490	7.688088	7.6807265	7.498059	7.478556
WRKY22	AT4G01250	1.4702057	1.2781469	0.8943532	1.0316354
AT4G01490	AT4G01490	-1.9111043	-3.309707	-4.598891	-4.683993
SAM-2	AT4G01850	7.3552837	7.404457	7.165405	7.2721734
AT4G01975	AT4G01975	-1.8468891	-4.693708	-4.9828916	-5.0679936
AtGH9B13	AT4G02290	2.9397528	2.779789	2.576305	2.6575181
AT4G02790	AT4G02790	4.6556215	4.4504395	4.4562826	4.2334533
AT4G03030	AT4G03030	3.819169	3.7148001	3.5755644	3.5821388
AT4G06744	AT4G06744	3.7069924	3.6681893	3.1118577	3.3541524
AT4G08280	AT4G08280	3.8057706	3.692269	3.387864	3.439813
AT4G08410	AT4G08410	1.2583964	1.297418	0.3700498	0.67732614
AT4G09150	AT4G09150	4.770902	4.6313863	4.5283103	4.561476
ATSPS4F	AT4G10120	3.4105222	3.2175713	2.8992736	2.8616552
AT4G11270	AT4G11270	4.318427	4.1450815	4.108829	4.0663443
WRKY19	AT4G12020	3.5572646	3.201827	3.0821016	2.9387405
AT4G13210	AT4G13210	0.15471825	0.12312353	-0.9026768	-0.40027878
ATTPS12	AT4G13280	1.2015213	1.3202858	0.31072992	0.880822
CYP71A19	AT4G13290	1.9434437	2.0526125	1.4219913	1.6226196
AT4G13780	AT4G13780	5.4052925	5.268806	5.202267	5.1499496
AT4G14090	AT4G14090	0.6006542	-0.7099467	-1.1151534	-2.331028
AT4G15960	AT4G15960	1.1529933	1.2823578	0.52140874	0.7048885
AT4G16150	AT4G16150	5.3783364	5.0820985	5.1626945	5.0829678
AT4G16155	AT4G16155	5.4695983	5.4511914	5.27733	5.2775474
AT4G16260	AT4G16260	5.219906	5.281275	4.818746	5.0567336
AT4G16540	AT4G16540	-2.1802225	-3.7072554	-4.932224	-5.0173264

AT4G16830	AT4G16830	4.8051305	4.7170243	4.5708046	4.5300198
AT4G16840	AT4G16840	0.7339408	0.617865	-0.29534292	0.2887593
AT4G18650	AT4G18650	0.114282824	0.4558598	-1.1878023	-0.3590683
BEH3	AT4G18890	1.6841078	1.767224	1.1452998	1.3713574
NIP1;2	AT4G18910	1.8940266	1.5448989	1.3965044	0.99172753
AT4G19020	AT4G19020	3.7719047	3.5178578	3.3078387	3278
AT4G20690	AT4G20690	-1.6640769	-1.8064489	-4.3025675	-3.859349
AT4G20930	AT4G20930	1.788741	1.5513153	0.87320375	1.0369469
AT4G21020	AT4G21020	-0.38507882	-2.8124228	-4.932224	-4.2999916
AT4G22620	AT4G22620	-1.9716877	-2.5541117	-4.598891	-4.4890056
AT4G22770	AT4G22770	1.4989825	1.2886852	0.94999987	0.905381
AtGH9B15	AT4G23560	1.0841182	0.011017094	0.021100571	0.19366117
RD26	AT4G27410	3.1718023	2.932872	2.7617238	2.624375
AT4G28300	AT4G28300	4.8309517	4.634272	4.466559	4.614256
AT4G29020	AT4G29020	3.7097619	3.628216	3.345685	3.39052
AT4G29950	AT4G29950	4.435843	4.220745	4.0897045	4.084562
ATEXO70G1	AT4G31540	2.6413555	2.512571	2.2237053	2.23648
CCD8	AT4G32810	-0.8533733	-1.6174355	-2.6359007	-2.859349
AT4G33280	AT4G33280	-1.1666752	-1.674077	-4.2148895	-3.859349
AT4G33390	AT4G33390	-2.2543535	-3.2530658	-4.598891	-2.947027
AT4G33720	AT4G33720	3.813693	3.762724	2.4380977	2.9333057
ATXDH2	AT4G34900	4.3875136	4.3202567	4.0905304	4.0653687
AT4G35190	AT4G35190	-0.5135558	-1.0716254	-2.7926273	-1.9592023
MCA1	AT4G35920	4.1125107	4.0422835	3.8682773	3.9382477
AT4G36140	AT4G36140	3.4075682	3.1944714	3.0498636	3.131902
ALDH3F1	AT4G36250	5.8738885	5.8805594	5.637842	5.6735806
AT4G36520	AT4G36520	3.935196	3.4366577	3.5088577	3.3320425
BEH2	AT4G36780	4.542385	4.5208354	4.3261623	4.52523
BLH2	AT4G36870	3.5358665	3.4492843	3.1859055	3.294562
AT4G37460	AT4G37460	4.5449815	4.420116	4.263498	4.3473644
AT4G38060	AT4G38060	2.0088248	1.7273449	1.5084428	1.5466223
AT4G38552	AT4G38552	1.389472	1.045207	0.8109939	0.9613716
AT4G38950	AT4G38950	3.17568	2.7230012	2.6921139	2.4461198
AT4G38960	AT4G38960	1.6903881	1.5187702	1.0859178	1.0318522
APL3	AT4G39210	2.5671194	2.2019804	2.0716848	1.8952087
BRI1	AT4G39400	6.0512276	5.8658986	5.857912	5.9050155
AT4G40045	AT4G40045	2.808152	2.8365061	2.4886572	2.5856369
AT5G01170	AT5G01170	1.4874629	1.2401549	0.8469765	0.58726776
AT5G01300	AT5G01300	-2.5876865	-3.498721	-4.9828916	-4.5826573
AT5G01320	AT5G01320	-1.3926992	-2.0492542	-4.598891	-4.5826573
AT5G01445	AT5G01445	0.60163206	0.42834857	-0.21246918	-0.36295593
AT5G01720	AT5G01720	4.1129627	3.9740589	3.8445342	3.745753
AT5G01890	AT5G01890	3.972482	3.8917735	3.6862926	3.7589042
AT5G02970	AT5G02970	2.7907522	2.7651434	2.3473835	2.4442332
CTR1	AT5G03730	5.713852	5.615916	5.372046	5.5197563
AT5G04120	AT5G04120	0.94460946	0.17445908	-0.12946482	-1.2131491
AT5G06330	AT5G06330	0.5401068	0.80434084	-0.3236883	0.16847749
AT5G06750	AT5G06750	2.5329592	2.5846243	2.170245	2.3621604
AT5G06980	AT5G06980	3.7541552	3.7003899	2.9765275	2.7967083
AT5G07330	AT5G07330	-2.1160076	-2.5999463	-4.932224	-3.4383373
AT5G07790	AT5G07790	1.5714642	1.4063059	1.0273784	0.8974162
AT5G08030	AT5G08030	-1.6937453	-1.1875998	-4.3025675	-1.7938832
AT5G10625	AT5G10625	2.3315685	2.2746236	1.8299013	2.0835066
AT5G13100	AT5G13100	3.9691935	3.9707973	3.7209213	3.8079815
SAG29	AT5G13170	0.37072578	-0.47216824	-0.785652	-1.4402195
AT5G13510	AT5G13510	6.6509757	6.676165	6.4544272	6.4745502
AT5G14390	AT5G14390	3.5650396	3.4549668	3.2659485	3.30198
AT5G14500	AT5G14500	2.8352635	2.7259429	2.4620712	2.528897
SNL2	AT5G15020	4.61562	4.403256	4.363866	4.3208137

AT5G16210	AT5G16210	4.5386214	4.4035783	4.157393	4.273167
ATGSTF12	AT5G17220	0.18928564	-1.3407437	-0.8189451	-1.7655869
AT5G17580	AT5G17580	1.1807727	0.99099034	0.3429784	0.35124552
AT5G17630	AT5G17630	4.4955115	4.3923573	4.288936	4.263371
AT5G18190	AT5G18190	4.9338436	4.81591	4.7000346	4.688119
ACL5	AT5G19530	3.9672184	3.988451	3.6917675	3.7526672
AT5G22470	AT5G22470	-2.1100335	-3.7813864	-4.9828916	-5.0679936
NF-YB13	AT5G23090	1.6825352	1.6113399	1.1141983	1.3535657
AT5G23110	AT5G23110	4.678989	4.1711917	4.370264	4.264956
AT5G23950	AT5G23950	-2.5000086	-3.0074103	-4.9828916	-5.0679936
AT5G24260	AT5G24260	4.0254135	3.9061959	3.6317947	3.6780179
GMI1	AT5G24280	2.5895758	1.8186302	2.0434966	1.883056
AT5G24990	AT5G24990	0.64173007	0.36470434	-0.3580952	0.062274914
CYP71B12	AT5G25130	0.7294082	0.7087696	-0.13253273	-0.08746467
AT5G26790	AT5G26790	-0.7610933	-0.8222917	-2.6669376	-2.085373
AT5G27750	AT5G27750	2.0224984	1.6752399	1.3507663	1.4569052
AT5G28320	AT5G28320	1.680366	0.6716347	0.9937436	0.7597694
AT5G35170	AT5G35170	5.586788	5.513332	5.257587	5.1180882
AT5G35180	AT5G35180	5.435236	5.341225	5.2237554	5.3094597
PMI15	AT5G38150	2.6426163	2.2547407	2.106353	1.9847454
AT5G40390	AT5G40390	4.5158973	4.6469965	4.1436234	4.3602576
AT5G40800	AT5G40800	-2.305021	-4.360375	-4.932224	-4.2999916
RPP8	AT5G43470	3.3980763	3.2323825	2.9802554	3.0773141
PDF1.2c	AT5G44430	-0.18210475	-1.2841021	-3.0002708	-1.5004104
CML43	AT5G44460	-0.10257765	0.06305692	-1.5407668	-1.0181617
CHR4	AT5G44800	5.1593356	4.805927	4.818961	4.7454147
RPS4	AT5G45250	2.5568998	2.2281077	2.0621798	2.0178385
AT5G45472	AT5G45472	1.2576698	0.37524566	0.25046703	0.4178121
KAT1	AT5G46240	2.4680736	2.2849486	1.9372554	2.0876207
AT5G46250	AT5G46250	5.092259	4.88225	4.8924117	4.7859225
AT5G47160	AT5G47160	-0.41974482	-1.1381359	-1.9617783	-2.06191
AT5G47480	AT5G47480	5.1732774	5.0033774	4.976382	5.0144577
TED7	AT5G48920	1.2038121	1.0848154	0.4591609	0.46257916
HCT	AT5G48930	5.7780113	5.864943	5.586717	5.6862583
AT5G49560	AT5G49560	2.4199932	2.3022785	1.9282588	1.861518
AT5G50760	AT5G50760	2.2564704	2.4392745	1.8229319	2.177805
CLPC	AT5G50920	8.827933	8.719802	8.632476	8.574771
AT5G51795	AT5G51795	0.61015177	0.30806258	-0.26722842	-0.47723007
AT5G51910	AT5G51910	1.627143	1.3196388	1.0275556	1.1460153
AT5G52540	AT5G52540	4.7539835	4.578295	4.468921	4.483606
AT5G53048	AT5G53048	-1.1258764	-1.0614293	-3.2284367	-2.0112422
GLT1	AT5G16150	8.7386055	8.519573	8.508411	8.400384
UF3GT	AT5G54060	-0.80971974	-3.6430404	-3.4975548	-4.9666586
GPT1	AT5G54800	4.249693	4.3054028	4.0142922	4.171278
ATET2	AT5G56780	1.6411285	1.536429	1.0396236	1.3303853
AT5G57070	AT5G57070	2.1383793	2.185862	1.5937343	1.890512
ATCOL5	AT5G57660	5.0151343	5.0143814	4.6970983	4.7608285
AT5G58110	AT5G58110	4.688065	4.6872506	4.43648	4.537767
AT5G58340	AT5G58340	1.9326366	1.66506	1.382703	1.2429248
AT5G58490	AT5G58490	4.6560473	4.5805297	4.3678794	4.339503
AT5G58575	AT5G58575	2.5219796	2.3757474	1.9863563	2.1785185
LAC17	AT5G60020	2.889761	2.813831	2.5275156	2.6021001
OBP4	AT5G60850	3.4381263	3.4838188	3.0759432	3.2770035
AT5G61480	AT5G61480	3.6237123	3.2269156	3.2735984	3.0491421
AT5G62580	AT5G62580	3.3058465	3.2587624	2.962621	3.1919048
TUB3	AT5G62700	7.373047	7.444597	7.1622295	7.2447224
AT5G63640	AT5G63640	3.3726857	3.4952443	3.048005	3.221385
SNRK2-5	AT5G63650	2.8815613	3.055813	2.5018134	2.8587666
MUM2	AT5G63800	3.9678233	3.8043642	3.733841	3.4939353

AtMC3	AT5G64240	3.2152646	3.0750268	2.8931484	2.831481
AT5G64600	AT5G64600	2.6519058	2.693576	2.3031728	2.4424326
CPR5	AT5G64930	2.8480692	2.7741823	2.4996612	2.4861658
AT5G66670	AT5G66670	-1.6937453	-2.7247448	-4.0199018	-3.0347052
AT5G66780	AT5G66780	-2.4803772	-3.1147196	-4.9828916	-5.0173264
SKIP2	AT5G67250	3.5791578	3.5070994	3.2402966	3.25706
NAD5C	ATMG00060	1.2333404	0.5564073	0.16314562	0.73171276
NAD9	ATMG00070	0.1372885	-1.0802904	-1.4409136	-0.92023593
RPL16	ATMG00080	1.697014	0.29086223	-0.06851008	0.6047569
ATMG00090	ATMG00090	3.811763	2.7639344	2.3464098	2.701396
COX2	ATMG00160	1.686937	1.4912745	0.97201806	1.3690375
NAD7	ATMG00510	-0.37790117	-1.2657548	-1.7594486	-0.9685405
ORF25	ATMG00640	0.19003177	-1.1457562	-1.171795	-0.38641903
ATP9	ATMG01080	0.49408498	-0.29479533	-0.7803381	-0.11507533
COX1	ATMG01360	1.052431	-0.37439215	-0.23386808	0.807158
PSBA	ATCG00020	6.329146	5.14432	5.0855813	6.2262535
PSBK	ATCG00070	2.0555382	0.90132904	-0.04761046	0.9436218
TRNS.1	ATCG00090	1.457015	0.43697476	-0.23723851	0.25356314
ATPA	ATCG00120	5.5782795	4.2482677	3.5033953	3.9225357
ATPF	ATCG00130	4.96015	3.6331654	3.060912	3.4398296
ATPH	ATCG00140	3.6515868	2.231451	1.6687384	2.1110227
ATPI	ATCG00150	3.9405606	2.386962	2.2579892	2.5435107
RPS2	ATCG00160	2.6192443	1.1043957	0.81238264	1.2419747
RPOC1	ATCG00180	4.3016977	2.7755272	2.8606873	3.1228135
YCF6	ATCG00210	-0.36370206	-1.742894	-2.1386166	-1.1360406
PSBD	ATCG00270	5.5394115	4.175215	3.6300576	4.1783614
PSBC	ATCG00280	5.977562	4.611661	4.348863	5.031735
TRNS.2	ATCG00290	0.9330608	-0.41253212	-1.0282888	-0.32783827
YCF9	ATCG00300	1.6615046	0.13046561	-0.541281	0.38668182
RPS14	ATCG00330	3.1834917	1.7951183	1.4777417	1.9184628
PSAB	ATCG00340	5.761713	4.2247076	4.1000724	4.6374383
PSAA	ATCG00350	5.4649987	4.0987926	3.8634675	4.407907
RPS4	ATCG00380	1.8790417	0.21555133	0.21274227	0.6196899
NDHC	ATCG00440	1.6158594	0.4192039	-0.13861658	0.40392712
ATPE	ATCG00470	3.5675867	2.7069123	2.0293255	2.468751
ATPB	ATCG00480	5.474897	4.4298835	3.749449	4.2680264
RBCL	ATCG00490	6.797438	5.5121274	5.1161785	5.8190618
ACCD	ATCG00500	2.9542172	1.5395256	1.2982712	1.6446441
PSAI	ATCG00510	0.5439438	-1.4471148	-1.1975178	-0.05480628
YCF4	ATCG00520	3.2678077	1.9016128	1.4533124	1.9253601
PETA	ATCG00540	3.9815273	2.6433456	2.314701	2.690686
PSBJ	ATCG00550	1.4043163	0.27927378	-0.18064241	0.16290502
PSBL	ATCG00560	1.021604	-0.08611826	-0.6709617	-0.13999934
PSBF	ATCG00570	1.3318597	0.30105835	-0.43345752	0.37060192
PSBE	ATCG00580	2.7639961	1.6914068	1.0081398	1.8026576
PETG	ATCG00600	-0.13050044	-1.8542665	-1.4442648	-1.0708989
RPL20	ATCG00660	2.010638	0.7207988	-0.34921682	0.6866371
RPS12A	ATCG00065	0.43577638	-1.0074104	-1.8384619	-0.99992627
PSBB	ATCG00680	4.74634	3.4542236	3.212943	3.7905414
PETB	ATCG00720	4.609789	3.3295233	2.818402	3.361228
PETD	ATCG00730	3.6730213	2.394863	1.8468019	2.3524795
RPOA	ATCG00740	4.3015685	2.7693374	2.241685	2.673375
RPS11	ATCG00750	3.7379615	2.2824237	1.7948729	2.1055982
RPL36	ATCG00760	1.8221487	0.34750393	-0.044854578	0.060613792
RPS8	ATCG00770	4.130884	2.8141286	2.22136	2.6780987
RPL14	ATCG00780	4.6429763	3.3721201	2.6130784	3.0565388
RPL16	ATCG00790	5.9932847	4.8691854	4.1080437	4.463078
ATCG00800	ATCG00800	5.1129937	3.8674676	3.2558727	3.6615686
RPL22	ATCG00810	4.567368	3.283064	2.7161882	2.8486478

RPS19	ATCG00820	3.301514	1.8543228	1.2154888	1.5538257
RPL32	ATCG01020	2.824314	1.602806	1.4325123	1.9448937
NDHD	ATCG01050	3.8254507	2.1981308	2.0931985	2.6705348
PSAC	ATCG01060	2.2344663	0.8554945	0.378935	0.6938841
NDHE	ATCG01070	1.7624254	0.005301634	-0.015021801	0.5174781
NDHG	ATCG01080	2.4828472	0.98078346	0.4071397	1.1108652
NDHI	ATCG01090	2.2622163	0.6880495	0.5096696	0.8561032
NDHA	ATCG01100	5.154258	3.6208827	3.2278004	3.4808133
NDHH	ATCG01110	4.139919	2.6263359	2.0419252	2.175379
RPS15	ATCG01120	1.8049256	0.518651	-0.46449396	0.14275979
YCF1.2	ATCG01130	5.80155	4.497286	3.5703087	3.9857912