

Cluster 2. 462 genes					
Probe	ID	Sample 1	Sample 2	Sample 3	Sample 4
KCS1	AT1G01120	4.5224247	4.983749	4.549017	4.594504
AT1G01260	AT1G01260	2.7492492	2.7652977	2.5189264	2.389198
AT1G01490	AT1G01490	4.509184	4.5747867	4.390865	4.3620186
CYP86A4	AT1G01600	1.740141	1.9791956	1.4050832	1.4406885
ATAF1	AT1G01720	4.2319484	4.171524	4.0313087	3.9315288
AT1G02270	AT1G02270	3.16175	3.1922483	2.9067726	2.8541172
HFR1	AT1G02340	1.0414122	1.6190876	0.41507193	0.7477762
AT1G02360	AT1G02360	2.4303513	2.9216623	2.1605477	2.3468397
AT1G02820	AT1G02820	0.34777614	0.8112033	-0.3694738	-0.100425385
POR C	AT1G03630	5.384011	5.326579	5.261159	5.116451
ATHM1	AT1G03680	6.2099533	6.3343315	6.0810323	6.103056
YUC9	AT1G04180	0.10577109	0.71889424	-0.8093076	-0.09237411
emb2394	AT1G05190	7.427685	7.493656	7.3203597	7.2323513
RCI3	AT1G05260	4.268927	4.4637623	4.132108	4.0892873
LPA19	AT1G05385	2.5667534	2.6345677	2.4038079	2.198296
AT1G06350	AT1G06350	0.5834243	1.1997267	0.38304412	0.17943238
AT1G06630	AT1G06630	2.6666927	2.7112665	2.3911111	2.2881112
AT1G06960	AT1G06960	2.3829272	2.4392412	2.0458946	2.0027745
RTFL3	AT1G07490	-1.2308903	-0.8474836	-2.4719498	-2.557052
MT1C	AT1G07610	4.7968864	5.10341	4.602327	4.806352
ATRBOHB	AT1G09090	2.6230087	2.5508573	2.1075552	1.9536358
AT1G09230	AT1G09230	2.811416	2.8871937	2.6114829	2.4776676
AT1G09310	AT1G09310	8.601675	8.788959	8.48011	8.459805
AT1G09380	AT1G09380	-2.4035065	-1.4095606	-3.3902457	-3.526016
ATRAB11C	AT1G09630	3.4383285	3.5839167	3.2800324	3.1979702
AT1G10610	AT1G10610	1.2102889	1.3663802	0.67716974	0.5433958
AT1G11120	AT1G11120	0.058431447	0.46457398	-0.20092706	-0.48984075
PIRL3	AT1G12970	2.2931805	2.368077	1.9395384	1.950437
CYP71B2	AT1G13080	3.4806979	3.6466935	3.191741	3.2198713
CYP71B28	AT1G13090	3.4497268	3.4420779	3.2195895	3.0471365
AT1G13470	AT1G13470	-1.8975569	-1.1048039	-2.7235792	-2.7520397
AT1G15380	AT1G15380	2.3062546	1.9668311	1.6886498	1.2846674
AT1G16840	AT1G16840	3.8826091	4.0888853	3.8268309	3.832937
SRG1	AT1G17020	1.6404606	1.9681946	1.2950574	1.3778774
AT1G17100	AT1G17100	4.524116	4.5584064	4.3715186	4.191006
AT1G17130	AT1G17130	3.9013033	3.9826925	3.726489	3.7054107
AT1G17970	AT1G17970	2.9935462	2.9933329	2.998789	2.5107973
BEE1	AT1G18400	3.775055	3.602951	3.5697854	3.290754
AT1G18810	AT1G18810	1.3347012	1.5914993	1.0664457	0.7865922
ATCDPK1	AT1G18890	3.4238746	3.5534103	3.197322	3.1837456
ARR7	AT1G19050	2.2317898	2.3984373	1.8961405	1.6076851
APS2	AT1G05610	5.570535	5.6090546	5.4400635	5.392969
AT1G20990	AT1G20990	-2.3926992	-1.8630905	-3.774247	-4.5826573
AT1G21010	AT1G21010	1.7945188	1.8882784	1.3878222	1.3390855
AT1G21400	AT1G21400	3.9758797	3.9782321	3.6675844	3.6458404
AT1G22160	AT1G22160	0.18628931	0.7147277	-0.21455044	-0.41178492
ATMYB3	AT1G22640	2.7646134	3.089772	2.4871988	2.5873508
AT1G24580	AT1G24580	-2.059366	-1.7557812	-4.3532352	-4.9666586
MAP65-8	AT1G27920	0.029562986	0.23553221	-0.84494597	-0.7228853
SCPL45	AT1G28110	2.7836883	2.478049	2.5554552	1.895639
AtRLP4	AT1G28340	4.113379	4.0981345	3.9431384	3.8279896
AT1G28570	AT1G28570	1.7522637	1.3944631	1.4445285	0.77264977
COR414-TM1	AT1G29395	3.3561738	4.057581	3.0766175	3.4510882
AT1G29450	AT1G29450	-0.8848452	-0.74521154	-2.1211274	-2.3222039
AT1G29460	AT1G29460	-0.9568896	-0.26607645	-1.3519846	-1.9888706
AT1G29490	AT1G29490	-3.782674	-2.3407438	-4.9828916	-5.0679936

AT1G29500	AT1G29500	0.2770467	0.39574075	0.056296688	-0.8352303
SAUR68	AT1G29510	-0.46093854	0.13653827	-0.19400753	-1.2002556
AT1G29660	AT1G29660	4.12801	4.395744	4.447166	3.9673595
CAB3	AT1G29910	10.643051	10.872748	10.101387	10.148391
CYP97A3	AT1G31800	4.921712	4.935902	4.7385545	4.602815
ATPRR1	AT1G32100	2.5808911	2.7980187	2.1813402	2.2087395
AT1G35180	AT1G35180	0.6899169	1.4356527	0.22138946	0.07212303
AT1G35340	AT1G35340	4.1785235	4.1886353	4.065592	3.897323
AT1G43670	AT1G43670	5.274375	5.32613	5.1409607	4.9563527
AT1G47580	AT1G47580	2.4396408	2.4731903	2.110837	1.8113683
GLN1;5	AT1G48470	-2.5135558	-1.8124229	-4.1642213	-4.438338
ACT8	AT1G49240	6.7202086	6.817875	6.574303	6.598818
AT1G49310	AT1G49310	0.9466081	1.3111335	0.31559202	0.4585077
AT1G49975	AT1G49975	4.0977397	4.2036595	3.9081032	3.8488553
AT1G50180	AT1G50180	-0.37007174	-0.33082792	-1.2537822	-1.7520396
ATHX	AT1G50320	5.0637813	5.198292	4.858898	4.8759904
AT1G51140	AT1G51140	2.1922681	2.1468885	1.8439584	1.4812092
AT1G51340	AT1G51340	1.9683646	2.1466293	1.5931954	1.4942757
AT1G51400	AT1G51400	6.236791	6.5165253	6.076223	6.178497
AT1G51580	AT1G51580	3.3083966	3.45214	3.0600202	3.145954
AT1G51890	AT1G51890	0.3019416	0.6566113	-0.0155386655	-0.2547552
AT1G53070	AT1G53070	2.5907629	2.2744465	2.2621882	1.7682041
AT1G53520	AT1G53520	3.890311	3.971094	3.7908375	3.7056274
ATPME2	AT1G53830	1.4298605	1.7219337	1.0662867	1.1033893
ESP	AT1G54040	1.1368723	1.4657078	0.7956352	0.8423297
AT1G54120	AT1G54120	1.5443364	1.3133622	1.2154888	0.4380037
AT1G54500	AT1G54500	5.2606564	5.2861676	5.103949	5.0531526
PDF1.5	AT1G55010	-1.1235809	-0.81906414	-2.4409132	-3.1185515
AT1G56150	AT1G56150	-1.0359026	-1.3087689	-2.9496028	-3.4753478
AT1G56423	AT1G56423	2.0403984	2.1667128	1.6374422	1.6636709
PP2A-1	AT1G59830	4.068687	4.177798	4.0469437	3.962429
AT1G60000	AT1G60000	5.9234176	5.838148	5.751597	5.581465
AT1G61170	AT1G61170	0.62112635	1.1513363	0.5500266	0.5147833
ATCDS1	AT1G62430	2.97388	3.0902233	2.7530737	2.6734836
FMO GS-OX2	AT1G62540	0.49704728	0.98412484	0.55179137	0.265624
AT1G63080	AT1G63080	1.0792851	1.337706	0.5498405	0.6295982
AT1G63220	AT1G63220	3.4261532	3.6487577	3.2903516	3.3607304
AT1G63295	AT1G63295	0.2934785	0.5041861	-0.18761742	-0.45759884
AT1G63630	AT1G63630	-2.782674	-1.7247447	-4.9828916	-4.683993
EGL3	AT1G63650	2.4476814	2.4123518	2.1204684	1.9197868
LACS3	AT1G64400	2.4886463	2.5756757	2.2116354	2.1313784
AT1G64405	AT1G64405	-0.12381949	0.2884991	-0.5029864	-0.6212671
AT1G64510	AT1G64510	6.8528557	7.0099907	6.747928	6.7350535
BDG1	AT1G64670	3.1982243	3.4078217	3.1447792	2.9980135
NDF2	AT1G64770	4.4669013	4.3812447	4.29748	4.052659
AT1G65000	AT1G65000	0.8756253	1.0098405	0.4109358	0.23494953
AT1G65220	AT1G65220	4.9886117	5.061086	4.8175855	4.797357
AT1G65450	AT1G65450	0.038228076	0.56792945	-0.8274956	-1.0468806
AT1G66760	AT1G66760	2.9393852	3.2891314	2.8057241	2.8478222
MIR414	AT1G67195	2.6864555	2.624943	2.5401793	1.9743376
AT1G67820	AT1G67820	1.1346222	1.1002058	0.59077555	0.43077263
ENDO 2	AT1G68290	0.9493831	1.1701498	0.5484221	0.538082
AT1G68440	AT1G68440	3.8760102	3.9471045	3.5916853	3.5450401
CUT1	AT1G68530	6.7287707	6.758241	6.716959	6.455604
AT1G68660	AT1G68660	3.9645615	3.9497375	3.7487164	3.5873096
AT1G68780	AT1G68780	2.9053524	2.968413	2.6223903	2.3961415
AT1G69610	AT1G69610	0.3997043	0.87708044	-0.2106231	-0.25404328
AT1G69730	AT1G69730	1.182063	1.2979658	0.692713	0.59284246
AT1G70180	AT1G70180	3.494262	3.5214503	3.3667967	3.2500165

HWI1	AT1G70690	1.3163849	1.52446	0.74602336	0.94992995
AT1G70780	AT1G70780	6.468776	6.614305	6.2926955	6.2339363
AT1G70782	AT1G70782	6.468776	6.614305	6.2926955	6.2339363
AT1G70860	AT1G70860	-2.134388	-1.3206319	-3.774247	-3.5766833
AT1G72230	AT1G72230	1.60076	2.0436327	1.2416916	1.3345022
ATKI1	AT1G73260	4.3627353	4.092194	3.8552496	3.7759628
AT1G74670	AT1G74670	6.1899133	6.724978	5.9474716	6.1728272
RPS9	AT1G74970	6.579803	6.622982	6.420105	6.352093
PR5	AT1G75040	-0.47321746	-0.3627157	-1.5407668	-1.6447301
AT1G75460	AT1G75460	4.793106	4.977263	4.5996556	4.4957805
AT1G75960	AT1G75960	0.5288755	0.9144346	-0.31747207	-0.21970026
EMB1793	AT1G76060	2.062847	2.2539659	1.6911097	1.5251948
AT1G76110	AT1G76110	3.160237	3.1775525	2.953622	2.759703
AT1G76570	AT1G76570	1.9056449	2.1109512	1.5858831	1.3978142
AT1G76610	AT1G76610	-3.1666753	-1.150792	-3.6359012	-3.1420145
AT1G77540	AT1G77540	3.1830122	3.2765534	2.968681	2.818002
AT1G78100	AT1G78100	3.2559528	3.488537	3.0347593	3.1379707
AtkdsA1	AT1G79500	3.961998	4.0664496	3.7602375	3.7007158
CRR3	AT2G01590	3.260308	3.342681	3.1879396	2.9706373
AT2G01755	AT2G01755	2.0905032	2.2116325	1.7728906	1.7718464
AT2G02400	AT2G02400	2.3875506	2.5557935	2.0851715	2.0306494
AT2G03540	AT2G03540	-3.0283296	-2.3717802	-4.9828916	-5.0173264
AT2G05310	AT2G05310	5.3767304	5.452784	5.2274265	5.0432544
RBP36B	AT2G15400	-1.5876867	-1.7343012	-2.9692342	-4.633325
AT2G15960	AT2G15960	4.577097	4.7574716	4.305679	4.3937907
PDV2	AT2G16070	2.9299343	3.0038328	2.8452587	2.6634865
AT2G17740	AT2G17740	-0.6776243	-0.9247678	-2.0002708	-3.1420145
AtPPa2	AT2G18230	2.4385583	2.5396204	2.167489	2.1300943
AT2G18480	AT2G18480	-2.0593657	-1.0631138	-4.0199018	-4.054336
AT2G18890	AT2G18890	1.4249052	1.3825647	1.1739448	0.7124954
AT2G19060	AT2G19060	0.7637727	0.96868014	0.16899411	0.08079936
AT2G20340	AT2G20340	1.7376035	1.9875011	1.3263631	1.1420156
AT2G21187	AT2G21187	0.04533158	0.30204642	-0.58831924	-0.8202788
AT2G21210	AT2G21210	3.836715	4.0078197	3.6655197	3.660075
CYP96A5	AT2G21910	-3.1160076	-2.512268	-4.9828916	-5.0679936
AT2G22420	AT2G22420	1.7871355	2.119752	1.4957968	1.6448773
AT2G22510	AT2G22510	0.51118976	1.1642267	0.40844408	0.4208084
IAA8	AT2G22670	5.503845	5.5689197	5.360434	5.266027
YCF37	AT2G23670	4.93751	5.016402	4.8497677	4.794145
BLH4	AT2G23760	2.8419893	2.909097	2.5374763	2.482961
AT2G23840	AT2G23840	2.3068917	2.750192	2.0937881	2.261289
3BETAHSD/logenase/decar		3.0446155	3.1047344	2.752966	2.7487295
AT2G26500	AT2G26500	6.790442	6.90159	6.7567677	6.609101
ATEXPA6	AT2G28950	4.5274696	4.751415	4.3853545	4.3730073
AT2G29180	AT2G29180	3.969797	4.043666	3.7756014	3.6674283
ATGSTU7	AT2G29420	5.0078316	5.2510676	4.7255874	4.7980056
PCNA2	AT2G29570	3.8167584	3.9121923	3.6238854	3.6276715
AT2G31490	AT2G31490	5.052566	5.2138863	4.8700128	4.905735
ATGPX2	AT2G31570	5.511753	5.6827826	5.30382	5.4131093
AT2G32500	AT2G32500	3.2828286	3.445569	2.9365425	2.9345353
ATGRP23	AT2G32690	5.772377	5.825707	5.587518	5.536646
ZFN2	AT2G32930	1.5120684	1.7255274	1.0774426	1.1176866
AT2G33330	AT2G33330	3.4384181	3.3482864	3.256158	2.8569863
AT2G34620	AT2G34620	3.3415039	3.6954463	3.0074494	3.006469
EDA18	AT2G34920	1.0048962	1.019318	0.39244226	0.27711472
AT2G35000	AT2G35000	0.92166233	1.3820904	0.71109056	0.62438816
AT2G35490	AT2G35490	5.1794424	5.232092	4.993031	4.956157
AT2G35830	AT2G35830	4.085801	4.2433944	3.9398105	3.9067051
XTH32	AT2G36870	3.8678055	3.5730324	3.6623867	3.051459

AT2G37100	AT2G37100	0.475794	0.76430625	0.24866688	-0.025403216
TTG2	AT2G37260	0.7385184	0.72060937	0.16669863	-0.270598
LP1	AT2G38540	7.889714	7.8913665	7.8616676	7.63822
AT2G39080	AT2G39080	5.3280516	5.286947	5.194117	5.054313
AT2G40480	AT2G40480	2.7273686	2.796705	2.4386303	2.4352787
FL3-27	AT2G40880	3.9961898	4.2590594	3.783017	3.8858407
AT2G41040	AT2G41040	2.0347235	2.3847897	1.9653416	1.9726859
AT2G41760	AT2G41760	2.6351805	2.7598178	2.3605356	2.3199227
ATINT1	AT2G43330	3.0257218	3.1228411	2.8671958	2.7955034
OASB	AT2G43750	6.3873916	6.356523	6.260484	6.1234226
AT2G43860	AT2G43860	-2.5876865	-1.3914113	-4.0199018	-4.155672
MTHFR2	AT2G44160	5.766909	5.8450737	5.689747	5.629638
AT2G44220	AT2G44220	-1.3582311	-0.56797147	-2.700116	-2.2803602
AT2G46100	AT2G46100	3.451266	3.6506054	3.3104537	3.3116763
AT2G46760	AT2G46760	-0.20173596	0.095874764	-1.1717952	-1.1778842
AT2G46915	AT2G46915	3.6955745	3.6909068	3.48405	3.4297059
MIR408	AT2G47015	0.7363527	1.24531	0.22138946	0.35301027
AT2G47485	AT2G47485	1.3143444	1.4206233	0.8228679	0.85422546
AT2G47630	AT2G47630	3.9280388	4.0032163	3.7097156	3.6944988
AT3G01175	AT3G01175	-3.2543533	-1.2874533	-3.2284367	-3.1926823
AT3G01190	AT3G01190	2.8316362	3.0213501	2.6896362	2.5714607
RGF7	AT3G02240	0.46672344	0.34403396	-0.11874495	-0.947027
AT3G03830	AT3G03830	-2.782674	-2.3407438	-3.6359007	-5.0679936
AT3G05230	AT3G05230	3.3022525	3.443307	3.0448782	3.109267
AT3G05345	AT3G05345	2.1639402	2.2431846	2.011176	1.670878
AT3G05400	AT3G05400	1.2855798	1.3500415	0.62961465	0.6497558
AT3G05727	AT3G05727	4.9055552	4.770738	4.3393283	4.407307
SFR2	AT3G06510	4.7818274	4.646063	4.608196	4.390289
AT3G06750	AT3G06750	3.8061378	3.933324	3.570901	3.4752378
AT3G08740	AT3G08740	6.6640983	6.6598816	6.600781	6.4305778
AT3G09050	AT3G09050	3.2134593	3.20315	3.0950434	2.854089
ATEXO70H4	AT3G09520	-0.8643784	-0.45372185	-2.7682726	-1.8593489
AT3G10130	AT3G10130	3.6892202	3.834535	3.6115544	3.5290337
LYC	AT3G10230	4.7044096	4.752676	4.5254207	4.4691525
LBD21	AT3G11090	1.7380733	2.023247	1.3896114	1.3783749
HSP70	AT3G12580	5.188328	4.993604	4.371989	4.264816
ALIS1	AT3G12740	4.0634007	4.1814	3.9579504	3.8954804
AT3G13610	AT3G13610	3.956382	3.9753017	3.836568	3.6282845
TBL41	AT3G14850	0.7102701	1.055267	0.23551564	0.19084889
SPA3	AT3G15354	4.1005073	3.9976327	3.8648121	3.5196545
IAA19	AT3G15540	-0.1269321	0.70074505	-0.5997262	-0.41658196
AT3G15650	AT3G15650	1.3638972	1.6827418	1.0031608	0.95288825
AT3G15780	AT3G15780	0.82797265	0.9917319	0.26913375	0.24456716
FAD5	AT3G15850	5.6145706	5.615474	5.5220246	5.342247
NDF4	AT3G16250	4.289435	4.335914	4.0474133	3.850829
JAL31	AT3G16430	4.388555	4.4077168	4.152537	4.1255383
CTL2	AT3G16920	1.7746296	1.8469208	1.4910396	1.3424946
AT3G17070	AT3G17070	2.1037495	2.1654775	1.6999239	1.6638308
BGLU43	AT3G18070	1.7381449	1.8251529	1.082174	1.2348423
WNK6	AT3G18750	2.653242	2.6344604	2.4316404	2.241972
AT3G18890	AT3G18890	5.947262	5.9729385	5.776613	5.7253623
AT3G19380	AT3G19380	1.2395798	1.5672144	1.0753247	0.97418207
AT3G21030	AT3G21030	-3.5566502	-2.5863988	-4.9828916	-5.0679936
AT3G22800	AT3G22800	1.7361912	2.2176788	1.5640022	1.7167044
AT3G23170	AT3G23170	1.5899817	2.2359877	1.5128899	1.7138075
ckl10	AT3G23340	2.8225954	2.9572766	2.7479827	2.578264
FIB4	AT3G23400	5.569468	5.6418705	5.413176	5.3990455
ATFAO3	AT3G23410	2.330962	2.0218132	2.0222745	1.4878422
AT3G24100	AT3G24100	5.017406	5.124248	4.867377	4.8425965

AMT1;3	AT3G24300	2.6317146	2.8431976	2.4425275	2.4244528
MBF1C	AT3G24500	3.2921002	2.8123362	2.5371065	2.3494632
AT3G25130	AT3G25130	1.016096	1.4541392	1.0080322	0.88190955
AT3G25210	AT3G25210	1.6907336	1.8381726	1.2842581	1.1352988
AT3G25470	AT3G25470	4.9977756	5.035835	4.837263	4.667498
CCB1	AT3G26710	5.3053575	5.267814	5.1797414	5.01938
TBL22	AT3G28150	-1.172344	-0.9452348	-3.1717951	-3.4383373
AT3G28200	AT3G28200	3.9112034	4.113618	3.7197444	3.7694304
AT3G28940	AT3G28940	5.279712	5.482013	5.082176	5.226739
ATEXPA5	AT3G29030	2.4640377	2.7627716	2.475214	2.380544
CYP85A2	AT3G30180	5.7647977	5.6921945	5.6933084	5.4301014
AT3G44630	AT3G44630	2.2220132	2.3242702	1.9572363	1.907173
PSK3	AT3G44735	1.9861627	2.3735046	1.7570748	1.7232729
ATCHX4	AT3G44900	-1.3517469	-1.1641368	-1.9496031	-3.613694
UGT76E11	AT3G46670	2.7096796	2.5145879	2.7671492	2.0346866
AT3G46930	AT3G46930	1.1315974	1.3402084	0.6448825	0.67847854
AT3G47070	AT3G47070	5.2791524	5.44791	5.115893	4.895357
AT3G47590	AT3G47590	3.0546472	3.187947	2.8752785	2.7669156
AT3G47610	AT3G47610	3.076563	3.1545343	2.9134884	2.7394295
CYP71A22	AT3G48310	2.8534348	2.955618	2.8661602	2.5648048
AT3G48720	AT3G48720	4.090892	4.3369946	3.8993218	3.877161
AT3G49160	AT3G49160	-0.45094022	-0.32195476	-0.9496031	-1.8162546
AT3G50560	AT3G50560	-0.026220733	0.40219593	-0.22713035	-0.9178727
AT3G51330	AT3G51330	2.6789696	2.920552	2.3564622	2.5591013
AT3G52230	AT3G52230	5.260837	5.2458434	5.0679364	4.957599
AT3G52360	AT3G52360	2.0312595	2.4214814	1.8150791	1.9527744
CAH1	AT3G52720	3.952321	3.8278034	3.8859756	3.3243363
AT3G52900	AT3G52900	2.0616016	2.008449	1.7368631	1.4519734
AT3G54160	AT3G54160	-0.97672325	-0.3839554	-1.4153084	-1.8208566
AT3G54200	AT3G54200	1.8785435	2.161593	1.699804	1.7067674
PIP2D	AT3G54820	2.0827067	2.3013473	1.700966	1.6658769
AT3G55420	AT3G55420	1.8416038	1.998753	1.5795999	1.5028116
AT3G56010	AT3G56010	4.61844	4.715898	4.6084175	4.478466
AT3G56080	AT3G56080	2.6683834	2.6594446	2.4436247	2.1748981
AT3G56270	AT3G56270	1.489262	1.4014388	0.94875985	0.6033833
AT3G56320	AT3G56320	1.6206216	1.6289893	1.277535	1.0713176
BHLH038	AT3G56970	2.4357336	2.3644211	1.7717854	1.4951786
AT3G57920	AT3G57920	0.17260893	0.005440742	-0.49943733	-1.1420145
AT3G58270	AT3G58270	0.30816358	0.3254531	0.0013960997	-0.5570521
AT3G59380	AT3G59380	3.3558655	3.4172537	3.1205919	2.9915493
AT3G59480	AT3G59480	-0.13321845	0.112750076	-0.84712696	-0.9489093
AT3G59980	AT3G59980	4.128114	4.173999	4.0132337	3.8839538
AT3G60080	AT3G60080	2.6258142	2.7715492	2.3636143	2.303076
CDS5	AT3G60620	3.3712301	3434	3.2401698	3.1453617
AT3G61220	AT3G61220	3.6774337	3.853822	3.4261572	3.3595707
CYP78A9	AT3G61880	-0.7185766	-0.68165034	-1.723579	-2.06191
AT3G62460	AT3G62460	-0.21040101	-0.26516595	-0.8039493	-1.4829211
AT3G62860	AT3G62860	2.7216651	2.725624	2.482296	2.2503176
AT3G63160	AT3G63160	6.3501754	6.385382	6.1285815	6.000351
AT4G00390	AT4G00390	-1.9716878	-1.9615759	-4.0199018	-5.017326
TMP-C	AT4G00430	5.943737	6.02055	5.828032	5.7367578
AT4G01940	AT4G01940	4.890062	4.948814	4.678637	4.5854173
AT4G02800	AT4G02800	3.290718	3.2144794	2.8922374	2.761262
ATHM2	AT4G03520	6.744518	6.775931	6.641005	6.554168
ATABC1	AT4G01660	4.8613353	4.946247	4.7599587	4.684124
ATMSRB6	AT4G04840	3.1305609	3.3624785	2.8407347	2.8875563
KEA3	AT4G04850	4.054083	3.9890823	3.8343656	3.6997821
AT4G04925	AT4G04925	2.0449994	2.1542027	1.7615814	1.6203638
AT4G04990	AT4G04990	-2.3616629	-1.1789347	-4.598891	-4.249324

AT4G05010	AT4G05010	0.06709361	0.49604583	-0.8916275	-0.7871003
AT4G05090	AT4G05090	2.8230603	2.9297533	2.5302184	2.5684478
ACS11	AT4G08040	1.7175131	2.531463	1.6892885	2.098106
AT4G08220	AT4G08220	1.759744	1.9882259	1.264089	1.2883421
EXO	AT4G08950	4.8972063	4.753521	4.134485	4.268534
AT4G09620	AT4G09620	3.9407294	4.0408616	3.7609203	3.6410503
AT4G09950	AT4G09950	0.68018657	0.8112946	0.13807505	0.0345924
AT4G10800	AT4G10800	0.8450168	0.93547803	0.38342962	-0.012747244
KELP	AT4G10920	3.8171942	3.8823397	3.6241796	3.534643
AT4G10970	AT4G10970	3.1234567	3.1534245	2.8314831	2.8119233
AT4G11211	AT4G11211	2.1405232	2.4455237	1.800378	1.7972465
AT4G12490	AT4G12490	4.2444415	3.9138393	3.4500048	2.8830535
AT4G13500	AT4G13500	3.7327585	3.8751507	3.5318534	3.5213547
AT4G13620	AT4G13620	0.8536162	1.2267915	0.4948715	0.47069883
AT4G13650	AT4G13650	1.2290171	1.3611168	1.1810942	0.7414899
AT4G13680	AT4G13680	-3.143212	-2.5863988	-4.932224	-5.0679936
AT4G13800	AT4G13800	-0.98523504	-0.6633032	-1.994957	-2.1827667
NF-YB3	AT4G14540	3.254586	3.3495867	3.0960567	2.9503686
AT4G14740	AT4G14740	2.6258414	2.6391773	2.297807	2.1479244
AT4G16410	AT4G16410	5.050905	5.0893173	4.875678	4.8420672
AT4G16790	AT4G16790	1.7922277	1.9047941	1.4080514	1.3721884
AT4G17010	AT4G17010	2.5079076	2.711396	2.4308074	2.3502605
AT4G17050	AT4G17050	4.2040954	4.309318	3.9770339	3.7844703
NS1	AT4G17300	4.7337255	4.6969905	4.5677676	4.464603
AT4G17350	AT4G17350	0.04740888	0.27961862	-0.7708151	-0.8122637
RAB1C	AT4G17530	5.1629214	5.3141327	4.981737	5.054478
SYP23	AT4G17730	4.233008	4.226647	4.0108504	3.949189
AT4G18280	AT4G18280	0.83675647	1.0643733	0.20233707	0.32037064
AT4G18970	AT4G18970	3.7565362	4.2010016	3.6842442	3.790437
AT4G19810	AT4G19810	2.9959517	2.9754124	2.7634687	2.610916
AT4G19830	AT4G19830	2.7849913	2.8953476	2.451421	2.5368652
ENDO5	AT4G21600	3.3812644	3.3924801	3.155337	3.0547075
AT4G21740	AT4G21740	1.1972193	1.5591211	0.7570305	0.6084993
AT4G22520	AT4G22520	1.7612581	1.7497439	0.696698	0.9830982
CRK21	AT4G23290	2.5485036	2.9879234	2.3061306	2.3740137
AT4G23493	AT4G23493	-0.10670551	0.105872996	-1.0249376	-1.0317088
AT4G23690	AT4G23690	3.252588	3.5202637	3.0081768	3.209747
VATG3	AT4G25950	-3.8333418	-1.4912647	-4.3532352	-4.1926827
AT4G26520	AT4G26520	3.136792	3.1497898	2.9293683	2.7713306
AT4G26530	AT4G26530	3.8539505	4.2649064	3.9237814	3.6501236
AT4G26790	AT4G26790	-0.16153687	-0.10438242	-1.1751465	-1.158253
AT4G28730	AT4G28730	3.0561001	3.1310031	2.8654823	2.756075
AT4G28780	AT4G28780	3.3109426	3.543587	3.2345216	2.8422482
AT4G28940	AT4G28940	0.864042	1.0541114	0.48720726	-0.047265977
AT4G29960	AT4G29960	3.241473	3.3221266	3.1282158	2.9757397
GAE1	AT4G30440	4.763057	4.954317	4.685688	4.715139
AT4G31080	AT4G31080	4.697366	4.7270846	4.492268	4.485665
AT4G32220	AT4G32220	-2.620865	-2.492637	-4.9828916	-5.0679936
AT4G32290	AT4G32290	2.4652326	2.6625397	2.2266462	2.1624377
VTE1	AT4G32770	2.0704281	1.91005	1.632609	1.2258942
ATHB-8	AT4G32880	3.9583066	3.9135382	3.7598574	3.6330602
AT4G33110	AT4G33110	4.3205457	4.407971	4.2507706	4.132861
CYCD3;1	AT4G34160	3.8003244	3.751766	3.6148489	3.368495
AT4G34540	AT4G34540	4.3795676	4.5786796	4.1694546	4.299696
BLH6	AT4G34610	3.4719913	3.4957304	3.2593582	3.1090662
SQS2	AT4G34650	2.2897892	2.1877997	1.8423953	1.6710547
AT4G34760	AT4G34760	1.9794396	2.539694	1.7753462	1.7747917
AT4G34930	AT4G34930	-1.1654245	-0.14692643	-2.333604	-2.2493238
AGF1	AT4G35390	-0.24284542	-0.054335605	-0.7594487	-1.261933

HB-4	AT4G35550	2.2189667	2.0853965	1.9256454	1.5021824
AT4G35785	AT4G35785	3.8678608	3.9923964	3.6792285	3.5983722
FAH1	AT4G36220	5.2079635	5.0693016	5.011175	4.7751393
BEE2	AT4G36540	4.3719625	4.5198746	4.233493	4.138499
CP1	AT4G36880	2.7250264	2.7147748	2.1865623	2.0156674
AT4G37560	AT4G37560	1.6894883	1.7288879	1.4075847	1.1787096
AT4G37700	AT4G37700	-1.1518772	-0.8766379	-1.7877941	-3.1420145
AT4G38300	AT4G38300	-0.5620815	-0.59545875	-3.996439	-3.6975403
AT4G38860	AT4G38860	2.634412	2.877237	2.2418735	2.1322653
FKBP16-2	AT4G39710	3.8904335	3.8741171	3.774408	3.529358
AT4G39730	AT4G39730	5.684814	5.860981	5.486337	5.4402404
AT4G39970	AT4G39970	3.7671738	3.9087384	3.6569614	3.5341885
AT5G01870	AT5G01870	3.498596	3.509142	3.297435	3.1591084
AT5G03370	AT5G03370	1.8636128	2.1230803	1.5928391	1.5416651
AT5G04180	AT5G04180	-1.1666752	-1.2912798	-3.1075802	-4.1556716
NAMT1	AT5G04370	-0.04659607	0.3149984	-0.6413322	-0.5728948
ATEXPA2	AT5G05290	-3.0048664	0.8923025	-4.9828916	-5.017326
AT5G06770	AT5G06770	2.2506642	2.2924027	1.9505725	1.6483598
AT5G06790	AT5G06790	0.34211263	-0.15079184	-0.4024211	-1.2155509
AT5G08460	AT5G08460	-1.6693908	-1.2849934	-3.9692342	-5.0173264
AT5G09720	AT5G09720	-2.28539	-1.2221464	-3.5792592	-3.085373
AT5G10745	AT5G10745	2.7168913	2.8212872	2.3916657	2.3998883
SYTD	AT5G11100	1.1292343	1.2521311	0.549275	0.44879818
AT5G11840	AT5G11840	3.2130458	3.3978913	2.9425848	2.8696816
AT5G12940	AT5G12940	2.8491147	3.1741526	2.5400903	2.8062134
AT5G14410	AT5G14410	1.9468683	1.9904865	1.5541004	1.3956083
MIR398C	AT5G14565	2.7171977	2.793911	2.4015484	2.2179914
EDL1	AT5G15440	2.5383663	2.3789823	2.1951864	1.9459766
AT5G16010	AT5G16010	4.6780515	4.762743	4.6245093	4.49815
RTFL18	AT5G16023	-3.1666753	-2.1134691	-4.932224	-5.017326
AT5G16190	AT5G16190	0.8734041	0.65351623	0.21594828	-0.22072245
AT5G16810	AT5G16810	3.1877868	3.395786	2.9348316	2.887575
ENH1	AT5G17170	3.841675	4.0756097	3.6479461	3.3160183
AT5G17560	AT5G17560	4.4696717	4.6224456	4.367509	4.3752627
AT5G17600	AT5G17600	1.0315021	1.0398682	0.4318477	0.09247577
PSRP6	AT5G17870	4.6674933	4.798298	4.485752	4.478383
MYR1	AT5G18240	1.7252043	1.9331394	1.3491114	1.2792463
AT5G18520	AT5G18520	5.438434	5.5518107	5.258987	5.346252
AT5G19760	AT5G19760	6.5352745	6.6091194	6.371865	6.333964
AT5G19850	AT5G19850	2.4125202	2.610858	2.0554018	1.7710768
AT5G19855	AT5G19855	3.9889066	4.161199	3.853688	3.8030796
AT5G20190	AT5G20190	5.594374	5.7921085	5.3339057	5.3973413
HHP1	AT5G20270	3.1711347	3.344114	3.0315063	2.8068917
AT5G20790	AT5G20790	0.4531122	0.9309618	-0.32614812	-0.37423983
ATRAD51	AT5G20850	1.4770117	1.7335113	1.230622	1.1020412
AT5G22140	AT5G22140	2.9235601	3.0001612	2.6236198	2.5956361
AT5G22355	AT5G22355	-0.74649936	0.11421108	-1.0002707	-1.3802137
AT5G23350	AT5G23350	0.72589797	1.2086515	0.38607273	0.49526587
AT5G23820	AT5G23820	6.7487245	6.630696	6.5796266	6.2602997
AT5G25460	AT5G25460	7.7182355	7.6032453	7.5506663	7.3244433
RD22	AT5G25610	5.5810966	5.7096767	5.3211837	5.043038
AT5G26010	AT5G26010	1.8779598	2.2486327	1.654064	1.7925612
AT5G26220	AT5G26220	0.19344926	0.3855609	-0.74715966	-0.57520133
AT5G26582	AT5G26582	-2.7592113	-2.2841022	-4.9828916	-5.0679936
AT5G27400	AT5G27400	2.9898853	2.9374857	2.7667038	2.5666082
CYSD2	AT5G28020	3.9078739	3.913102	3.792554	3.577715
AT5G28520	AT5G28520	-2.002724	-0.93694323	-3.1952581	-3.0347052
AT5G28750	AT5G28750	5.553295	5.6317964	5.431412	5.394207
AT5G35460	AT5G35460	3.784352	4.008981	3.7160866	3.6658905

AT5G36160	AT5G36160	4.7804656	4.443298	4.638634	4.117776
ATPGLP1	AT5G36700	-0.7750333	-0.6484718	-1.7357544	-2.0347052
ATGSL09	AT5G36870	-1.6519016	-1.3087689	-2.7235792	-3.3876698
AT5G37290	AT5G37290	1.1244729	1.4812818	0.9101689	0.79289746
ACYB-1	AT5G38630	3.0629845	3.1526086	2.9329643	2.7992904
CDF2	AT5G39660	1.9709717	2.1309206	1.6801282	1.5012565
AT5G39800	AT5G39800	1.7247099	1.7395201	1.2605103	1.1783888
AT5G39860	AT5G39860	0.33950606	1.3741778	-1.0714053	-0.7489603
AT5G40330	AT5G40330	-0.33074364	0.10895529	-0.92044884	-0.9546004
AT5G40380	AT5G40380	2.6013348	2.987292	2.4827697	2.577534
AT5G42310	AT5G42310	3.9331942	3.9738533	3.8246555	3.689914
AT5G43260	AT5G43260	2.2852614	2.3480198	2.0012174	1.8729157
AT5G43530	AT5G43530	0.1970631	0.5148191	-0.2982043	-0.36924228
ATARD4	AT5G43850	3.782224	3.9912918	3.7032611	3.5759878
ATCLH2	AT5G43860	0.98426247	1.126998	0.35652566	0.25356323
AT5G44050	AT5G44050	0.47579405	0.67466116	0.10058347	-0.23589402
AT5G44250	AT5G44250	3.8992703	4.00988	3.6346836	3.5795372
AT5G44390	AT5G44390	2.5225537	2.601704	2.1547065	1.9807072
AT5G44440	AT5G44440	-3.0283291	-2.2787883	-4.9828916	-5.0679936
AT5G44565	AT5G44565	-2.3420315	-1.5897502	-3.4409134	-3.859349
AT5G44568	AT5G44568	0.83401567	1.0084113	0.19873525	-0.06526101
AT5G44580	AT5G44580	2.8715627	2.8923025	2.5765834	2.423948
AT5G45410	AT5G45410	4.68548	4.8418884	4.569838	4.584561
AT5G45670	AT5G45670	3.9125092	4.3892345	3.7271004	4.02804
AT-HSFA4C	AT5G45710	1.7836691	1.8607966	1.3337926	1.224558
AT5G45760	AT5G45760	1.747615	1.8579473	1.3457626	1.1915051
APE2	AT5G46110	8.036628	8.138871	7.892881	7.8837657
AT5G47000	AT5G47000	-2.3926992	-1.5999461	-4.164222	-4.0543365
AT5G47440	AT5G47440	-0.6462106	-0.3523413	-1.9261398	-1.6447302
AT5G48220	AT5G48220	3.7571418	3.7583969	3.5567894	3.3468769
AT5G48490	AT5G48490	2.5931501	2.926448	2.19059	2.320007
ATCP1	AT5G49480	4.6892204	4.73744	4.2735577	4.173511
AT5G51110	AT5G51110	6.2458396	6.266765	6.0931563	6.012851
AT5G51440	AT5G51440	1.7978077	1.6874151	1.2111715	0.8254438
AT5G53380	AT5G53380	-1.7260326	-1.352919	-3.4409134	-3.859349
AT5G54290	AT5G54290	4.2301784	4.2190633	4.0733953	3.9818382
AT5G54760	AT5G54760	5.7045555	5.8431544	5.630354	5.588324
AT5G55720	AT5G55720	-1.4110798	-0.7598054	-2.0334494	-2.3876698
AT5G55770	AT5G55770	-2.9541986	-1.8713242	-4.9828916	-5.0679936
ATNAS2	AT5G56080	0.16712749	0.39703873	-4.3532352	-4.5826573
PFN3	AT5G56600	3.3732207	3.413287	3.2468445	3.124809
AT5G57150	AT5G57150	2.954902	3.242239	2.6511958	2.743539
AT5G57270	AT5G57270	3.125117	3.2000399	2.8562915	2.8943875
ZIP2	AT5G59520	2.574958	2.9813404	2.5064385	2.5584526
AT5G60750	AT5G60750	3.4571426	3.5064719	3.2576044	3.1310527
EXL2	AT5G64260	5.88767	6.003313	5.7812734	5.782284
AT5G64770	AT5G64770	1.503734	2.3839366	1.6036501	1.6035633
XTH6	AT5G65730	4.3160377	4.6332283	4.1481442	4.1738834
AT5G66080	AT5G66080	1.7585624	2.1542418	1.5043955	1.5548412
AT5G66900	AT5G66900	2.928961	3.003104	2.7989776	2.646158
AT5G67210	AT5G67210	1.2917618	1.4094595	0.7722001	0.5162431
AT5G67390	AT5G67390	1.7415494	2.148596	1.2305042	1.4838747