

Cluster 1. 505 genes					
Probe	ID	Sample 1	Sample 2	Sample 3	Sample 4
AT1G01300	AT1G01300	5.438282	5.680371	5.8365903	6.046599
PGP12	AT1G02530	-4.55665	-3.6430404	-1.3754479	-1.5335889
CALS1	AT1G05570	4.821655	4.710134	5.26588	5.2599373
UGT74E2	AT1G05680	1.7573404	1.6731313	2.7519913	2.2356024
AT1G06650	AT1G06650	3.5224495	3.5755024	4.0656686	3.9956884
AT1G06720	AT1G06720	4.468238	4.1976686	4.871572	4.5938106
AT1G07070	AT1G07070	3.4609501	3.5620391	3.9231346	3.8642807
AT1G07590	AT1G07590	8.215949	8.360531	8.65771	8.728143
ATAMI1	AT1G08980	4.0340314	3.8869016	4.5524693	4.3031397
RPT5B	AT1G09100	3.8068173	3.8730404	4.295728	4.2473626
NIMIN-3	AT1G09415	2.1872394	2.5110776	2.7716076	2.7151568
AT1G09660	AT1G09660	3.906622	3.910978	4.3498464	4.3088565
AT1G10090	AT1G10090	3.274947	3.3923388	3.7687597	3.750511
AT1G10490	AT1G10490	4.0117216	3.749501	4.4339714	4.1968985
AT1G11220	AT1G11220	-0.529711	-0.16772819	0.70986223	0.5010469
AT1G11740	AT1G11740	0.117241144	0.29588735	1.2023371	1.0881013
ADT1	AT1G11790	2.697183	2.6828501	3.2920382	3.1128988
CLPR2	AT1G12410	5.361173	5.4574914	5.733204	5.719748
AT1G12650	AT1G12650	3.0583508	3.047735	3.5764961	3.3739147
UGE1	AT1G12780	4.1877303	4.068445	4.6241817	4.375023
AT1G13030	AT1G13030	2.3758667	2.339751	2.983167	2.8335094
ATST4B	AT1G13420	-1.3542067	-1.8456014	0.41279614	-0.59798574
AT1G13730	AT1G13730	4.0851226	4.140157	4.610706	4.4739475
AT1G14642	AT1G14642	-4.55665	-3.4480531	-1.7311524	-2.1827667
AT1G14960	AT1G14960	-0.018567005	0.281176	1.5759753	1.4643192
AT1G16650	AT1G16650	1.8597704	1.7794814	2.4535642	2.3729184
AT1G18090	AT1G18090	2.2890918	2.2296371	2.8258104	2.5770419
AT1G19130	AT1G19130	3.4330413	3.5562038	3.9346917	3.9178832
OPCL1	AT1G20510	3.169327	3.301328	3.6614344	3.6976883
HMGB2	AT1G20693	6.104454	6.1978345	6.548185	6.5480385
HMGB3	AT1G20696	5.8301163	5.892109	6.1902046	6.203686
SCL1	AT1G21450	2.863674	2.8267272	3.4170628	3.320116
PTAC6	AT1G21600	5.4448857	5.3352513	5.8569274	5.718308
ATFBP7	AT1G21760	2.3479753	2.3499436	2.8822901	2.8509052
AT1G22110	AT1G22110	-4.6073184	-3.498721	-1.7311525	-3.0543365
AT1G22520	AT1G22520	3.1628196	3.3239295	3.6595325	3.5838299
AT1G23280	AT1G23280	4.1831813	4.0241714	4.685757	4.39444
AT1G23390	AT1G23390	4.58773	4.698521	5.099605	5.3485284
CAF2	AT1G23400	4.2832103	4.2462974	4.766837	4.6588087
AT1G24147	AT1G24147	-2.9210198	-2.0481622	-0.72924787	-0.5162532
AT1G27030	AT1G27030	3.4392645	3.1192648	3.935077	3.4935048
AT1G27300	AT1G27300	2.3124566	2.3997924	2.9400203	2.8459728
AT1G28190	AT1G28190	1.4801215	1.2352912	2.2807014	1.7136202
PUP1	AT1G28230	-0.5831992	-0.6592789	0.4948715	-0.22039069
AT1G30540	AT1G30540	1.9482185	2.0831811	2.6235209	2.591703
WRKY14	AT1G30650	1.8075849	1.937438	2.5270002	2.5050287
AT1G30870	AT1G30870	2.3652973	2.7011359	3.3199232	3.5135124
AT1G30960	AT1G30960	2.2563229	1.9220816	2.8472595	2.4357147
OSB4	AT1G31010	1.1346222	0.99359053	1.8752699	1.6338129
ATPP2-A9	AT1G31200	0.055103436	0.25775585	1.0499835	1.0278362
AT1G31710	AT1G31710	4.683171	4.59677	5.0616264	5.141798
AT1G31940	AT1G31940	2.1272843	2.3881876	2.7227833	2.7728722
XTR4	AT1G32170	1.8805238	2.0825918	2.5243387	2.5564868
AT1G32860	AT1G32860	2.2925842	2.4472952	2.884783	2.8375432
AT1G34030	AT1G34030	6.083777	6.1157756	6.448971	6.3933964
AT1G34160	AT1G34160	0.74297804	0.58186954	1.6099143	1.294051

AT1G34640	AT1G34640	1.7607604	1.8774124	2.5345223	2.3348138
AT1G35190	AT1G35190	2.922865	2.9876032	3.4138906	3.428645
AT1G35330	AT1G35330	-1.6383543	-1.4974699	0.03064827	-0.32494417
CINV1	AT1G35580	5.7062583	5.6004987	6.11277	6.0002303
AT1G36590	AT1G36590	-5.0419865	-5.128377	-2.3667827	-2.7520397
UGT80B1	AT1G43620	2.6791732	2.686387	3.2521229	3.2363348
AT1G45110	AT1G45110	1.1534864	1.240489	2.014325	1.8085684
THO5	AT1G45233	1.6085515	1.8076807	2.2594473	2.262461
AT1G48095	AT1G48095	-5.0419865	-5.077709	-1.9125925	-2.9470272
TOM6	AT1G49410	4.4146767	4.4779243	4.827197	4.736009
AT1G49650	AT1G49650	2.9176161	2.9088328	3.424352	3.3879888
AT1G50120	AT1G50120	3.380976	3.3775616	3.827294	3.784294
AT1G50710	AT1G50710	2.976938	3.1052983	3.4378738	3.4696438
Y14	AT1G51510	4.8324	4.8422194	5.3205123	5.260719
ATPDIL1-5	AT1G52260	0.6394513	0.7827098	1.4259372	1.2860674
AT1G52450	AT1G52450	-2.8333418	-2.8456013	-0.7892992	-0.70620507
AT1G52550	AT1G52550	-0.08048656	0.03667052	1.0436816	0.54544663
AT1G52750	AT1G52750	-0.051909912	0.57328933	0.9878643	0.943693
AT1G52930	AT1G52930	4.2908235	4.262966	4.6734776	4.5317035
AT1G53180	AT1G53180	2.3143706	2.4055853	2.836877	2.9414616
AT1G54410	AT1G54410	8.134491	8.007409	8.48973	8.285042
AtIDD7	AT1G55110	2.3929312	2.3664052	2.9574232	2.6415365
NOP56	AT1G56110	6.708674	6.5987916	7.142282	6.9345245
AT1G56570	AT1G56570	0.6110432	0.5634702	1.3806773	1.0286521
AT1G57790	AT1G57790	0.2964456	0.7925863	1.4438037	1.2245442
ATGSTU16	AT1G59700	1.5344815	1.5824324	2.2234144	1.8795285
AT1G61730	AT1G61730	3.6505642	3.7562091	4.081552	4.063726
AT1G61740	AT1G61740	4.811511	4.703056	5.2659345	5.1294246
BGLU45	AT1G61810	-0.78267425	-0.6174353	0.4961222	0.12148922
AT1G62085	AT1G62085	0.3621324	0.52521175	1.3839945	1.2891402
AT1G62975	AT1G62975	1.4229608	1.651832	2.1192248	2.219721
AT1G64710	AT1G64710	3.9065354	4.0570226	4.3615823	4.3722816
CYP89A5	AT1G64950	3.0833871	3.2120273	3.602026	3.4791996
AT1G65030	AT1G65030	3.339186	3.2829132	3.9099452	3.7392588
AT1G65080	AT1G65080	1.1354389	1.2942432	1.8877006	1.4140358
AT1G65560	AT1G65560	0.9597817	0.89888144	1.7690176	1.3813556
AT1G65700	AT1G65700	2.2864592	2.412834	2.9209678	2.8344858
AT1G65820	AT1G65820	5.2565	5.337402	5.6405773	5.607592
ATPAO4	AT1G65840	4.640709	4.387166	5.028853	4.78569
AT1G66070	AT1G66070	3.7802622	3.8315792	4.1950145	4.129499
BGLU22	AT1G66280	6.4143233	6.1880136	6.8839893	6.642433
pde194	AT1G66520	2.4008875	2.3907049	2.9979513	2.8926964
AT1G67650	AT1G67650	0.5339347	0.7630779	1.338077	1.3613014
AT1G68160	AT1G68160	1.519021	1.618351	2.1630538	2.0102282
AT1G68310	AT1G68310	3.136013	3.1929445	3.5845826	3.6121647
AT1G69460	AT1G69460	4.3622117	4.4285264	4.7580132	4.814832
EXPA1	AT1G69530	4.5841565	5.2517505	5.1314235	5.643946
HO3	AT1G69720	-3.1666753	-2.8690643	-0.89510345	-0.89756316
RHS10	AT1G70460	1.2587966	1.3913136	1.9987735	2.1362875
MLP43	AT1G70890	4.948527	5.3039365	5.585174	5.5421004
AT1G71900	AT1G71900	3.1501496	3.3634377	3.7402093	3.7079113
HRE1	AT1G72360	0.44463956	0.88867307	1.4272366	1.5137275
TIR	AT1G72930	3.242511	3.299554	4.30015	4.3206124
AT1G72940	AT1G72940	1.6438688	1.7988187	2.392989	2.1795607
NRP1	AT1G74560	5.9147334	5.807583	6.366909	6.149038
AT1G75670	AT1G75670	2.3000672	2.1237915	2.8792217	2.6498184
AT1G75900	AT1G75900	1.7564434	2.1046422	2.6702063	2.572074
AT1G77360	AT1G77360	-0.80971974	-0.32485396	0.57870525	0.14275976
ATGGH3	AT1G78670	4.4491076	4.688713	5.0646534	5.034928

AT1G79075	AT1G79075	3.1476076	3.3175738	3.713014	3.4751387
AtOCT5	AT1G79410	2.7636254	2.9242048	3.2630184	3.0701523
AT1G80150	AT1G80150	1.4417272	1.362302	2.0977926	1.8970743
PSF1	AT1G80190	1.8346729	2.0029268	2.651288	2.402355
atnudt17	AT2G01670	3.9056766	3.8195457	4.389937	4.0919876
AT2G03310	AT2G03310	1.4941773	1.6555678	2.4626768	2.2523172
AT2G03350	AT2G03350	3.1668396	3.3437593	3.6746962	3.56241
AT2G03370	AT2G03370	-5.0419865	-5.128377	-1.717605	-2.9159906
AT2G03420	AT2G03420	4.0881457	4.237783	4.7346787	4.493341
PAA2	AT2G05840	4.737581	4.7824016	5.14973	5.021771
EXGT-A1	AT2G06850	7.4922523	7.717262	8.044974	8.074622
TSPLA2-ALPH	AT2G06925	3.3535664	3.363716	3.9798238	3.826748
PR1	AT2G14610	-1.3050212	-1.9005822	0.70647526	1.2659283
KCS8	AT2G15090	3.6593513	3.7428534	4.157028	3.9352634
ROC3	AT2G16600	7.6137023	7.5713353	8.033298	7.9049172
AT2G16750	AT2G16750	2.1398687	1.9785322	2.753062	2.5996664
AT2G16930	AT2G16930	3.6149578	3.7334597	4.170149	4.1225224
AT2G17140	AT2G17140	0.90855294	0.83975095	1.6645793	1.4684048
EMB2762	AT2G17250	3.6424	3.5584085	4.123487	3.9082105
AT2G17720	AT2G17720	4.283579	4.2671556	4.750101	4.618981
NIP2	AT2G17730	2.113737	2.4140718	2.8805072	2.8964818
ERD7	AT2G17840	4.01817	4.0915155	4.4293303	4.5261254
AT2G18220	AT2G18220	4.1371193	3.967635	4.5699406	4.386033
PNP-A	AT2G18660	-2.4433668	-1.5572447	0.29663035	0.94477487
AT2G18900	AT2G18900	4.243583	4.078319	4.7225947	4.5163746
AT2G19385	AT2G19385	2.998668	3.0150535	3.4954054	3.2827175
AT2G19740	AT2G19740	4.8296905	4.89064	5.2968	5.288586
MAN2	AT2G20680	1.6645508	1.9768791	2.2948492	2.3275483
PSB29	AT2G20890	6.713209	6.7505593	7.1715126	7.130591
AT2G22190	AT2G22190	2.008417	2.2165105	2.7764807	2.6197667
EMB2001	AT2G22870	3.220412	3.1488419	3.8278883	3.5400724
SNRK2-9	AT2G23030	1.3609734	1.3455354	2.083688	1.9694128
AT2G25150	AT2G25150	-1.2181785	-1.4691738	0.5900056	-0.06260605
CYP82F1	AT2G25160	-0.0035597633	-0.17024732	1.0589797	0.72057796
AT2G25450	AT2G25450	3.1429663	3.386954	3.9456692	3.7954352
AT2G26200	AT2G26200	3.248069	3.287913	3.8434198	3.7128613
AT2G26230	AT2G26230	3.341747	3.4534018	3.8324459	3.8491802
AT2G26900	AT2G26900	5.9023337	5.861805	6.3647995	6.230643
AT2G27285	AT2G27285	2.563952	2.7015884	3.2883537	3.1278334
AT2G27480	AT2G27480	-0.4418849	-0.043482464	0.7787879	0.74226713
AT2G28720	AT2G28720	3.12889	3.3659408	3.6459816	3.641945
ENOC	AT2G29560	3.9345715	3.9570704	4.3436184	4.366597
AT2G29590	AT2G29590	1.6359882	1.8385395	2.257421	2.1788228
THIC	AT2G29630	5.63891	5.6628337	6.0699687	5.92717
TBL45	AT2G30010	3.4803054	3.7925873	4.1124043	4.162438
AT2G30990	AT2G30990	3.17427	3.1752079	3.6326497	3.589445
AT2G31060	AT2G31060	4.8092847	4.631639	5.36711	5.094203
AT2G31140	AT2G31140	3.0093803	3.3092644	3.569743	3.4072087
FRS2	AT2G32250	1.9942983	2.0481539	2.5658486	2.5804713
AT2G32960	AT2G32960	2.387042	2.661129	3.0695097	3.1055954
DAL1	AT2G33430	5.764498	5.627365	6.1572614	5.993796
AT2G34010	AT2G34010	-0.34429097	0.14673437	0.7844791	0.8825459
AT2G34260	AT2G34260	3.2291129	3.1454744	3.7603834	3.5166864
ACD11	AT2G34690	3.6781442	3.7798471	4.1819673	4.088408
AT2G35880	AT2G35880	4.305235	4.4386044	4.678751	4.644831
SBE2.1	AT2G36390	5.0052705	4.9343915	5.4351068	5.26286
AT2G36410	AT2G36410	3.5542352	3.7929604	4.163842	4.207887
UGT73C1	AT2G36750	0.9322596	0.609058	2.199793	1.4382286
ADK	AT2G37250	4.915628	5.0143356	5.360212	5.304957

AT2G37400	AT2G37400	3.8480027	3.8427184	4.28193	4.2400393
AT2G37770	AT2G37770	2.221115	2.616148	3.0427902	3.0322037
AtIPCS2	AT2G37940	3.9770992	4.207683	4.371626	4.48595
AT2G39820	AT2G39820	-3.1160076	-1.4556265	-0.38094378	-0.5185597
AT2G39950	AT2G39950	3.2334976	3.2077138	3.692341	3.5816917
AT2G40360	AT2G40360	5.654634	5.452723	6.052035	5.765722
AT2G44510	AT2G44510	2.204717	2.1346223	2.8996181	2.6040924
AT2G44860	AT2G44860	5.0198183	4.925901	5.4693694	5.2791576
AT2G45240	AT2G45240	4.158376	4.089102	4.5850143	4.488734
CYP76C1	AT2G45560	3.131984	3.1657238	3.6195958	3.3255424
AT2G45750	AT2G45750	1.4527165	1.7127901	2.1692142	2.1750238
AT2G46170	AT2G46170	3.9035056	4.004254	4.3482833	4.2794375
AT2G46580	AT2G46580	2.4471977	2.5980768	2.99553	2.8474634
AT2G47300	AT2G47300	0.9983738	1.0995921	1.8393186	1.6589006
HRE2	AT2G47520	-4.6073184	-3.1147196	-1.4442648	-2.2925355
AT2G47800	AT2G47800	4.3070197	4.2122188	4.7216725	4.702638
AT3G02250	AT3G02250	3.6960924	3.522044	4.1393456	3.8564165
AT3G02330	AT3G02330	0.46560374	0.21392389	1.2973279	0.83885425
AT3G04010	AT3G04010	1.5725346	1.667236	2.296509	2.3160021
AT3G04220	AT3G04220	-3.8899834	-2.5357313	-1.3842717	-1.7421237
ATLTL1	AT3G04290	4.3067174	4.354276	4.790373	4.731916
AT3G05210	AT3G05210	2.2084358	2.4350626	2.9003	2.8550625
AtRLP31	AT3G05370	1.3043724	1.3642979	2.1031237	1.7945639
AT3G05730	AT3G05730	6.7315927	6.785067	7.1821785	7.2844753
RCI2A	AT3G05880	5.1564183	5.5799174	5.898472	5.8543563
PDK	AT3G06483	4.3958335	4.5061545	4.8256464	4.708473
AT3G06770	AT3G06770	3.0292275	3.0944679	3.500611	3.427201
AT3G06950	AT3G06950	2.3495443	2.3457537	2.9319313	2.8615038
AT3G07010	AT3G07010	3.4799356	3.9535182	4.020224	4.3008466
AT3G07460	AT3G07460	4.670921	4.936419	5.1545334	5.1232142
AT3G07470	AT3G07470	4.2237425	4.5944796	4.730453	4.763476
AT3G07570	AT3G07570	2.1326458	2.4735801	2.7996578	2.7528563
AT3G08820	AT3G08820	0.3191184	0.42920807	1.1637229	0.92261714
AT3G09700	AT3G09700	1.9102373	1.9343971	2.594989	2.4173067
SCPL49	AT3G10410	4.9700027	5.0084643	5.4431624	5.3956547
anac053	AT3G10500	2.5463464	2.6198318	3.079483	3.0517752
SUN2	AT3G10730	2.7556865	2.7632606	3.234166	3.2065516
DREB2B	AT3G11020	-1.5876867	-0.71482897	0.05204716	-0.023197254
AT3G11560	AT3G11560	5.4282756	5.2862144	5.813785	5.706139
AT3G11800	AT3G11800	4.0686016	4.269724	4.4721055	4.521181
scpl17	AT3G12203	-3.4493408	-3.3407438	-1.0399336	-1.3417214
AT3G12340	AT3G12340	2.4789474	2.2816164	3.0747907	2.8014238
AT3G13150	AT3G13150	2.1784775	2.1163251	2.7696638	2.583483
AT3G13230	AT3G13230	3.7897873	3.8003016	4.360377	4.17209
AT3G13910	AT3G13910	1.7850595	2.0809877	2.3887258	2.3715057
AT3G13930	AT3G13930	5.916098	5.9687333	6.351902	6.35288
AT3G14530	AT3G14530	-3.5000086	-2.7813864	-1.2594733	-1.0359089
CYP72A13	AT3G14660	5.5383606	5.5506263	6.0572047	5.9130616
AT3G15630	AT3G15630	3.846264	3.9221773	4.4121757	4.361259
AT3G15710	AT3G15710	3.3664901	3.6061065	3.8015497	3.7368593
AT3G15750	AT3G15750	0.5682158	0.91116375	1.7120775	1.5118742
DELTA-TIP	AT3G16240	8.03701	8.393481	8.464923	8.615259
AT3G16370	AT3G16370	6.2059956	6.695885	6.8568707	7.0248513
ATMLP		7.4307647	7.426431	8.139308	8.094885
UGT88A1	AT3G16520	4.0347857	4.1066823	4.4748306	4.4716077
AT3G16690	AT3G16690	0.9305149	1.2433019	1.7808652	1.8677119
MTO3	AT3G17390	8.324876	8.408141	8.775569	8.799071
AT3G18320	AT3G18320	-5.0419865	-4.7443757	-2.1952581	-2.5260155
AT3G18420	AT3G18420	3.865097	3.7967675	4.32553	4.076197

AT3G18680	AT3G18680	5.611449	5.5898857	6.0310974	5.9052777
ACT2	AT3G18780	7.1943965	7.3901806	7.541094	7.6840158
AT3G19000	AT3G19000	3.7728117	3.8138206	4.2714705	4.160975
AT3G19010	AT3G19010	3.8358698	4.134557	4.341786	4.5901446
KRP6	AT3G19150	0.43414855	0.5950413	1.383613	1.0917543
AT3G19340	AT3G19340	3.880722	3.9950838	4.2973237	4.2774644
AT3G19400	AT3G19400	2.3475637	2.4748843	3.0071285	2.9800494
AT3G19508	AT3G19508	1.5428457	1.6233867	2.2122848	2.0155704
AT3G19520	AT3G19520	3.3894112	3.4247086	3.870409	3.8141012
NDR1	AT3G20600	-0.680198	-0.08063672	0.690018	0.43461064
AT3G20810	AT3G20810	2.4533684	2.5679145	3.5792506	3.4103594
AT3G21770	AT3G21770	3.8770561	4.119044	4.4571266	4.4587917
PMH1	AT3G22310	4.457786	4.2642555	4.9316216	4.7447815
ATRPABC24.3	AT3G22320	4.819673	4.8841424	5.2224174	5.100675
AT3G22845	AT3G22845	4.530765	4.651629	4.911812	4.826635
ARFC1	AT3G22950	3.1024425	3.3175888	3.5709229	3.6293974
AtRLP38	AT3G23120	-5.0419865	-5.128377	-2.4409134	-4.054336
RNR2	AT3G23580	2.9760406	2.6735942	3.4945176	3.1080396
AT3G23620	AT3G23620	5.0308914	4.9866967	5.4314475	5.288051
AT3G23740	AT3G23740	1.5470146	1.9029468	2.2306132	2.0970967
SBP3	AT3G23800	2.243447	2.1799304	2.7916985	2.6961746
RTFL16	AT3G25717	3.1266098	3.3628693	3.8312855	3.5541108
AT3G26020	AT3G26020	3.0441885	3.0803688	3.5446093	3.546198
AT3G26115	AT3G26115	1.1794168	1.1271046	1.952804	1.7361518
CYP71B20	AT3G26180	3.0666082	3.322273	3.694785	3.6958177
CYP71B23	AT3G26210	1.7967978	1.9884924	2.4383137	2.5678062
CYP71B37	AT3G26330	1.6583852	1.9314022	2.428724	2.4760542
AT3G26780	AT3G26780	4.324741	4.435999	4.694367	4.7481823
AT3G27770	AT3G27770	5.0640264	5.197383	5.5191445	5.451901
AT3G29410	AT3G29410	3.4205344	3.6002655	4.0848074	4.0929403
AT3G44590	AT3G44590	3.7668488	3.7811763	4.2556295	4.2195306
AT3G45080	AT3G45080	0.1975772	0.42565897	1.4256209	1.2319702
AT3G46020	AT3G46020	0.030568143	0.2663814	1.0298256	1.0499105
AT3G46330	AT3G46330	-0.95366216	-1.5379906	0.2803031	-0.2636535
AT3G47347	AT3G47347	-3.607318	-2.576483	-0.4620342	-0.79790753
AT3G47370	AT3G47370	5.733874	5.7843184	6.265186	6.189901
CHL	AT3G47860	3.9810226	4.120678	4.4991326	4.478321
CYP71A21	AT3G48320	1.4393525	1.8291813	2.5266044	2.3729334
PDE312	AT3G48500	5.707504	5.540329	6.1169086	5.8946786
AT3G48740	AT3G48740	5.314781	5.08246	5.825447	5.5565915
EMB2261	AT3G49170	1.7023449	1.6103595	2.3906424	2.1776068
AT3G49740	AT3G49740	0.13562164	0.20660688	1.0082527	0.7901676
MAPKKK20	AT3G50310	-2.8333418	-1.9839472	-0.69663984	-0.58690256
HR3	AT3G50470	-2.9541986	-3.1147196	-0.77612895	-1.6383606
AT3G51100	AT3G51100	2.782114	2.8420162	3.327322	3.19788
AT3G51450	AT3G51450	1.6821756	1.8528681	2.4163542	2.5800874
AT3G52040	AT3G52040	3.7420228	3.7816849	4.218759	4.057279
BGAL2	AT3G52840	4.721786	4.836122	5.3323064	5.1858273
AT3G53250	AT3G53250	0.59637624	1.3816243	1.6588186	1.8761021
AT3G53530	AT3G53530	1.5065917	1.5202513	2.3502135	2.142197
AT3G53990	AT3G53990	5.0385985	5.2425346	5.443876	5.474483
ATFER3	AT3G56090	4.3358912	4.314214	4.7858844	4.6314583
AT3G56720	AT3G56720	3.9667552	3.9384882	4.478271	4.3228154
AT3G57340	AT3G57340	3.7040346	3.7387683	4.1332545	4.127131
MBF1B	AT3G58680	5.7222276	5.8213296	6.1324563	6.1473618
ATMRP14	AT3G59140	2.9087012	2.6149511	3.500825	2.9592354
UCC3	AT3G60280	-1.6208652	-1.3483171	0.0023519595	-0.21609838
AT3G60660	AT3G60660	0.7682368	1.1171498	1.6305262	1.6967983
AT3G61100	AT3G61100	2.1396875	2.0644546	2.8094347	2.6047525

ATBZIP53	AT3G62420	4.237368	4.298012	4.6836953	4.601374
CPuORF3	AT3G62422	4.237368	4.298012	4.6836953	4.601374
AT3G62550	AT3G62550	5.2081046	5.3561497	5.8692985	5.7238426
AT3G62630	AT3G62630	2.812271	2.982867	3.3615677	3.3575246
PRP3	AT3G62680	2.9625652	3.2839584	3.9090474	4.1415
AT3G62840	AT3G62840	4.8410373	4.9311824	5.2710757	5.2438602
AT4G00238	AT4G00238	2.9191914	2.8386433	3.4368503	3.2883947
AT4G01870	AT4G01870	5.3916817	5.841046	6.06869	6.2869473
SUS3	AT4G02280	0.9678545	1.0310459	1.7381138	1.7650924
XTH9	AT4G03210	4.9445705	4.6811085	5.4253087	5.038996
APR1	AT4G04610	4.3658714	4.433639	4.809336	4.8454137
ATG8B	AT4G04620	1.704753	1.7021307	2.488956	2.2752326
AT4G04745	AT4G04745	0.03164031	0.6827194	1.1322241	1.3854837
AT4G05400	AT4G05400	3.4808986	3.5042098	3.9117396	3.7865517
AT4G08555	AT4G08555	0.36289632	0.81800294	1.4427704	1.3736973
ATPUP13	AT4G08700	1.6308609	1.6177435	2.4773333	2.2528532
ATMES12	AT4G09900	1.8925434	1.6344256	2.6188323	2.2613523
CYTC-2	AT4G10040	3.3920279	3.5867708	3.9249136	3.9596918
AT4G10650	AT4G10650	-0.147044	-0.27801812	0.81765383	0.24456716
AT4G11290	AT4G11290	3.968795	3.9752476	4.512466	4.3727174
AT4G12170	AT4G12170	0.47078824	0.6409896	1.864006	1.3368893
AT4G13495	AT4G13495	5.3980193	5.3745427	5.967175	5.8387465
MIR850A	AT4G13493	1.538383	1.7124509	2.3485432	2.1591551
NOV	AT4G13750	2.9327385	2.6153831	3.4361517	3.130184
ATGRP2	AT4G13850	6.34791	6.3382263	6.854507	6.7378006
AT4G14230	AT4G14230	3.3267305	3.2727616	3.8379743	3.6304293
XBAT34	AT4G14365	-0.3305235	-0.052269023	0.80708414	1.1205312
ATBET12	AT4G14455	1.8889246	1.919911	2.5417986	2.4114492
AT4G14500	AT4G14500	4.2964253	4.3553066	4.664074	4.646736
AT4G14840	AT4G14840	1.3681222	1.519629	2.0939248	1.9987592
ATCSLB05	AT4G15290	-0.8137107	-0.3056154	0.4974587	0.5674458
AT4G15920	AT4G15920	2.2728312	2.6522195	2.939602	2.9972696
AT4G15975	AT4G15975	-3.223317	-3.428422	-0.95931846	-1.411086
AT4G16563	AT4G16563	1.3669776	1.1707988	2.0415857	1.7891933
PSD1	AT4G16700	1.1010096	1.0350108	1.8418957	1.7408724
AT4G17720	AT4G17720	3.3414814	3.4384854	3.7875392	3.7344475
AT4G17910	AT4G17910	2.3012927	2.3219988	2.844301	2.725958
WRKY28	AT4G18170	0.046438333	0.09486339	1.0102172	0.86521006
AT4G18220	AT4G18220	0.8792731	0.4986981	1.7413858	1.1859053
AT4G18340	AT4G18340	2.0053787	1.9286698	2.6314704	2.3229268
AT4G18590	AT4G18590	3.045271	3.1555688	3.6253784	3.5724869
ERD3	AT4G19120	3.9875317	4.098598	4.485534	4.5444446
AT4G19140	AT4G19140	2.0937498	2.224417	2.6673079	2.7001574
AT4G19880	AT4G19880	5.148855	5.3598123	5.533612	5.5894413
AT4G20330	AT4G20330	3.587038	3.7187521	4.0619807	4.0712776
TUB9	AT4G20890	5.9411902	6.023205	6.3302765	6.36417
AT4G21450	AT4G21450	4.290383	4.4347005	4.8525867	4.825339
AT4G21570	AT4G21570	4.44123	4.4993424	5.0232244	4.8832345
ENDO3	AT4G21590	-2.305021	-1.9332795	0.1258998	-0.61936253
AT4G22110	AT4G22110	-4.078997	-3.3407438	-1.1063294	-1.557052
AT4G22310	AT4G22310	4.8731256	4.95092	5.295849	5.3043933
AT4G23430	AT4G23430	4.2297673	4.3313518	4.6551585	4.6694136
AT4G23450	AT4G23450	-0.89010096	-0.6987438	0.36441198	0.23527108
VHA-G2	AT4G23710	4.188915	4.450752	4.6844444	4.819708
SLY1	AT4G24210	2.5646837	2.2570267	3.2156343	2.6541734
AT4G24860	AT4G24860	-1.3779011	-1.2874533	-0.069521405	-0.23129208
AT4G25090	AT4G25090	2.2915404	2.735326	2.9835637	3.0945299
AT4G26010	AT4G26010	3.4256897	3.6103284	4.216928	4.464867
AT4G26120	AT4G26120	0.09050321	0.052559327	1.0054222	0.9203536

UKL4	AT4G26510	4.106626	4.1548314	4.5137544	4.4749165
AT4G26810	AT4G26810	0.84230036	0.9930826	1.9174489	1.6477183
AT4G27100	AT4G27100	0.8235132	0.9035101	1.6487385	1.5753622
AT4G27130	AT4G27130	5.0578675	5.1385064	5.490027	5.4634767
AT4G27380	AT4G27380	2.9432907	2.9994733	3.4284592	3.2719715
BGLU9	AT4G27820	2.642484	2.7053204	3.2053623	3.0001528
AT4G28450	AT4G28450	4.047655	3.9559133	4.5087	4.2962875
AT4G28820	AT4G28820	0.8036223	1.1525165	1.6316046	1.4427913
AT4G29700	AT4G29700	3.354122	3.7969177	4.017053	4.305251
RUXF	AT4G30220	4.4754834	4.505051	4.8528147	4.8255906
AT4G30500	AT4G30500	1.1915671	1.2583079	1.8993746	1.6464485
AT4G30530	AT4G30530	5.290837	5.366611	5.7288795	5.7009277
AT4G30650	AT4G30650	3.479088	3.640928	4.1959844	4.132913
AT4G30993	AT4G30993	3.3357747	3.4189737	3.8992298	3.6798525
AT4G31050	AT4G31050	1.8861092	2.0115535	2.492891	2.279173
AT4G31600	AT4G31600	1.9309689	2.0474145	2.507937	2.3865287
AT4G32350	AT4G32350	1.9917184	2.0591586	2.6431053	2.5680516
AtLa1	AT4G32720	5.1064763	5.0136976	5.484464	5.33951
AT4G33625	AT4G33625	4.061191	4.2609115	4.680708	4.6018867
AT4G33980	AT4G33980	1.0633483	1.1262162	2.0233514	1.8403789
AT4G33985	AT4G33985	-0.4844016	-0.1714788	0.6448825	0.6656206
COW1	AT4G34580	1.8529619	2.029393	2.5076494	2.6503003
ATB2	AT4G34590	3.439453	3.1684234	3.9026186	3.5631268
CPuORF2	AT4G34588	3.439453	3.1684234	3.9026186	3.5631268
AT4G34770	AT4G34770	2.3320227	2.4197488	2.9393914	2.9155557
AT4G34910	AT4G34910	3.4654863	3.4231682	3.9033089	3.6633737
AT4G34950	AT4G34950	4.6624475	4.578501	5.3765693	5.066698
MSI3	AT4G35050	3.2366211	3.1243286	3.7369916	3.5864174
XCP1	AT4G35350	2.9288712	2.9349575	3.44259	3.3755968
MRPL11	AT4G35490	3.867281	3.883632	4.313616	4.2715664
AT4G35850	AT4G35850	4.8123965	4.723012	5.171535	5.044867
ROT3	AT4G36380	3.5995567	3.69493	4.0295634	3.9356077
ACD2	AT4G37000	3.095101	3.3026552	3.5658052	3.4661396
AT4G37190	AT4G37190	2.3770316	2.4187777	2.920943	2.8466272
AT4G37230	AT4G37230	-5.0419865	-4.360375	-2.5051284	-4.633325
NAGS2	AT4G37670	1.4742867	1.4038461	2.2685993	2.1056235
AT4G38010	AT4G38010	-0.31111243	-0.26063892	0.71734065	0.45787415
AT4G38020	AT4G38020	2.1803827	2.1986315	2.8058157	2.6586
AT4G38370	AT4G38370	2.283163	2.3349793	2.8149192	2.7506378
AT4G38890	AT4G38890	4.3514476	4.2075524	4.7488275	4.6067452
AT4G39740	AT4G39740	1.1973385	1.18966	1.9245925	1.7370113
DHS1	AT4G39980	5.4156895	5.2357864	5.7727885	5.61606
AT4G40065	AT4G40065	1.6204262	1.6661109	2.2497835	2.0124338
AT5G01015	AT5G01015	0.23075569	0.63577443	1.1763363	1.1684775
AT5G01350	AT5G01350	4.388083	4.4008174	4.8326554	4.7415357
ATROPGEF7	AT5G02010	2.081978	2.0422304	2.6412802	2.4997146
AT5G03285	AT5G03285	-1.7382078	-1.8164471	0.103687376	-0.36206457
ATRAB8C	AT5G03520	4.097388	4.2493258	4.542784	4.538521
AT5G03610	AT5G03610	3.8893774	3.7969437	4.354922	4.202035
ATMDAR2	AT5G03630	6.1643066	6.2822757	6.502142	6.6104965
NAS1	AT5G04950	4.805535	4.8689055	5.358605	5.161017
AT5G04960	AT5G04960	2.5300748	2.5759056	3.3001373	3.6476133
AT5G06550	AT5G06550	2.755036	2.5494258	3.3693192	3.0470793
AT5G07580	AT5G07580	3.3399143	3.405227	3.911967	3.8694465
AT5G08180	AT5G08180	5.32884	5.3217683	5.777872	5.6993504
AT5G08330	AT5G08330	3.2683325	3.729497	3.8126452	4.0620017
AT5G08350	AT5G08350	0.23575325	0.78814656	1.2819251	1.2204925
AtAGAL1	AT5G08380	3.3651514	3.3958023	3.860323	3.8089235
PEP7	AT5G09978	-0.6815662	-0.5812605	0.6317279	0.20974624

AT5G10600	AT5G10600	-0.08324238	0.2724817	0.8787551	1.0360256
KNAT4	AT5G11060	2.805046	2.8424733	3.3108728	3.0116894
AT5G11070	AT5G11070	2.129488	1.9469151	2.8126297	2.2322276
AT5G11240	AT5G11240	3.857128	3.7525065	4.292313	4.041001
AGP15	AT5G11740	6.4983463	6.678552	7.021045	7.076756
AT5G12950	AT5G12950	4.6488285	4.6227794	5.1750584	4.96242
PBS3	AT5G13320	-2.782674	-1.49747	-0.7298185	-1.2388717
AT5G14360	AT5G14360	-0.5927223	-0.9839473	0.529051	0.0035559486
AT5G16930	AT5G16930	2.9789398	2.9365094	3.5257463	3.3477976
AT5G18180	AT5G18180	-2.7260325	-1.7159208	-0.6709617	-1.307406
AT5G18490	AT5G18490	1.7381926	1.8340273	2.427271	2.3029845
AT5G18540	AT5G18540	0.7016978	0.83858794	1.7685852	1.5316948
AT5G19550	AT5G19550	5.302763	5.248198	5.7369857	5.6167583
AT5G21100	AT5G21100	3.3382118	3.0575993	3.9311235	3.4182446
AT5G21482	AT5G21482	1.7566538	1.6672899	2.5954654	2.2142868
AT5G22100	AT5G22100	3.3613608	3.4427035	3.9072955	3.8281946
AT5G22920	AT5G22920	4.5695667	4.5403724	5.1565228	5.037742
PYRD	AT5G23300	3.7174196	3.6227367	4.164455	4.042658
MIA40	AT5G23395	2.2925375	2.361227	3.1102886	2.8356457
AT5G23510	AT5G23510	1.4209124	1.6037288	2.2062247	2.1756842
VSP2	AT5G24770	-2.2085187	-1.83991	0.15478201	0.33296996
AT5G25210	AT5G25210	1.3342584	1.064535	2.0301037	1.621987
AT5G25930	AT5G25930	1.987485	2.2696075	2.685423	2.677914
AT5G26300	AT5G26300	-3.8899834	-3.1789348	-0.58711547	-1.011242
AT5G26690	AT5G26690	-4.991319	-3.3914115	-2.2262948	-2.613694
AT5G27280	AT5G27280	3.2680016	3.427035	3.8262126	3.873399
DES1	AT5G28030	0.44323233	0.28856674	1.3920225	0.9180587
AT5G35190	AT5G35190	1.9502143	2.3857758	3.0997436	3.4487982
AT5G35220	AT5G35220	4.7554564	4.682277	5.1770835	5.0060554
AT5G35490	AT5G35490	0.38873276	0.61640406	1.6960527	1.3911501
AT5G35910	AT5G35910	4.4307194	4.339888	4.805704	4.6935782
CAM1	AT5G37780	5.231477	5.170385	5.6360145	5.5111756
AT5G40530	AT5G40530	2.2500582	2.3610332	2.8311756	2.6821544
PBB2	AT5G40580	4.2989006	4.494152	4.6928654	4.7743115
AT5G41040	AT5G41040	2.4344938	2.7359924	3.0466652	2.8545742
AT5G41060	AT5G41060	2.8185303	2.7784967	3.302824	3.2344043
AT5G41080	AT5G41080	2.0200622	2.2009513	2.6876287	2.5836632
AT5G42150	AT5G42150	3.5225255	3.5348854	4.0246177	3.9313595
AT5G42420	AT5G42420	3.5563872	3.6399033	4.0521636	4.043939
AT5G43580	AT5G43580	3.4356089	3.5129735	4.0393624	4.004387
AT5G43780	AT5G43780	4.3966837	4.42956	4.838442	4.8835893
AT5G44005	AT5G44005	0.7324748	0.93011135	1.6116058	1.3734742
AT5G44010	AT5G44010	0.2705742	0.37499127	1.2844545	1.060429
AT5G44020	AT5G44020	6.53994	6.7490807	7.1159725	7.0627894
EDA23	AT5G44700	-2.1666753	-1.4136238	-0.56083184	-0.8643846
OSB3	AT5G44785	3.9622166	3.860729	4.354571	4.0052934
NRPC2	AT5G45140	4.0255313	3.6752548	4.4616256	4.1157093
AT5G46550	AT5G46550	2.768054	2.7360477	3.2699363	3.1630375
AT5G46850	AT5G46850	0.7788064	0.8947118	1.6048037	1.4258361
VAM3	AT5G46860	4.039532	4.1350684	4.4985924	4.50811
GATA27	AT5G47140	2.236077	2.4814165	2.8223827	2.6696548
CYP705A5	AT5G47990	3.4375584	3.9891236	5.0131783	4.984533
CYP708A2	AT5G48000	3.5580084	3.7489374	4.8718104	4.750965
AT5G48655	AT5G48655	2.5127914	2.6117601	3.047984	2.9941757
AT5G48790	AT5G48790	3.049163	3.2022953	3.7626379	3.65895
AT5G49015	AT5G49015	1.0965027	1.1666528	1.9393158	1.8599826
AT5G49080	AT5G49080	1.182352	1.4301463	2.4264786	2.7090538
AT5G49410	AT5G49410	0.7837053	0.7726324	1.6459398	1.3457035
UBC33	AT5G50430	2.9488442	3.0849113	3.459077	3.5004027



AT5G50460	AT5G50460	4.6798763	4.707215	5.0487976	4.9477496
ERD1	AT5G51070	5.194916	5.205813	5.5770364	5.6004148
AT5G51310	AT5G51310	-0.68985766	-0.048162255	0.71163225	0.8202336
AT5G51960	AT5G51960	2.4314747	2.6148872	2.9808357	2.912358
AT5G52450	AT5G52450	2.1541622	1.7653681	2.7747688	2.2876434
ATCNGC4	AT5G54250	3.4551556	2.9580486	4.0615373	3.2511795
AT5G54530	AT5G54530	0.7057629	0.93534154	1.5276499	1.5764953
AT5G54870	AT5G54870	3.6723251	3.7441723	4.1532083	4.166364
CNX5	AT5G55130	2.908123	2.916087	3.4854314	3.325733
FTSZ1-1	AT5G55280	5.18734	5.156734	5.5852923	5.5231957
AT5G55510	AT5G55510	2.8659198	2.9588041	3.442786	3.1808898
AT5G55960	AT5G55960	2.6671827	2.6863778	3.1871436	3.0894804
PFK7	AT5G56630	4.1947465	4.2892594	4.722899	4.713184
CYP81F2	AT5G57220	-0.14604314	-0.113781355	1.0097728	0.8095271
CIPK21	AT5G57630	3.239762	3.3483016	3.9404328	3.7323267
AT5G57780	AT5G57780	2.6352117	3.1284177	3.276904	3.425193
APO2	AT5G57930	5.0844655	5.0167236	5.5241637	5.3821683
PMR5	AT5G58600	2.1739042	2.3269107	2.8322906	2.7146533
AT5G59530	AT5G59530	-2.1160076	-1.49747	-0.35198465	-0.229289
AALP	AT5G60360	6.5562587	6.6223216	7.014362	6.9774437
ARF4	AT5G60450	3.8428414	3.4764726	4.352836	3.8229733
AT5G60610	AT5G60610	-1.599862	-1.0762273	-0.18064241	-0.25070545
AT5G61820	AT5G61820	5.4658923	5.5491257	6.008614	5.8229213
TUB2	AT5G62690	6.569994	6.62714	6.986545	7.0417023
AT5G63290	AT5G63290	1.2577292	1.2517432	1.988133	1.5967745
FLS5	AT5G63600	4.3718305	4.184052	5.007893	4.648123
MRH3	AT5G65090	0.09474856	-0.2410077	1.0461706	0.6089429
AT5G65205	AT5G65205	0.42627573	0.3905547	1.35014	0.91930056
AT5G66470	AT5G66470	4.5786357	4.525786	5.030918	4.9178033
AT5G66530	AT5G66530	4.7096596	4.7919593	5.2816434	5.167178
DAR3	AT5G66640	-3.9406512	-2.9763737	-1.3152571	-1.0975481
AT5G66790	AT5G66790	0.5169099	0.83800536	1.3605442	1.5174408
skS17	AT5G66920	4.3863354	4.3967094	4.761804	4.6273084
RHS19	AT5G67400	3.26171	3.4658864	4.366518	4.5991073
ATARLA1D	AT5G67560	3.925854	4.096679	4.3904986	4.29265
AT5G67630	AT5G67630	3.5894651	3.4036329	4.048729	3.850331