

Appendix A. Differentially expressed genes (DEGs) identified in *Minc03329* ectopic expressing *Arabidopsis thaliana* lines.

GeneID	logFC	PValue	FDR
At5G65080	3.976350799	1.50E-20	1.38E-16
At3G56600	2.279972268	0.001154836	0.068754011
At3G11340	2.167759991	5.71E-06	0.001280792
At4G37990	2.002147294	0.005233407	0.1626525
At5G65070	1.986602988	0.000245863	0.023853869
At1G18310	1.985201659	0.00083132	0.054637704
At2G07708	1.965555502	0.00649793	0.185307214
At3G26830	1.96204015	2.01E-08	1.23E-05
At4G04223	1.938760777	7.70E-05	0.009866146
At5G50360	1.917821492	0.014515561	0.283161536
At5G51990	1.870498531	4.66E-09	3.89E-06
At1G10585	1.85281892	0.004817129	0.155829358
At4G25490	1.795420395	4.94E-17	2.94E-13
At4G12735	1.778614402	0.001244359	0.072066519
At2G14247	1.671980482	0.004387088	0.148488835
At1G36622	1.666365311	4.74E-06	0.001129397
At5G12020	1.656866172	0.009741586	0.227522526
At4G25480	1.646960797	2.60E-05	0.004310793
AtCG00950	1.625319744	0.000947091	0.060092788
At4G25780	1.602116414	1.23E-07	5.77E-05
At3G10280	1.599846176	0.008535515	0.213819314
At1G19210	1.543421817	6.40E-17	2.94E-13
At4G25470	1.511158945	1.55E-14	5.69E-11
AtMG01330	1.489209915	0.002549449	0.108466915
At3G15420	1.486643865	0.009206789	0.221323825
At3G02840	1.48323875	1.33E-13	3.48E-10
At3G48480	1.470533069	0.006941589	0.189584589
At2G27420	1.464193696	8.96E-13	1.64E-09
At1G62510	1.462455899	1.15E-11	1.62E-08
AtMG00580	1.460506028	0.005499319	0.168609382
At5G46295	1.459954096	3.54E-06	0.000954334
At1G60190	1.432612466	1.08E-24	1.98E-20
At1G06283	1.428911636	0.003688606	0.1357223
At5G06790	1.419738693	2.46E-07	0.00010244
At1G26790	1.415911489	0.001789363	0.087497462
At1G60460	1.402709021	0.035717492	0.433455762
At3G14630	1.397875277	0.000183997	0.018744194
At1G69485	1.381404833	0.009866775	0.228732043
At5G03395	1.380178424	0.003498762	0.132009882
At3G47660	1.364310201	0.0090719	0.22033301

At4G21323	1.353072343	0.011565461	0.249794894
At3G56790	1.35013856	5.85E-05	0.008006709
At1G59920	1.347373209	0.002653545	0.111857599
At3G01940	1.342332034	0.019366864	0.325807504
At2G35070	1.340879746	0.003768446	0.138051397
At3G21890	1.330406714	0.0130665	0.268911789
At2G44995	1.309496348	0.018249131	0.316588761
At3G21660	1.296197148	0.007078943	0.190722075
At3G03025	1.292661473	0.0259556	0.377436831
At5G42450	1.291235796	0.008288088	0.211153587
At3G44350	1.286923543	0.002145941	0.097401281
At3G13590	1.278454909	0.010244002	0.234219786
At2G06002	1.271433087	0.094621887	0.631370996
At1G42980	1.267446451	0.001311866	0.07424597
At1G33612	1.251959649	0.068404195	0.564331132
AtCG00100	1.242264944	0.004166392	0.144969901
At5G60100	1.23109957	0.024275335	0.364957972
At1G14260	1.222808496	0.006772846	0.18732079
At1G73040	1.202899125	0.019516556	0.326856412
At1G65500	1.201854482	0.000397381	0.033226726
At5G03210	1.199331731	2.64E-12	4.03E-09
At1G15580	1.189877172	0.019252794	0.32459921
At1G61470	1.186912069	6.20E-11	8.13E-08
At4G24580	1.186017574	3.44E-05	0.005345698
At3G48240	1.181721001	0.00011678	0.013526699
At1G47395	1.171286405	0.020658644	0.337026299
At2G30424	1.146371385	0.001053418	0.063750914
At5G42760	1.143586181	0.000217585	0.021336144
At1G61550	1.136455337	0.127839818	0.688232076
At1G01520	1.131933496	7.09E-07	0.000251337
At5G44568	1.118424654	1.56E-08	1.06E-05
At1G57630	1.111639362	0.016993451	0.307296326
At5G55950	1.111623209	0.038678053	0.452898755
At4G27657	1.104866094	4.98E-14	1.52E-10
At5G51440	1.101731308	0.000114199	0.013466072
At3G01840	1.098871747	0.000368086	0.031540139
At4G13800	1.090812232	0.003364434	0.127995072
At3G04060	1.090695041	0.009039266	0.220142761
At5G66740	1.084732672	0.001038879	0.063079212
At3G09870	1.084277768	0.000964333	0.060973944
At5G45630	1.081492249	1.61E-12	2.68E-09
At4G05685	1.080913031	0.03317189	0.420950131
At1G74453	1.0769626	0.003318972	0.127322165

At5G10280	1.075108964	0.048137516	0.497132035
At3G25880	1.073458336	0.052679487	0.512730232
At5G63130	1.065384633	6.07E-07	0.000227058
AtMG00180	1.065055458	0.015434175	0.291090337
AtCG00030	1.058764729	0.021109517	0.340906213
At3G55580	1.056686864	0.000419325	0.034326636
At4G14450	1.055225011	0.000657238	0.045824258
At1G30860	1.047554467	0.014046476	0.278454312
At2G42280	1.047098459	0.001432212	0.077470399
At5G35480	1.046716028	0.000571748	0.041603757
At3G03965	1.046052267	0.046783289	0.49161328
At5G05300	1.041547632	0.002702209	0.112871104
At4G12470	1.036501014	0.000416738	0.034326636
At4G11910	1.035999116	0.086439297	0.607759736
At1G74930	1.030377773	5.46E-13	1.11E-09
At2G46790	1.020797401	2.73E-08	1.46E-05
At3G02850	1.020084758	0.04448454	0.480679441
At1G04220	1.013997241	0.100734477	0.640070978
At2G46940	1.012399277	0.009976973	0.229833869
At4G14548	1.012331264	0.0091233	0.220704427
At4G15248	1.009884718	5.73E-06	0.001280792
At4G12320	1.008421634	6.73E-09	5.28E-06
At5G55010	1.007706112	0.07331762	0.576017652
AtMG00160	1.006360348	0.077937335	0.587063772
At3G10910	1.005681933	0.019662649	0.327181484
At5G26731	1.005561496	0.023714243	0.362071668
At3G17185	1.004251556	4.29E-05	0.006402703
AtCG00580	1.003335071	0.048110857	0.497132035
At1G50910	1.001548784	0.012492967	0.262409549
At1G13710	-1.00040974	0.004134094	0.144476134
At5G11620	-1.00187645	0.077921273	0.587063772
At3G09940	-1.00188844	0.000969593	0.060973944
At1G62440	-1.00552266	1.38E-05	0.00263933
At1G26820	-1.00584707	0.05761233	0.529769567
At5G03790	-1.00738973	0.067256109	0.560559762
At2G26310	-1.00764498	0.085757842	0.605272505
At4G16447	-1.01038479	0.025287612	0.372448953
At2G27880	-1.01197277	0.238793892	0.819300091
At1G13600	-1.01253385	0.007614841	0.199811317
At5G02515	-1.01834481	0.028558857	0.395436615
At1G64260	-1.02622665	0.051452608	0.509297695
At5G51480	-1.02704941	0.068790011	0.564331132
At5G19110	-1.03101643	0.001025053	0.062446501

At3G04030	-1.03456831	0.024942069	0.371235977
At1G52820	-1.03584156	0.062580686	0.543994904
At5G48170	-1.0389251	0.118401926	0.674588982
At5G06250	-1.04136313	0.064929138	0.552485201
At3G24860	-1.04993862	0.000847537	0.055307085
At5G55250	-1.05903367	0.00032689	0.028818224
At4G11140	-1.06186363	0.006667675	0.18732079
At1G35230	-1.06245118	0.016778399	0.305476294
At1G04660	-1.06481266	0.002257587	0.100912029
At3G62020	-1.06570656	0.001335643	0.07460227
At2G34790	-1.07127857	0.047010964	0.492594315
At1G69180	-1.07262293	0.289464683	0.862514445
At1G76930	-1.07577031	3.74E-06	0.000978558
At3G47340	-1.08389397	3.78E-10	3.85E-07
At2G46970	-1.0854685	0.035575907	0.432972404
At5G67550	-1.0864521	0.094443901	0.631370996
At5G24780	-1.0886636	0.00044484	0.035934039
At1G66830	-1.08946216	0.098889248	0.638272489
At1G53160	-1.09140154	0.038946987	0.454220816
At2G41240	-1.09800708	0.253487772	0.829734534
At5G63090	-1.0981997	0.002125392	0.096948536
At1G53700	-1.09903615	0.001309647	0.07424597
At3G17280	-1.1013211	0.041672024	0.464522734
At4G09950	-1.10134268	0.003891126	0.138909646
At5G43890	-1.10183191	0.04740306	0.493673442
At3G05980	-1.10403341	0.034429903	0.426870267
At1G12160	-1.1046417	0.024731448	0.369300131
At5G41160	-1.10669788	0.133204731	0.69615136
At5G47600	-1.11142116	0.097466917	0.634538145
At3G11050	-1.11285003	0.032293289	0.4149699
At1G05260	-1.11883177	0.019196764	0.32459921
At5G38940	-1.12118231	0.066169218	0.557347242
At3G48185	-1.13514355	0.015597391	0.292445227
At2G48090	-1.13592569	0.033032371	0.420388586
At5G39220	-1.14318331	0.040926035	0.461836503
At1G29430	-1.14511396	0.002258635	0.100912029
At1G05420	-1.14926313	0.052517516	0.511425223
At1G21310	-1.15099924	1.92E-05	0.00331305
At2G45220	-1.154396	0.00030977	0.027981543
At3G05790	-1.18938773	0.083036901	0.597587272
At4G03450	-1.20253605	0.019469661	0.326856412
At5G19100	-1.20322081	0.000145655	0.015821934
At5G62360	-1.20624958	0.000213062	0.021004943

At4G12500	-1.20796236	0.009537969	0.225575023
At4G18250	-1.21299901	0.012512866	0.262526806
At2G34530	-1.21432859	0.014586438	0.28364225
At3G55970	-1.21766217	0.000199458	0.019986157
At1G29270	-1.21989662	0.009358401	0.222863625
At2G23620	-1.22938236	0.051765472	0.509297695
At1G44970	-1.23709783	0.015144393	0.288522226
At5G52900	-1.23900974	1.73E-09	1.59E-06
At4G15280	-1.24155327	0.009818521	0.227907466
At1G22340	-1.26030649	0.009462688	0.224763361
At5G26220	-1.26444524	0.004670006	0.153191245
At3G27150	-1.26548044	0.012462162	0.262062688
At1G47560	-1.26879859	0.012688905	0.264104941
At4G18960	-1.2691265	0.025911101	0.377088771
At4G12870	-1.27093672	0.02081866	0.33813266
At2G19970	-1.28167738	0.001209899	0.070881535
At1G67260	-1.28512223	0.033355032	0.421814642
At1G14240	-1.29811811	0.002275757	0.101287767
At5G61120	-1.31469377	0.041559956	0.463837439
At2G47670	-1.32576162	0.014669809	0.284821271
At1G13320	-1.32715145	2.76E-13	6.33E-10
At5G64910	-1.33203555	0.002782027	0.115283289
At5G49120	-1.34134058	0.004577963	0.152416493
At1G34460	-1.34637678	5.12E-05	0.007338351
At1G32970	-1.37013101	0.007452953	0.197207497
At1G50040	-1.37755543	0.000780751	0.052634664
At3G59270	-1.38363107	0.029543183	0.400230934
At4G28720	-1.38513975	0.003820457	0.138724194
At3G03850	-1.38873652	0.010859938	0.239926117
At2G48130	-1.39974479	0.004388992	0.148488835
At1G24577	-1.40009507	0.014929666	0.286965708
At2G44910	-1.40347359	6.91E-09	5.28E-06
At4G38860	-1.40596482	9.76E-09	7.16E-06
At2G32100	-1.41205131	2.55E-10	2.76E-07
At1G24260	-1.43218321	0.021440599	0.343561671
At5G20240	-1.43443044	0.035219111	0.431693068
At1G69120	-1.4364703	0.077140736	0.584516396
At1G33960	-1.44866249	0.009568889	0.225649121
At3G59190	-1.46731109	0.011730119	0.252163179
At3G54340	-1.47820823	0.071482656	0.570338334
At4G32280	-1.4878878	2.61E-05	0.004310793
At3G03820	-1.51268799	5.61E-06	0.001280792
At5G18020	-1.51896924	4.39E-06	0.001079523

At5G18030	-1.52335675	2.04E-05	0.003467337
At5G51950	-1.53593434	0.001984004	0.093357724
At1G02065	-1.56457722	0.00048603	0.037764127
At1G29160	-1.57181734	0.000873821	0.056419912
At3G05727	-1.59770572	3.58E-05	0.005519408
At4G15160	-1.61107364	0.040387461	0.460849324
At1G70880	-1.614025	0.025899901	0.377088771
At4G20050	-1.62365819	0.014189246	0.279471758
At3G59930	-1.68508852	0.020770137	0.337643613
At5G48920	-1.68817047	0.013317546	0.271337601
At3G55940	-1.6962247	0.001349103	0.074965144
At5G18050	-1.71134718	0.000347221	0.030318988
At5G44540	-1.72896883	0.010324591	0.235475166
At3G03200	-1.73805036	0.0084132	0.212130771
At5G20820	-1.8976119	0.002379492	0.104009504
At4G22517	-1.93985443	0.008535131	0.213819314
At3G46280	-1.94461918	0.007083042	0.190722075
At3G27940	-1.99540275	1.55E-05	0.00280664
At1G04180	-2.00094593	2.00E-08	1.23E-05
At1G17030	-2.05162899	0.010814144	0.239517602
At2G39030	-2.13569887	1.80E-07	8.06E-05
At4G15210	-2.13959569	0.004779152	0.155657742
At2G16910	-2.15958758	0.03174418	0.412104179
At5G52160	-2.19588948	0.082925687	0.597518951
At3G55720	-2.38900157	1.19E-05	0.00234638
At2G26010	-2.53723078	0.024513382	0.366940308
At1G43800	-2.54243771	0.003337809	0.127777454
At3G13220	-2.5440889	0.001176195	0.069474441
At5G44420	-2.65730638	0.009626175	0.225748863
At4G34850	-2.67510036	0.00123045	0.071729659
At5G26730	-2.7827225	0.001440959	0.077714289
At2G14610	-3.07706611	8.24E-05	0.010284085
At3G42960	-3.11742568	0.001702593	0.085770462
At3G15400	-3.13206812	8.24E-06	0.001736114
At1G62940	-3.28952561	0.002481067	0.10704783
At1G69500	-3.56461934	0.000931125	0.059412468
At5G62080	-3.6585029	0.00129421	0.073723931
At3G11980	-3.8479091	0.000577357	0.041690588
At4G14080	-4.10875932	0.002507649	0.107436356
At3G01345	-4.24880701	2.09E-07	8.93E-05
At5G07230	-4.26344425	0.00028172	0.026222875
At4G18190	-4.50741244	0.000129424	0.014559751
At4G28395	-7.07773911	7.65E-06	0.00163196

At1G47980	-7.8356502	6.05E-07	0.000227058
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Appendix B. Pathways enrichment of differentially expressed genes (DEGs) which identified in *Minc03329* ectopic expressing *Arabidopsis thaliana* lines.

Bincode	Bin name	GeneID	Type	Descript	LogFC
hormone signaling					
auxins					
17.2.2	hormone metabolism. auxin. signal transduction	At3G25880	Transcript	auxin-resistance protein, putative chr3:9469713-9470033 REVERSE	1.0734583
17.2.3	hormone metabolism. auxin. induced-regulated-responsive-activated	At3G03850	Transcript	auxin-responsive protein, putative chr3:983121-983751 FORWARD	-1.3887365
17.2.3	hormone metabolism. auxin. induced-regulated-responsive-activated	At5G20820	Transcript	auxin-responsive protein-related chr5:7046751-7047396 REVERSE	-1.8976119
17.2.3	hormone metabolism. auxin. induced-regulated-responsive-activated	At3G03820	Transcript	auxin-responsive protein, putative chr3:976933-977223 REVERSE	-1.512688
17.2.3	hormone metabolism. auxin. induced-regulated-responsive-activated	At1G53700	Transcript	Symbols: WAG1, PK3AT WAG1 (WAG 1); kinase/ protein serine/threonine kinase chr1:20048586-20050115 FORWARD	-1.0990361
17.2.3	hormone metabolism. auxin. induced-regulated-responsive-activated	At4G38860	Transcript	auxin-responsive protein, putative chr4:18130268-18131060 FORWARD	-1.4059649
17.2.3	hormone metabolism. auxin. induced-regulated-responsive-activated	At1G29430	Transcript	auxin-responsive family protein chr1:10302650-10303335 REVERSE	-1.145114
17.2.3	hormone metabolism. auxin. induced-regulated-responsive-activated	At5G18050	Transcript	auxin-responsive protein, putative chr5:5974567-5975054 REVERSE	-1.7113472
17.2.3	hormone metabolism. auxin. induced-regulated-responsive-activated	At3G09870	Transcript	auxin-responsive family protein chr3:3027424-3027957 REVERSE	1.0842777
17.2.3	hormone metabolism. auxin. induced-regulated-responsive-activated	At5G18020	Transcript	auxin-responsive protein, putative chr5:5966183-5966677 REVERSE	-1.5189693

17.2.3	hormone metabolism. auxin. induced-regulated-responsive-activated	At5G18030	Transcript	auxin-responsive protein, putative chr5:5968435-5968938 FORWARD	-1.5233568
17.8.1	hormone metabolism. salicylic acid. synthesis-degradation	At5G55250	Transcript	Symbols: IAMT1 IAMT1 (IAA CARBOXYLMETHYLTRANSFERASE 1); S-adenosylmethionine-dependent methyltransferase/ indole acetic acid carboxyl methyltransferase chr5:22407473-22410944 REVERSE	-1.0590336
Signaling and MAPK					
30.2.3	signalling. receptor kinases. leucine rich repeat III	At1G66830	Transcript	leucine-rich repeat transmembrane protein kinase, putative chr1:24930665-24932918 REVERSE	-1.0894622
30.2.15	signalling. receptor kinases. thaumatin like	At4G18250	Transcript	receptor serine/threonine kinase, putative chr4:10087343-10091963 REVERSE	-1.212999
30.2.24	signalling. receptor kinases. S-locus glycoprotein like	At1G61550	Transcript	S-locus protein kinase, putative chr1:22704198-22707826 REVERSE	1.1364553
30.2.99	signalling. receptor kinases. misc	At3G46280	Transcript	protein kinase-related chr3:17005483-17008424 REVERSE	-1.9446192
30.2.99	signalling. receptor kinases. misc	At3G01840	Transcript	protein kinase family protein chr3:296582-298648 REVERSE	1.0988717
30.4	signalling. phosphoinositides	At3G56600	Transcript	inositol or phosphatidylinositol kinase/ phosphotransferase, alcohol group as acceptor chr3:20968444-20970913 FORWARD	2.2799723
30.4.4	signalling. phosphoinositides. phosphoinositide phospholipase C	At3G55940	Transcript	phosphoinositide-specific phospholipase C, putative chr3:20747787-20750184 FORWARD	-1.6962247
30.6	signalling. MAP kinases	At5G11620	Transcript	SWIM zinc finger family protein / mitogen-activated protein kinase kinase kinase	-1.0018765

				(MAPKKK)-related chr5:3739013-3740146 REVERSE	
30.8	signalling. misc	At2G48090	Transcript	unknown protein chr2:19669110-19669764 REVERSE	-1.1359257
30.99	signalling. unspecified	At4G24580	Transcript	Symbols: REN1 REN1 (ROP1 ENHANCER 1); Rho GTPase activator/ Rho GTPase binding / phosphoinositide binding chr4:12687879-12694248 REVERSE	1.1860176
20.1.3	stress.biotic.signalling	At1G33960	Transcript	Symbols: AIG1 AIG1 (AVRRPT2-INDUCED GENE 1); GTP binding chr1:12346232-12348513 FORWARD	-1.4486625
30.6	signalling. MAP kinases	At5G11620	Transcript	SWIM zinc finger family protein / mitogen-activated protein kinase kinase kinase (MAPKKK)-related chr5:3739013-3740146 REVERSE	-1.0018765
transcription factors					
ERF					
27.3.3	RNA. regulation of transcription. AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	At4G25470	Transcript	Symbols: CBF2, DREB1C, FTQ4, ATCBF2 CBF2 (C-REPEAT/DRE BINDING FACTOR 2); DNA binding / transcription activator/ transcription factor chr4:13015277-13016220 REVERSE	1.511159
27.3.3	RNA. regulation of transcription. AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	At1G19210	Transcript	AP2 domain-containing transcription factor, putative chr1:6626822-6627530 REVERSE	1.5434219
27.3.3	RNA. regulation of transcription. AP2/EREBP,	At5G51990	Transcript	Symbols: CBF4, DREB1D CBF4 (C-	1.8704985

	APETALA2/Ethylene-responsive element binding protein family			REPEAT-BINDING FACTOR 4); DNA binding / transcription activator/ transcription factor chr5:21117113-21117787 REVERSE	
27.3.3	RNA. regulation of transcription. AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	At4G25480	Transcript	Symbols: DREB1A, CBF3, ATCBF3 DREB1A (DEHYDRATION RESPONSE ELEMENT B1A); DNA binding / transcription activator/ transcription factor chr4:13018214-13019121 REVERSE	1.6469609
27.3.3	RNA. regulation of transcription. AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	At4G11140	Transcript	Symbols: CRF1 CRF1 (CYTOKININ RESPONSE FACTOR 1); DNA binding / transcription factor chr4:6794776-6795793 REVERSE	-1.0618637
27.3.3	RNA. regulation of transcription. AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	At1G74930	Transcript	Symbols: ORA47 ORA47; DNA binding / transcription factor chr1:28144132-28145049 FORWARD	1.0303777
27.3.3	RNA. regulation of transcription. AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	At4G25490	Transcript	Symbols: CBF1, DREB1B, ATCBF1 CBF1 (C-REPEAT/DRE BINDING FACTOR 1); DNA binding / transcription activator/ transcription factor chr4:13021780-13022725 REVERSE	1.7954204
27.3.35	RNA. regulation of transcription. bZIP transcription factor family	At1G13600	Transcript	Symbols: AtbZIP58 AtbZIP58 (Arabidopsis thaliana basic leucine-zipper 58); DNA binding / protein heterodimerization/ protein homodimerization/ transcription factor chr1:4650787-4651469 REVERSE	-1.0125339
27.3.25	RNA. regulation of transcription. MYB domain transcription factor family	At5G10280	Transcript	Symbols: MYB92, ATMYB92, ATMYB64 ATMYB92 (MYB DOMAIN PROTEIN 92); DNA binding / transcription factor chr5:3232569-3234210 FORWARD	1.075109

27.3.25	RNA. regulation of transcription. MYB domain transcription factor family	At3G04030	Transcript	myb family transcription factor chr3:1042882-1044697 REVERSE	-1.0345683
27.3.25	RNA. regulation of transcription. MYB domain transcription factor family	At2G30424	Transcript	Symbols: TCL2 TCL2 (TRICHOMELESS 2); DNA binding chr2:12964506-12965468 REVERSE	1.1463714
27.3.26	RNA. regulation of transcription. MYB-related transcription factor family	At1G01520	Transcript	myb family transcription factor chr1:190596-192139 FORWARD	1.1319335
27.3.8	RNA. regulation of transcription. C2C2(Zn) DOF zinc finger family	At1G26790	Transcript	Dof-type zinc finger domain-containing protein chr1:9273857-9275312 REVERSE	1.4159114
27.3.8	RNA. regulation of transcription. C2C2(Zn) DOF zinc finger family	At1G29160	Transcript	Dof-type zinc finger domain-containing protein chr1:10183797-10184324 REVERSE	-1.5718174
abiotic stress					
20.2.1	stress. abiotic. heat	At5G47600	Transcript	heat shock protein-related chr5:19299782-19300499 REVERSE	-1.1114211
20.2.1	stress. abiotic. heat	At5G51440	Transcript	23.5 kDa mitochondrial small heat shock protein (HSP23.5-M) chr5:20891163-20892211 FORWARD	1.1017313
20.2.1	stress. abiotic. heat	At5G12020	Transcript	Symbols: HSP17.6II HSP17.6II (17.6 KDA CLASS II HEAT SHOCK PROTEIN) chr5:3882237-3882938 REVERSE	1.6568662
20.2.2	stress. abiotic. cold	At1G05260	Transcript	Symbols: RCI3, RCI3A RCI3 (RARE COLD INDUCIBLE GENE 3); peroxidase chr1:1529767-1531439 FORWARD	-1.1188318
20.2.99	stress. abiotic. unspecified	At3G62020	Transcript	Symbols: GLP10 GLP10 (GERMIN-LIKE PROTEIN 10); manganese ion binding / nutrient	-1.0657066

				reservoir chr3:22971358-22972268 REVERSE	
20.2.99	stress. abiotic. unspecified	At1G70880	Transcript	Bet v I allergen family protein chr1:26722881-26723778 REVERSE	-1.614025
20.2.99	stress. abiotic. unspecified	At5G38940	Transcript	manganese ion binding / nutrient reservoir chr5:15588757-15589666 FORWARD	-1.1211823
cell wall					
10.5.1	cell wall. cell wall proteins. AGPs	At1G35230	Transcript	Symbols: AGP5 AGP5 (ARABINO GALACTAN-PROTEIN 5) chr1:12917149-12917763 FORWARD	-1.0624511
10.5.3	cell wall. cell wall proteins. LRR	At1G62440	Transcript	Symbols: LRX2 LRX2 (LEUCINE-RICH REPEAT/EXTENSIN 2); protein binding / structural constituent of cell wall chr1:23111818-23115293 FORWARD	-1.0055226
10.5.4	cell wall. cell wall proteins. HRGP	At1G21310	Transcript	Symbols: ATEXT3, RSH ATEXT3 (EXTENSIN 3); structural constituent of cell wall chr1:7453236-7455009 REVERSE	-1.1509992
10.5.4	cell wall. cell wall proteins. HRGP	At1G76930	Transcript	Symbols: ATEXT4, ORG5, ATEXT1 ATEXT4 (EXTENSIN 4); structural constituent of cell wall chr1:28895301-28896883 REVERSE	-1.0757703
10.8.99	cell wall. pectin esterases. misc	At2G45220	Transcript	pectinesterase family protein chr2:18644084-18646447 REVERSE	-1.154396
26.4.1	misc. beta 1,3 glucan hydrolases. glucan endo-1,3-beta-glucosidase	At4G14080	Transcript	Symbols: MEE48 MEE48 (maternal effect embryo arrest 48); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds chr4:8118537-8120358 REVERSE	-4.1087594

proteolysis					
29.5.1	protein. degradation. subtilases	At1G32970	Transcript	subtilase family protein chr1:11948721-11951982 REVERSE	-1.370131
29.5.1	protein. degradation. subtilases	At4G21323	Transcript	subtilase family protein chr4:11342494-11345632 FORWARD	1.3530723
29.5.3	protein. degradation. cysteine protease	At2G27420	Transcript	cysteine proteinase, putative chr2:11726144-11727614 REVERSE	1.4641937
29.5.5	protein. degradation. serine protease	At3G05790	Transcript	Symbols: LON4 LON4 (LON PROTEASE 4); ATP binding / ATP-dependent peptidase/ nucleoside-triphosphatase/ nucleotide binding / serine-type endopeptidase/ serine-type peptidase chr3:1720154-1725182 REVERSE	-1.1893877
29.5.11	protein. degradation. ubiquitin	At3G21660	Transcript	UBX domain-containing protein chr3:7624495-7626654 REVERSE	1.2961972
29.5.11.4.2	protein. degradation. ubiquitin. E3. RING	At1G14260	Transcript	zinc finger (C3HC4-type RING finger) family protein chr1:4872856-4874907 FORWARD	1.2228085
29.5.11.4.2	protein. degradation. ubiquitin. E3. RING	At1G60190	Transcript	armadillo/beta-catenin repeat family protein / U-box domain-containing protein chr1:22198403-22200678 FORWARD	1.4326124
29.5.11.4.2	protein. degradation. ubiquitin. E3. RING	At1G30860	Transcript	protein binding / zinc ion binding chr1:10986523-10989504 REVERSE	1.0475545
29.5.11.4.2	protein. degradation. ubiquitin. E3. RING	At3G10910	Transcript	zinc finger (C3HC4-type RING finger) family protein chr3:3412911-3414019 REVERSE	1.005682
29.5.11.4.3.2	protein. degradation. ubiquitin. E3. SCF. FBOX	At3G17280	Transcript	F-box family protein chr3:5903453-5904613 REVERSE	-1.1013211

29.5.11.4.3.2	protein. degradation. ubiquitin. E3. SCF. FBOX	At5G48170	Transcript	Symbols: SLY2 SLY2 (SLEEPY2) chr5:19532537-19533265 REVERSE	-1.038925
29.5.11.4.3.2	protein. degradation. ubiquitin. E3. SCF. FBOX	At3G59190	Transcript	F-box family protein chr3:21884527-21886776 FORWARD	-1.4673111
29.5.11.4.3.2	protein. degradation. ubiquitin. E3. SCF. FBOX	At3G27150	Transcript	kelch repeat-containing F-box family protein chr3:10009442-10011641 REVERSE	-1.2654804
Resporatory burst					
21.2.1	redox. ascorbate and glutathione. ascorbate	At3G09940	Transcript	Symbols: MDHAR, ATMDAR3 MDHAR (MONODEHYDROASCORBATE REDUCTASE); monodehydroascorbate reductase (NADH) chr3:3056375-3059148 REVERSE	-1.0018884
26.12	misc. peroxidases	At1G44970	Transcript	peroxidase, putative chr1:17002117-17003688 FORWARD	-1.2370979
PR-protein					
20.1.7	stress. biotic. PR-proteins	At1G57630	Transcript	disease resistance protein (TIR class), putative chr1:21345639-21346157 FORWARD	1.1116394
20.1.7.12	stress. biotic. PR-proteins. plant defensins	At5G44420	Transcript	Symbols: PDF1.2, PDF1.2A, LCR77 PDF1.2 chr5:17907069-17907598 REVERSE	-2.6573064
20.1.7.12	stress. biotic. PR-proteins. plant defensins	At3G59930	Transcript	Encodes a defensin-like (DEFL) family protein. chr3:22139551-22140320 REVERSE	-1.6850885
20.1.7.12	stress. biotic. PR-proteins. plant defensins	At2G26010	Transcript	Symbols: PDF1.3 PDF1.3 (plant defensin 1.3) chr2:11087348-11087944 FORWARD	-2.5372307
heat shock protein					

20.2.1	stress. abiotic. heat	At5G47600	Transcript	heat shock protein-related chr5:19299782-19300499 REVERSE	-1.1114211
20.2.1	stress. abiotic. heat	At5G51440	Transcript	23.5 kDa mitochondrial small heat shock protein (HSP23.5-M) chr5:20891163-20892211 FORWARD	1.1017313
20.2.1	stress. abiotic. heat	At5G12020	Transcript	Symbols: HSP17.6II HSP17.6II (17.6 KDA CLASS II HEAT SHOCK PROTEIN) chr5:3882237-3882938 REVERSE	1.6568662
secondary metabolism					
16.2	secondary metabolism. phenylpropanoids	At1G62940	Transcript	Symbols: ACOS5 ACOS5 (ACYL-COA SYNTHETASE 5); 4-coumarate-CoA ligase/ long-chain-fatty-acid-CoA ligase/ medium-chain-fatty-acid-CoA ligase chr1:23310535-23312747 FORWARD	-3.2895255
16.2.1.10	secondary metabolism. phenylpropanoids. lignin biosynthesis. CAD	At4G37990	Transcript	Symbols: ELI3-2, ELI3, ATCAD8, CAD-B2 ELI3-2 (ELICITOR-ACTIVATED GENE 3-2); aryl-alcohol dehydrogenase/ mannitol dehydrogenase chr4:17855876-17857639 FORWARD	2.0021472
16.8.1	secondary metabolism. flavonoids. anthocyanins	At3G55970	Transcript	oxidoreductase, 2OG-Fe(II) oxygenase family protein chr3:20766735-20769324 REVERSE	-1.2176622
16.8.2	secondary metabolism. flavonoids. chalcones	At4G34850	Transcript	chalcone and stilbene synthase family protein chr4:16608313-16609829 FORWARD	-2.6751003
receptor					
30.2.99	signalling. receptor kinases. misc	At3G46280	Transcript	protein kinase-related chr3:17005483-17008424	-1.9446192

				REVERSE	
30.2.15	signalling. receptor kinases. thaumatin like	At4G18250	Transcript	receptor serine/threonine kinase, putative chr4:10087343-10091963 REVERSE	-1.212999
30.2.3	signalling. receptor kinases. leucine rich repeat III	At1G66830	Transcript	leucine-rich repeat transmembrane protein kinase, putative chr1:24930665-24932918 REVERSE	-1.0894622
30.2.99	signalling. receptor kinases. misc	At3G01840	Transcript	protein kinase family protein chr3:296582-298648 REVERSE	1.0988717
30.2.24	signalling. receptor kinases. S-locus glycoprotein like	At1G61550	Transcript	S-locus protein kinase, putative chr1:22704198-22707826 REVERSE	1.1364553
cellular response					
biotic stress					
20.1	stress. biotic	At3G02840	Transcript	immediate-early fungal elicitor family protein chr3:618409-619686 FORWARD	1.4832387
20.1	stress. biotic	At2G14610	Transcript	Symbols: PR1, PR 1, ATPR1 PR1 (PATHOGENESIS-RELATED GENE 1) chr2:6241704-6242463 REVERSE	-3.0770662
20.1	stress. biotic	At4G09950	Transcript	avirulence-responsive family protein / avirulence induced gene (AIG1) family protein chr4:6234762-6236312 FORWARD	-1.1013427
20.1	stress. biotic	At2G19970	Transcript	pathogenesis-related protein, putative chr2:8623730-8624476 REVERSE	-1.2816774
20.1	stress. biotic	At4G25780	Transcript	pathogenesis-related protein, putative chr4:13121068-13121955 FORWARD	1.6021165
20.1.3	stress. biotic. signalling	At1G33960	Transcript	Symbols: AIG1 AIG1 (AVRRPT2-INDUCED	-1.4486625

				GENE 1); GTP binding chr1:12346232-12348513 FORWARD	
20.1.7	stress. biotic. PR-proteins	At1G57630	Transcript	disease resistance protein (TIR class), putative chr1:21345639-21346157 FORWARD	1.1116394
20.1.7.12	stress. biotic. PR-proteins. plant defensins	At5G44420	Transcript	Symbols: PDF1.2, PDF1.2A, LCR77 PDF1.2 chr5:17907069-17907598 REVERSE	-2.6573064
20.1.7.12	stress. biotic. PR-proteins. plant defensins	At3G59930	Transcript	Encodes a defensin-like (DEFL) family protein. chr3:22139551-22140320 REVERSE	-1.6850885
20.1.7.12	stress. biotic. PR-proteins. plant defensins	At2G26010	Transcript	Symbols: PDF1.3 PDF1.3 (plant defensin 1.3) chr2:11087348-11087944 FORWARD	-2.5372307
31.2	cell. division	At3G55580	Transcript	regulator of chromosome condensation (RCC1) family protein chr3:20612700-20615920 FORWARD	1.0566869
31.2	cell. division	At3G47660	Transcript	Ran GTPase binding / chromatin binding / zinc ion binding chr3:17571192-17574805 FORWARD	1.3643101
33.1	development. storage proteins	At5G24780	Transcript	Symbols: VSP1, ATVSP1 VSP1 (VEGETATIVE STORAGE PROTEIN 1); acid phosphatase/ transcription factor binding chr5:8507590-8508957 REVERSE	-1.0886636
33.3	development. squamosa promoter binding like (SPL)	At1G53160	Transcript	Symbols: SPL4 SPL4 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 4); DNA binding / transcription factor chr1:19806419-19807608 FORWARD	-1.0914016
33.3	development. squamosa promoter binding like (SPL)	At1G02065	Transcript	Symbols: SPL8 SPL8 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 8); DNA binding chr1:365209-367340 FORWARD	-1.5645772

33.99	development. unspecified	At3G15400	Transcript	Symbols: ATA20 ATA20 chr3:5201644-5203197 FORWARD	-3.1320682
33.99	development. unspecified	At2G27880	Transcript	Symbols: AGO5 AGO5 (ARGONAUTE 5); nucleic acid binding chr2:11871488-11876894 FORWARD	-1.0119728
33.99	development. unspecified	At3G54340	Transcript	Symbols: AP3, ATAP3 AP3 (APETALA 3); DNA binding / transcription factor chr3:20119173-20121170 REVERSE	-1.4782082
33.99	development. unspecified	At5G49120	Transcript	senescence-associated protein-related chr5:19908626-19909399 REVERSE	-1.3413405
33.99	development. unspecified	At3G03200	Transcript	Symbols: anac045 anac045 (Arabidopsis NAC domain containing protein 45); transcription factor chr3:736141-738527 REVERSE	-1.7380503
33.99	development. unspecified	At4G18960	Transcript	Symbols: AG AG (AGAMOUS); DNA binding / transcription factor chr4:10382856-10388539 FORWARD	-1.2691265
33.99	development. unspecified	At1G05420	Transcript	Symbols: ATOFP12, OFP12 OFP12 (OVATE FAMILY PROTEIN 12) chr1:1590073-1590753 FORWARD	-1.1492631
33.99	development. unspecified	At3G04060	Transcript	Symbols: anac046 anac046 (Arabidopsis NAC domain containing protein 46); transcription factor chr3:1053366-1055163 REVERSE	1.090695
33.99	development. unspecified	At5G20240	Transcript	Symbols: PI PI (PISTILLATA); DNA binding / transcription factor chr5:6829042-6831515 FORWARD	-1.4344305
33.99	development. unspecified	At3G11980	Transcript	Symbols: MS2, FAR2 MS2 (MALE STERILITY	-3.8479092

				2); fatty acyl-CoA reductase (alcohol-forming)/ oxidoreductase, acting on the CH-CH group of donors, NAD or NADP as acceptor chr3:3814236-3817117 FORWARD	
33.99	development. unspecified	At1G69120	Transcript	Symbols: AP1, AGL7 AP1 (APETALA1); DNA binding / protein binding / protein heterodimerization/ transcription activator/ transcription factor chr1:25982330-25986313 REVERSE	-1.4364703
33.99	development. unspecified	At3G44350	Transcript	Symbols: anac061 anac061 (Arabidopsis NAC domain containing protein 61); transcription factor chr3:16022836-16024487 REVERSE	1.2869235
26.7	misc. oxidases - copper, flavone etc.	At5G51480	Transcript	Symbols: SKS2 SKS2 (SKU5 SIMILAR 2); copper ion binding / oxidoreductase chr5:20910244-20913451 FORWARD	-1.0270494
26.7	misc. oxidases - copper, flavone etc.	At1G04180	Transcript	flavin-containing monooxygenase family protein / FMO family protein chr1:1104623-1105988 FORWARD	-2.000946
26.7	misc. oxidases - copper, flavone etc.	At4G28720	Transcript	flavin-containing monooxygenase family protein / FMO family protein chr4:14192583-14194256 FORWARD	-1.3851397
26.7	misc. oxidases - copper, flavone etc.	At1G12160	Transcript	flavin-containing monooxygenase family protein / FMO family protein chr1:4126066-4128310 FORWARD	-1.1046417
26.7	misc. oxidases - copper, flavone etc.	At5G43890	Transcript	Symbols: YUC5, SUPER1 YUCCA5; monooxygenase chr5:17648857-17650131	-1.1018319

				REVERSE	
26.8	misc. nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases	At2G23620	Transcript	Symbols: ATMES1, MES1 MES1 (METHYL ESTERASE 1); hydrolase, acting on ester bonds / methyl indole-3-acetate esterase/ methyl jasmonate esterase/ methyl salicylate esterase chr2:10047379-10049291 REVERSE	-1.2293824
26.8	misc. nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases	At5G51950	Transcript	glucose-methanol-choline (GMC) oxidoreductase family protein chr5:21105909-21108605 REVERSE	-1.5359343
26.8	misc. nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases	At2G34790	Transcript	Symbols: MEE23, EDA28 MEE23 (MATERNAL EFFECT EMBRYO ARREST 23); FAD binding / catalytic/ electron carrier/ oxidoreductase chr2:14673840-14677270 REVERSE	-1.0712786
16.2	secondary metabolism. phenylpropanoids	At1G62940	Transcript	Symbols: ACOS5 ACOS5 (ACYL-COA SYNTHETASE 5); 4-coumarate-CoA ligase/ long-chain-fatty-acid-CoA ligase/ medium-chain-fatty-acid-CoA ligase chr1:23310535-23312747 FORWARD	-3.2895255
16.2.1.10	secondary metabolism. phenylpropanoids. lignin biosynthesis. CAD	At4G37990	Transcript	Symbols: ELI3-2, ELI3, ATCAD8, CAD-B2 ELI3-2 (ELICITOR-ACTIVATED GENE 3-2); aryl-alcohol dehydrogenase/ mannitol dehydrogenase chr4:17855876-17857639 FORWARD	2.0021472
transcription factors					
27.3.1	RNA. regulation of transcription. ABI3/VP1-related	At5G06250	Transcript	transcription factor chr5:1892714-1894124	-1.0413631

	B3-domain-containing transcription factor family			REVERSE	
27.3.3	RNA. regulation of transcription. AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	At4G25470	Transcript	Symbols: CBF2, DREB1C, FTQ4, ATCBF2 CBF2 (C-REPEAT/DRE BINDING FACTOR 2); DNA binding / transcription activator/ transcription factor chr4:13015277-13016220 REVERSE	1.511159
27.3.3	RNA. regulation of transcription. AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	At1G19210	Transcript	AP2 domain-containing transcription factor, putative chr1:6626822-6627530 REVERSE	1.5434219
27.3.3	RNA. regulation of transcription. AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	At5G51990	Transcript	Symbols: CBF4, DREB1D CBF4 (C-REPEAT-BINDING FACTOR 4); DNA binding / transcription activator/ transcription factor chr5:21117113-21117787 REVERSE	1.8704985
27.3.3	RNA. regulation of transcription. AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	At4G25480	Transcript	Symbols: DREB1A, CBF3, ATCBF3 DREB1A (DEHYDRATION RESPONSE ELEMENT B1A); DNA binding / transcription activator/ transcription factor chr4:13018214-13019121 REVERSE	1.6469609
27.3.3	RNA. regulation of transcription. AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	At4G11140	Transcript	Symbols: CRF1 CRF1 (CYTOKININ RESPONSE FACTOR 1); DNA binding / transcription factor chr4:6794776-6795793 REVERSE	-1.0618637
27.3.3	RNA. regulation of transcription. AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	At1G74930	Transcript	Symbols: ORA47 ORA47; DNA binding / transcription factor chr1:28144132-28145049 FORWARD	1.0303777
27.3.3	RNA. regulation of transcription. AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	At4G25490	Transcript	Symbols: CBF1, DREB1B, ATCBF1 CBF1 (C-REPEAT/DRE BINDING FACTOR 1); DNA binding / transcription activator/ transcription factor chr4:13021780-13022725 REVERSE	1.7954204

27.3.6	RNA. regulation of transcription. bHLH, Basic Helix-Loop-Helix family	At2G42280	Transcript	basic helix-loop-helix (bHLH) family protein chr2:17611185-17613519 REVERSE	1.0470985
27.3.6	RNA. regulation of transcription. bHLH, Basic Helix-Loop-Helix family	At2G16910	Transcript	Symbols: AMS AMS (ABORTED MICROSPORES); DNA binding / transcription factor chr2:7331721-7334254 FORWARD	-2.1595876
27.3.6	RNA. regulation of transcription. bHLH, Basic Helix-Loop-Helix family	At1G10585	Transcript	transcription factor chr1:3493940-3495144 REVERSE	1.852819
27.3.6	RNA. regulation of transcription. bHLH, Basic Helix-Loop-Helix family	At2G46970	Transcript	Symbols: PIL1 PIL1 (PHYTOCHROME INTERACTING FACTOR 3-LIKE 1); transcription factor chr2:19295490-19297826 REVERSE	-1.0854685
27.3.6	RNA. regulation of transcription. bHLH, Basic Helix-Loop-Helix family	At2G41240	Transcript	Symbols: BHLH100 BHLH100 (BASIC HELIX-LOOP-HELIX PROTEIN 100); DNA binding / transcription factor chr2:17198331-17199320 REVERSE	-1.0980071
27.3.7	RNA. regulation of transcription. C2C2(Zn) CO-like, Constans-like zinc finger family	At3G21890	Transcript	zinc finger (B-box type) family protein chr3:7709113-7709733 REVERSE	1.3304067
27.3.8	RNA. regulation of transcription. C2C2(Zn) DOF zinc finger family	At1G26790	Transcript	Dof-type zinc finger domain-containing protein chr1:9273857-9275312 REVERSE	1.4159114
27.3.8	RNA. regulation of transcription. C2C2(Zn) DOF zinc finger family	At1G29160	Transcript	Dof-type zinc finger domain-containing protein chr1:10183797-10184324 REVERSE	-1.5718174
27.3.10	RNA. regulation of transcription. C2C2(Zn) YABBY family	At1G69180	Transcript	Symbols: CRC CRC (CRABS CLAW); transcription factor chr1:26007465-26009059 REVERSE	-1.0726229
27.3.20	RNA. regulation of transcription. G2-like transcription factor family, GARP	At3G04030	Transcript	myb family transcription factor chr3:1042882-1044697 REVERSE	-1.0345683
27.3.22	RNA. regulation of transcription. HB, Homeobox	At5G03790	Transcript	Symbols: ATHB51, LMI1, HB51 HB51; DNA	-1.0073898

	transcription factor family			binding / sequence-specific DNA binding / transcription factor chr5:1004983-1006373 FORWARD	
27.3.22	RNA. regulation of transcription. HB, Homeobox transcription factor family	At2G44910	Transcript	Symbols: ATHB4, ATHB-4 ATHB4 (ARABIDOPSIS THALIANA HOMEBOX-LEUCINE ZIPPER PROTEIN 4); DNA binding / transcription factor chr2:18517887-18519525 REVERSE	-1.4034736
27.3.24	RNA. regulation of transcription. MADS box transcription factor family	At1G24260	Transcript	Symbols: SEP3, AGL9 SEP3 (SEPALLATA3); DNA binding / protein binding / transcription factor chr1:8593642-8596098 REVERSE	-1.4321831
27.3.24	RNA. regulation of transcription. MADS box transcription factor family	At5G65080	Transcript	Symbols: MAF5, AGL68 MAF5 (MADS AFFECTING FLOWERING 5); transcription factor chr5:25997504-26002465 FORWARD	3.9763508
27.3.24	RNA. regulation of transcription. MADS box transcription factor family	At5G65070	Transcript	Symbols: MAF4, FCL4 MAF4 (MADS AFFECTING FLOWERING 4); transcription factor chr5:25992260-25996134 FORWARD	1.986603
27.3.25	RNA. regulation of transcription. MYB domain transcription factor family	At5G10280	Transcript	Symbols: MYB92, ATMYB92, ATMYB64 ATMYB92 (MYB DOMAIN PROTEIN 92); DNA binding / transcription factor chr5:3232569-3234210 FORWARD	1.075109
27.3.25	RNA. regulation of transcription. MYB domain transcription factor family	At3G04030	Transcript	myb family transcription factor chr3:1042882-1044697 REVERSE	-1.0345683
27.3.25	RNA. regulation of transcription. MYB domain transcription factor family	At2G30424	Transcript	Symbols: TCL2 TCL2 (TRICHOMELESS 2); DNA binding chr2:12964506-12965468 REVERSE	1.1463714

27.3.26	RNA. regulation of transcription. MYB-related transcription factor family	At1G01520	Transcript	myb family transcription factor chr1:190596-192139 FORWARD	1.1319335
27.3.27	RNA. regulation of transcription. NAC domain transcription factor family	At3G03200	Transcript	Symbols: anac045 anac045 (Arabidopsis NAC domain containing protein 45); transcription factor chr3:736141-738527 REVERSE	-1.7380503
27.3.27	RNA. regulation of transcription. NAC domain transcription factor family	At3G44350	Transcript	Symbols: anac061 anac061 (Arabidopsis NAC domain containing protein 61); transcription factor chr3:16022836-16024487 REVERSE	1.2869235
27.3.29	RNA.regulation of transcription.TCP transcription factor family	At1G67260	Transcript	Symbols: TCP1 TCP1; DNA binding / transcription factor chr1:25168228-25169307 REVERSE	-1.2851223
27.3.30	RNA. regulation of transcription. Trihelix, Triple-Helix transcription factor family	At3G24860	Transcript	hydroxyproline-rich glycoprotein family protein chr3:9073623-9074682 FORWARD	-1.0499387
27.3.35	RNA. regulation of transcription. bZIP transcription factor family	At1G13600	Transcript	Symbols: AtbZIP58 AtbZIP58 (Arabidopsis thaliana basic leucine-zipper 58); DNA binding / protein heterodimerization/ protein homodimerization/ transcription factor chr1:4650787-4651469 REVERSE	-1.0125339
27.3.37	RNA. regulation of transcription. AS2, Lateral Organ Boundaries Gene Family	At5G63090	Transcript	Symbols: LOB LOB (LATERAL ORGAN BOUNDARIES) chr5:25308572-25310973 REVERSE	-1.0981997
27.3.37	RNA. regulation of transcription. AS2, Lateral Organ Boundaries Gene Family	At3G27940	Transcript	Symbols: LBD26 LBD26 (LOB DOMAIN-CONTAINING PROTEIN 26) chr3:10373251-10376461 FORWARD	-1.9954028
27.3.40	RNA. regulation of transcription. Aux/IAA family	At1G15580	Transcript	Symbols: IAA5, ATAUX2-27, AUX2-27 IAA5 (INDOLE-3-ACETIC ACID INDUCIBLE 5);	1.1898772

				transcription factor chr1:5365665-5366497 REVERSE	
27.3.40	RNA. regulation of transcription. Aux/IAA family	At4G32280	Transcript	Symbols: IAA29 IAA29 (INDOLE-3-ACETIC ACID INDUCIBLE 29); transcription factor chr4:15583387-15584769 FORWARD	-1.4878879
27.3.66	RNA. regulation of transcription. Psudo ARR transcription factor family	At5G60100	Transcript	Symbols: APRR3, PRR3 APRR3 (ARABIDOPSIS PSEUDO-RESPONSE REGULATOR 3); transcription regulator/ two-component response regulator chr5:24197999-24201364 REVERSE	1.2310996
27.3.66	RNA. regulation of transcription. Psudo ARR transcription factor family	At2G46790	Transcript	Symbols: APRR9, PRR9, TL1 APRR9 (ARABIDOPSIS PSEUDO-RESPONSE REGULATOR 9); protein binding / transcription regulator/ two-component response regulator chr2:19232649-19235087 FORWARD	1.0207974
27.3.70	RNA. regulation of transcription. Silencing Group	At3G17185	Transcript	Symbols: TASIR-ARF, TAS3, ATTAS3 TAS3/TASIR-ARF (TRANS-ACTING SIRNA3); other RNA chr3:5861491-5862437 FORWARD	1.0042516
27.3.99	RNA. regulation of transcription. unclassified	At1G64260	Transcript	zinc finger protein-related chr1:23847756-23849915 FORWARD	-1.0262266
27.3.99	RNA. regulation of transcription. unclassified	At5G06250	Transcript	transcription factor chr5:1892714-1894124 REVERSE	-1.0413631
Protein degradation					
29.5.1	protein. degradation. subtilases	At1G32970	Transcript	subtilase family protein chr1:11948721-11951982 REVERSE	-1.370131
29.5.1	protein. degradation. subtilases	At4G21323	Transcript	subtilase family protein chr4:11342494-11345632	1.3530723

				FORWARD	
29.5.3	protein. degradation. cysteine protease	At2G27420	Transcript	cysteine proteinase, putative chr2:11726144-11727614 REVERSE	1.4641937
29.5.5	protein. degradation. serine protease	At3G05790	Transcript	Symbols: LON4 LON4 (LON PROTEASE 4); ATP binding / ATP-dependent peptidase/ nucleoside-triphosphatase/ nucleotide binding / serine-type endopeptidase/ serine-type peptidase chr3:1720154-1725182 REVERSE	-1.1893877
29.5.11	protein. degradation. ubiquitin	At3G21660	Transcript	UBX domain-containing protein chr3:7624495-7626654 REVERSE	1.2961972
29.5.11.4.2	protein. degradation. ubiquitin. E3. RING	At1G14260	Transcript	zinc finger (C3HC4-type RING finger) family protein chr1:4872856-4874907 FORWARD	1.2228085
29.5.11.4.2	protein. degradation. ubiquitin. E3. RING	At1G60190	Transcript	armadillo/beta-catenin repeat family protein / U-box domain-containing protein chr1:22198403-22200678 FORWARD	1.4326124
29.5.11.4.2	protein. degradation. ubiquitin. E3. RING	At1G30860	Transcript	protein binding / zinc ion binding chr1:10986523-10989504 REVERSE	1.0475545
29.5.11.4.2	protein. degradation. ubiquitin. E3. RING	At3G10910	Transcript	zinc finger (C3HC4-type RING finger) family protein chr3:3412911-3414019 REVERSE	1.005682
29.5.11.4.3.2	protein. degradation. ubiquitin. E3. SCF. FBOX	At3G17280	Transcript	F-box family protein chr3:5903453-5904613 REVERSE	-1.1013211
29.5.11.4.3.2	protein. degradation. ubiquitin. E3. SCF. FBOX	At5G48170	Transcript	Symbols: SLY2 SLY2 (SLEEPY2) chr5:19532537-19533265 REVERSE	-1.038925
29.5.11.4.3.2	protein. degradation. ubiquitin. E3. SCF. FBOX	At3G59190	Transcript	F-box family protein chr3:21884527-21886776 FORWARD	-1.4673111
29.5.11.4.3.2	protein. degradation. ubiquitin. E3. SCF. FBOX	At3G27150	Transcript	kelch repeat-containing F-box family protein	-1.2654804

				chr3:10009442-10011641 REVERSE	
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