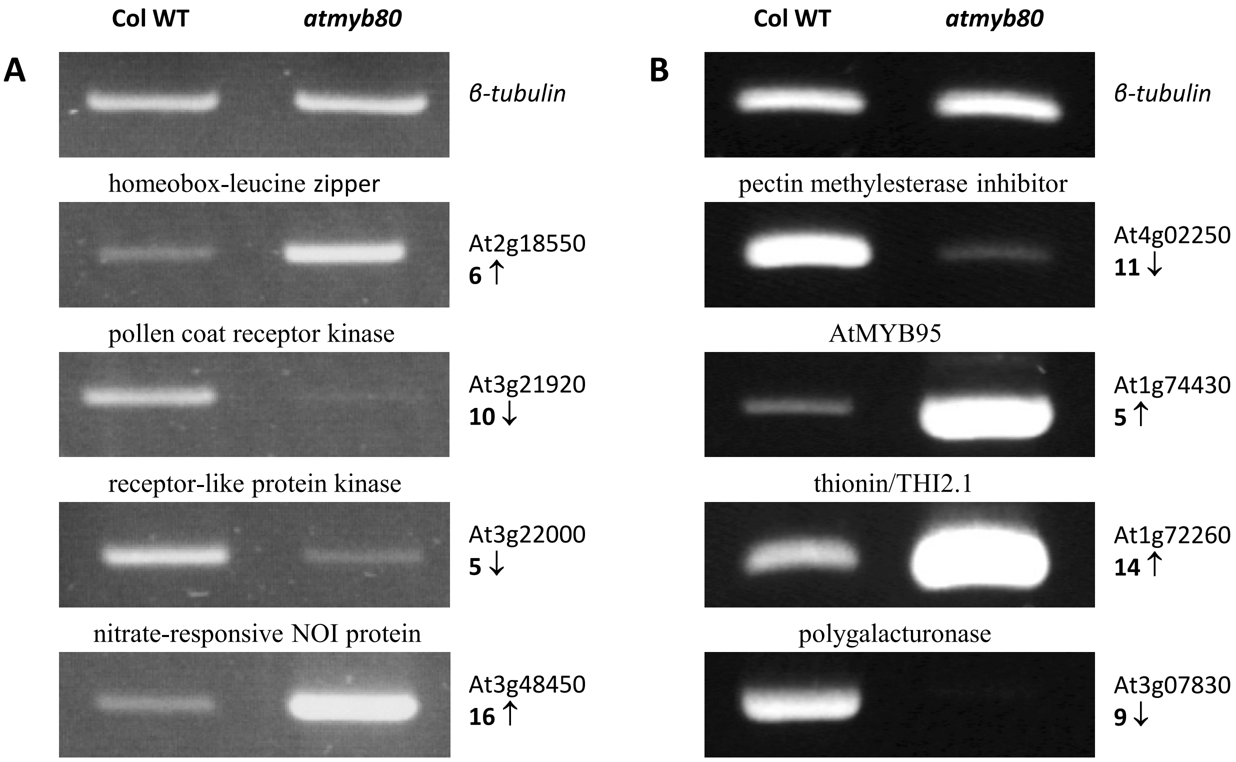
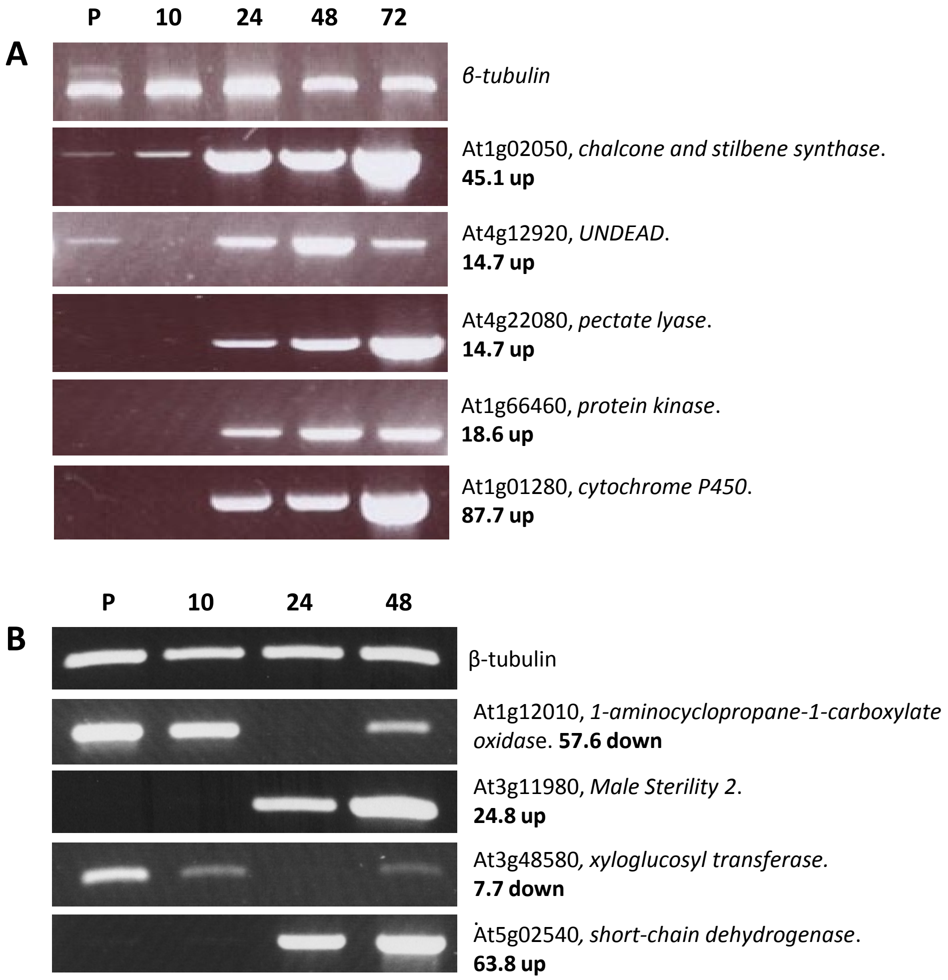
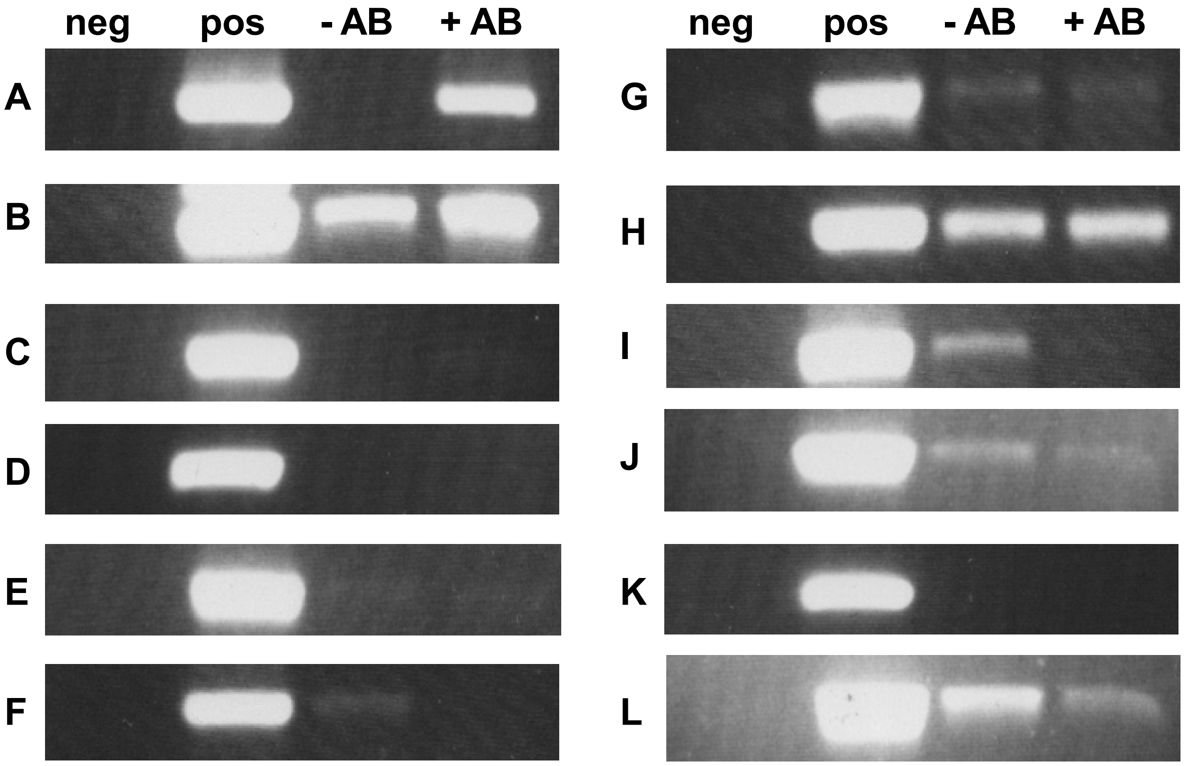
Supplemental Data



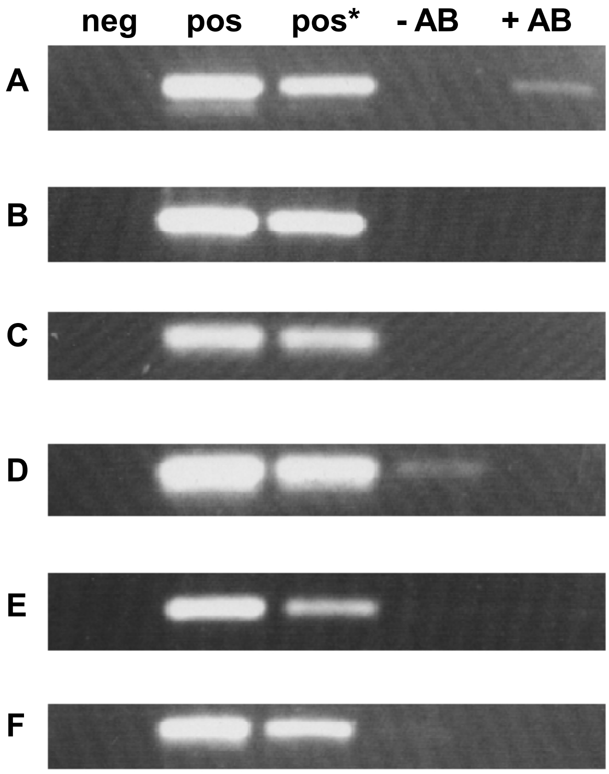
Supplemental Figure 1. RT-PCR analysis to validate the microarray data. RNA was obtained from dissected anthers of stages 5-8. To balance for input cDNA volume, *β-tubulin* amplification was used as a control. Three replicates were performed. A) 30 cycles. B) 32 cycles. Numbers and arrows represent the fold changes based on the microarray data. The RT-PCR result correlates with the fold changes as indicated by the microarray analysis. Primers are presented in Supplemental Table 5 online.



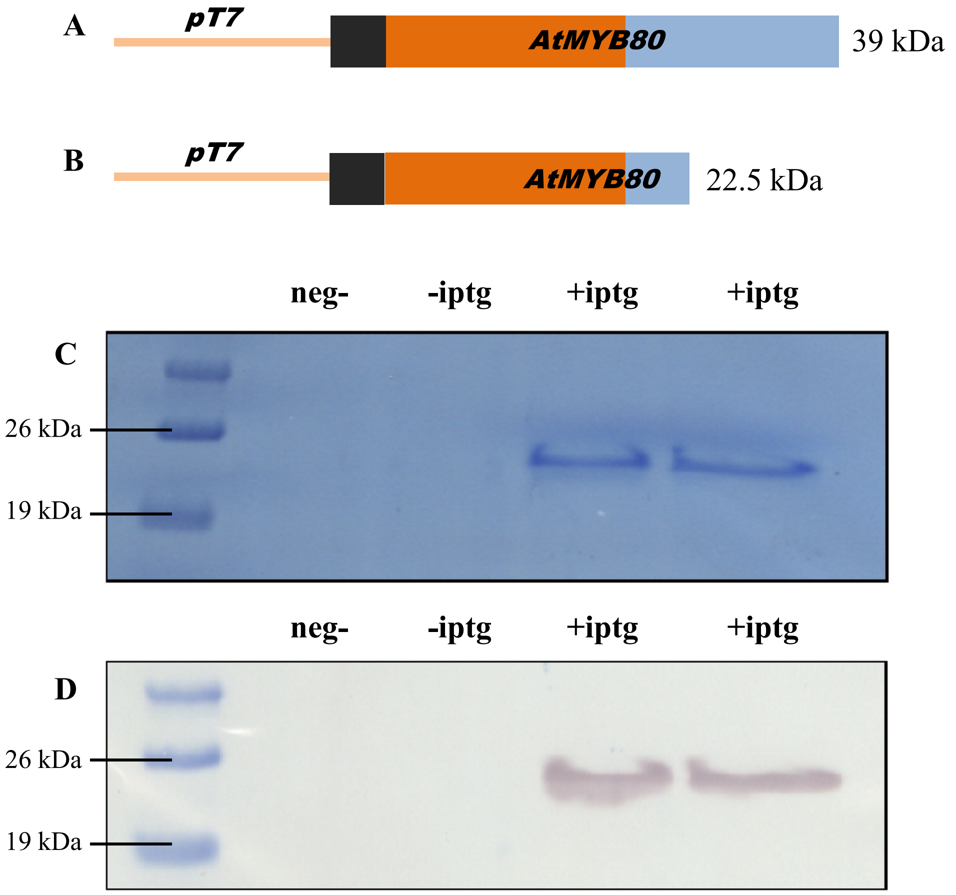
Supplemental Figure 2. RT-PCR analysis to validate the inducible microarray data. RNA was obtained from dissected anthers of stages 5-8. To balance for input cDNA volume, *β-tubulin* amplification was used as a control. Three replicates were performed. A) 32 cycles. B) 30 cycles. Bolded numbers represent the fold changes based on the microarray data at 24 hrs post-DEX induction. The RT-PCR result correlates with the fold changes as indicated by the microarray analysis. P, pre-DEX; 10, 8-10 hrs post-DEX; 24, 22-24 hrs post-DEX; 48, 46-48 hrs post-DEX; 72, 70-72 hrs post-DEX. Primers are presented in Supplemental Table 5 online.



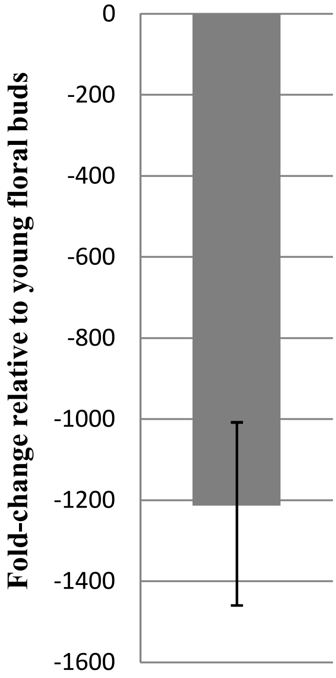
Supplemental Figure 3. ChIP assay using floral buds as input material. Two biological and three technical replicates were performed. A) At4g12920, *Aspartic protease/UNDEAD* is positively enriched. B) At1g67290, *glyoxal oxidase/GLOX1* is positively enriched. C) At5g22260, *Male Sterility 1*. D) At4g14080, *A6* putative callase. E) At3g62180, pectin methylesterase. F) At5g52160, *protease inhibitor*. G) At4g22080*, pectate lyase*. H) At5g09550, *Rab-GDP dissociation inhibitor*. I) At2g47030, *vanguard1 homolog.* J) At3g23770, *glycosyl hydrolase.* K) At4g30040, *aspartyl protease*. L) At5g56110, *MYB80*. neg, no template control; pos, sonicated chromatin control; - AB, no AB final elution; + AB, with anti-GR PA-516 AB final elution. Primers are presented in Supplemental Table 5 online.



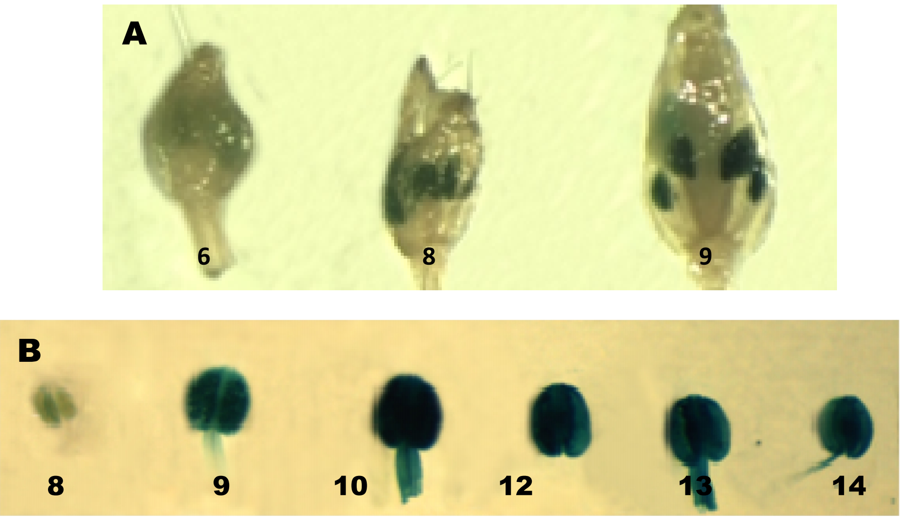
Supplemental Figure 4. ChIP assay using dissected anthers (stages 5 to 8) as input material. Two biological and three technical replicates were performed. A) At2g47040, *VANGUARD1* is enriched in the + AB treatment. B) At1g01280, *Cytochrome p450*. C) At3g11980, *Male Sterility 2*. D) At4g11760, *PCP* pollen coat protein. E) At3g01700, *AGP11* arabinogalactan-protein 11. F) At1g02790, *PGA4* polygalacturonase 4. neg, no template control; pos, sonicated chromatin control; pos*, supernatant from post incubation with protein-A/agarose beads in no AB treatment; - AB, no AB final elution; + AB, with anti-GR PA-516 AB final elution. Primers are presented in Supplemental Table 5 online.



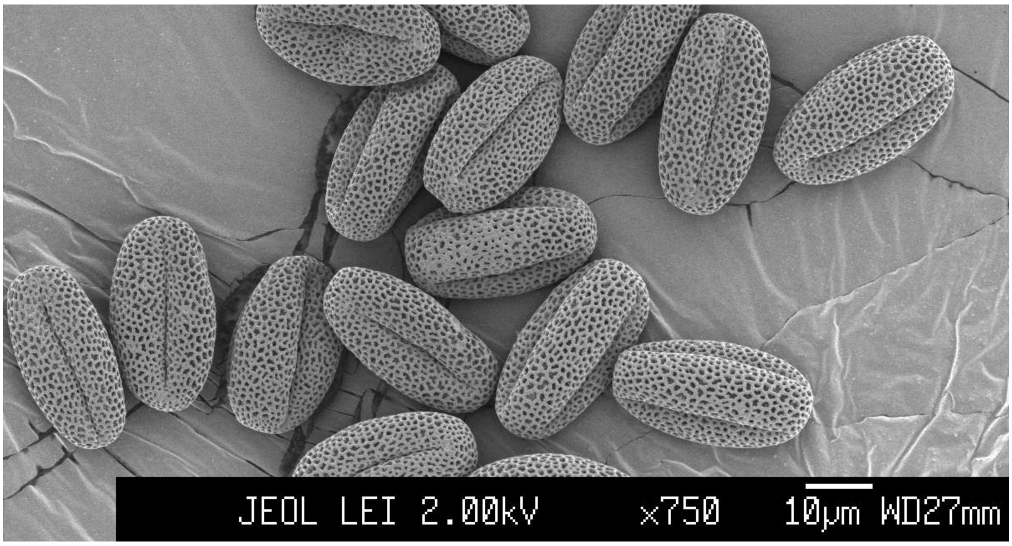
Supplemental Figure 5. Recombinant MYB80 protein expression and purification. A) Full-length *Arabidopsis thaliana MYB80* cDNA was cloned into pRSET-B. B) *MYB80* cDNA truncated in the C-terminal region after the MYB domain was cloned into pRSET-B. C) SDS-PAGE analysis of purified truncated MYB80 protein from *E. coli* resulted in a single band of ~23 kDA in the induced samples but not in the empty vector (neg-) or non induced (-iptg) samples. D) Western blot analysis using the anti-T7 antibody specific for the leader peptides of the recombinant MYB80 protein. Black bar, T7 leader peptides and histidine tag; orange bar, MYB domain; blue bar, MYB80 C-terminal region. The predicted size of both proteins are indicated in kDa.



Supplemental Figure 6. Comparative RT-qPCR analysis of *MYB80* transcript levels in wild-type mature (anther stages 10-12) vs. young (anther stages ≤ 9) floral buds. qPCR data was gathered from 3 replicates. Error bar represent SD. *MYB80* transcript level is lower in mature floral buds.



Supplemental Figure 7. Promoter:*GUS* expression analysis. A) The *UNDEAD* promoter drives GUS activity in anthers at developmental stages 6 to 9. B) The *GLOX1* promoter directs GUS activity in anthers from developmental stage 8 onwards, reaching a peak at stage 10 and persisting to anther dehiscence at stage 14.



Supplemental Figure 8. Scanning electron micrograph of wild-type Arabidopsis pollen grain.

Supplemental Table 1. Summary of T-DNA insertion mutants analysed for phenotypic changes in male fertility. Genes were selected from the *myb80* (10 genes) and the inducible microarray datasets (12 genes). T-DNA lines were germinated on media containing either kanamycin or sulfadiazine to select for transgenic plants. PCR was used to screen for the presence of the T-DNA and to identify homozygous lines. Pollen from homozygous plants were examined for phenotypic changes in morphology and tested for pollen viability by Alexander's staining. Silique elongation was also observed. The primers used in PCR screening are listed. a; gene-specific primers used to identify homozygous lines. Gene specific primer and left border primer (LBa1 or LBb1 for SALK lines and pAC161 8760 primer for GABI-Kat lines) was used to verify the presence of the T-DNA. b; contains T-DNA insertion but failed to grow in the presence of kanamycin.

Locus ID	**Gene description**	**T-DNA line**	**Primers**[a]	**Pollen phenotype**	**Silique phenotype**
At1g02470	expressed protein	SALK_123221	1g024, F & R	Wt	Wt
At1g12010	ACC oxidase, putative	SALK_007181	1g120, F & R	Wt	Wt
At1g23760	polygalacturonase, putative	SALK_086372	1g237, F & R	Wt	Wt
At1g49000	expressed protein	SALK_023230	1g490, F & R	Wt	Wt
At1g52410	protein binding	GABI-Kat 299G09	1g524, F & R	Wt	Wt
At1g74430	MYB95	NASC_314F0	74430+1F, +1710R	Wt	Wt
At2g13570	CCAAT-box	SALK_130081[b]	13570-429F, +648R	Wt	Wt
At2g18550	transcription factor	SAIL_790_D09	2g185, F & R	Wt	Wt
At2g35930	U-box domain protein	SALK_063470	2g359, F & R	Wt	Wt
At3g17220	pectin methylesterase inhibitor	NASC_227H0	17220+1F, +522R	Wt	Wt
At3g21920	pollen coat	SALK_050491	3g219, F & R	Wt	Wt
At3g22000	protein kinase	GABI_215A11	3g220, F & R	Wt	Wt
At3g25730	AP2	SALK_007234[b]	25730+1F, +1115R	Wt	Wt
At3g23770	glycosyl hydrolase family 17	SALK_033100	3g237, F & R	Wt	Wt
At3g48450	nitrate response	SALK_077128	3g484, F & R	Wt	Wt
At3g62230	F-box	SALK_020875	62230+1F, +1386R	Wt	Wt
At4g02250	pectin methylesterase inhibitor	SALK_139236	02250+1F, +438R	Wt	Wt
At5g02540	short-chain hydrogenase reductase	SALK_103967	5g025, F & R	Wt	Wt
At5g24870	zinc finger family protein	SALK_015310	5g248, F & R	Wt	Wt
At5g45840	LRR protein kinase	SALK_054077	5g458, F & R	Wt	Wt
At5g48880	PKT1, 3-ketoacyl-CoA thiolase	SALK_144464	5g488, F & R	Wt	Wt
At5g51830	pfkB-type kinase family protein	SALK_046463	5g518, F & R	Wt	Wt

Supplemental Table 2. Genes identified to be differentially expressed 24 hrs post-dexamethasone induction of functional MYB80 compared to non-induced and *myb80* mutant.

Probe ID	**Locus**	**Gene Description**	**Dex24**		**p-value**
246968_at	At5g24870	zinc finger (C3HC4-type RING finger)	2.39	up	0.001104
247293_at	At5g64510	expressed protein	2.26	up	0.017253
248110_at	At5g55320	membrane bound O-acyl transferase (MBOAT)	7.66	up	0.001277
248368_at	At5g51950	glucose-methanol-choline (GMC)	6.88	up	0.001309
248381_at	At5g51830	pfkB-type carbohydrate kinase family protein	2.96	up	0.001924
248625_at	At5g48880	acetyl-CoA C-acyltransferase 1	3.23	up	0.002413
248697_at	At5g48370	thioesterase family protein	2.24	up	0.012563
248916_at	At5g45840	leucine-rich transmembrane protein kinase	2.22	up	0.001081
250082_at	At5g17200	polygalacturonase (pectinase)	4.29	up	0.009879
250541_at	At5g09520	hydroxyproline-rich glycoprotein family protein	2.26	up	0.017994
251013_at	At5g02540	short-chain dehydrogenase	63.84	up	4.39E-06
251940_at	At3g53450	hypothetical protein	2.19	up	0.001283
248350_at	At5g52160	protease inhibitor/seed storage protein	5.97	up	0.0028878
252527_at	At3g46440	NAD-dependent epimerase	2.25	up	0.002744
253294_at	At4g33750	expressed protein	2.86	up	0.001447
253638_at	At4g30470	cinnamoyl-CoA reductase-related	4.02	up	0.001137
253652_at	At4g30040	aspartyl protease family	9.85	up	0.006218
254090_at	At4g25010	nodulin MtN3 family protein	5.76	up	0.007241
254338_s_at	At4g22080	pectate lyase family protein	14.69	up	0.003593
254792_at	At4g12920	aspartyl protease/UNDEAD	14.67	up	0.003295
256359_at	At1g66460	protein kinase family protein	18.63	up	0.001708
256662_at	At3g11980	male sterility protein 2 (MS2)	24.85	up	0.011961
256962_at	At3g13560	glycosyl hydrolase family 17 protein	3.06	up	0.001163
257170_at	At3g23770	glycosyl hydrolase family 17 protein	37.49	up	0.00277
260056_at	At1g78140	methyltransferase-related	2.08	up	0.018037
260287_at	At1g80440	kelch repeat-containing F-box family protein	7.72	up	0.001816
260546_at	At2g43520	trypsin inhibitor, putative	2.15	up	0.014175
260693_at	At1g32450	proton-dependent oligopeptide transport (POT)	2.68	up	0.003949
260754_at	At1g49000	expressed protein	6.85	up	3.52E-04
260883_at	At1g29270	expressed protein	13.14	up	2.18E-05
260933_at	At1g02470	expressed protein	4.214	up	0.005961
261051_at	At1g01280	cytochrome P450 family protein	87.68	up	0.001727
263005_at	At1g54540	hypothetical protein	10.16	up	7.89E-05
263496_at	At2g42570	expressed protein	2.89	up	0.004921
263935_at	At2g35930	U-box domain-containing protein	5.94	up	0.010747
264039_at	At2g03740	LEA domain-containing protein	2.15	up	0.003771
264175_at	At1g02050	chalcone and stilbene synthase family protein	45.11	up	2.68E-05
265131_at	At1g23760	BURP domain-containing polygalacturonase	24.84	up	8.99E-05
265263_at	At2g42940	DNA-binding family protein	56.97	up	4.00E-06
266273_at	At2g29410	zinc transporter, putative	4.96	up	0.004739
266321_at	At2g46660	cytochrome P450, putative	2.6	up	0.001934

267150_at	At2g23510	transferase family protein	5.99	up	2.25E-05
267483_at	At2g02810	UDP-galactose/UDP-glucose transporter	2.52	up	7.94E-04
267541_at	At2g32750	exostosin family protein	2.16	up	0.002524
259986_at	At1g75050	thaumatin-like protein, putative	7.73	up	7.56E-04
259987_at	At1g75030	pathogenesis-related thaumatin family protein	6.53	up	3.87E-04
245232_at	At4g25590	actin-depolymerizing factor, putative	6.03	down	0.0105804
245335_at	At4g16160	import inner membrane translocase	4.27	down	0.0125576
245912_at	At5g19600	sulfate transporter, putative	2.92	down	9.05E-04
248211_at	At5g54010	glycosyltransferase family protein	2.62	down	0.0067784
248227_at	At5g53820	expressed protein	22.07	down	0.0020433
248484_at	At5g51030	short-chain dehydrogenase/reductase (SDR)	3.42	down	0.0133266
250514_at	At5g09550	Rab GDP dissociation inhibitor, putative	7.65	down	0.0057648
250561_at	At5g08030	glycerophosphoryl diester phosphodiesterase	8.87	down	6.51E-04
251250_at	At3g62180	invertase/pectin methylesterase inhibitor family	2.25	down	0.0022099
252440_at	At3g47440	major intrinsic family protein	13.68	down	1.81E-04
254886_at	At4g11760	expressed protein	11.75	down	0.0166252
255580_at	At4g01470	major intrinsic family protein	7.52	down	0.0067914
256581_at	At3g28830	expressed protein	46.7	down	0.0014606
256588_at	At3g28790	expressed protein	23.16	down	0.0068463
257102_at	At3g25050	xyloglucan:xyloglucosyl transferase, putative	18.58	down	0.0012607
257691_at	At3g12660	fasciclin-like arabinogalactan family protein	2.083	down	3.90E-04
258058_at	At3g28980	expressed protein	31.41	down	0.0025556
258498_at	At3g02480	ABA-responsive protein-related	5.26	down	0.0139488
259189_at	At3g01700	arabinogalactan-protein (AGP11)	3.41	down	0.0081282
261462_at	At1g07850	fringe-related protein	2.024	down	0.0068629
262122_at	At1g02790	exopolygalacturonase	21.22	down	0.0010092
263950_at	At2g36020	abscisic acid-responsive HVA22 family protein	2.04	down	0.0174042
264124_at	At1g79360	transporter-related	2.29	down	0.0191997
264993_at	At1g67290	glyoxal oxidase/AtGLOX1	2.91	down	0.0051945
265405_at	At2g16750	protein kinase family protein	7.73	down	0.0040933
266750_s_at	At2g47040	Pectinesterase/VANGUARD1	29.19	down	0.0066573
266764_at	At2g47050	invertase/pectin methylesterase inhibitor family	8.85	down	0.0139459
252320_at	At3g48580	xyloglucan:xyloglucosyl transferase	7.76	down	1.74E-05
259272_at	At3g01290	band 7 family protein	2.12	down	0.007131
262119_s_at	At1g02930	glutathione S-transferase, putative	2.62	down	0.007567
264346_at	At1g12010	1-aminocyclopropane-1-carboxylate oxidase	57.6	down	1.54E-05
265983_at	At2g18550	homeobox-leucine zipper family protein	5.18	down	0.007386
263475_at	At2g31945	expressed protein	2.74	down	0.004911

Supplemental Table 3. List of overlapping genes (30) present in both the *ms1* (Yang et al. 2007) and *myb80* microarray dataset.

Locus	Function or description	FC in *ms1*	FC in *myb80*
AT1G06990	GDSL-motif lipase/hydrolase family protein	-5.708	-2.1
AT1G24400	lysine and histidine specific transporter, putative	-3.647	-2.8
AT1G52400	glycosyl hydrolase family 1 protein	2.86	4.5
AT1G54870	short-chain dehydrogenase/reductase (SDR)	-2.691	-5.1
AT1G55560	multi-copper oxidase type I family protein	-7.646	-3.9
AT1G63180	UDP-glucose 4-epimerase, putative	-3.617	-2.5
AT1G75910	family II extracellular lipase 4 (EXL4)	-43.098	-2.8
AT1G77210	sugar transporter, putative	-2.054	-4.2
AT1G80660	ATPase 9, plasma membrane-type, putative	-5.894	-7.6
AT2G03200	aspartyl protease family protein	-6.04	-2.8
AT2G03850	LEA domain-containing protein	-14.985	-6.6
AT2G18550	homeobox-leucine zipper family protein	-4.578	-5.18
AT2G41040	methyltransferase-related	-4.292	-2.5
AT3G25050	xyloglucosyl transferase, putative	-36.233	-18.58
AT3G52160	beta-ketoacyl-CoA synthase family protein	-13.885	-3.6
AT4G01430	nodulin MtN21 family protein	-2.274	-2
AT4G14270	expressed protein	-2.69	-2
AT4G16160	import inner membrane translocase	-3.132	-4.27
AT4G26830	glycosyl hydrolase family 17 protein	-3.149	-2
AT4G27260	auxin-responsive GH3 family protein	-3.768	3.6
AT4G35190	expressed protein	-2.884	-2.5
AT5G14980	esterase/lipase/thioesterase family protein	-2.578	-2.5
AT5G15140	aldose 1-epimerase family protein	5.202	4.2
AT5G44400	FAD-binding domain-containing protein	-15.714	-5.8
AT5G49070	beta-ketoacyl-CoA synthase family protein	-3.135	-5.9
AT5G53190	nodulin MtN3 family protein	2.591	4.3
AT5G54510	auxin-responsive GH3 protein, putative (DFL-1)	-2.779	5
AT5G63070	40S ribosomal protein S15, putative	-2.701	-2.1
AT5G65660	hydroxyproline-rich glycoprotein family protein	-2.128	-2.3
AT5G66020	phosphoinositide phosphatase family protein	-2.202	-4.3

Supplemental Table 4. List of overlapping genes (66) present in both the *ams* (Xu et al. 2010) and *myb80* microarray dataset.

Locus	**Function or description**	**FC in *myb80***
At1g06990	GDSL-motif lipase/hydrolase family protein	-2.1
At1g13970	expressed protein	3.2
At1g22990	copper chaperone (CCH)-related	4
At1g26480	14-3-3 protein GF14 iota (GRF12)	-7.6
At1g32450	proton-dependent oligopeptide transport (POT) family	-3.3
At1g32780	alcohol dehydrogenase, putative	-3.8
At1g44800	nodulin MtN21 family protein	4.9
At1g52400	glycosyl hydrolase family 1 protein	4.5
At1g55560	multi-copper oxidase type I family protein	-3.9
At1g63180	UDP-glucose 4-epimerase, putative	-2.5
At1g70810	C2 domain-containing protein	-2.1
At1g71680	lysine and histidine specific transporter, putative	-13.3
At1g71810	ABC1 family protein	-2.6
At1g71880	sucrose transporter (SUC1)	-8.2
At1g73220	sugar transporter family protein	-3.3
At1g75050	pathogenesis-related protein, putative	-3.4
At1g75750	gibberellin-regulated protein 1 (GASA1)	2.3
At1g75910	family II extracellular lipase 4 (EXL4)	-2.8
At1g77210	sugar transporter, putative	-4.2
At1g77590	long-chain-fatty-acid--CoA ligase family protein	-2.1
At1g80130	expressed protein	-4.1
At2g03850	LEA domain-containing protein	-6.6
At2g07040	leucine-rich repeat transmembrane protein kinase	-2.4
At2g07180	protein kinase, putative	-3
At2g18550	homeobox-leucine zipper family protein	-5.18
At2g19000	expressed protein	-8.9
At2g41040	methyltransferase-related	-2.5
At2g46140	LEA domain-containing protein	-4.4
At3g01240	expressed protein	10.4
At3g01700	arabinogalactan-protein (AGP11)	-3.4
At3g03430	calcium-binding pollen allergen, putative	-10.1
At3g13390	multi-copper oxidase type I family protein	-12.7
At3g25050	xyloglucosyl transferase, putative	-18.58
At3g28810	hypothetical protein	-4.9
At3g52160	beta-ketoacyl-CoA synthase family protein	-3.6
At3g62230	F-box family protein	-11.4
At4g00040	chalcone and stilbene synthase family protein	-5.1
At4g00350	MATE efflux family protein	-2.4
At4g00750	dehydration-responsive family protein	3.3
At4g01430	nodulin MtN21 family protein	-2
At4g08290	nodulin MtN21 family protein	-2.3

At4g13230	LEA domain-containing protein	-7.5
At4g13790	auxin-responsive protein, putative	-4.8
At4g16160	import inner membrane translocase	-4.27
At4g20050	expressed protein	-2
At4g25040	integral membrane family protein	-10.1
At4g26260	expressed protein	-2.3
At4g30810	serine carboxypeptidase S10 family protein	-2.4
At4g35010	glycosyl hydrolase family 35 protein	-11.5
At4g35180	amino acid transporter family protein	-3.4
At5g07430	pectinesterase family protein	-17.9
At5g11420	expressed protein	2.4
At5g20230	plastocyanin-like domain-containing protein	-8.3
At5g24655	expressed protein	-2.7
At5g44400	FAD-binding domain-containing protein	-5.8
At5g45340	cytochrome P450 family protein	-3.5
At5g46940	invertase/pectin methylesterase inhibitor family protein	-6.7
At5g47000	peroxidase, putative	-9.2
At5g48880	acetyl-CoA C-acyltransferase 1	3.23
At5g49070	beta-ketoacyl-CoA synthase family protein	-5.9
At5g49900	expressed protein	3.6
At5g51950	glucose-methanol-choline (GMC)	6.88
At5g53190	nodulin MtN3 family protein	4.3
At5g59120	subtilase family protein	-7.6
At5g62080	seed storage/lipid transfer protein (LTP) family	4.3
At5g62850	nodulin MtN3 family protein	-8.3

Supplemental Table 5. Primer sequences used in this article.

Name	*Gene / Vector*	*Nucleotide sequence*
Vectors/Probes		
103GR-F	AtMYB80:GR Forward	5’-CTCGTCGACGGCAAGGAGCTTCTATGGCCAA-3’
103GR-R	AtMYB80:GR Reverse	5’CTCCTGCAGTGGCTTGCTGAACCATATGATTGATGAGATCATC-3’
AspF-BamH1	siRNA pUNDEAD Forward	5’-AATTGGATCCCTTTGCAAATATTGAAATAAGCC-3’
AspR-Hind3	siRNA pUNDEAD Reverse	5’-AATTAAGCTTCATTGTGGTTTTCATTTAAACTG-3’
Asp121+F	siRNA 121 Forward	5’AATTAAGCTTAAAGTTGTTTCTCTTCCACTCTTCAAGAGAGAGTGGAAGAGAAACAACTTTTTTTAAACTAGTTTAA-3’
Asp121+R	siRNA 121 Reverse	5’TTAAACTAGTTTAAAAAAAGTTGTTTCTCTTCCACTCTCTCTTGAAGAGTGGAAGAGAAACAACTTTAAGCTTAATT-3’
Asp297+F	siRNA 297 Forward	5’AATTAAGCTTAAAATACCGACCAGCAGCTTCTTCAAGAGAGAAGCTGCTGGTCGGTATTTTTTTTAAACTAGTTTAA-3’
Asp297+R	siRNA 297 Reverse	5’TTAAACTAGTTTAAAAAAAATACCGACCAGCAGCTTCTCTCTTGAAGAAGCTGCTGGTCGGTATTTTAAGCTTAATT-3’
pUndeadF	Undead promoter:*GUS* For.	5’-CACCCTTTGCAAATATTGAAATAAGCC-3’
pUndeadR	Undead promoter:*GUS* Rev.	5’-CAAAATTCATTGTGGTTTTCAT-3’
pVGD1F	Vanguard1 promoter:*GUS* For.	5’-CACCCGCTGATTTTACTTTTGTGGATTTG-3’
pVGD1R	Vanguard1 promoter:*GUS* Rev.	5’-ATCGGAGAGGGAGGGGCTTTATTAG-3’
pGLOX1F	AtGLOX1 promoter:*GUS* For.	5’-CACCCGTAAACTAATCAATTTCAAG-3’
pGLOX1R	AtGLOX1 promoter:*GUS* Rev.	5’-AGAGTCTTGTTGACTTTTTCAT-3’
AtPr-KpnF	AtMYB80 Protein Forward	5’-TACCAAGGTACCATGGGTCGGATTCCATGTTGT-3’
AtPr896R	AtMYB80 Protein Reverse (+896)	5’-TGTTATAAGCTTCTAAGGCTTGTGGGTCACCGGATC-3’
AtPr1015R	AtMYB80 Protein Reverse (+1015)	5’-TGTTATAAGCTTCTAAGGAAACTTGGTGAGCAAGTG-3’
eVANF	EMSA VGD1 Probe For.	5’-ATCCGCAACTAAGCAATTACA-3’
eVANR	EMSA VGD1 Probe Rev.	5’-CTATTGTGATGGATGCTGGAG-3’
eGLOXF	EMSA AtGLOX1 Probe For.	5’-GAAAGGCAAACGTATAGAGGA-3’
eGLOXR	EMSA AtGLOX1 Probe Rev.	5’-GGACAATAAGGAATGATGTCT-3’
eAspF	EMSA UNDEAD Probe For.	5’-GATATGATATTAGATGATCTAC-3’
eAspR	EMSA UNDEAD Probe Rev.	5’-GTAGTTTGACACTAAAGTAAGAG-3’
RT-PCR/qPCR		
β-TUB R3 Rev	β-tubulin For.	5’-GGCTCTGTATTGCTGTGATCCACG-3’
β-TUB F2 For	β-tubulin Rev.	5’-GGACATACACTGAAGGTGCTGAG-3’
3g11980F	MS2 For.	5’-ATCAGTTTCCTCCAAGGGAAGAAGTT-3’
3g11980R	MS2 Rev.	5’-ATTACCGGGCCCTCTTGTGTTGATGT-3’
1g01280+1F	Cytochrome p450 For.	5’-ATGATTTTGGTGCTAGCCTCCCTCTTC-3’
1g01280+1533R	Cytochrome p450 Rev.	5’-TTATGTGTACAAATGAGCTGCCAATCG-3’
1g02050+1F	Chalcone and stilbene synth For.	5’-ATGTCGAATTCTAGGATGAATGGTGTT-3’
1g02050+1188R	Chalcone and stilbene synth Rev.	5’-TTAGGAAGAGGTGAGGCTGCGGATGAG-3’
4g12920+1F	Aspartyl protease UNDEAD For.	5’-ATGAAAACCACAATGAATTTTGTTTTTC-3’
4g12920+1170R	Aspartyl protease UNDEAD Rev.	5’-CTACATATCACAATCTTGTTTATTAAT-3’
4g22080+90F	Pectate lyase For.	5’-ACCCCCACGGTTGCCAACTACGTCCCCGAG-3’
4g22080+1185R	Pectate lyase Rev.	5’-CTAATAACAAGGGCCGTTGCGGTTGCA-3’
1g66460+1F	Protein kinase For.	5’-ATGATTCTTGATTTGGGTTTTCCTTGT-3’
1g66460+1404R	Protein kinase Rev.	5’-CTACAAAAGATCATCAGCTTCAAATTC-3’
At1g12010F	ACC oxidase For.	5’-ACCATGGCTTTGATCGACGATGCTTG-3’
At1g12010R	ACC oxidase Rev.	5’-CTCTGGTTTAGGACATGGTGGATAGT-3’
At3g48580F	Xyloglucosyl transferase For.	5’-AACCTCTGAGCTCCAGCTCACCCTCG-3’
At3g48580F	Xyloglucosyl transferase Rev.	5’-CTTGCTGTACACCCTGATCGGTGTAT-3’
At5g02540F	Short-chain dehydrogenase For.	5’-AGGAAGAAGAGGACCAAGTGGATTTG-3’
At5g02540R	Short-chain dehydrogenase Rev.	5’-TAAGACCAGGGTGAACTGAATTTGCT-3’
3g07830+1F	Pectinase SALK 035568 For.	5’-ATGGGTTCATATTTTGGAATTTCTACA-3’
3g07830+1194R	Pectinase SALK 035568 Rev.	5’-TTACTTAGGTTGGGTCAGCACGGGTGG-3’
4g02250+1F	Pectin methylesterase inhibitor For.	5’-ATGAAAATGGCCGGAAGGATCTTTCTC-3’
4g02250+438R	Pectin methylesterase inhibitor Rev	5’-TTAGGGAGTTAAAATAGTGTTAATGAG-3’
1g74430+1F	MYB95 NASC_314F0 For.	5’-ATGGGGTGGACGACGTGGTTCGACGTT-3’
1g74430+1710R	MYB95 NASC_314F0 Rev.	5’-TCAAAGAAGGAACAGGTCAAGGTGTTC-3’

1g72260-370F	Thionin SALK 039929 For.	5’-GAAAACTTTAAACGTTGGCCTACG-3’
1g72260+405R	Thionin SALK 039929 Rev.	5’-TTACAACAGTTTAGGCGGCCCAGGTGG-3’
UBQ10F	Ubiquitin 10 (At4g05320) For.	5'-TCCGGATCAGCAGAGGCTTA-3'
UBQ10R	Ubiquitin 10 (At4g05320) Rev.	5'-TCAGAACTCTCCACCTCAAG-3'
qAsp+72F	UNDEAD qPCR For.	5’-CACTCTACATATCCCTCTTGTGC-3’
qAsp+219R	UNDEAD qPCR Rev.	5’-CTGCTACCCGTATCCATGTGA-3’
qGLOXF	AtGLOX1 qPCR For.	5’-GTCGATATTAACACCGGAGACATC-3’
qGLOXR	AtGLOX1 qPCR Rev.	5’-GTTTGCTCCTCCTTGGAATCCTC-3’
qVANF	VGD1 qPCR For.	5’-CAGCCCTGGAACCACCACTTCC-3’
qVANR	VGD1 qPCR Rev.	5’-CCGTTCACTCTGATAGCCACAG-3’
qMYB80F	AtMYB80 qPCR For.	5’-GTTTCACTCTGTTCTTGGTAACC-3’
qMYB80R	AtMYB80 qPCR Rev.	5’-CGGATCTATTCCCATTCCTGAC-3’

TDNA/RT-PCR

pAC161 8760	pAC161 T-DNA left border	5’-GGGCTACACTGAATTGGTAGCTC-3’
LBa1	SALK T-DNA left border	5’-TGGTTCACGTAGTGGGCCATCG-3’
LBb1	SALK T-DNA left border	5’-GCGTGGACCGCTTGCTGCAACT-3’
1g524F	Protein binding	5’-ACAGTGTTCTTCGTCATCTTTGTC-3’
1g524R	Protein binding	5’-TGTTGCGTTGCTCTTTAAGTTTAG-3’
2g185F	Transcription factor (RT-PCR)	5’-TGTTTTTACAAGATGATGGACACC-3’
2g185R	Transcription factor (RT-PCR)	5’-TACAATTTGGATGCTTTGACATTC-3’
3g219F	Pollen coat (RT-PCR)	5’-AAGGAGTCTGATTCGATTATTCCC-3’
3g219R	Pollen coat (RT-PCR)	5’-CCATATCAGGTTCTTTACCGTAGG-3’
3g220F	Protein kinase (RT-PCR)	5’-TCTTTATTATTTGCTTTCAACGCC-3’
3g220R	Protein kinase (RT-PCR)	5’-TTCTCTTTTACAACGTTCTCGTTTG-3’
3g484F	Nitrate response (RT-PCR)	5’-TAGCACACATGACACAAACCTATG-3’
3g484R	Nitrate response (RT-PCR)	5’-CGAGCTTTATTGAAAATGACAGTG-3’
1g024F	Expressed protein	5’-CTCCATAAACGGTTTCATTGC-3’
1g024R	Expressed protein	5’-CCAAATCGACTCACCGTTAAC-3’
1g120F	ACC oxidase	5’-TTACCCAATCGGATCAAAGTG-3’
1g120R	ACC oxidase	5’-ACCCAAGCTTTGTGTTTGATG-3’
1g237F	BURP domain, polygalac.	5’-CTCGTCGTATGCCAAGAACTC-3’
1g237R	BURP domain, polygalac.	5’-ATTCTCGTAGAACCGGTTTGC-3’
1g490F	Expressed protein	5’-CGGACACTAGAGATTACATCGG-3’
1g490R	Expressed protein	5’-TTGTCCCCAAAACAAAACAAG-3’
2g185F	Homeobox-leucine zipper	5’-TCTTTTAATCAAGAGTTCCTATTTGTG-3’
2g185R	Homeobox-leucine zipper	5’-GGATGCTTTGACATTCACATG-3’
2g359F	U-box domain-containing	5’-TCACCCCGAATCACACTCTAC-3’
2g359R	U-box domain-containing	5’-CAGCATCTCTCATATATGTGATTGC-3’
3g237F	Glycosyl hydrolase	5’-ACATGTTGCATTGCTTCTTCC-3’
3g237R	Glycosyl hydrolase	5’-AAAACCATTAAAGCAGGCCAC-3’
5g025F	Short-chain dehydrogenase	5’-GCAATTCGATTCCATCTTCAG-3’
5g025R	Short-chain dehydrogenase	5’-AGGACCAAGTGGATTTGGTTC-3’
5g248F	Zinc finger family protein	5’-TTATGTTGGCAAGGCAAAGTC-3’
5g248R	Zinc finger family protein	5’-AGCAGCTCTTCGAGTAGAGGG-3’
5g458F	LRR protein kinase	5’-AAATGGGTTAAAAAGAAGCCG-3’
5g458R	LRR protein kinase	5’-CTTAACCGATGATTACGCAGC-3’
5g488F	3-ketoacyl-CoA thiolase 1	5’-TCAACGTCAGCGATATTGATC-3’
5g488R	3-ketoacyl-CoA thiolase 1	5’-TACTCAATGGCAACAACATCG-3’
5g518F	pfkB-type kinase family	5’-CCATTGAAAGTTGACTCAGGG-3’
5g518R	pfkB-type kinase family	5’-AGCAGCTCTTCGAGTAGAGGG-3’
74430+1F	MYB95 NASC_314F0	5’-ATGGGGTGGACGACGTGGTTCGACGTT-3’
74430+1710R	MYB95 NASC_314F0	5’-TCAAAGAAGGAACAGGTCAAGGTGTTC-3’
13570-429F	CCAAT-Box SALK 130081	5’-CCAAAGTTTCAAAATAGTGCCTTT-3’
13570+648R	CCAAT-Box SALK 130081	5’-TCACCAGTGAATTGAATCAATGTTATT-3’
17220+1F	Pectin methylesterase inhibitor	5’-ATGGCAGCATACCTGACGAACAGAGTT-3’
17220+522R	Pectin methylesterase inhibitor	5’-TCACATCATGTTTGAGATGACAAGTAC-3’
25730+1F	AP2 SALK 007234	5’-ATGGATGCCATGAGTAGCGTAGACGAG
25730+1115R	AP2 SALK 007234	5’-TAATTTTTTCCACTTGTTACAACTTAC-3’
62230+1F	F-box SALK 020875	5’-ATGGACTCAGGAAGTGCAGTGGACATC-3’

62230+1386R	F-box SALK 020875	5’-TTAGTAAAAAGTAACGACCAAATTCTC-3’
02250+1F	Pectin methylesterase inhibitor	5’-ATGAAAATGGCCGGAAGGATCTTTCTC-3’
02250+438R	Pectin methylesterase inhibitor	5’-TTAGGGAGTTAAAATAGTGTTAATGAG-3’

ChIP/qChIP

At4g12920F	Aspartyl protease	5’-TGGTGTTACATACTTTTATATCC-3’
At4g12920R	Aspartyl protease	5’-CTCTTACTTTAGTGTCAAACTAC-3’
At1g67290F	Glyoxal oxidase	5’-GGTAGAAGCTTTCCACTTTAT-3’
At1g67290R	Glyoxal oxidase	5’-AGACATCATTCCTTATTGTCC-3’
At2g47040F	Vanguard	5’-GTAACTCGGTTTTATACAAGT-3’
At2g47040R	Vanguard	5’-CTCCAGCATCCATCACAATAG-3’
At2g47050F	Vanguard homolog	5’-CATACAAATTAAAACATTCTTTTAC-3’
At2g47050R	Vanguard homolog	5’-TCCATTCCTTTCCAATCCACGT-3’
At3g23770F	Glycosyl hydrolase 17	5’-GCAATACGTTCTACCAAGTTTGA-3’
At3g23770R	Glycosyl hydrolase 17	5’-ACACACTTCCTTAATCTCTTCT-3’
At3g62180F	Pectin methylesterase	5’-GTTCGAATTTCAAATATACCACA-3’
At3g62180R	Pectin methylesterase	5’-TCCGAGATCCGTTCCTTTCCG-3’
At4g16160F	Inner membrane translocase	5’-AGCGGAGATGACACGTGTCACGT-3’
At4g16160R	Inner membrane translocase	5’-AGAGAGAAGCAACAAGTGAAGA-3’
At4g22080F	Pectate lyase	5’-TGGCTTGATACCGGTTCGGTTT-3’
At4g22080R	Pectate lyase	5’-ACACCTTCTAATCTTTCCGACAC-3’
At5g09550F	Rab GDP dissociation inhibitor	5’-ACCACCTGTTCGTCTAATTATAG-3’
At5g09550R	Rab GDP dissociation inhibitor	5’-CAATAACGGAGATAGAGATCGA-3’
At5g52160F	Protease inhibitor	5’-CAACTAGTCTGTCTCCATTATCA-3’
At5g52160R	Protease inhibitor	5’-CACTAAACACTTAAATAAATCA-5’
At1g01280F	Cytochrome p450	5’-ACTATGATGTTCGTGCACACC-3’
At1g01280R	Cytochrome p450	5’-ACTTAGCTACTAGTCTTCCAT-3’
At1g02790F	Polygalacturonase 4	5’-AGCTATGACGCTCCGACATAA-3’
At1g02790R	Polygalacturonase 4	5’-AGCATACTAACTAGCACTATA-3’
At3g01700F	Arabinogalactan protein 11	5’-AACCTTTTGTGGTGGGCTTGA-3’
At3g01700R	Arabinogalactan protein 11	5’-AACCTTTTGTGGTGGGCTTGA-3’
At4g11760F	Pollen coat protein	5’-CAAGTAAACAGAATCGATGTAG-3’
At4g11760R	Pollen coat protein	5’-TAGTCCATATGTTTTTTCCTT-3’
At3g11980F	MS2	5’-CATCATCTTTTGTCCTTAGAA-3’
At3g11980R	MS2	5’-CTTCTGTTTCCTCAAAAGATA-3’
At4g30030F	Aspartyl protease	5’-GATTTATGTTTATCAGAGATC-3’
At4g30030R	Aspartyl protease	5’-GGATTGGAAGAAAACCACATTC-3’
At4g30040F	Aspartyl protease	5’-GTATCATGATCATGGATACCAC-3’
At4g30040R	Aspartyl protease	5’-GTCAATGTGTATGTGAAGTGT-3’
A6F	A6 callase (At4g14080)	5’-CTACATAAATTGTTTTCATCG-3’
A6R	A6 callase (At4g14080)	5’-GTCTTTGTGTTTGTGTCTGGT-3’
At5g56110F	AtMYB80	5’-TCCAAGTCGTTCTACCAATCC-3’
At5g56110R	AtMYB80	5’-ATATCAAAGATTGCCCCACCC-3’
At1g02930F	Glutathione S-transferase	5’-CTCTCGTTCTATCGAATGATC-3’
At1g02930R	Glutathione S-transferase	5’-CAAACGGCGCCACCAAGCTTG-3’
At3g02480F	LEA, ABA-responsive	5’-ACGACAGTACAAGAAGAAGG-3’
At3g02480F	LEA, ABA-responsive	5’-ATGATTGGAGCATTGGGTTGC-3’
At3g01290F	Band 7 family protein	5’-ATTCGATTCTCTTACTACAG-3’
At3g01290R	Band 7 family protein	5’-GAGAAGAAAGTCGCAGGAGTG-3’
At2g43520F	Trypsin inhibitor	5’-TTGGTAAGGACTCACATAAG-3’
At2g43520R	Trypsin inhibitor	5’-ACTTTGGAGTTAACGTATGTG-3’
At2g42570F	Expressed protein	5’-TCAGCTTATTTGAACCAAGCT-3’
At2g42570R	Expressed protein	5’- TGAGAGCGAGATTGGTGTGAG-3’
At2g02810F	UDP-galatose transporter 1	5’-GAACATACGAGTTTTATTCAG-3’
At2g02810R	UDP-galatose transporter 1	5’-GGTTAACGATGACGCGTGTAC-3’
At2g46660F	Cytochrome P450	5’- CAACGTCGATCGATTCTCATG-3’
At2g46660R	Cytochrome P450	5’- AGATGAGCAGATGGCTTTGG-3’
At2g03740F	LEA, late embryogenesis	5’-GATTCTCACTTTGTCCTTCTTAC-3’
At2g03740R	LEA, late embryogenesis	5’-GTTAGAGGAACCAAGTGAGTC-3’

At1g29270F	Expressed protein	5’-AGCTACCAGTTTATCACCAAC-3’
At1g29270R	Expressed protein	5’-TCTGCATAATAACTCATTGGC-3’
At1g78140F	Methyltransferase	5’-AACATGTAATCTACTAAGCCC-3’
At1g78140R	Methyltransferase	5’-GCAGCCTATTGAGCACGAAGC-3’
At1g54540F	LEA, late embryogenesis	5’-GTTGTTGCTGAACATAGAGATG-3’
At1g54540R	LEA, late embryogenesis	5’-TAGTAATACTAATGCACCAAC-3’
At5g22260F	MS1	5’-CCAGTTTCTAATATTACAGAAG-3’
At5g22260R	MS1	5’-GAATAGGAATATGATAGATTTGG-3’
At5g48880F	Acetyl-CoA C-acyltransferase 1	5’-ATCCGATATGAATTCTTGTGG-3’
At5g48880R	Acetyl-CoA C-acyltransferase 1	5’-TGCCAAAACCTTGTCTTGTCG-3’