

Supplemental Figure 1. The *CDM1* gene and protein structures, mRNA expression levels in wild type and the T-DNA insertional mutant, wild type and *cdm1* mutant siliques phenotype, and genotype of *CDM1* in transgenic line and *cdm1* mutant. (A) A diagram showing the *CDM1* gene structure. Solid boxes indicate exons. The thin line represents the intron. The open triangle indicates the T-DNA insertion (SALK_065040) site. Below the gene structure, the approximate regions of RT-PCR products were shown for the following primers. fa: oMC7506/oMC7395, and fb: oMC7506/oMC7507. (B) An illustrated *CDM1* protein structure. Two CCCH domains are indicated. The T-DNA insertion disrupts the intact protein after the first CCCH domain (arrow). (C) RT-PCR results with primer pairs of fa and fb for wild type and *cdm1* inflorescences. The ubiquitin gene was used as a control. (D) A dissected wild type silique (upper) shows plenty of seeds inside. No seeds were seen in a *cdm1* mutant silique (lower). (E) PCR results with primer pairs of fa for *CDM1-GR/cdm1* and *cdm1* genomic DNA, showing *CDM1* was detected in the transgenic line.

Supplemental Figure 2. Comparison of wild type and *cdm1* tapetum development.

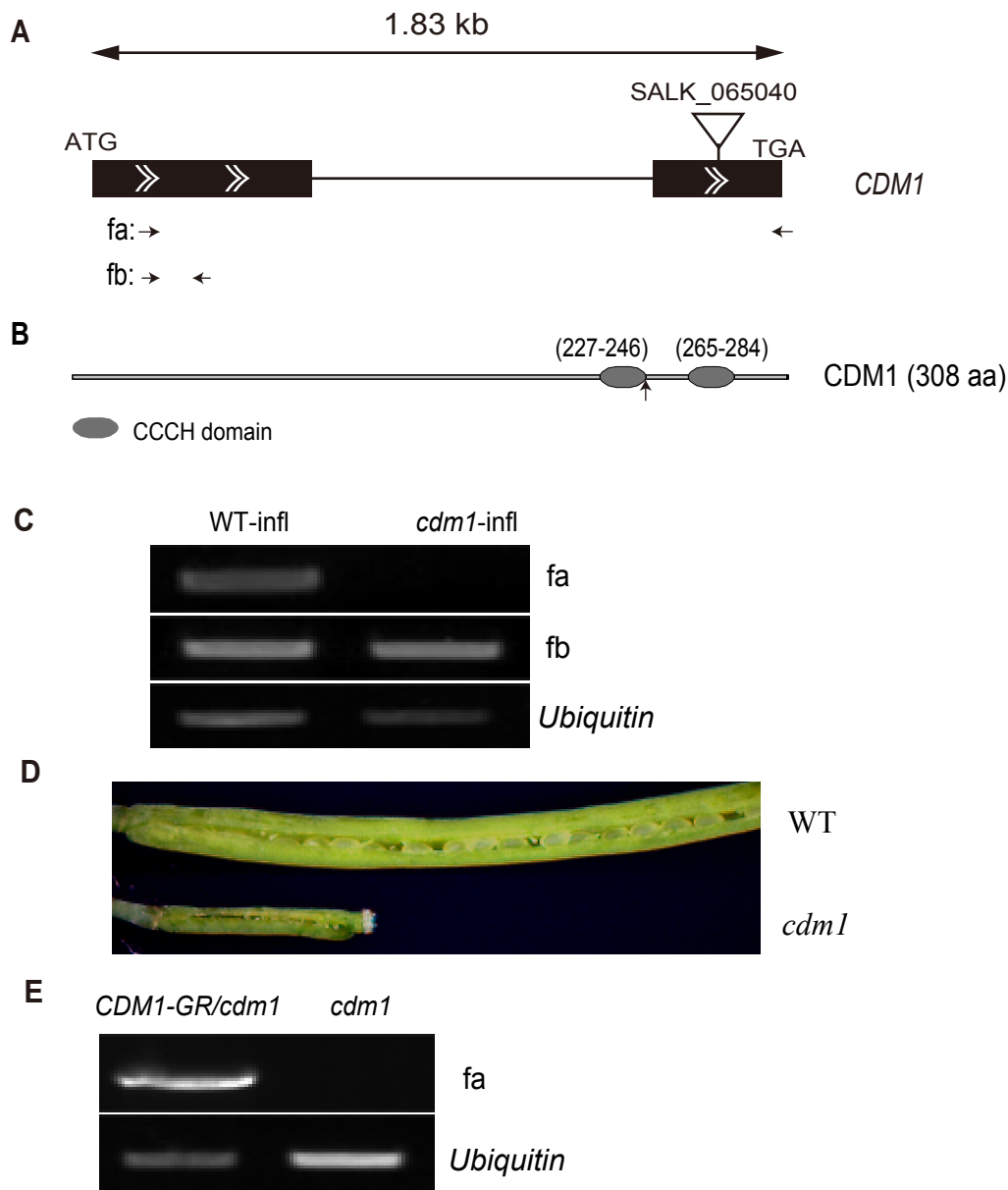
Semi-thin anther sections were stained with toluidine blue, with part of one locule shown in each panel. (A) A stage 7 wild type anther section. (B) A stage 7 *cdm1* anther section. (C) A stage 9 wild type anther section. (D) A stage 9 *cdm1* anther section. Scale bars = 10 um.

Supplemental Figure 3. Aniline blue staining for callose in wild type and *cdm1*. (A, C, E and G) bright field; (B, D, F and H) UV light. (A, B) A wild type stage 5 anther section, showing callose was initially deposited on the meiocyte primary wall. (C, D) A *cdm1* stage 5 anther section, showing callose wall was also initially synthesized and deposited

to meiocyte primary wall. Bright field view (E) and UV light view (F) of a wild type tetrad. Bright field view (G) and UV light view (H) of *cdm1* tetrads. Scale bars = 50 μm (A-C), 10 μm (E-H).

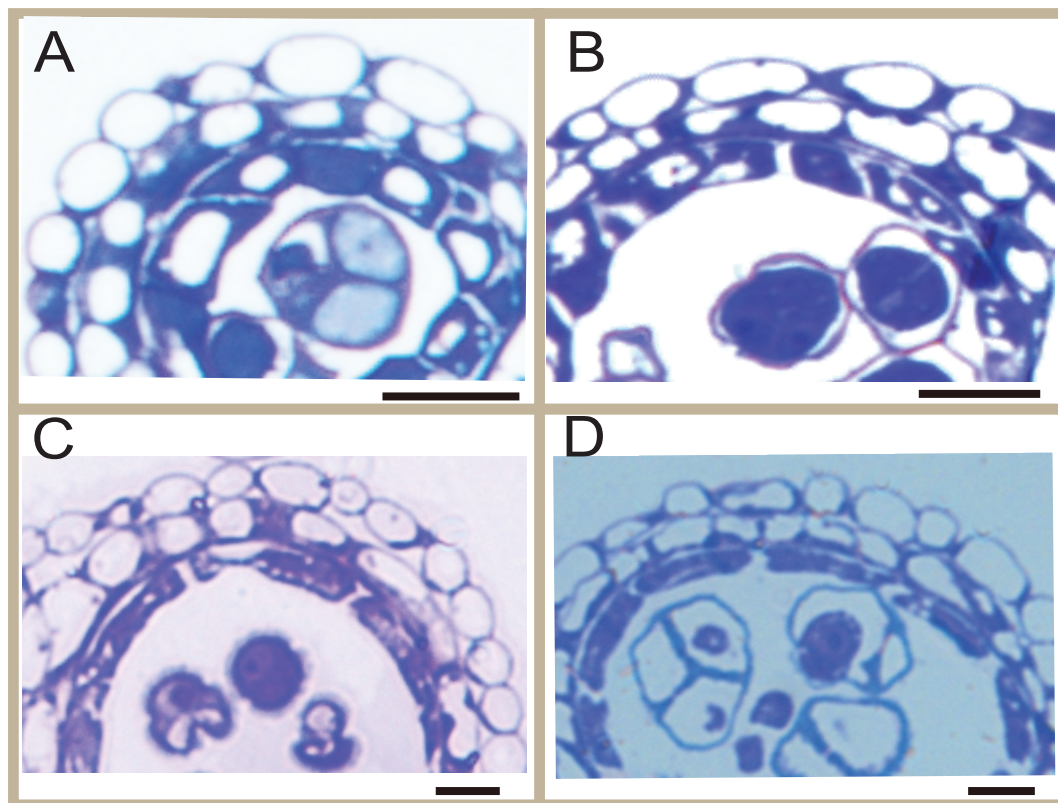
Supplemental Figure 4. qRT-PCR analyses of different genes expression in wild type and *cdm1* young inflorescences. (A) Expression of *At3g24330*, *At3g55780*, and *At3g61810*. (B) Expression of *MS2*, *DEX1*, *NEF1* and *FLP1*. (C) Expression of *IMPA-8*, *BT3*, *AtPV42a*, *ROXY2*, *KOM*, and *SHT*. *Arabidopsis ACTIN1* was used as a normalizer control. Error bars indicate SD.

Figure S1



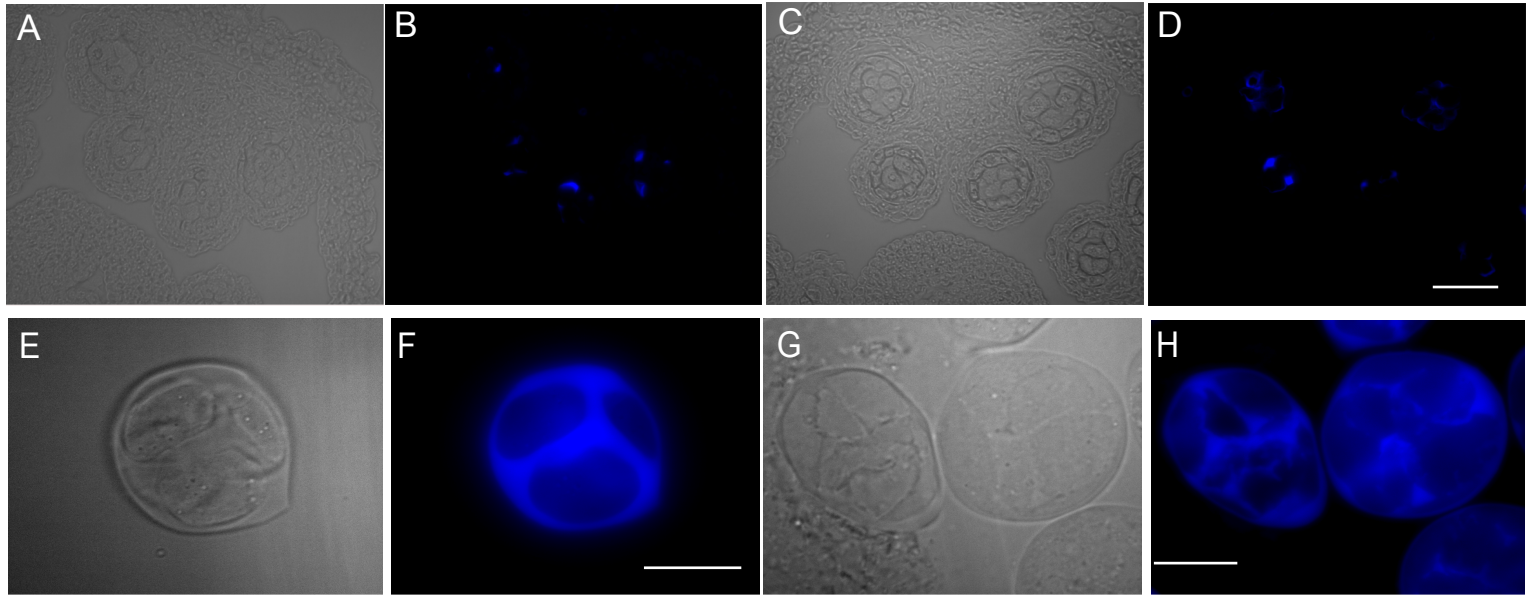
Supplemental Figure 1. The *CDM1* gene and protein structures, mRNA expression levels in wild type and the T-DNA insertional mutant, wild type and *cdm1* mutant siliques phenotype, and genotype of *CDM1* in transgenic line and *cdm1* mutant. (A) A diagram showing the *CDM1* gene structure. Solid boxes indicate exons. The thin line represents the intron. The open triangle indicates the T-DNA insertion (SALK_065040) site. Below the gene structure, the approximate regions of RT-PCR products were shown for the following primers. fa: oMC7506/oMC7395, and fb: oMC7506/oMC7507. (B) An illustrated *CDM1* protein structure. Two CCCH domains are indicated. The T-DNA insertion disrupts the intact protein after the first CCCH domain (arrow). (C) RT-PCR results with primer pairs of fa and fb for wild type and *cdm1* inflorescences. The ubiquitin gene was used as a control. (D) A dissected wild type silique (upper) shows plenty of seeds inside. No seeds were seen in a *cdm1* mutant silique (lower). (E) PCR results with primer pairs of fa for *CDM1-GR/cdm1* and *cdm1* genomic DNA, showing *CDM1* was detected in the transgenic line.

Figure S2



Supplemental Figure 2. Comparison of wild type and *cdm1* tapetum development. Semi-thin anther sections were stained with toluidine blue, with part of one locule shown in each panel. (A) A stage 7 wild type anther section. (B) A stage 7 *cdm1* anther section. (C) A stage 9 wild type anther section. (D) A stage 9 *cdm1* anther section. Scale bars = 10 μm .

Figure S3

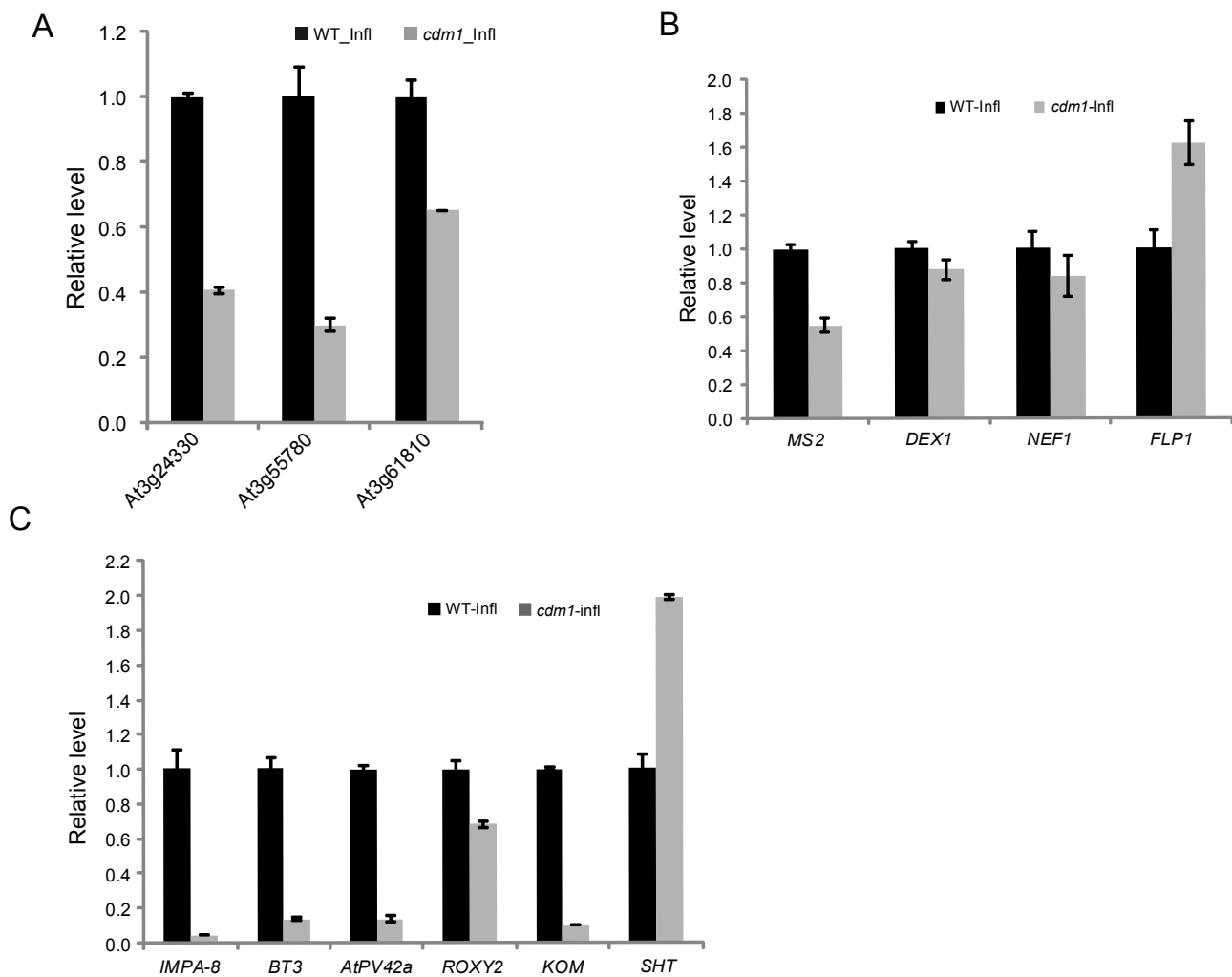


Supplemental Figure 3. Aniline blue staining for callose in wild type and *cdm1*.

(A, C, E and G) bright field; (B, D, F and H) UV light. (A, B) A wild type stage 5 anther section, showing callose was initially deposited on the meicyote primary wall. (C, D) A *cdm1* stage 5 anther section, showing callose wall was also initially synthesized and deposited to meicyote primary wall.

Bright field view (E) and UV light view (F) of a wild type tetrad. Bright field view (G) and UV light view (H) of *cdm1* tetrads. Scale bars = 50 μm (A-C), 10 μm (E-H).

Figure S4



Supplemental Figure 4. qRT-PCR analyses of different genes expression in wild type and *cdm1* young inflorescences. (A) Expression of *At3g24330*, *At3g55780*, and *At3g61810*. (B) Expression of *MS2*, *DEX1*, *NEF1* and *FLP1*. (C) Expression of *IMPA-8*, *BT3*, *AtPV42a*, *ROXY2*, *KOM*, and *SHT*. *Arabidopsis ACTIN1* was used as a normalizer control. Error bars indicate SD.

Supplemental Table 1. Down-regulated genes with expression level changed greater than 1.5-fold in the *cdm1* mutant.

Classification	Probe ID	Locus	Fold change	p-Value	Anther specific	Gene description
Carbohydrate metabolism	265477_at	At2g46480	-2.35	0.007358	-	GAUT2_LGT2__galacturonosyltransferase 2
	267280_at	At2g19450	-1.55	0.047464	-	ABX45_ACYL-COA__diacylglycerol acyltransferase (DGAT)
Sucrose biosynthesis and transport	262460_s_at	At1g50390	-1.60	0.026023	-	pfkB-like carbohydrate kinase family protein
	260517_at	At1g51420	-1.53	0.000681	-	ATSPP1_SPP1__sucrose-phosphatase 1
Pectin biosynthesis	259033_at	At3g09410	-2.19	0.002636	-	Pectinacetyltransferase family protein
	252221_at	At3g49830	-3.46	0.017067	-	P-loop containing nucleoside triphosphate hydrolases superfamily protein
	257585_at	At3g12420	-2.22	0.035580	Yes	Polynucleotidyl transferase, ribonuclease H-like superfamily protein
	261674_at	At1g18270	-1.98	0.032623	-	ketose-bisphosphate aldolase class-II family protein
Other metabolism	256616_at	At3g22260	-1.96	0.015817	-	Cysteine proteinases superfamily protein
	247381_at	At5g63390	-1.91	0.000800	Yes	O-fucosyltransferase family protein
	262358_at	At1g73050	-1.82	0.008582	-	Glucose-methanol-choline (GMC) oxidoreductase family protein
	266058_at	At2g40690	-1.64	0.020323	-	GLY1_SFD1__NAD-dependent glycerol-3-phosphate dehydrogenase family protein
	264742_at	At1g62130	-1.60	0.014134	Yes	AAA-type ATPase family protein
	253971_at	At4g26530	-1.54	0.020109	-	Aldolase superfamily protein
	252570_at	At3g45300	-1.52	0.041414	-	ATIVD_IVD_IVDH__isovaleryl-CoA-dehydrogenase
Hydrolases	266475_at	At2g31100	-1.55	0.018839	-	alpha/beta-Hydrolases superfamily protein
	249323_at	At5g40940	-2.45	0.037023	Yes	FLA20__putative fasciclin-like arabinogalactan protein 20
Cell wall related	257419_at	At1g30800	-1.84	0.018650	Yes	Fasciclin-like arabinogalactan family protein
	262606_at	At1g15190	-1.73	0.024225	Yes	Fasciclin-like arabinogalactan family protein
	262393_at	At1g49490	-1.50	0.032925	-	Leucine-rich repeat (LRR) family protein
	247661_at	At5g60080	-2.55	0.011509	Yes	Protein kinase superfamily protein
Protein phosphorylation and	265168_at	At1g23700	-2.54	0.006175	Yes	Protein kinase superfamily protein
	250699_at	At5g06820	-2.39	0.012233	-	SRF2__STRUBBELIG-receptor family 2
	263416_at	At2g17170	-2.07	0.003661	Yes	Protein kinase superfamily protein
	258095_at	At3g23610	-1.99	0.011443	-	DSPTP1__dual specificity protein phosphatase 1
	260239_at	At1g74360	-1.95	0.014437	-	Leucine-rich repeat protein kinase family protein
	247831_at	At5g58540	-1.94	0.005852	-	Protein kinase superfamily protein
	247662_at	At5g60090	-1.90	0.002762	Yes	Protein kinase superfamily protein

dephosphorylation

248441_at	At5g51270	-1.85	0.043913	-	U-box domain-containing protein kinase family protein
255875_s_at	At2g40500	-1.74	0.000958	-	Protein kinase superfamily protein
258029_at	At3g27580	-1.69	0.000404	-	ATPK7_D6PKL3__Protein kinase superfamily protein
262353_at	At1g64210	-1.59	0.007509	-	Leucine-rich repeat protein kinase family protein
248055_at	At5g55830	-1.59	0.012094	-	Concanavalin A-like lectin protein kinase family protein
249223_at	At5g42120	-1.58	0.025622	-	Concanavalin A-like lectin protein kinase family protein
255221_at	At4g05150	-1.50	0.037247	-	Octicosapeptide/Phox/Bem1p family protein
258667_at	At3g08750	-3.90	0.009880	-	F-box and associated interaction domains-containing protein
250036_at	At5g18340	-3.78	0.002464	-	ARM repeat superfamily protein
255275_at	At4g05310	-3.46	0.000400	-	Ubiquitin-like superfamily protein
267594_at	At2g33000	-3.23	0.007399	Yes	Ubiquitin-associated (UBA)/TS-N domain-containing protein-related
255289_at	At4g04690	-3.16	0.013727	-	F-box and associated interaction domains-containing protein
251441_at	At3g60020	-2.79	0.010848	Yes	ASK5_SK5__SKP1-like 5
245902_at	At5g11080	-2.65	0.001172	-	Ubiquitin-like superfamily protein
257454_at	At1g65170	-2.58	0.010566	-	Ubiquitin carboxyl-terminal hydrolase family protein
267598_at	At2g33010	-2.38	0.013350	-	Ubiquitin-associated (UBA) protein
266248_at	At2g27650	-2.18	0.010384	-	Ubiquitin carboxyl-terminal hydrolase-related protein
266564_at	At2g24000	-2.03	0.044483	-	scpl22__serine carboxypeptidase-like 22
253716_at	At4g29420	-1.89	0.008245	-	F-box/RNI-like superfamily protein
262152_s_at	At1g52450	-1.88	0.024952	Yes	Ubiquitin carboxyl-terminal hydrolase-related protein
255426_at	At4g03370	-1.85	0.003180	-	Ubiquitin family protein
257920_at	At3g23260	-1.65	0.020889	-	F-box and associated interaction domains-containing protein
251440_at	At3g60010	-1.54	0.017912	-	ASK13_SK13__SKP1-like 13
251366_at	At3g61340	-1.52	0.041065	-	F-box and associated interaction domains-containing protein
247670_at	At5g60190	-1.50	0.018049	-	Cysteine proteinases superfamily protein

Proteolysis**Protein biosynthesis**

259776_s_at	At1g29550	-1.66	0.014933	-	Eukaryotic initiation factor 4E protein
249338_at	At5g41090	-4.03	0.006421	-	NAC095__NAC domain containing protein 95
266111_at	At2g02060	-3.51	0.003879	-	Homeodomain-like superfamily protein
264273_s_at	At1g60300	-3.44	0.004057	-	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein
246556_at	At5g15480	-3.36	0.005884	-	C2H2-type zinc finger family protein
255416_at	At4g03170	-2.93	0.003360	-	AP2/B3-like transcriptional factor family protein
264269_at	At1g60240	-2.43	0.005376	-	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein
246788_at	At5g27580	-2.21	0.019461	-	AGL89__AGAMOUS-like 89

	257369_at	At2g35550	-1.93	0.013883	-	ATBPC7_BBR_BPC7__basic pentacysteine 7
	257400_s_at	At1g23810	-1.91	0.022893	Yes	Paired amphipathic helix (PAH2) superfamily protein
Transcription factor	246962_s_at	At5g24800	-1.80	0.034770	-	ATBZIP9_BZIP9_BZO2H2__basic leucine zipper 9
	260998_at	At1g26590	-1.77	0.003977	-	C2H2-like zinc finger protein
	255903_at	At1g17950	-1.77	0.026746	-	ATMYB52_BW52_MYB52__myb domain protein 52
	259992_at	At1g67970	-1.76	0.017012	-	AT-HSFA8_HSFA8__heat shock transcription factor A8
	249463_s_at	At5g39690	-1.75	0.023771	-	ANAC093_NAC093__NAC domain containing protein 93
	264726_at	At1g22985	-1.67	0.015306	-	ERF (ethylene response factor) subfamily B-5 of ERF/AP2 transcription factor family protein
	249419_s_at	At5g39810	-1.65	0.024250	-	AGL98__AGAMOUS-like 98
	253064_at	At4g37730	-1.63	0.010177	-	AtbZIP7_bZIP7__basic leucine-zipper 7
	257930_at	At3g17010	-1.60	0.014006	-	AP2/B3-like transcriptional factor family protein
	256742_at	At3g29380	-1.54	0.021275	-	TFIIB-related protein
	263378_at	At2g40180	-2.80	0.007484	-	ATHPP2C5_PP2C5__phosphatase 2C5
	257460_at	At1g75580	-1.83	0.003798	-	SAUR-like auxin-responsive protein family
Hormone response	266139_at	At2g28085	-1.75	0.034852	-	SAUR-like auxin-responsive protein family
	252367_at	At3g48360	-1.62	0.042039	-	ATBT2_ TAZ domain protein 2; an essential component of the TAC1-mediated telomerase activation pathway
	253439_at	At4g32540	-1.53	0.002151	-	Flavin Monooxygenase-Like Enzyme
	249706_at	At5g35600	-2.47	0.011046	Yes	HDA7__histone deacetylase7
Histone deacetylation	246881_at	At5g26040	-1.53	0.018619	-	HDA2__histone deacetylase 2
	254946_at	At4g10950	-4.41	0.000107	Yes	SGNH hydrolase-type esterase superfamily protein
Fatty acid-lipid biosynthesis	251255_at	At3g62280	-1.81	0.003385	-	GDSL-like Lipase/Acylhydrolase superfamily protein
	263482_at	At2g03980	-1.54	0.026602	-	GDSL-like Lipase/Acylhydrolase superfamily protein
	249645_at	At5g36910	-3.11	0.009242	-	THI2.2__thionin 2.2
	262366_at	At1g72890	-2.16	0.004510	-	Disease resistance protein (TIR-NBS class)
	267191_at	At2g44110	-2.01	0.036977	-	ATMLO15_MLO15__Seven transmembrane MLO family protein
Stress response	255331_at	At4g04330	-1.79	0.001871	-	Chaperonin-like RbcX protein
	253627_at	At4g30650	-1.67	0.048294	-	Low temperature and salt responsive protein family
	253313_at	At4g33870	-1.59	0.003748	Yes	Peroxidase superfamily protein
	251919_at	At3g53800	-1.58	0.026771	-	Orthologs of the human Hsp70-binding protein 1 (HspBP-1) and yeast Fes1p
	263275_at	At2g14170	-1.53	0.029790	-	ALDH6B2__aldehyde dehydrogenase 6B2
Electron transport	262793_at	At1g13110	-1.75	0.002886	-	CYP71B7__cytochrome P450, family 71 subfamily B, polypeptide 7
	265227_s_at	At2g07695	-1.57	0.047555	-	Cytochrome C oxidase subunit II-like, transmembrane domain

Ion transport	262213_at	At1g74870	-3.59	0.000211	-	RING/U-box superfamily protein
	246968_at	At5g24870	-1.82	0.005574	-	RING/U-box superfamily protein
	257380_at	At2g28090	-1.64	0.001059	Yes	Heavy metal transport/detoxification superfamily protein
Oligopeptide transport	265323_at	At2g18260	-3.58	0.003220	-	ATSYP112_SYP112__syntaxin of plants 112
	249535_at	At5g38820	-2.20	0.004263	-	Transmembrane amino acid transporter family protein
Other transporters	250052_at	At5g17830	-4.60	0.003411	Yes	Plasma-membrane choline transporter family protein
	258835_at	At3g07250	-1.92	0.025338	Yes	nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein
	257593_at	At3g24840	-1.58	0.001935	-	Sec14p-like phosphatidylinositol transfer family protein
Meiosis	254435_at	At4g20900	-4.75	0.002234	-	MS5_TDM1__Tetratricopeptide repeat (TPR)-like superfamily protein
	256517_at	At1g66170	-2.61	0.036614	Yes	MMD1__RING/FYVE/PHD zinc finger superfamily protein
	265266_at	At2g42890	-1.65	0.036979	-	AML2_ML2__MEI2-like 2
	248699_at	At5g48390	-1.63	0.012743	-	AtZIP4. Defective in meiotic chromosome segregation
	245419_at	At4g17380	-1.61	0.000938	Yes	ATMSH4_MSH4_MSH4__MUTS-like protein 4
RNA binding protein	248215_at	At5g53680	-4.35	0.002879	-	RNA-binding (RRM/RBD/RNP motifs) family protein
	259377_at	At3g16380	-2.04	0.000327	-	PAB6__poly(A) binding protein 6
	265205_at	At2g36660	-1.79	0.017115	-	PAB7__poly(A) binding protein 7
	259864_at	At1g72800	-1.73	0.009746	-	RNA-binding (RRM/RBD/RNP motifs) family protein
	265449_at	At2g46610	-1.58	0.001481	-	RNA-binding (RRM/RBD/RNP motifs) family protein
Nucleic acid binding(other)	259494_at	At1g15850	-2.77	0.000521	-	Transducin/WD40 repeat-like superfamily protein
	248278_at	At5g52890	-2.01	0.031900	-	AT hook motif-containing protein
	259552_at	At1g21320	-1.72	0.007079	-	nucleotide binding;nucleic acid binding
	264971_at	At1g67210	-1.65	0.023200	-	Proline-rich spliceosome-associated (PSP) family protein / zinc knuckle (CCHC-type) family protein
Anther and pollen development	248390_at	At5g52000	-3.35	0.033601	-	IMPA-8__importin alpha isoform 8
	257451_at	At1g05690	-2.95	0.002348	-	BT3__BTB and TAZ domain protein 3
	262580_at	At1g15330	-2.85	0.025430	-	Cystathionine beta-synthase (CBS) protein
	250223_at	At5g14070	-1.54	0.021751	-	glutaredoxin ROXY2
	262178_at	At1g77860	-1.51	0.028109	-	KOM__Rhomboid-related intramembrane serine protease family protein
Cyclin	251651_at	At3g57370	-2.97	0.014788	Yes	Cyclin family protein

Cyclin

245043_at	At2g26430	-1.53	0.010804	-	ATRCY1_RCY1__arginine-rich cyclin 1
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Putative beta-1, 3-glucanase

257165_at	At3g24330	-2.08	0.034071	Yes	O-Glycosyl hydrolases family 17 protein
251754_at	At3g55780	-1.77	0.012575	Yes	Glycosyl hydrolase superfamily protein
261004_at	At1g26450	-1.70	0.004230	-	Carbohydrate-binding X8 domain superfamily protein
251280_at	At3g61810	-1.60	0.001122	-	Glycosyl hydrolase family 17 protein

Others

260659_s_at	At1g19470	-7.10	0.011718	-	Galactose oxidase/kelch repeat superfamily protein
266667_at	At2g29770	-5.15	0.001256	-	Galactose oxidase/kelch repeat superfamily protein
255464_s_at	At4g02970	-4.96	0.000028	-	AT7SL-1__7SL RNA1
249041_at	At5g44330	-4.71	0.001768	Yes	Tetratricopeptide repeat (TPR)-like superfamily protein
266677_at	At2g29820	-3.25	0.007310	-	Galactose oxidase/kelch repeat superfamily protein
254567_s_at	At4g19260	-3.12	0.000414	-	Galactose oxidase/kelch repeat superfamily protein
256975_at	At3g21000	-3.02	0.004770	Yes	Gag-Pol-related retrotransposon family protein
265213_at	At1g05020	-3.00	0.012585	-	ENTH/ANTH/VHS superfamily protein
264610_at	At1g04645	-2.98	0.015980	-	Plant self-incompatibility protein S1 family
257693_at	At3g12850	-2.91	0.008471	-	COP9 signalosome complex-related / CSN complex-related
266666_at	At2g29780	-2.88	0.014302	-	Galactose oxidase/kelch repeat superfamily protein
265007_s_at	At1g61566	-2.62	0.026665	-	RALFL9__ralf-like 9
251568_at	At3g58280	-2.58	0.017035	Yes	Arabidopsis phospholipase-like protein (PEARLI 4) with TRAF-like domain
259904_at	At1g74150	-2.55	0.001618	Yes	Galactose oxidase/kelch repeat superfamily protein
251238_at	At3g62430	-2.41	0.003814	Yes	Protein with RNI-like/FBD-like domains
266390_at	At2g32310	-2.28	0.005679	-	CCT motif family protein
266664_at	At2g29800	-2.03	0.018292	-	Galactose oxidase/kelch repeat superfamily protein
251904_at	At3g54130	-1.87	0.001496	-	Josephin family protein
255086_at	At4g09300	-1.85	0.030007	-	LisH and RanBPM domains containing protein
248124_at	At5g54730	-1.76	0.027291	-	ATATG18F_ATG18F_G18F__homolog of yeast autophagy 18 (ATG18) F
259411_at	At1g13410	-1.65	0.003960	-	Tetratricopeptide repeat (TPR)-like superfamily protein
264583_at	At1g05170	-1.60	0.002445	-	Galactosyltransferase family protein
259387_at	At1g13370	-1.55	0.026611	-	Histone superfamily protein
252873_at	At4g40020	-1.54	0.014398	-	Myosin heavy chain-related protein;
262579_at	At1g15320	-3.44	0.004175	-	Unknown protein
256519_at	At1g66110	-2.97	0.002180	-	Family of unknown function (DUF577)
261251_at	At1g05920	-2.84	0.005208	-	Domain of unknown function (DUF313)
248702_at	At5g48420	-2.80	0.006283	-	Unknown protein
248600_at	At5g49390	-2.64	0.004633	Yes	Unknown protein

	251339_at	At3g60780	-2.60	0.002411	-	Protein of unknown function (DUF1442)
	254287_at	At4g22960	-2.34	0.002236	-	Protein of unknown function (DUF544)
	245591_at	At4g14530	-2.32	0.005703	-	Unknown protein
	262836_at	At1g14680	-2.30	0.007553	Yes	Unknown protein
	257589_at	At1g55050	-2.28	0.003476	Yes	Unknown protein
	267039_at	At2g34270	-2.19	0.007458	-	Unknown protein
	254322_at	At4g22600	-2.07	0.019211	-	Unknown protein
	258424_at	At3g16750	-2.01	0.017727	-	Unknown protein
	249615_x_at	At5g37420	-1.98	0.022555	Yes	Family of unknown function (DUF577)
	255339_at	At4g04480	-1.97	0.024326	-	Unknown protein
	257391_at	At2g32050	-1.87	0.033883	-	Family of unknown function (DUF572)
	266092_at	At2g37880	-1.76	0.015567	-	Protein of unknown function, DUF617
Unknown protein	254369_at	At4g21720	-1.76	0.017601	-	unknown protein
	261461_at	At1g07860	-1.72	0.017377	Yes	Unknown protein
	251535_at	At3g58540	-1.67	0.003585	Yes	Unknown protein
	252655_at	At3g44760	-1.66	0.021869	-	Unknown protein
	266504_at	At2g47820	-1.66	0.047543	-	Unknown protein
	265495_at	At2g15695	-1.66	0.014512	-	Protein of unknown function DUF829, transmembrane 53
	250372_at	At5g11460	-1.65	0.021539	-	Protein of unknown function (DUF581)
	256957_at	At3g13420	-1.64	0.013262	-	Unknown protein
	263246_at	At2g31460	-1.63	0.007106	-	Domain of unknown function (DUF313)
	266686_at	At2g19700	-1.62	0.030549	-	Unknown protein
	266479_at	At2g31160	-1.58	0.029481	-	LSH3__Protein of unknown function (DUF640)
	259709_at	At1g77655	-1.58	0.000063	-	Unknown protein
	245261_at	At4g14385	-1.57	0.028296	-	Unknown protein
	251279_at	At3g61800	-1.56	0.008539	-	Unknown protein
	245497_at	At4g16460	-1.56	0.015478	-	Unknown protein
	249365_at	At5g40600	-1.55	0.029575	-	Unknown protein
	267022_at	At2g34230	-1.53	0.017201	-	Protein with domains of unknown function (DUF627 and DUF629)
	254179_at	At4g23910	-1.53	0.045298	-	Unknown protein

Supplemental Table 2. Up-regulated genes with expression level changed greater than 1.5-fold in the *cdm1* mutant.

Classification	Probe ID	Locus	Fold change	p-Value	Anther specific	Gene description
Carbohydrate metabolism	253631_at	At4g30440	1.97	0.026842	–	GAE1__UDP-D-glucuronate 4-epimerase 1
	251455_at	At3g60100	1.62	0.030938	–	CSY5__citrate synthase 5
Sucrose biosynthesis and transport	261072_at	At1g07340	2.45	0.034534	Yes	ATSTP2__sugar transporter 2
	264482_at	At1g77210	1.99	0.026194	–	AtSTP14_STP14__sugar transporter 14
	248211_at	At5g54010	1.96	0.004364	–	UDP-Glycosyltransferase superfamily protein
	249150_at	At5g43340	1.89	0.023038	–	PHT1;6_PHT6__phosphate transporter 1;6
	251192_at	At3g62720	1.63	0.015888	–	ATXT1_XT1_XXT1__xylosyltransferase 1
	261877_at	At1g50580	1.59	0.013922	–	UDP-Glycosyltransferase superfamily protein
	249057_at	At5g44480	1.50	0.033763	–	DUR__NAD(P)-binding Rossmann-fold superfamily protein
Pectin biosynthesis	255524_at	At4g02330	2.13	0.028705	–	ATPMEPCRB__Plant invertase/pectin methylesterase inhibitor superfamily
	249431_at	At5g39910	1.79	0.040332	–	Pectin lyase-like superfamily protein
	248968_at	At5g45280	1.51	0.015029	–	Pectinacetyltransferase family protein
Other metabolism	262369_at	At1g73010	3.04	0.008775	–	ATPS2_PS2__phosphate starvation-induced gene 2
	254926_at	At4g11280	2.11	0.044948	–	ATACS6__1-aminocyclopropane-1-carboxylic acid (acc) synthase 6
	257947_at	At3g21720	1.88	0.022361	–	ICL__isocitrate lyase
	250100_at	At5g16570	1.86	0.007305	–	GLN1;4__glutamine synthetase 1;4
	250892_at	At5g03760	1.81	0.049963	–	ATCSLA09__Nucleotide-diphospho-sugar transferases superfamily protein
	266089_at	At2g38010	1.75	0.035824	–	Neutral/alkaline non-lysosomal ceramidase
	263134_at	At1g78570	1.73	0.012400	–	ATRHM1_RHM1_ROL1__rhamnose biosynthesis 1
	259905_s_at	At1g74140	1.65	0.043988	Yes	Rhomboid-related intramembrane serine protease family protein
	258856_at	At3g02040	1.60	0.000823	–	Glycerophosphodiester phosphodiesterase (GDPD) family protein
	267541_at	At2g32750	1.58	0.001481	–	Exostosin family protein
	251827_at	At3g55120	1.58	0.041359	–	A11_CFL_TT5__Chalcone-flavanone isomerase family protein
	252967_at	At4g38880	1.51	0.013296	–	ASE3_ATASE3__GLN phosphoribosyl pyrophosphate amidotransferase 3
	252121_at	At3g51160	1.50	0.048340	–	F24M12.200, GDP-D-MANNOSE-4,6-DEHYDRATASE 2
	257203_at	At3g23730	2.43	0.016630	–	XTH16__xyloglucan endotransglucosylase/hydrolase 16

Hydrolases	259507_at	At1g43910	1.90	0.005661	-	P-loop containing nucleoside triphosphate hydrolases superfamily protein
	254158_at	At4g24380	1.81	0.027513	-	Serine hydrolase
	259786_at	At1g29660	1.68	0.040813	-	GDSL-like Lipase/Acylhydrolase superfamily protein
	261825_at	At1g11545	1.66	0.029508	-	XTH8_xyloglucan endotransglucosylase/hydrolase 8
	250604_at	At5g07830	1.58	0.003409	-	AtGUS2_GUS2_glucuronidase 2
	249657_at	At5g37140	1.57	0.036243	-	P-loop containing nucleoside triphosphate hydrolases superfamily protein
	249917_at	At5g22460	1.54	0.041370	-	alpha/beta-Hydrolases superfamily protein
	253608_at	At4g30290	1.50	0.032940	-	ATXTH19_XTH19_xyloglucan endotransglucosylase/hydrolase 19
Cell wall related	254785_at	At4g12730	1.92	0.006885	-	FLA2_FASCICLIN-like arabinogalactan 2
	247189_at	At5g65390	1.85	0.016356	-	AGP7_arabinogalactan protein 7
	256964_at	At3g13520	1.75	0.010608	-	ATAGP12_arabinogalactan protein 12
	267260_at	At2g23130	1.69	0.028621	-	ATAGP17_arabinogalactan protein 17
	255080_at	At4g09030	1.64	0.020114	-	AGP10_ATAGP10_arabinogalactan protein 10
	263927_s_at	At2g21890	1.63	0.016363	-	ATCAD3_CAD3_cinnamyl alcohol dehydrogenase homolog 3
	259664_at	At1g55330	1.61	0.011144	-	AGP21_ATAGP21_arabinogalactan protein 21
	245674_at	At1g56680	1.60	0.031618	-	Chitinase family protein
	264007_at	At2g21140	1.59	0.004897	-	ATPRP2_PRP2_proline-rich protein 2
	258415_at	At3g17390	1.58	0.044462	-	MAT4_MTO3_SAMS3_S-adenosylmethionine synthetase family protein
Protein phosphorylation and dephosphorylation	250358_at	At5g11740	1.54	0.001707	-	AGP15_ATAGP15_arabinogalactan protein 15
	254111_at	At4g24890	5.64	0.008483	-	ATPAP24_purple acid phosphatase 24
	261341_s_at	At1g52940	3.30	0.040813	-	ATPAP5_purple acid phosphatase 5
	259635_at	At1g56360	3.22	0.010690	Yes	ATPAP6_purple acid phosphatase 6
	259399_at	At1g17710	3.01	0.020803	-	Pyridoxal phosphate phosphatase-related protein
	253087_at	At4g36350	2.99	0.031652	Yes	ATPAP25_purple acid phosphatase 25
	251491_at	At3g59480	2.20	0.037607	-	pfkB-like carbohydrate kinase family protein
	265038_at	At1g03920	1.84	0.022743	-	Protein kinase family protein
	265405_at	At2g16750	1.62	0.014916	-	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain
	250360_at	At5g11360	1.55	0.035183	-	Interleukin-1 receptor-associated kinase 4 protein
248179_at	At5g54380	1.54	0.047856	-	THE1_protein kinase family protein	
265216_at	At1g05100	1.50	0.006043	-	MAPKKK18_mitogen-activated protein kinase kinase kinase 18	

	255345_at	At4g04460	1.77	0.016701	-	Saposin-like aspartyl protease family protein
	249000_at	At5g44980	1.75	0.004132	-	F-box/RNI-like/FBD-like domains-containing protein
	262087_at	At1g56030	1.74	0.004157	-	RING/U-box superfamily protein
	267056_at	At2g32470	1.71	0.022508	-	F-box associated ubiquitination effector family protein
	256108_at	At1g16940	1.68	0.002580	-	F-box/RNI-like/FBD-like domains-containing protein
Proteolysis	251239_at	At3g62440	1.67	0.017858	-	F-box/RNI-like superfamily protein
	253651_at	At4g30030	1.64	0.008477	-	Eukaryotic aspartyl protease family protein
	258431_at	At3g16580	1.61	0.016547	-	F-box and associated interaction domains-containing protein
	253579_at	At4g30610	1.58	0.043677	-	BRS1_SCPL24_alpha/beta-Hydrolases superfamily protein
	256767_at	At3g13680	1.56	0.019513	-	F-box and associated interaction domains-containing protein
	267264_at	At2g22970	1.53	0.017314	-	SCPL11_serine carboxypeptidase-like 11
	252144_at	At3g51190	2.31	0.007769	-	Ribosomal protein L2 family
	251572_at	At3g58390	2.29	0.009385	-	Eukaryotic release factor 1 (eRF1) family protein
Protein Biosynthesis	247739_at	At5g59240	1.96	0.002371	-	Ribosomal protein S8e family protein
	266972_at	At2g39590	1.79	0.031850	-	Ribosomal protein S8 family protein
	262132_at	At1g02830	1.77	0.033130	-	Ribosomal protein L13e family protein
	252283_at	At3g48960	1.71	0.009667	-	Ribosomal protein L13e family protein
	247224_at	At5g65080	3.18	0.009640	-	AGL68_MAF5_K-box region and MADS-box transcription factor family protein
	247666_at	At5g60140	2.08	0.012270	-	AP2/B3-like transcriptional factor family protein
	255014_at	At4g09960	2.05	0.028994	-	AGL11_STK_K-box region and MADS-box transcription factor family protein
	258385_at	At3g15510	2.03	0.012982	-	ANAC056_ATNAC2_NAC2_NARS1_NAC domain containing protein 2
Transcription factors	266597_at	At2g46130	1.97	0.009462	-	ATWRKY43_WRKY43_WRKY DNA-binding protein 43
	264882_at	At1g61110	1.84	0.033509	-	NAC025_NAC domain containing protein 25
	252193_at	At3g50060	1.83	0.044658	-	MYB77_myb domain protein 77
	263463_at	At2g31770	1.65	0.042392	-	ATARI9_RING/U-box superfamily protein
	251861_at	At3g54810	1.58	0.047847	-	BME3_BME3-L1_GAI18_Piant-specific GAI1A-type zinc finger transcription factor family protein
	258960_at	At3g10590	1.54	0.017428	-	Duplicated homeodomain-like superfamily protein
	260427_at	At1g72430	2.34	0.002835	-	SAUR-like auxin-responsive protein family
Hormone response	247657_at	At5g59845	2.25	0.008782	-	Gibberellin-regulated family protein
	258399_at	At3g15540	1.69	0.046016	-	IAA19_MSG2_indole-3-acetic acid inducible 19

Signal transduction(others)	249583_at	At5g37770	2.48	0.003746	-	CML24_TCH2_EF hand calcium-binding protein family
	263903_at	At2g36180	2.44	0.000810	-	EF hand calcium-binding protein family
	266447_at	At2g43290	2.20	0.001468	-	MSS3_Calcium-binding EF-hand family protein
	253571_at	At4g31000	1.78	0.007180	-	Calmodulin-binding protein
	245334_at	At4g15800	1.52	0.020917	-	RALFL33_ralf-like 33
Fatty acid - lipid biosynthesis	248638_at	At5g49070	3.26	0.040551	Yes	KCS21_3-ketoacyl-CoA synthase 21
	250610_at	At5g07550	2.94	0.025952	-	ATGRP19_GRP19_glycine-rich protein 19
	263195_at	At1g36150	2.41	0.046607	-	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
	245322_at	At4g14815	1.91	0.002596	-	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
	256381_at	At1g66850	1.80	0.016599	Yes	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
	255732_at	At1g25450	1.65	0.004383	-	CER60_KCS5_3-ketoacyl-CoA synthase 5
Stress response	264648_at	At1g09080	5.82	0.001384	-	BIP3_Heat shock protein 70 (Hsp 70) family protein
	246418_at	At5g16960	2.43	0.044079	-	Zinc-binding dehydrogenase family protein
	262113_at	At1g02820	2.20	0.029844	-	Late embryogenesis abundant 3 (LEA3) family protein
	253839_at	At4g27890	2.19	0.003878	-	HSP20-like chaperones superfamily protein
	248434_at	At5g51440	1.80	0.004205	-	HSP20-like chaperones superfamily protein
	262911_s_at	At1g59860	1.76	0.039016	-	HSP20-like chaperones superfamily protein
	248719_at	At5g47910	1.71	0.001589	-	ATRBOHD_RBOHD_respiratory burst oxidase homologue D
	267069_at	At2g41010	1.69	0.017760	-	ATCAMP25_CAMBP25_calmodulin (CAM)-binding protein of 25 kDa
	260686_at	At1g17620	1.69	0.000358	-	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
	264436_at	At1g10370	1.67	0.034774	-	ATGSTU17_ERD9_GST30_GST30B_Glutathione S-transferase family protein
	254563_at	At4g19120	1.51	0.041998	-	ERD3_early-responsive to dehydration 3
258751_at	At3g05890	1.50	0.038262	-	RCI2B_Low temperature and salt responsive protein family	
Electron transport	260228_at	At1g74540	2.56	0.041783	Yes	CYP98A8_cytochrome P450, family 98, subfamily A, polypeptide 8
	265422_at	At2g20800	2.37	0.016256	-	NDB4_NAD(P)H dehydrogenase B4
	259852_at	At1g72280	2.05	0.035133	-	AERO1_ERO1_endoplasmic reticulum oxidoreductins 1
	257633_at	At3g26125	2.01	0.045400	-	CYP86C2_cytochrome P450, family 86, subfamily C, polypeptide 2
	262933_at	At1g65840	1.55	0.022588	-	ATPAO4_PAO4_polyamine oxidase 4
	262764_at	At1g13140	1.54	0.045919	Yes	CYP86C3_cytochrome P450, family 86, subfamily C, polypeptide 3

	265188_at	At1g23800	1.51	0.010417	-	ALDH2B_ALDH2B7__aldehyde dehydrogenase 2B7
	253915_at	At4g27280	3.61	0.007302	-	Calcium-binding EF-hand family protein
	254884_at	At4g11730	2.61	0.024809	-	Cation transporter/ E1-E2 ATPase family protein
	259327_at	At3g16460	2.18	0.003746	-	Mannose-binding lectin superfamily protein
Ion transport	246302_at	At3g51860	1.99	0.035034	-	ATCAX3_ATHCX1_CAX1-LIKE_CAX3__cation exchanger 3
	265460_at	At2g46600	1.96	0.002629	-	Calcium-binding EF-hand family protein
	254855_s_at	At4g12140	1.70	0.022233	-	RING/U-box superfamily protein
	263319_at	At2g47160	1.55	0.036325	-	BOR1__HCO3- transporter family
	251975_at	At3g53230	1.54	0.037119	-	ATPase, AAA-type, CDC48 protein
	265002_at	At1g24400	2.64	0.011178	-	AATL2_ATLHT2_LHT2__lysine histidine transporter 2
	248274_at	At5g53510	2.11	0.021368	-	ATOPT9_oligopeptide transporter 9
Oligopeptide transport	262912_at	At1g59740	1.84	0.016025	-	Major facilitator superfamily protein
	245740_at	At1g44100	1.72	0.004759	-	AAP5__amino acid permease 5
	257671_at	At3g20450	1.68	0.036703	-	B-cell receptor-associated protein 31-like
	258760_at	At3g10780	1.68	0.027512	-	emp24/gp25L/p24 family/GOLD family protein
	265064_at	At1g61630	2.04	0.046975	-	ATENT7_equilibrative nucleoside transporter 7
Other transporters	253193_at	At4g35380	1.93	0.014487	-	SEC7-like guanine nucleotide exchange family protein
	254120_at	At4g24570	1.85	0.029046	-	DIC2__dicarboxylate carrier 2
	261926_at	At1g22530	1.57	0.011419	-	PATL2__PATELLIN 2
	255575_at	At4g01430	2.12	0.028343	-	Nodulin MtN21 /EamA-like transporter family protein
Nodulin proteins	261335_at	At1g44800	1.99	0.036179	-	Nodulin MtN21 /EamA-like transporter family protein
	255576_at	At4g01440	1.61	0.027334	-	nodulin MtN21 /EamA-like transporter family protein
	250110_at	At5g15350	1.60	0.010991	-	AtENODL17_ENODL17__early nodulin-like protein 17
Pollen development	267440_at	At2g19070	3.32	0.046943	-	SHT__spermidine hydroxycinnamoyl transferase
	252364_at	At3g48450	2.96	0.042199	-	RPM1-interacting protein 4 (RIN4) family protein
	251498_at	At3g59070	2.87	0.002265	-	Cytochrome b561/ferric reductase transmembrane with DOMON related domain
	265881_at	At2g42480	2.64	0.019325	-	TRAF-like family protein

Others

247961_at	At5g56570	2.56	0.010292	-	Leucine-rich repeat (LRR) family protein
252944_at	At4g39320	2.19	0.044770	-	Microtubule-associated protein-related
252160_at	At3g50570	2.07	0.017824	-	hydroxyproline-rich glycoprotein family protein
250677_at	At5g06520	2.03	0.013749	-	SWAP (Suppressor-of-White-APricot)/surp domain-containing protein
261586_at	At1g01640	2.02	0.009986	-	BTB/POZ domain-containing protein
254212_at	At4g23580	1.95	0.008177	-	Galactose oxidase/kelch repeat superfamily protein
251569_at	At3g58290	1.95	0.025007	-	TRAF-like superfamily protein
257442_at	At2g28680	1.89	0.046103	-	RmlC-like cupins superfamily protein
252615_at	At3g45230	1.80	0.019653	-	hydroxyproline-rich glycoprotein family protein
254570_s_at	At4g19330	1.71	0.002017	-	Galactose oxidase/kelch repeat superfamily protein
245559_at	At4g15460	1.68	0.007546	-	Glycine-rich protein
257900_at	At3g28420	1.68	0.013643	-	Putative membrane lipoprotein
266549_at	At2g35150	1.67	0.019044	-	EXL1__EXORDIUM like 1
250535_at	At5g08480	1.61	0.022658	-	VQ motif-containing protein
245058_at	At2g39790	1.58	0.017796	-	Mitochondrial glycoprotein family protein
253169_at	At4g35120	1.58	0.009954	-	Galactose oxidase/kelch repeat superfamily protein
256275_at	At3g12110	1.58	0.002096	-	ACT11__actin-11
264966_at	At1g60570	1.56	0.029473	-	Galactose oxidase/kelch repeat superfamily protein
265251_at	At2g01960	1.51	0.036724	-	TET14__tetraspanin14
248241_at	At5g53960	1.99	0.035419	-	ATP binding;DNA binding;DNA topoisomerase (ATP-hydrolyzing)s
247293_at	At5g64510	2.46	0.025705	-	Unknown protein;
253643_at	At4g29780	2.21	0.040071	-	Unknown protein
248716_at	At5g48210	2.16	0.024190	Yes	Protein of unknown function (DUF1278)
256867_at	At3g26390	2.14	0.023971	-	Unknown protein
256569_at	At3g19550	2.10	0.017261	-	Unknown protein
252161_at	At3g50580	2.06	0.031814	-	Unknown protein
257578_x_at	At3g30160	2.05	0.003392	-	Unknown protein
253165_at	At4g35320	2.02	0.010779	-	Unknown protein
265438_at	At2g20970	2.00	0.016996	-	Unknown protein
254793_at	At4g12930	1.93	0.040199	-	Unknown protein
264359_at	At1g03320	1.91	0.030834	-	Unknown protein
258397_at	At3g15357	1.88	0.008059	-	Unknown protein

Unknown protein	262910_at	At1g59710	1.70	0.015515	-	Protein of unknown function (DUF569)
	260883_at	At1g29270	1.69	0.014749	-	Unknown protein
	265186_at	At1g23560	1.65	0.031498	-	Domain of unknown function (DUF220)
	266550_s_at	At2g35070	1.65	0.006349	-	Unknown protein
	254823_at	At4g12580	1.62	0.029172	-	Unknown protein
	259433_at	At1g01570	1.57	0.007240	-	Protein of unknown function (DUF604)
	260761_at	At1g49150	1.57	0.001646	-	Unknown protein
	249211_at	At5g42680	1.56	0.001018	-	Protein of unknown function, DUF617
	265823_at	At2g35760	1.56	0.026118	-	Uncharacterised protein family (UPF0497)
	266635_at	At2g35470	1.55	0.010343	-	Unknown protein
	264902_at	At1g23060	1.53	0.038465	-	Unknown protein
	257555_at	At3g24780	1.53	0.027452	-	Uncharacterised conserved protein UCP015417
	264909_at	At2g17300	1.53	0.043793	-	Unknown protein
	253525_at	At4g31330	1.51	0.034161	-	Protein of unknown function, DUF599
	267633_at	At2g42180	1.51	0.010992	Yes	Unknown protein
	248904_at	At5g46295	1.50	0.036653	-	Unknown protein

Supplemental Table 3. The genes show differential expression levels between *cdm1* and the wild type, involved in callose dissolution and anther and pollen development.

Classification	Probe ID	Locus	Fold change	p-Value	Anther specific	Gene name/description
Putative beta-1, 3-glucanase	257165_at	At3g24330	-2.08	0.034071	Yes	O-Glycosyl hydrolases family 17 protein
	251754_at	At3g55780	-1.77	0.012575	Yes	Glycosyl hydrolase superfamily protein
	251280_at	At3g61810	-1.60	0.001122	–	Glycosyl hydrolase family 17 protein
Anther and pollen development	248390_at	At5g52000	-3.35	0.033601	–	IMPA-8__importin alpha isoform 8 (Borg et al., 2011)
	257451_at	At1g05690	-2.95	0.002348	–	BT3__BTB and TAZ domain protein 3 (Robert et al., 2009)
	262580_at	At1g15330	-2.85	0.025430	–	AtPV42a__Cystathionine beta-synthase (CBS) protein (Fang et al., 2011)
	250223_at	At5g14070	-1.54	0.021751	–	glutaredoxin ROXY2 (Xing and Zachgo, 2008)
	262178_at	At1g77860	-1.51	0.028109	–	KOM__Intramembrane serine protease family protein (Kanaoka et al., 2002, 2003)
	267440_at	At2g19070	3.32	0.046943	–	SHT__spermidine hydroxycinnamoyl transferase (Dobritsa et al., 2011)

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Supplemental Table 4. Primer sequences used in this study.

Stock Number	Nucleotide sequence	Gene	Purpose
oMC7506	5'-GTTGTGTTACACGCGTCTCC-3'	<i>CDM1</i> Forward	qRT-PCR
oMC7507	5'-AAATCGGTTCTGGATCGAAG-3'	<i>CDM1</i> Reverse	
oMC7508	5'-AAGCCATTTTCAGAGCCAAGT-3'	At2g13680 (<i>AtGSL2/CalS5</i>) Forward	qRT-PCR
oMC7509	5'-CACTTCGCTTCTGATTTCCA-3'	At2g13680 (<i>AtGSL2/CalS5</i>) Reverse	
oMC7510	5'-TGCCACATCTCTTATCCCAA-3'	AT5G13390 (<i>NEF1</i>) Forward	qRT-PCR
oMC7511	5'-TGTTACAACGATCAGGGCAT-3'	AT5G13390 (<i>NEF1</i>) Reverse	
oMC7512	5'-AAAGAAGGGTCTCACCATCG-3'	AT3G09090 (<i>DEX1</i>) Forward	qRT-PCR
oMC7513	5'-ACCGTCAACATTATCAGCCA-3'	AT3G09090 (<i>DEX1</i>) Reverse	
oMC7527	5'-GAAGAATCTTGGGTGGGAGA-3'	At5g24860 (<i>FLP1</i>) Forward	qRT-PCR
oMC7528	5'-GGAGAAGTCACGAGGGAGAG-3'	At5g24860 (<i>FLP1</i>) Reverse	
oMC7529	5'-CTGCTGCT AATACAACCT-3'	At3g11980 (<i>MS2</i>) Forward	qRT-PCR
oMC7530	5'-TGCTATAACAATCTCCATA-3'	At3g11980 (<i>MS2</i>) Reverse	
oMC7531	5'-TACCTAAACCGACGAACA-3'	At4g14080 (<i>A6</i>) Forward	qRT-PCR
oMC7532	5'-ATGCCAATAAATG GAGAC-3'	At4g14080 (<i>A6</i>) Reverse	
oMC7533	5'-GAAGAAGAAGTTGTCAGGAA-3'	At5g56110 (<i>AtMYB103</i>) Forward	qRT-PCR
oMC7534	5'-GTGAGCAAGTGAAGCATCT-3'	At5g56110 (<i>AtMYB103</i>) Reverse	
oMC7537	5'-TCAGCCTTTCAACAAGATCG-3'	At4g04970 (<i>AtGSL1/CalS11</i>) Forward	qRT-PCR
oMC7538	5'-TCGAGTAGCTCAACCTCCCT-3'	At4g04970 (<i>AtGSL1/CalS11</i>) Reverse	
oMC7541	5'-CCACCAGGAGTACATTCAGG-3'	At4g03550 (<i>AtGSL5/CalS12</i>) Forward	qRT-PCR
oMC7542	5'-TGAAGAAATCAAGCCTGTGC-3'	At4g03550 (<i>AtGSL5/CalS12</i>) Reverse	
oMC7589	5'-ACCAGTCTACTTCGGAGA-3'	At4g18340 Forward	qRT-PCR
oMC7590	5'-GCTCCTCTTTGCCTTAGTGG-3'	At4g18340 Reverse	
oMC7591	5'-AACGGTGGAGTCAACATCAA-3'	At3g24330 Forward	qRT-PCR
oMC7592	5'-TTCCTCTAGTGCTCGTTGGA-3'	At3g24330 Reverse	
oMC7593	5'-ACCACCGGAGTAAGATACCG-3'	At3g55780 Forward	qRT-PCR
oMC7594	5'-GAGCTAGGCCAACCAGTCTC-3'	At3g55780 Reverse	
oMC7635	5'-ATTCAACCACAGCAAGTCCA-3'	At1g26450 Forward	qRT-PCR
oMC7636	5'-CACTCGTGCTGCTAGATGGT-3'	At1g26450 Reverse	
oMC7597	5'-TGTAGGTCCACAAATCGGAA-3'	At3g61810 Forward	qRT-PCR
oMC7598	5'-CGATGGTATTGCTTCTGGTG-3'	At3g61810 Reverse	
oMC7599	5'-CTTCAACCCTAACCCCTGGAA-3'	At1g30080 Forward	qRT-PCR
oMC7600	5'-TCGATGTCTTTGAAGCCAAG-3'	At1g30080 Reverse	
oMC7609	5'-CATGGAGCAACAGTTTGGAC-3'	At1g77860 Forward	qRT-PCR
oMC7610	5'-GCAGCACCAGAAGAGATTGA-3'	At1g77860 Reverse	
oMC7611	5'-ACCATCCATGTTGTTGTTGG-3'	At4g24890 Forward	qRT-PCR
oMC7612	5'-GAGTGATCGGAAGCAGTCAA-3'	At4g24890 Reverse	
oMC7647	5'-TTTGGCTTGAGCAAGAGCTA-3'	At1g56360 Forward	qRT-PCR
oMC7648	5'-TAACGAGCCACGACTCAAAC-3'	At1g56360 Reverse	
oMC7651	5'-CATCACGCCACAATTAAGG-3'	At4g36350 Forward	qRT-PCR
oMC7652	5'-CACCAATAATGCCGAAAGTG-3'	At4g36350 Reverse	
oMC7617	5'-TGTTCCGAAATTGTTGGTGT-3'	At1g74540 Forward	qRT-PCR
oMC7618	5'-ATCTCTGCCATAGCCCATTG-3'	At1g74540 Reverse	
oMC7659	5'-GTGAACGCAATCGCTACAGT-3'	At1g07340 Forward	qRT-PCR
oMC7660	5'-TGTAGCGGTCATCTGGAGAG-3'	At1g07340 Reverse	
oMC7703	5'-GGGCTATGACTGCTGGAAAT-3'	At5g52000 (<i>IMPA-8</i>) Forward	qRT-PCR
oMC7704	5'-AGTCCCTGCAGTGATGTTG-3'	At5g52000 (<i>IMPA-8</i>) Reverse	
oMC7705	5'-GTCTCACTTCTGCCCCATT-3'	At1g05690 (<i>BT3</i>) Forward	qRT-PCR
oMC7706	5'-CTGCTTCAACAAGGAACTCCA-3'	At1g05690 (<i>BT3</i>) Reverse	
oMC7707	5'-TTGATTGAGTCTGCCTCTGC-3'	At1g15330 (<i>AtPV42a</i>) Forward	qRT-PCR
oMC7708	5'-TGGCGTAAACGGAATCATT-3'	At1g15330 (<i>AtPV42a</i>) Reverse	
oMC7709	5'-GTGTTTCATCGGAGGGAAGAT-3'	At5g14070 (<i>ROXY2</i>) Forward	qRT-PCR
oMC7710	5'-GCACTCATCAGAGCCAAAGA-3'	At5g14070 (<i>ROXY2</i>) Reverse	
oMC7711	5'-CATGGAGCAACAGTTTGGAC-3'	At1g77860 (<i>KOM</i>) Forward	qRT-PCR
oMC7712	5'-GCAGCACCAGAAGAGATTGA-3'	At1g77860 (<i>KOM</i>) Reverse	
oMC7713	5'-GAAGTAAAGCCAACGGAAGC-3'	At2g19070 (<i>SHT</i>) Forward	qRT-PCR
oMC7714	5'-ATTCTAGAGCCGTTGGTTG-3'	At2g19070 (<i>SHT</i>) Reverse	
oMC7715	5'-AATTGGTAGCCAGTGAAGG-3'	At2g42890 (<i>MEI2-like2</i>) Forward	qRT-PCR
oMC7716	5'-GAGCAGGAAGAATTGAAGCC-3'	At2g42890 (<i>MEI2-like2</i>) Reverse	

oMC1533	5'-GGTAACATTGTGCTCAGTGGTGG-3'	Actin Forward	
oMC1534	5'-AACGACCTTAATCTTCATGCTGC-3'	Actin Reverse	qRT-PCR
oMC2216	5'-ACCGGCAAGACCATCACTCT-3'	Ubiquitin Forward	
oMC2217	5'-AGGCCTCAACTGGTTGCTGT-3'	Ubiquitin Reverse	RT-PCR
oMC7395	TCATGTGATCAGCTTGAGGG	CDM1 Reverse	RT-PCR
oMC7489	5'-TAAATCTGGCATGCAAATGTG-3'	SALK_065040 LP	
oMC7490	5'-TGAATTCACCACATAACCGATG-3'	SALK_065040 RP	T-DNA Identification
oMC7545	5'-ATGAAAACAAAATCGCGCC-3'	<i>CDM1</i> RNA <i>In situ</i> Forward	
oMC7546	5'-TCTCTTCCTCCTGATCTTCT-3'	<i>CDM1</i> RNA <i>In situ</i> Reverse	<i>In situ</i> probe
oMC7495	5'- cctctagagtcgacctgcagTATGGTCCCAAGAAAA TGGCAGAG-3'	<i>CDM1</i> promoter forward, with 15bp overlapping with pCAMBIA1301 Pst I digested end	
oMC7494	5'-TTTCCCGGTGACAATTCTGTTACACA-3'	<i>CDM1</i> promoter reverse	
oMC7496	5'- attgtcaccgggaaaaATGAAAACAAAATCGCG CCGTTT-3'	<i>CDM1</i> CDS forward, with 15bp overlapping with its promoter region	The GR inducible construction for functional complementation of cdm1 mutant
oMC7497	5'- agtggcttgctgaatTGTGATCAGCTTGAGGGATG ACT-3'	<i>CDM1</i> CDS reverse, with 15bp overlapping with GR domain	
oMC7453	5'-ATTCAGCAAGCCACTGCAGG-3'	GR Sense primer	
oMC7456	5'- ACCTGTAATTCACACGTGTTACTTGTCATCG TCATCCTTGAATC-3'	3xFLAG Reverse primer, 5' add stop codon and 15 nt region complementary to pCAMBIA1301 vector PmlI end	