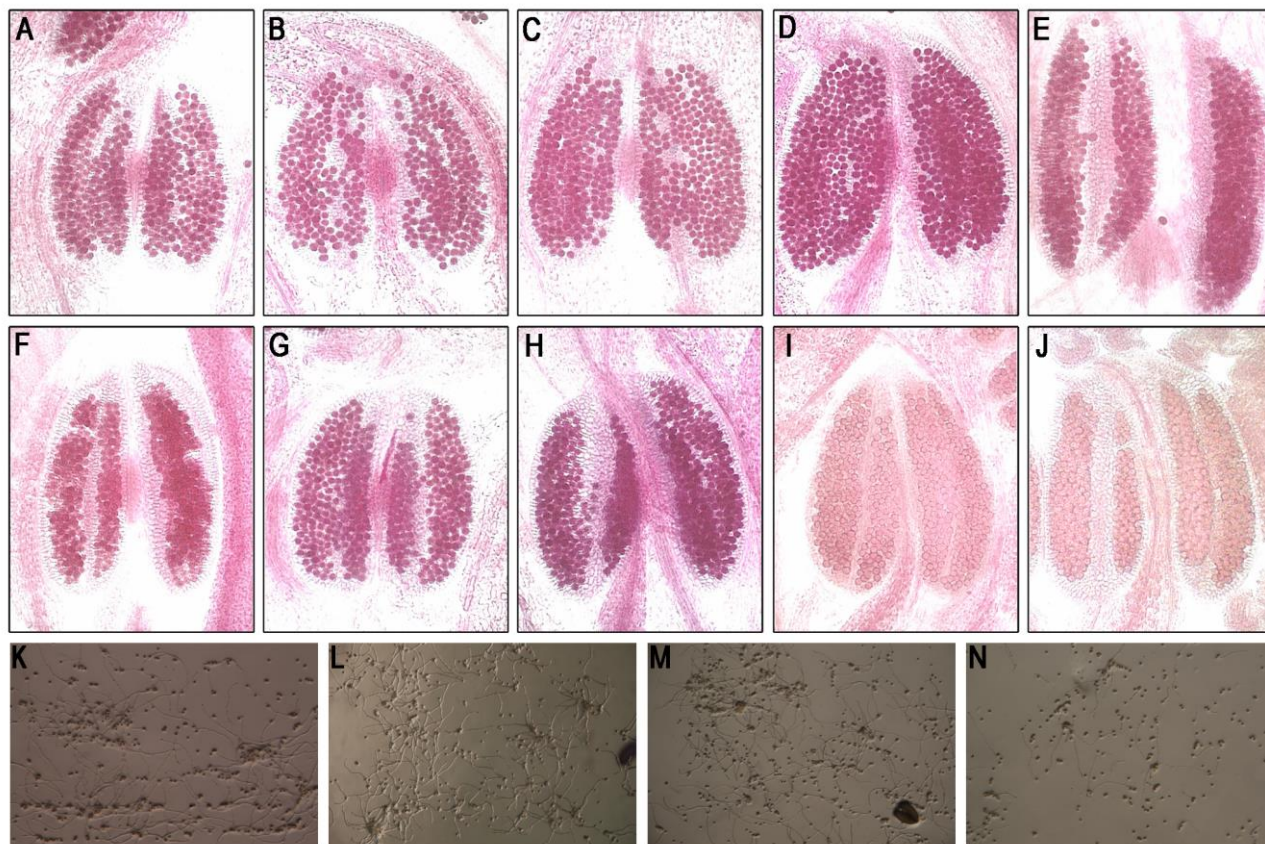


Supplemental Figure 1. Phenotypic Comparison of WW Plants and DT Plants.

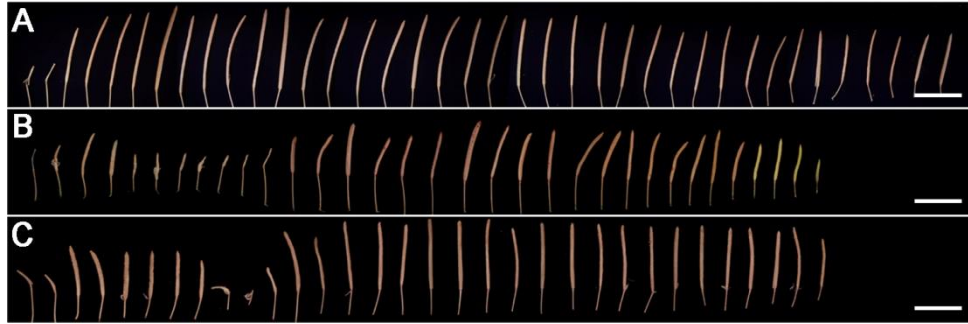
(A) The photo was taken after the plants were put inside the growth chamber for 18 days. (B) The photo was taken after the plants were put inside the growth chamber for 24 days. (C) The plant to be well-watered which has around 1 cm main stem at day 24. (D) The plant to be treated with drought which has around 1 cm main stem at day 24. (E) At C1/T1, the plants grew over 25 days and had been treated with drought for 1 day. (F) C2/T2. (G) C4/T4. (H) C6/T6. (I) C8/T8. (J) C9/T9. At this

time point, the plants grew over 34 days and had been treated for 10 day. Scale bars for A-J, 3 cm. **(K)-(Q)** The floral buds (stage 8-12) and 0-2 flowers from WW plants at C0(**K**), C3(**L**), C5(**M**), C7(**N**), C10(**O**), C12(**P**), and C15(**Q**). **(R)-(X)** The floral buds and 0-2 flowers from DT plant at T0(**R**), T3(**S**), T5(**T**), T7(**U**), T10(**V**), T12(**W**), and T15(**X**). Scale bars, 2 mm.



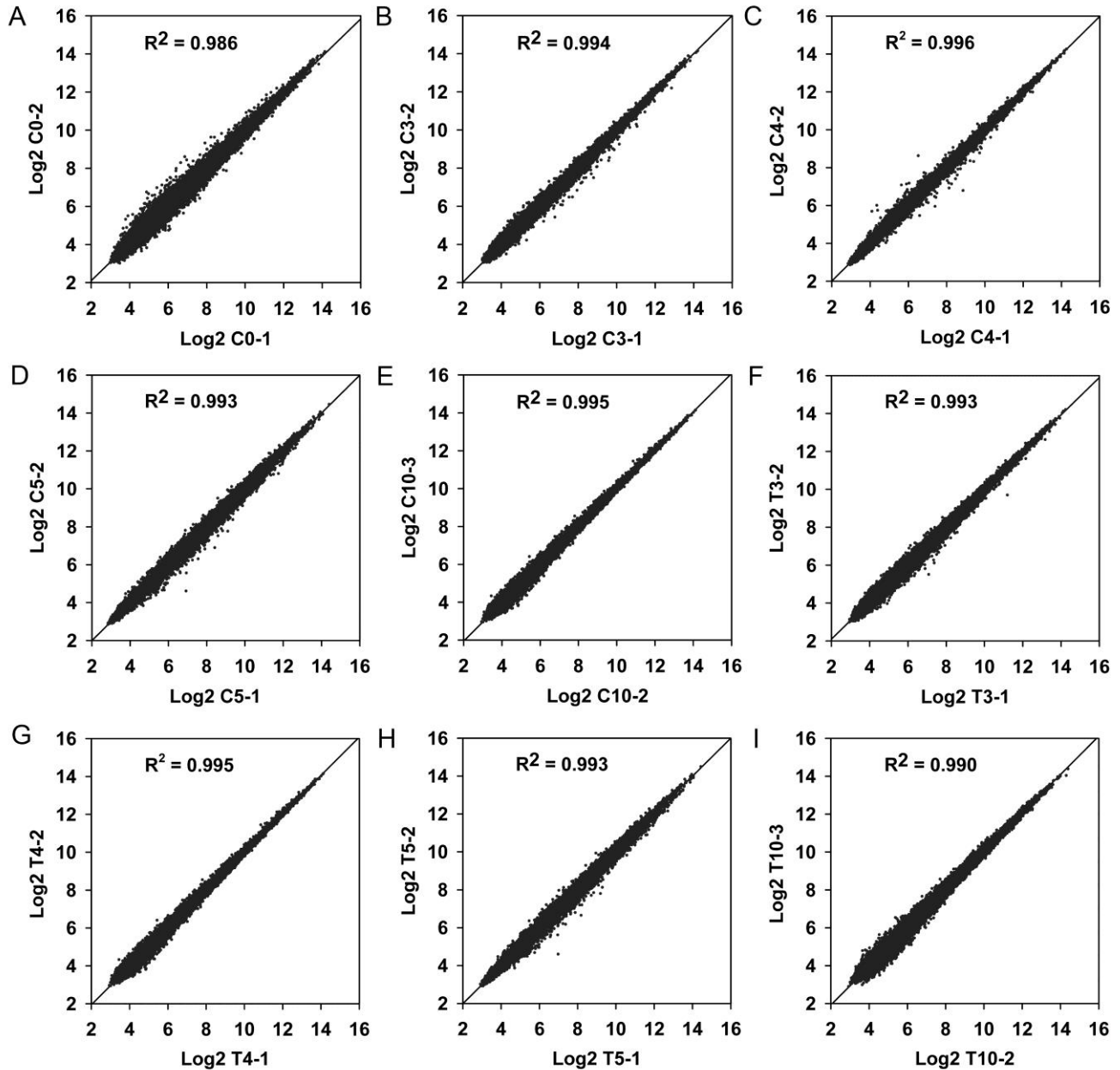
Supplemental Figure 2. Alexander Staining of the Anthers from WW Plants and DT Plants.

(A)-(E) The staining result of anthers collected from WW plants on C0, C3, C5, C7, C9. (F)-(J) The staining result of anthers collected from DT plants on T0, T3, T5, T7, T9. (K)-(N) The *in vitro* germination assay of the pollens from WW plants on C3(K) and C7(M) comparing with those from DT plants on T3(L) and T7(N).



Supplemental Figure 3. Silique Growth was Affected by Drought Stress.

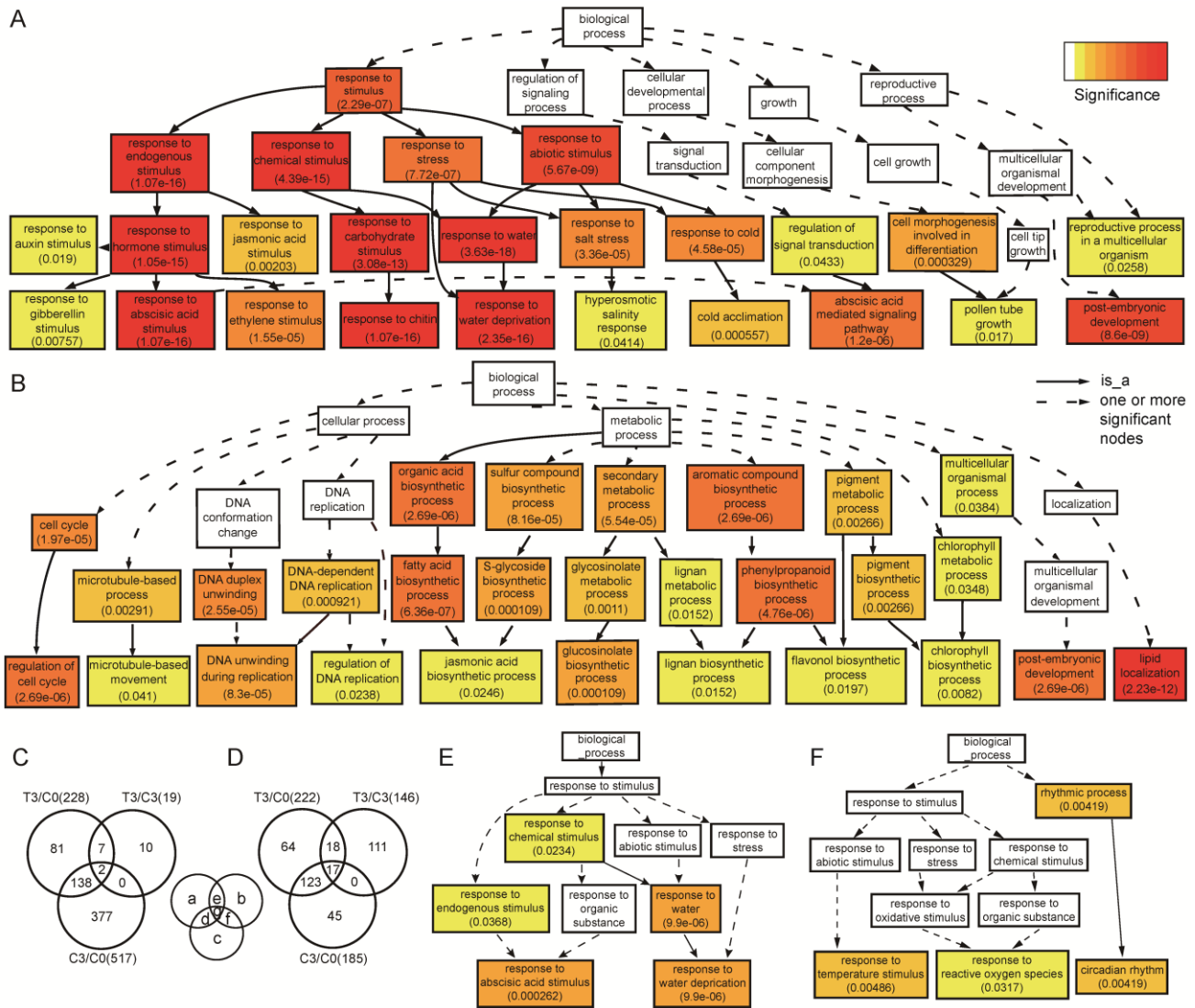
(A) All siliques from a WW plant. The siliques (left to right) were collected one at a time from the bottom to the top of the main inflorescence stem. (B) All siliques from a DT plant main inflorescence, similar to those in (A). (C) All siliques produced from the DT pistil (DPi) pollinated with pollen grains (WP) from WW plants.



Supplemental Figure 4. Correlation between Two Biological Replicates at Each Time Point.

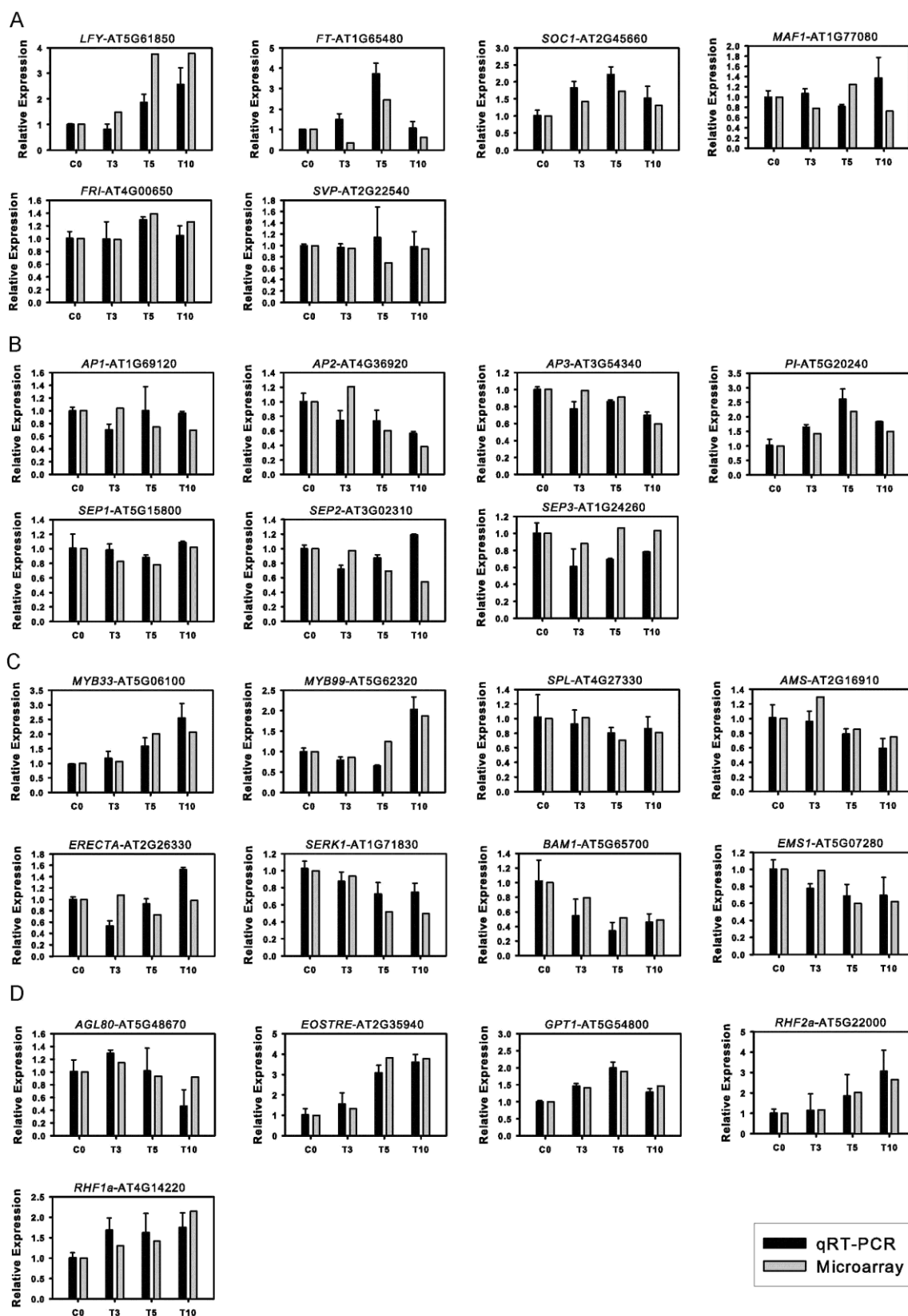
The data for the linear analysis are based on log 2 of the expression data. (A) C0 is the inflorescence from the plants grown on well watered condition for 24 days, we use this time point as our start point of the drought treatment; (B) C3 is the inflorescence from around 28-day-old plant with well watered condition; (C) C4 is the inflorescence from around 29-day-old plant with well watered condition; (D) C5 is the inflorescence from around 30-day-old plant with well watered condition; (E) C10 is the

inflorescence from around 34-day-old plant with well watered condition; **(F)** T3 is the inflorescence from the 28-day-old plant withholding water for 3 days; **(G)** T4 is the inflorescence from the 29-day-old plant withholding water for 4 days; **(H)** T5 is the inflorescence from the 30-day-old plant withholding water for 5 days; **(I)** T10 is the inflorescence from the 34-day-old plant withholding water for 10 days. R^2 is the square of the correlation coefficient which stands for the Pearson's coefficient between replicates.



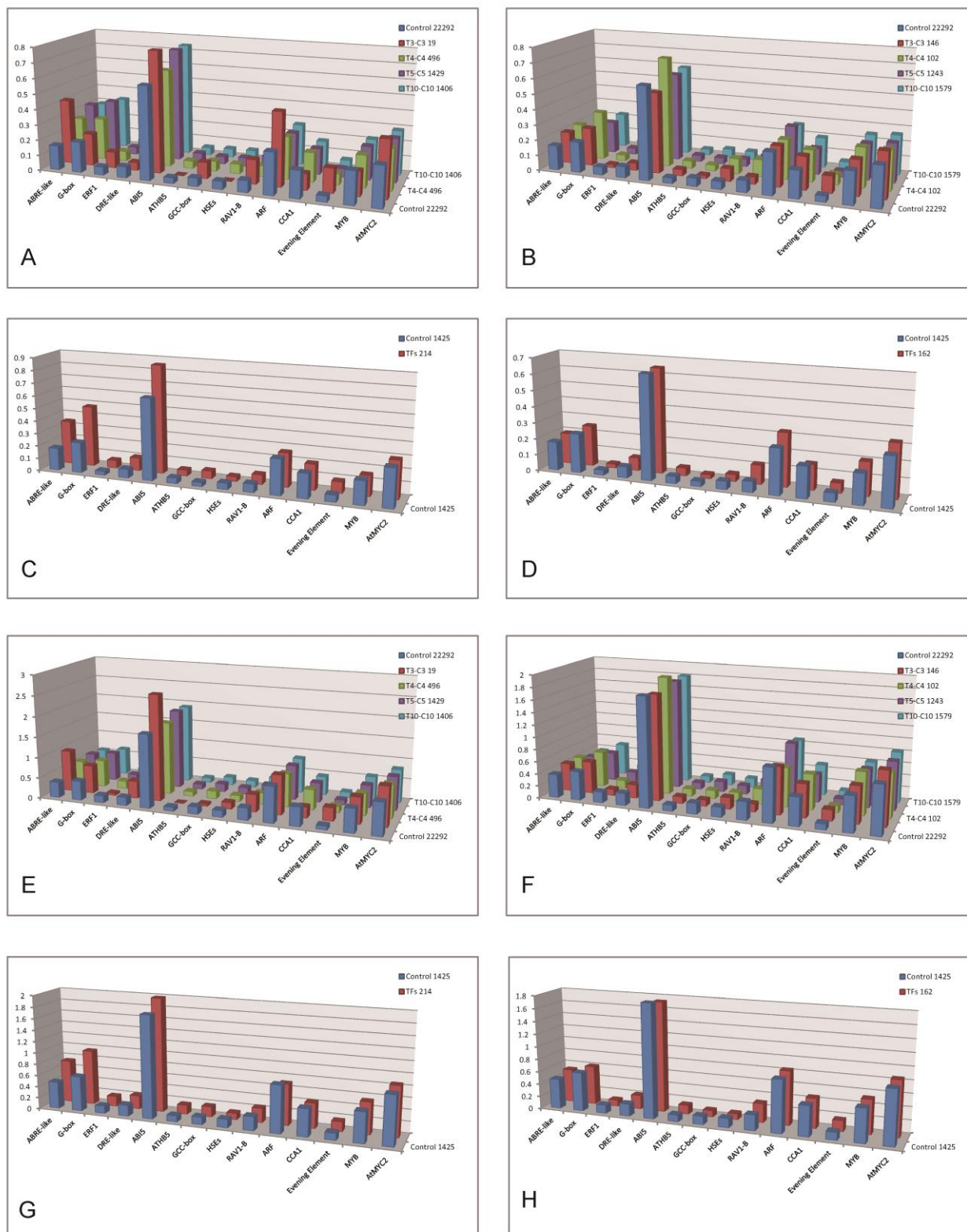
Supplemental Figure 5. The Venn Diagram and Enrichment Analysis of Differentially Expressed Genes.

(A) The enrichment analysis of all up-regulated genes with p-values. The reder the filled color is, the more significant the group is. (B) The enrichment analysis of all down-regulated genes with p-values. (C) The Venn Diagram of up-regulated genes differential expressed at T3 from 3 different comparing groups. (D) The Venn Diagram of down-regulated genes differential expressed at T3 from 3 different comparing groups. (E) The enrichment analysis of the genes combined from a b e groups (98 genes) of up-regulated genes at T3. (F) The enrichment analysis of the genes combined from a b e groups (193 genes) of down-regulated genes at T3.



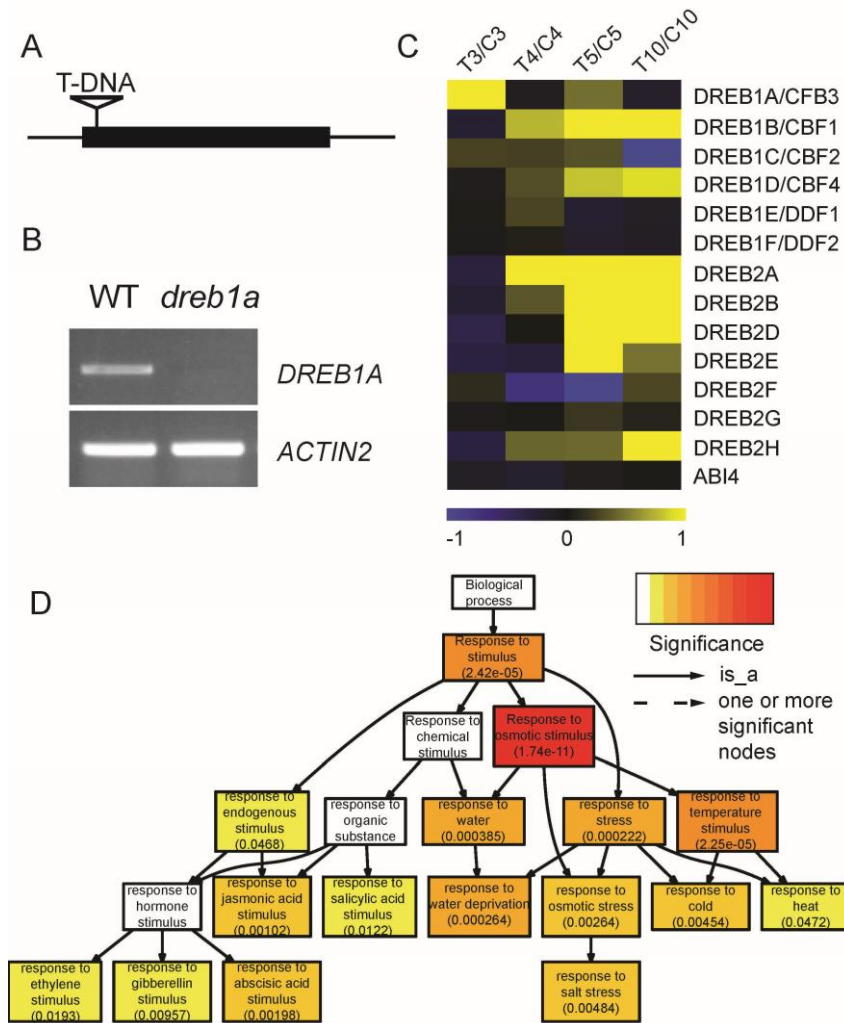
Supplemental Figure 6. QPCR Verification of Microarray Data.

(A) The flowering time related genes. **(B)** ABC model genes. **(C)** Anther development genes. **(D)** Pistil development genes.



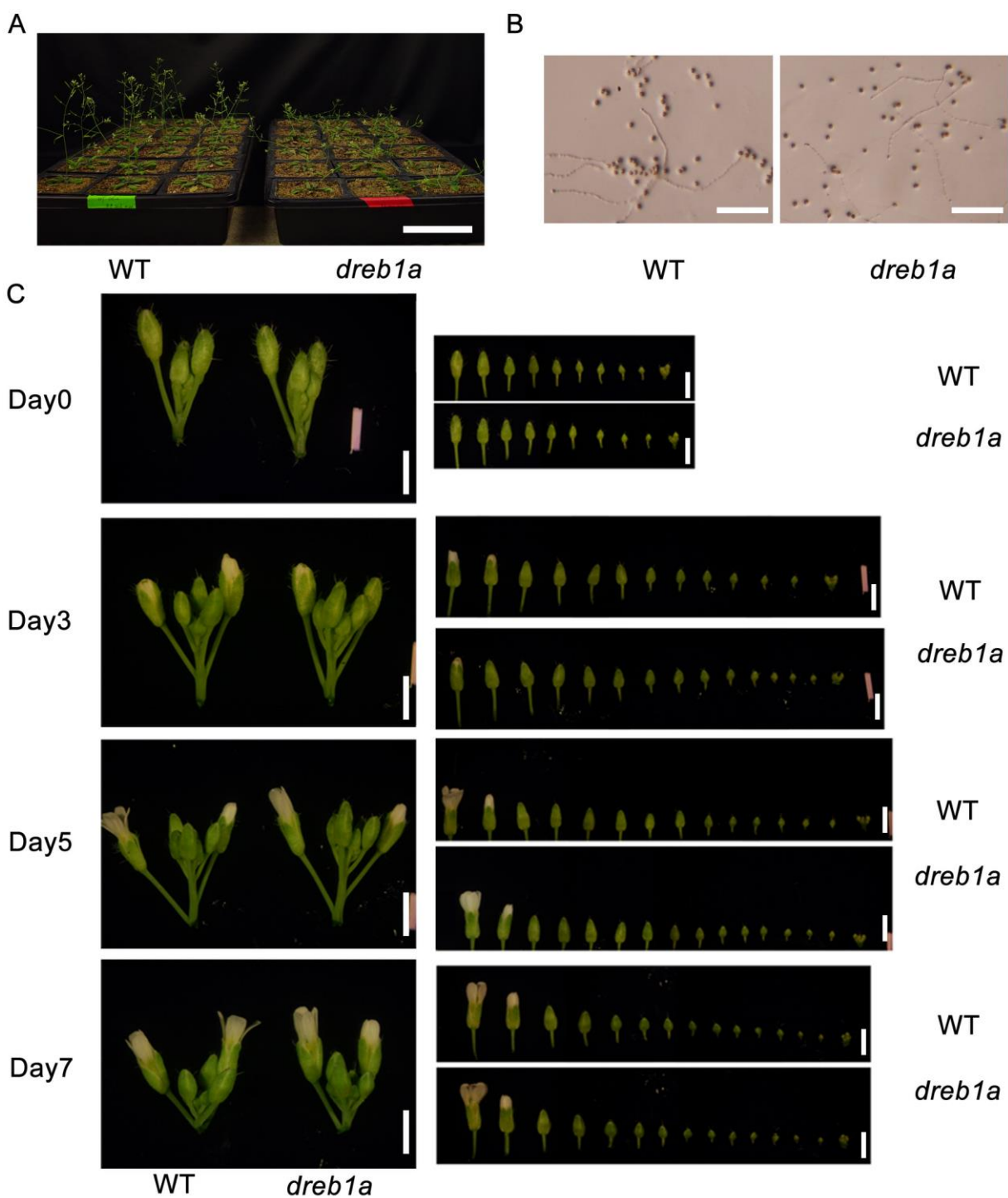
Supplemental Figure 7. *cis*-Regulatory Element Analysis of 1 kb and 3 kb Promoters of Differentially Expressed Genes.

(A) *cis*-regulatory element (CRE) analysis within 1000bp promoter of all up-regulated genes. (B) CRE analysis within 1000bp promoter of all down-regulated genes. (C) CRE analysis within 3000bp promoter of all up-regulated transcription factors. (D) CRE analysis within 3000bp promoter of all down-regulated transcription factors.



Supplemental Figure 8. The *dreb1a* T-DNA Mutant Information and *DREB* Genes Expression Pattern under Drought Stress in Flower.

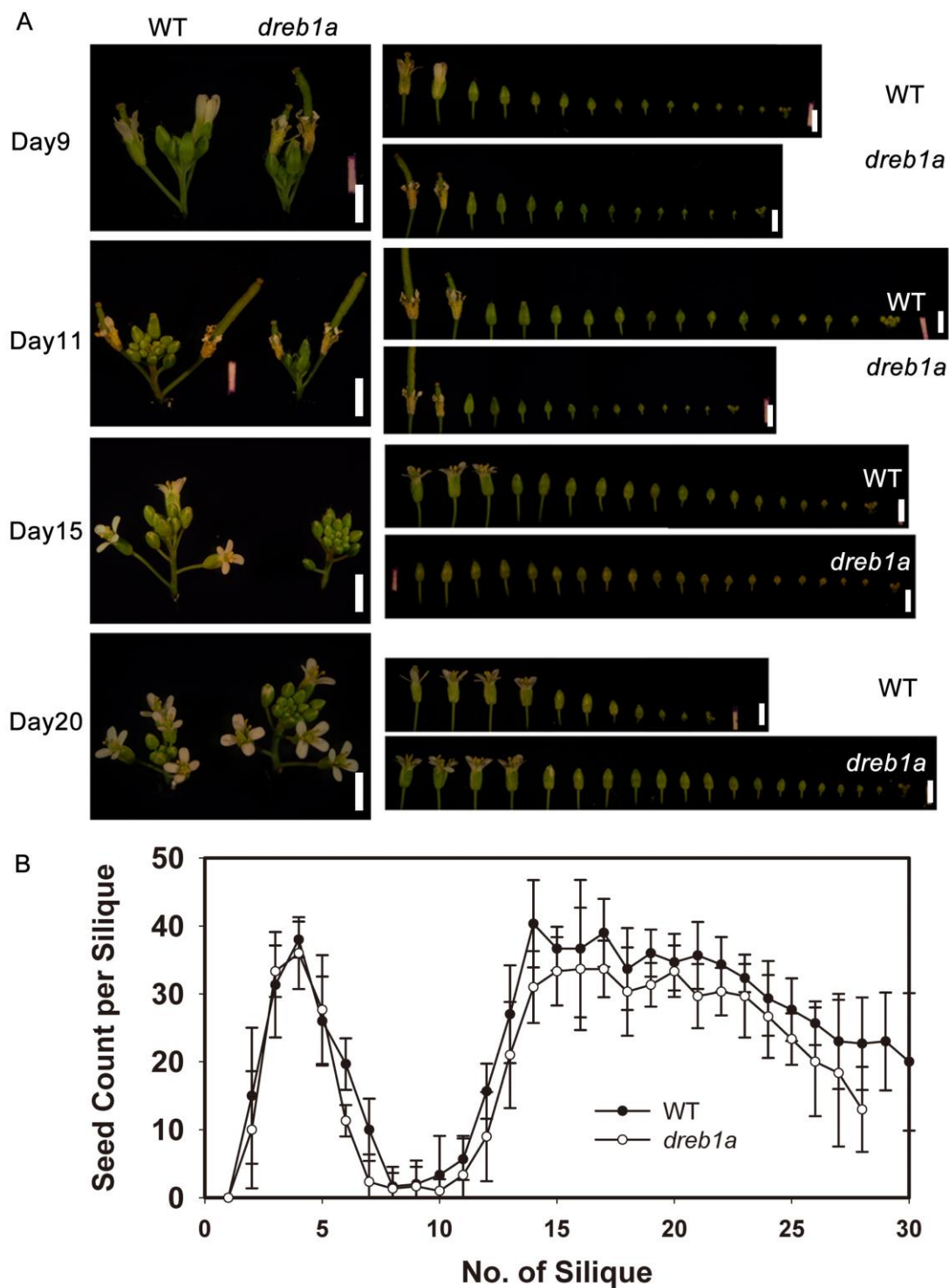
(A) T-DNA insertion of *dreb1a* (CS872453). (B) RT-PCR results of *DREB1A* gene expression in WT and *dreb1a* mutant. (C) The heat map of *DREB* family genes expression pattern in flower under drought stress. (D) Enrichment analysis of the genes that up-regulated in wild type T3 compared with *dreb1a* T3.



Supplemental Figure 9. Phenotypic Analyses of *dreb1a* Compared with WT under Early Drought Stress.

(A) WT and *dreb1a* plants after 7 days of drought treatment. Bars = 5 cm. (B) *in vitro* germination assay of the pollens from the newly open flowers of WT and *dreb1a* plants at T7. Bars = 500 μ m. (C)

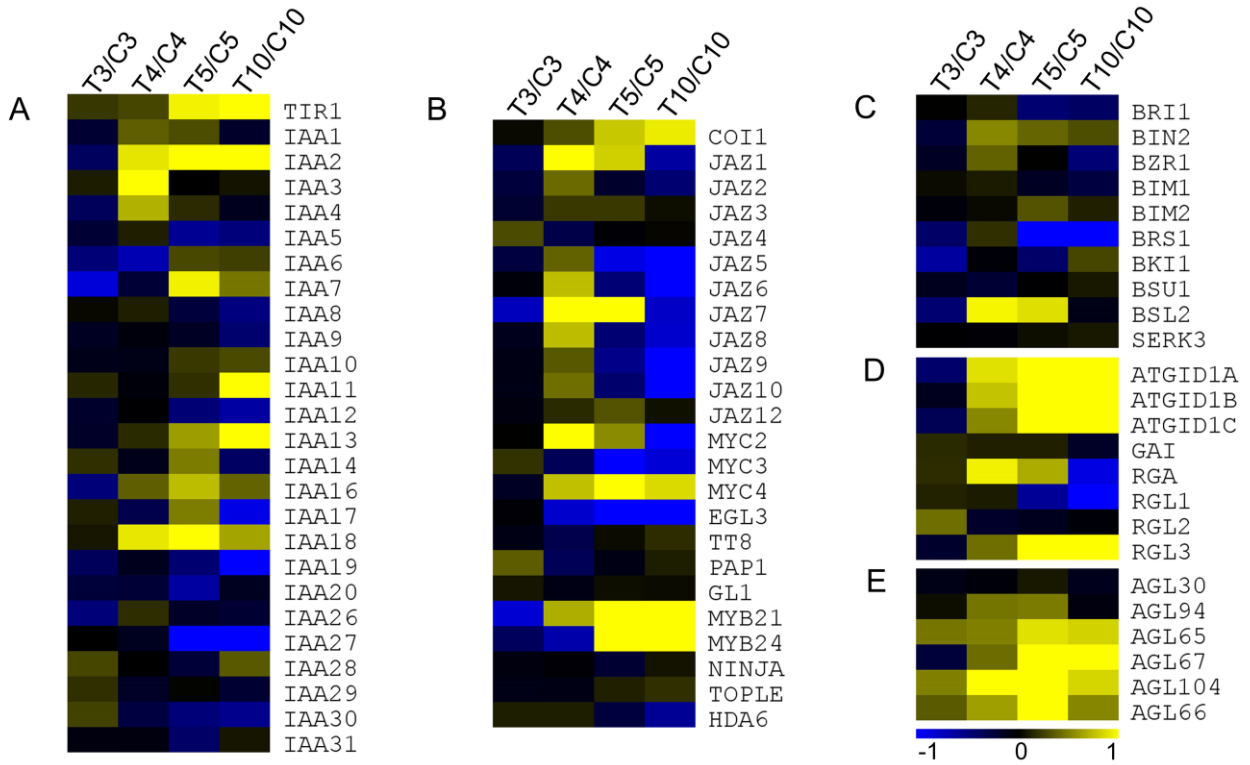
Inflorescence and floral buds phenotype characterization (From C0 to T7). WT inflorescence (left) and *drebla* inflorescence (right). The floral buds (stage 8-12) were dissected off with 0-2 open flowers from WW plants (Upper panel) and *drebla* (lower panel), Bars = 2 mm.



Supplemental Figure 10. Phenotypic Analyses of *dreb1a* Compared with WT under Prolonged Drought Stress.

(A) Inflorescence and floral buds phenotype characterization (From T9 to T20). WT inflorescence

(left) and *drebla* inflorescence (right). The floral buds (stage 8-12) were dissected off with 0-2 open flowers from WW plants (Upper panel) and *drebla* (lower panel). Bars = 2 mm. **(B)** Seeds count per silique from most bottom one to the top one.



Supplemental Figure 11. Expression Pattern Change of Key Phytohormone Pathway Genes under Drought Stress.

(A) Auxin pathway gene expression changes under drought. (B) JA pathway gene expression changes under drought. (C) BR pathway gene expression changes under drought. (D) GA pathway gene expression change under drought. (E) MADS-box family Mδ subfamily gene expression changes under drought.

Supplemental Table 1. The Number of Genes which Expression Levels Were Above the 50 Threshold (log₂ value > 5.64) in Each Dataset and The Number of Genes Which Were Differentially Expressed in Each Dataset Compared with Multiple Controls.

Sample	C0	C3	C4	C5	C10	T3	T4	T5	T10
Gene Count	15067	15244	15232	15230	15051	15168	15154	15158	15014
		T3/C3		T4/C4		T5/C5		T10/C10	
Up-regulated		19		462		1377		1395	
Down-regulated		145		101		1230		1567	
	T3/C0	T4/C0	T5/C0	T10/C0	T3/C3	T4/C3	T5/C3	T10/C3	
Up-regulated	228	955	1984	1825	19	710	1782	1511	
Down-regulated	222	341	1562	1794	145	384	1555	1682	
	C3/C0	C4/C0	C5/C0	C10/C0	C4/C3	C5/C3	C10/C3		
Up-regulated	517	469	262	467	205	130	216		
Down-regulated	185	218	106	275	271	167	398		

Supplemental Table 2. GO Annotation of Genes Differentially Expressed at T3 v. C3.

Gene ID	Gene Name and Description	T3/C3	Q Value
Transporter activity AT1G61800	Glucose-6-phosphate/phosphate translocator 2 (GPT2)	2.5	1.34E-05
Transcription factor activity AT4G25480	Dehydration response element binding protein 1a (DREB1A)	1.1	6.65E-03
DNA or RNA binding ATCG00660	Ribosomal protein L20 (RPL20)	1.28	1.14E-03
AT1G69260	ABI FIVE binding protein (AFP1)	1.43	2.34E-05
Transferase activity AT1G19640	Jasmonic acid carboxyl methyltransferase (JMT)	1.11	7.98E-03
Hydrolase activity AT1G07430	Highly ABA-induced PP2C gene (HAI2)	1.74	2.04E-04
AT1G62710	Beta vacuolar processing enzyme (BETA-VPE)	1.28	9.72E-04
Other binding AT3G53980	Lipid-transfer protein	1.27	1.18E-05
AT4G33550	Lipid-transfer protein	1.12	1.07E-03
AT5G03350	Legume lectin family protein	1.15	5.18E-03
AT5G55450	Lipid-transfer protein	1.02	8.39E-03
Unknown molecular functions AT1G52690	Late embryogenesis abundant 7 (LEA7)	2.03	7.42E-06
AT4G35190	Putative lysine decarboxylase family protein	1.08	5.96E-04
AT5G52310	Cold regulated 78 (COR78); Low-temperature-induced 78 (LTI78); Responsive to desiccation 29A (RD29A)	2.4	1.07E-05
AT5G52390	PAR1 protein	1.44	3.02E-05
AT1G80130	unknown protein	2.15	3.81E-06
AtCG00530	hypothetical protein	1.07	4.89E-04
AT1G19960	Unknown protein	1.76	8.95E-03
Other molecular functions ATCG00590	hypothetical protein (ORF31)	1.7	4.56E-03

Supplemental Table 3. The Expression of DREB Genes in *Arabidopsis* Flower under Drought Stress.

Gene ID	Name	cis element	Gene	T3/C3	Q Value	T4/C4	Q Value	T5/C5	Q Value	T10/C10	Q Value
AT4G25480	DREB1A/CBF3	DRE/CRT	<i>RD29A Cor15a</i>	1.10	0.01	-0.14	0.36	0.40	0.05	-0.48	0.01
AT4G25490	DREB1B/CBF1	DRE/CRT	<i>RD29A Cor15a</i>	-0.28	0.56	0.66	0.08	1.32	0.00	1.27	0.00
AT4G25470	DREB1C/CBF2	DRE/CRT	<i>RD29A Cor15a</i>	0.19	0.55	0.23	0.24	0.22	0.14	-0.99	0.00
AT5G51990	DREB1D/CBF4	DRE/CRT	<i>RD29A Cor15a</i>	-0.12	0.60	0.26	0.15	0.80	0.00	0.70	0.00
AT1G12610	DREB1E/DDF1			-0.04	0.69	0.07	0.37	-0.17	0.09	-0.08	0.14
AT1G63030	DREB1F/DDF2			0.08	0.66	0.24	0.17	-0.30	0.05	-0.31	0.02
AT5G05410	DREB2A	DRE	<i>RD29A</i>	-0.28	0.50	1.37	0.00	4.02	0.00	4.57	0.00
AT3G11020	DREB2B	DRE	<i>RD29A</i>	-0.13	0.65	0.23	0.27	0.87	0.00	1.98	0.00

Supplemental Table 4. Primers for QPCR.

Gene Name	AGI	oMC #	Sequence	Amplicon Size(bp)
ACTIN2	AT3G18780	oMC1533 oMC1534	GGTAACATTGTGCTCAGTGGTGG AACGACCTTAATCTTCATGCTGC	108
SPL	At4g27330	oMC2362 oMC2363	TCCAACGGTGGTGGATTTTC TGGTCCCCTATGATTTGTTGC	200
DYT1	At4g21330	oMC1872 oMC1834	ATGGGTGGAGGAAGCAGATTTTC TTATGGATTGCTTCTCATAACTTC	153
EMS1	At5g07280	oMC2364 oMC2365	CTCATCTCCTTCAAGCGCTCA AGACACGTAACGCCAACCCA	101
TPD1	At4g24972	oMC2366 oMC2367	GGTATCGGCGACTGCTCT CCAATTCTCTCCGGCTCTACA	201
AMS	At2g16910	oMC2368 oMC2369	TTCCCATCTTCCAGCTTCCA ACCACGTTCTGATCTTCAGCG	201
AG	AT4G18960	oMC7717 oMC7718	GAGCTCAGGAACTTGGAAAGG TCTTTGCACGAAGAATCTGG	145
AGL24	AT4G24540	oMC7719 oMC7720	AGTTCTTTGCGATGCTGATG AGCTGGAGAACTCGAAGAGC	71
AP1	AT1G69120	oMC7721 oMC7722	TCTCAACATGGGTGGTCTGT GCCAAGGTTGCAGTTGTA AAA	100
AP2	AT4G36920	oMC7723 oMC7724	ACTCAATGCCGAGTCATCAG GAATTAGCCGAATTTCCCAA	81
AP3	AT3G54340	oMC7725 oMC7726	GAGTGTTTGGACGAGCTTGA TTCTTGGTGGTCTCGATCTG	125
FRI	AT4G00650	oMC7727 oMC7728	TGGTTCACGGACAGAGACAT ACTGCGAGGAGACCTTTGAT	146
FT	AT1G65480	oMC7729 oMC7730	CCTTTGGCAATGAGATTGTG GCCAAGCTGTTCGAAACAATA	89
LFY	AT5G61850	oMC7731 oMC7732	AGAGCTGAACGGAGACGATT GCATCAAGAGCGTGATGAGT	110
MAF1	AT1G77080	oMC7733 oMC7734	GATCAAGCGAATCGAGAACA GAGCTTTGTGCGATGAGACCA	77
PI	AT5G20240	oMC7735 oMC7736	AGCTGCAACAACAGGAGATG GCTGAATCGGTTGCACTCTA	99
SEP1	AT5G15800	oMC7737 oMC7738	TCATATGGGAGGAGGAGGAG CCATTTGCAGAGTTGGATTG	119
SEP2	AT3G02310	oMC7739 oMC7740	GCTTTGTCAATGAAGCTGGA TGAGAATGAGCCTGAGGATG	116
SEP3	AT1G24260	oMC7741 oMC7742	ACTATGGAGCACCAGAACCC GGTCCAAGATCTTCTCCCAA	142
SOC1	AT2G45660	oMC7743 oMC7744	TCAGTGCTTTGTGATGCTGA TGGTGCTGACTCGATCCTTA	133
SVP	AT2G22540	oMC7745 oMC7746	CTGCTGTGTACGAGGAAGGA ATACGGTAAGCCGAGCCTAA	116
BAM1	AT5G65700	oMC7761 oMC7762	GTTCGTTTCCCGATGAGATT CCGGTAAATCTCCGGTTAGA	87
BAM2	AT3G49670	oMC7763 oMC7764	GTTCAATACCGATTTCGCTT GAAGAGCTCCTTTGGAATCG	95
BAM3	AT4G17090	oMC7765	TCTCAGGCAAGTTTCCTCCT	97

		oMC7766	ATCTGAACCGGAATCTGACC	
ERECTA	AT2G26330	oMC7767	TCACGGCTCACTGAGAAATC	147
		oMC7768	TGCCATTTCCATCACTTCAT	
MYB110	AT3G29020	oMC7769	ACTCAACCTTCCCTGCAGAT	98
		oMC7770	TGTTGATGATGATGGCAGTG	
MYB33	AT5G06100	oMC7771	TATCAAGAGGCGACAACGAG	74
		oMC7772	GACTCCACTCAAGTGCCTCA	
MYB65	AT3G11440	oMC7773	CATCGCAGGTAGAGGAGTCA	109
		oMC7774	ATCAACAAACTGTGCTTCGC	
MYB99	AT5G62320	oMC7775	ATCGTCGATTTGACCAACAA	113
		oMC7776	TGCTGACGTGTCATTCTTCA	
SERK1	AT1G71830	oMC7777	TGGGTGAAAGGATTGTTGAA	143
		oMC7778	TTTGGTCTTTCCATTGGTGA	
AGL23	AT1G65360	oMC7747	TGATGTTCTGCTTGACCACTT	130
		oMC7748	TTCTACTTCCGCCTTCACCT	
AGL80	AT5G48670	oMC7749	TCTCGACTCTTTGTGGCATC	81
		oMC7750	AATTTGATGGCCCACTTCA	
EOSTRE	AT2G35940	oMC7751	TGGTGATCTCTTCGTTTCGAG	103
		oMC7752	TCTTTCAAGCAACGGAAGT	
GPT1	AT5G54800	oMC7753	GGACCACAGTTTGTCTGGTG	133
		oMC7754	CGGAGATACGTTTCATGGTG	
MYB98	AT4G18770	oMC7755	AGTGTTACCGGGAAGAATCG	147
		oMC7756	ATCTCTGCCATTTGTTTCC	
RHF1a	AT4G14220	oMC7757	AAGGAGTGCAACGTGAGATG	121
		oMC7758	GCAGTAGCAGTGGAGGTTGA	
RHF2a	AT5G22000	oMC7759	CAGCCACCAACTTCTTCTCA	69
		oMC7760	AAGAGGCCTGCTGTTTGAAT	