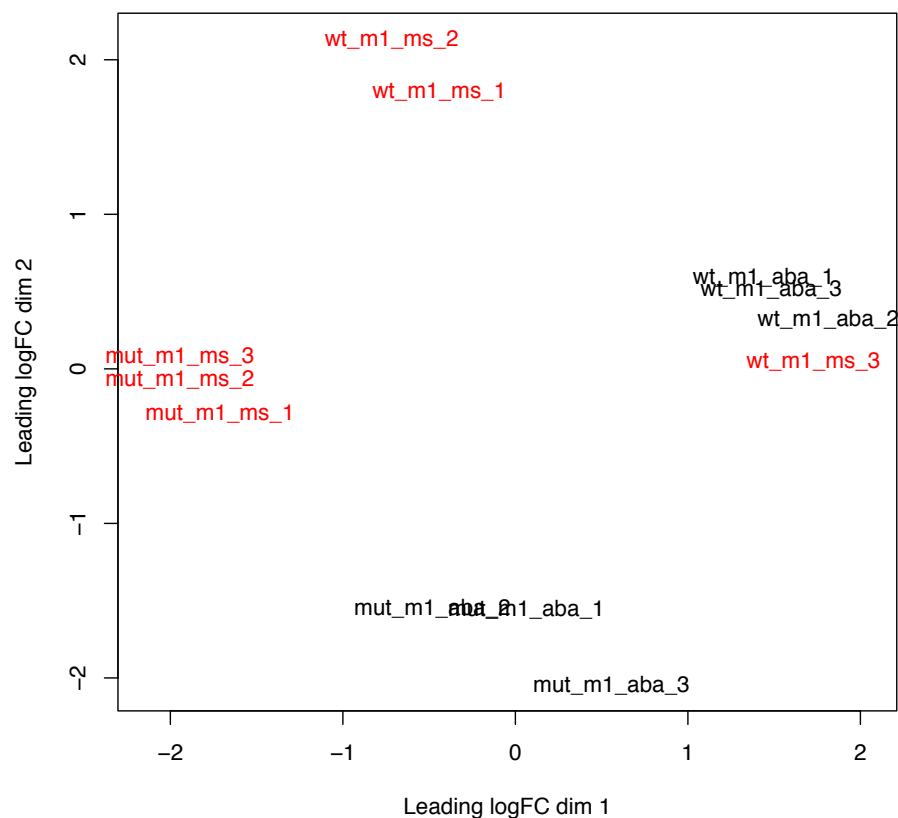
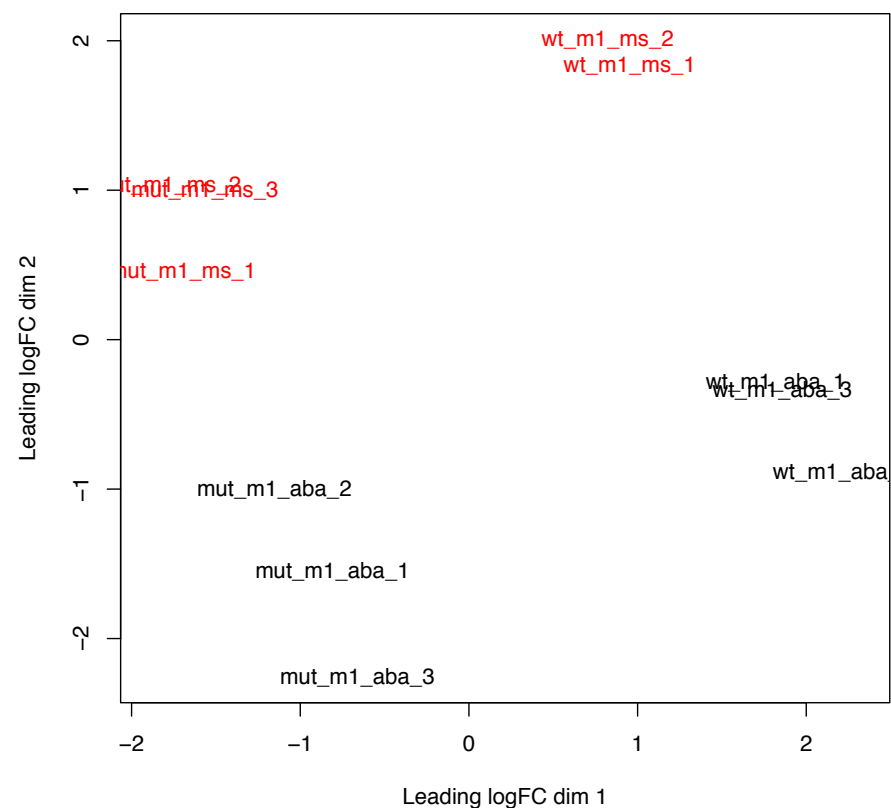


**Figure S1.** Reverse Transcriptase quantitative PCR (RT-qPCR) of the *Rab17* gene. Relative expression of the ABA-responsive *Rab17* gene (Zm00001d037894; *Dehydrin1*, *Dhn1*) in *Mop1* wildtype and *mop1-1* mutant under ABA and MS treatment. Three biological replicates were used per experiment. Error bars depict standard deviation. *Ubiquitin conjugase* was used as normalizer.

(a)



(b)

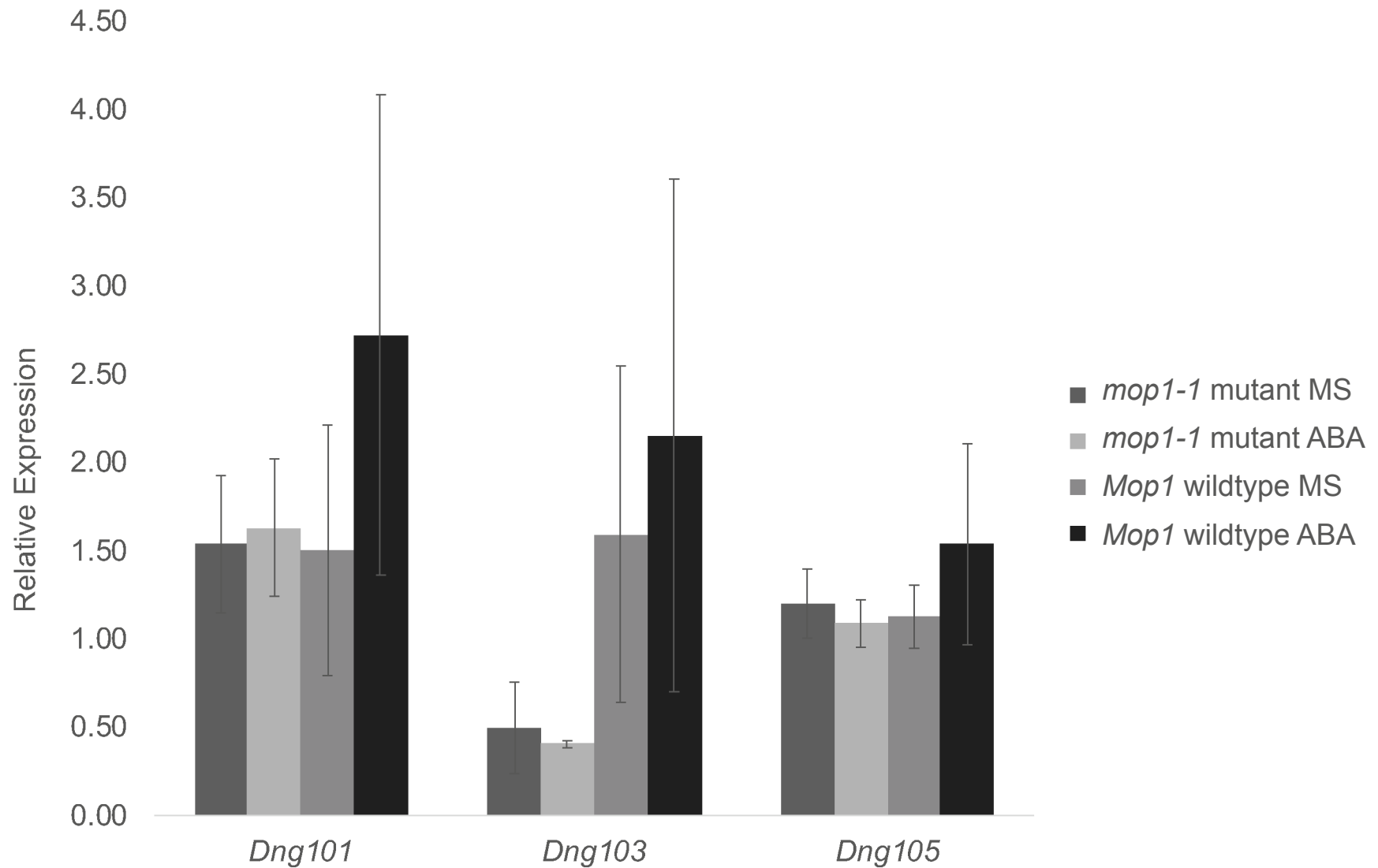


**Figure S2.** Multi-dimensional scaling (MDS) plots of RNA-seq samples.

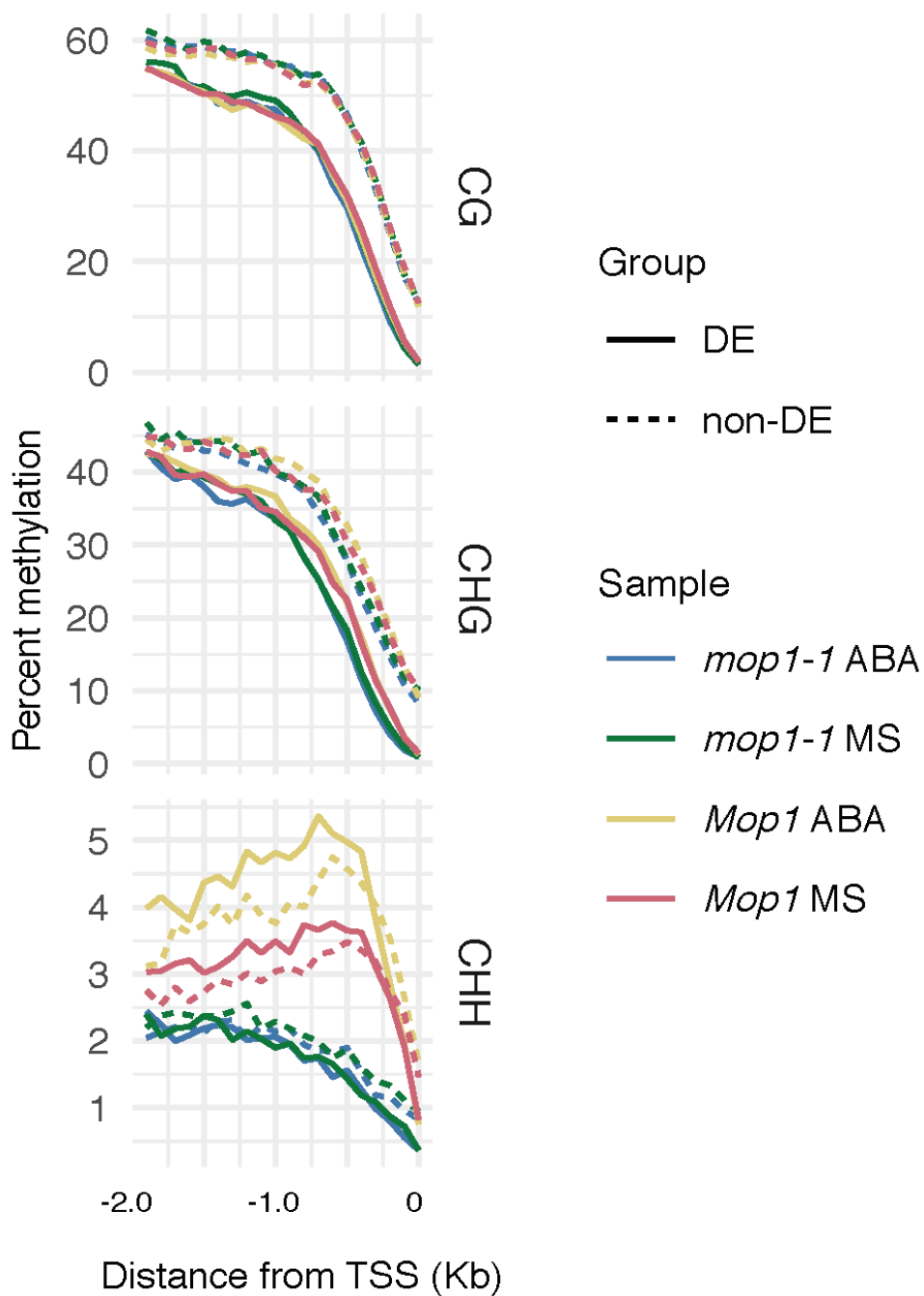
The MDS plots generated in 'edgeR' after differential expression analysis, visualizes the differences between expression profiles of the different samples in two dimensions.

(a) Complete set of 12 RNA-seq samples including two genotypes (wildtype (wt) and mutant (mut)) and two treatments (aba and ms) with three biological replicates each (1, 2, 3).

(b) MDS plot with the 11 samples after removal of the outlier (wt\_m1\_ms\_3).

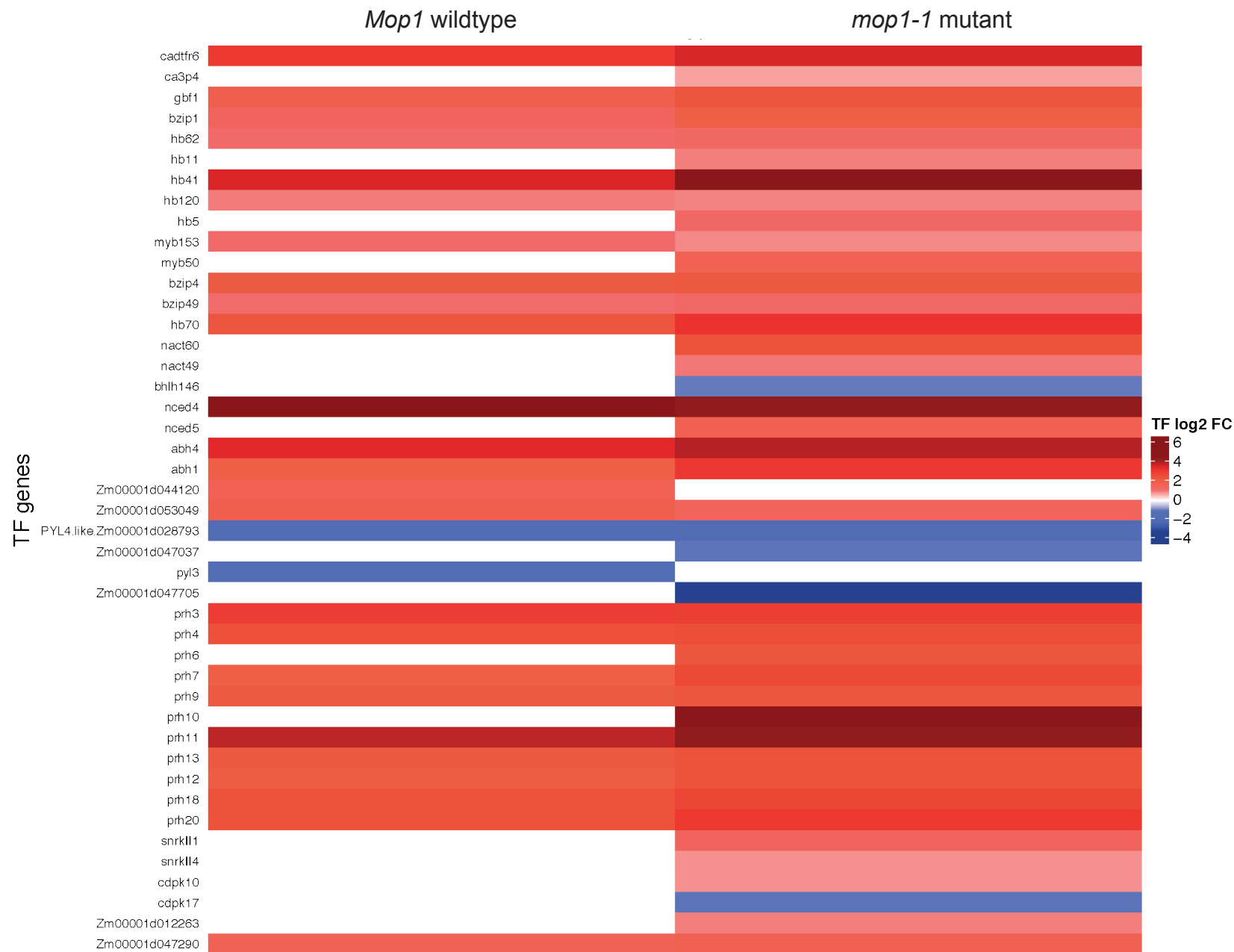


**Figure S3.** Reverse Transcriptase quantitative PCR (RT-qPCR) of the *DNG* genes. Relative expression of *Dng101* (Zm00010a020199), *Dng103* (Zm00001d038302), *Dng105* (Zm00001d016521) in *Mop1* wildtype and *mop1-1* mutant under ABA and MS treatment. Three biological replicates were used per experiment, except for *Mop1* wildtype MS for which the outlier wt ms 3 was removed. Error bars depict standard deviation. Ubiquitin conjugase was used for normalization.



**Figure S4.** Promoter DNA methylation for *Mop1* wildtype and *mop1-1* mutant seedlings in response to abscisic acid for differentially expressed (DE) genes and non-DE genes.

Promoter methylation (2 Kb upstream from TSS) for four samples (two genotypes and two treatments) *mop1-1* mutant ABA (blue), *mop1-1* mutant MS (green), *Mop1* WT ABA (yellow), and *Mop1* WT MS (red) for ABA-responsive DE genes (Groups I, II, V, VI; n = 1957) shown as a continuous line and non-DE genes (n = 3,028) shown as a dotted line.



**Figure S5.** Heatmap depicting the expression level of differentially expressed genes present in the maize transcription factor hierarchical network (Figure 3) in response to ABA in the two genotypes *Mop1* wildtype and *mop1-1* mutant. Gene expression change is presented in Log2 FC.

**Table S1. Differential Expression Analysis with different biological replicate number for each genotype/treatment**

- I. DEGs Published in this paper. Removal of one biological replicate for *Mop1* wildtype MS (wt\_m1\_ms\_3). Total of 11 samples.

DEGs	<i>mop1-1</i> mutant ABA vs <i>mop1-1</i> mutant MS	<i>Mop1</i> wildtype ABA vs <i>Mop1</i> wildtype MS	<i>mop1-1</i> mutant ABA vs <i>Mop1</i> wildtype ABA	<i>mop1-1</i> mutant MS vs <i>Mop1</i> wildtype MS
Downregulated	1,607	422	59	47
Non-significant	25,254	27,344	28,116	28,199
Upregulated	1,511	606	197	126
Total	3,118	1,028	256	173

- II. Additional removal of one biological replicate for *mop1-1* mutant MS (mut\_m1\_ms\_1). Total of 10 samples.

DEGs	<i>mop1-1</i> mutant ABA vs <i>mop1-1</i> mutant MS	<i>Mop1</i> wildtype ABA vs <i>Mop1</i> wildtype MS	<i>mop1-1</i> mutant ABA vs <i>Mop1</i> wildtype ABA	<i>mop1-1</i> mutant MS vs <i>Mop1</i> wildtype MS
Downregulated	1,345	400	64	30
Non-significant	25,829	27,284	28,022	28,138
Upregulated	1,078	568	166	84
Total	2,423	968	230	114

- III. Differential Expression Analysis using two biological replicates for each genotype/treatment

Genotype	ABA Treatment	MS Treatment (control)
<i>Mop1</i> wildtype	wt_m1_aba_1, wt_m1_aba_3	wt_m1_ms_1, wt_m1_ms_2
<i>mop1-1</i> mutant	mut_m1_aba_1, mut_m1_aba_2	mut_m1_ms_2, mut_m1_ms_3

DEGs	<i>mop1-1</i> mutant ABA vs <i>mop1-1</i> mutant MS	<i>Mop1</i> wildtype ABA vs <i>Mop1</i> wildtype MS	<i>mop1-1</i> mutant ABA vs <i>Mop1</i> wildtype ABA	<i>mop1-1</i> mutant MS vs <i>Mop1</i> wildtype MS
Downregulated	305	52	14	22
Non-significant	27,372	27,814	27,932	27,916
Upregulated	305	116	36	44
Total	610	168	50	66

**Table S2. Maize protein phosphatase class A (PP2C-A) differentially regulated genes in *Mop1* wildtype and *mop1-1* mutant.**

Protein phosphatase homolog	AGPv3 ID	AGPv4 ID	Alternative gene or protein names	Present in Group
<i>Prh3</i> †	GRMZM2G059453	Zm00001d042886	<i>prh3</i> , protein phosphatase 2C, ZmOrphan355, ZmPP2C3, ZmPP2C-A1	I, V
<i>Prh4</i> †	GRMZM2G166297	Zm00001d012401	PP2C20 probable protein phosphatase 2C 9, <i>prh4</i> , ZmOrphan11, ZmPP2C6, ZmPP2C-A2	I, V
<i>Prh5</i>	GRMZM2G010855	Zm00001d028574	PP2C14 2C-type protein phosphatase protein, <i>prh5</i> , ZmOrphan122, ZmPP2C14, ZmPP2C-A3	I, V
<i>Prh6</i> #	GRMZM2G308615	Zm00001d020100	<i>prh6</i> , ZmOrphan320, ZmPP2C11, ZmPP2C-A4	V
<i>Prh7</i> ‡§	GRMZM2G082487	Zm00001d005609	PP2C16, <i>prh7</i> , probable protein phosphatase 2C 68, ZmOrphan328, ZmPP2C16, ZmPP2C-A5	I, V
<i>Prh9</i> #	GRMZM5G818101	Zm00001d009626	PP2C12 putative protein phosphatase 2C family protein, <i>prh9</i> , ZmOrphan142, ZmPP2C12, ZmPP2C-A7	I, V
<i>Prh10</i> ‡§	GRMZM2G019819	Zm00001d004357	PP2C8, <i>prh10</i> , probable protein phosphatase 2C 37, ZmOrphan262, ZmPP2C8, ZmPP2C-A8	V
<i>Prh11</i> †‡§	GRMZM2G159811	Zm00001d025055	Orphan337 probable protein phosphatase 2C 37, PP2C13, <i>prh11</i> , ZmOrphan337, ZmPP2C13, ZmPP2C-A9	I, V
<i>Prh12</i>	GRMZM2G177386	Zm00001d038846	<i>pco092707</i> , <i>pco092707</i> (520), PHM2108, PP2C4 2C-type protein phosphatase protein, <i>prh12</i> , PZA01468, rs130444556, rs55625585, ss196416494, ZmOrphan249, ZmPP2C4, ZmPP2C-A10	I, V
<i>Prh13</i> ¶	GRMZM2G134628	Zm00001d044301	<i>magi100654</i> , <i>prh13</i> , ZmOrphan56, ZmPP2C2, ZmPP2C-A11	I, V
<i>Prh18</i>	GRMZM2G437575	Zm00001d011132	<i>prh18</i> , probable protein phosphatase 2C 50, ZmOrphan140, ZmPP2C5	I, V
<i>Prh20</i>	GRMZM2G300125	Zm00001d011495	<i>prh19</i> , protein phosphatase 2C ABI1, ZmOrphan154, ZmPP2C15	I, V

(Xiang et al., 2017)

- † Early stress response in shoot
- ‡ Early stress response in roots
- § Low basal expression across tissues
- ¶ High basal expression across tissues
- # Extremely susceptible to drought stress
- || Associated with drought tolerance. Its overexpression caused ABA signaling inhibition

**Table S3.** Number of differentially expressed genes (DEGs) in the four groups, number of identified annotated DEGs and number of significant GO terms found for each.

Pair-wise comparison	Analysis group	Expression pattern	2FC Significant Query DEGs	Annotated DEGs	Significant GO terms
<i>Mop1</i> wildtype ABA / MS	I	upregulated	506	470	17
	II	downregulated	352	304	11
<i>mop1-1</i> mutant MS /	III	upregulated	126	57	0
<i>Mop1</i> wildtype MS	IV	downregulated	47	32	0
<i>mop1-1</i> mutant ABA / MS	V	upregulated	965	894	22
	VI	downregulated	994	892	28
<i>mop1-1</i> mutant ABA /	VII	upregulated	194	83	0
<i>Mop1</i> wildtype ABA	VIII	downregulated	58	44	0

**Table S4.** High-confidence miRNAs from miRbase *Zea mays* B73\_v4 ([http://www.mirbase.org/cgi-bin/mirna\\_summary.pl?org=zma](http://www.mirbase.org/cgi-bin/mirna_summary.pl?org=zma)) used to normalize 24-nt siRNA presence in *mop1-1* mutant.

miRNA	Chromosomal coordinates
zma-MIR399f	6:163860157-163860261
zma-MIR172c	4:174154928-174155050
zma-MIR390a	1:298107396-298107576
zma-MIR396f	5:220211653-220211769
zma-MIR171e	1:7976712-7976837
zma-MIR160g	6:94036699-94036784
zma-MIR160b	5:44296768-44296888
zma-MIR171l	1:249547375-249547452
zma-MIR167e	7:10115799-10115917
zma-MIR171d	9:128212960-128213080
zma-MIR167c	5:4414244-4414375
zma-MIR159f	3:25007834-25008048
zma-MIR167i	9:113476123-113476252
zma-MIR529	5:164370906-164371031
zma-MIR156g	7:119411284-119411404
zma-MIR159a	8:10753073-10753318
zma-MIR167h	6:95985872-95986014
zma-MIR319b	3:2038966-2039178
zma-MIR166n	4:181112182-181112277
zma-MIR166j	7:128589394-128589547
zma-MIR166i	1:244940015-244940097
zma-MIR168b	4:244520636-244520739
zma-MIR166g	1:13782628-13782753
zma-MIR166m	5:216484037-216484192
zma-MIR166k	5:216483766-216483933
zma-MIR166a	6:87381728-87381940
zma-MIR156e	2:33005026-33005151
zma-MIR166d	5:22443534-22443637
zma-MIR156l	5:188595332-188595421
zma-MIR156i	4:140280587-140280703