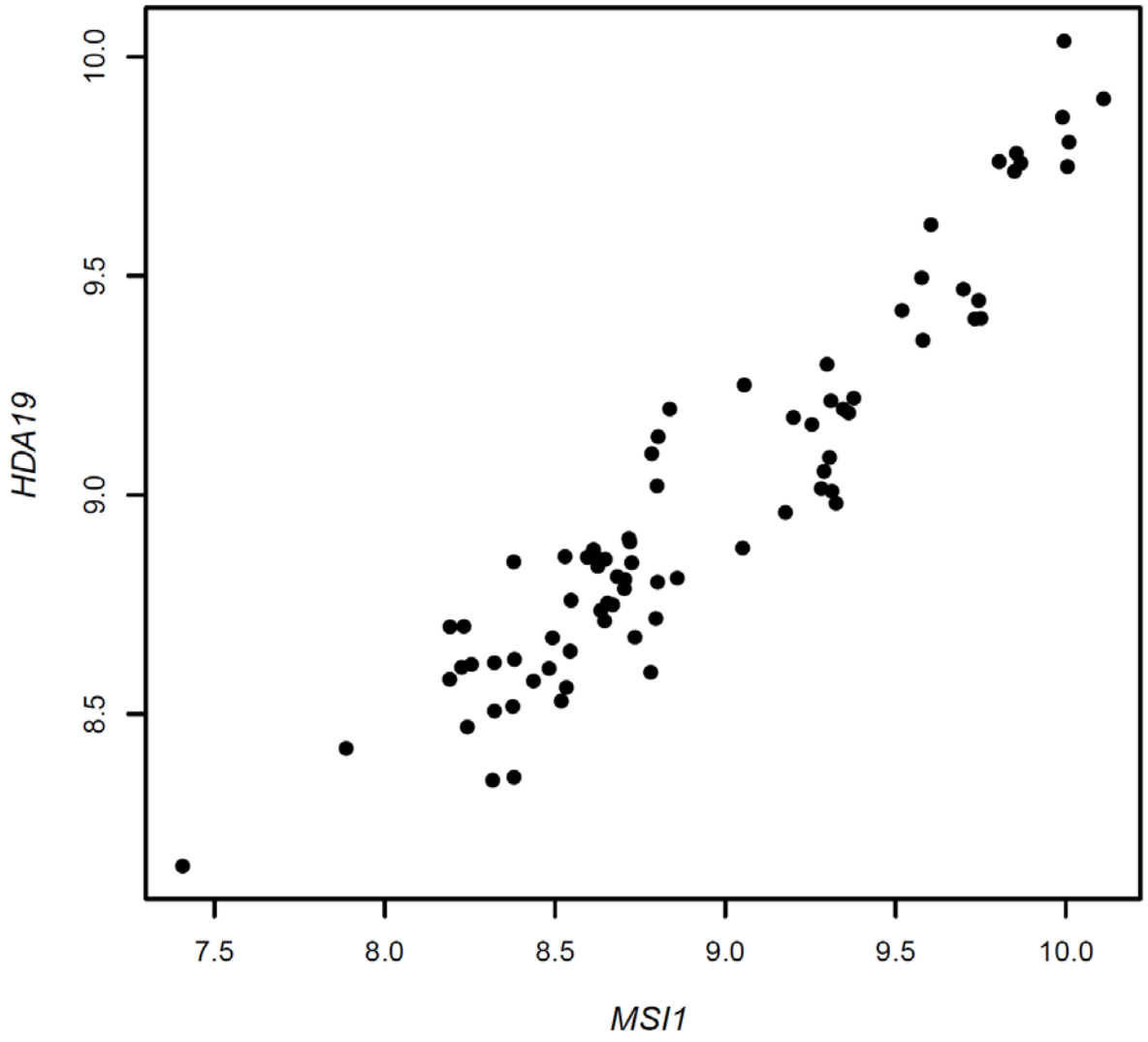
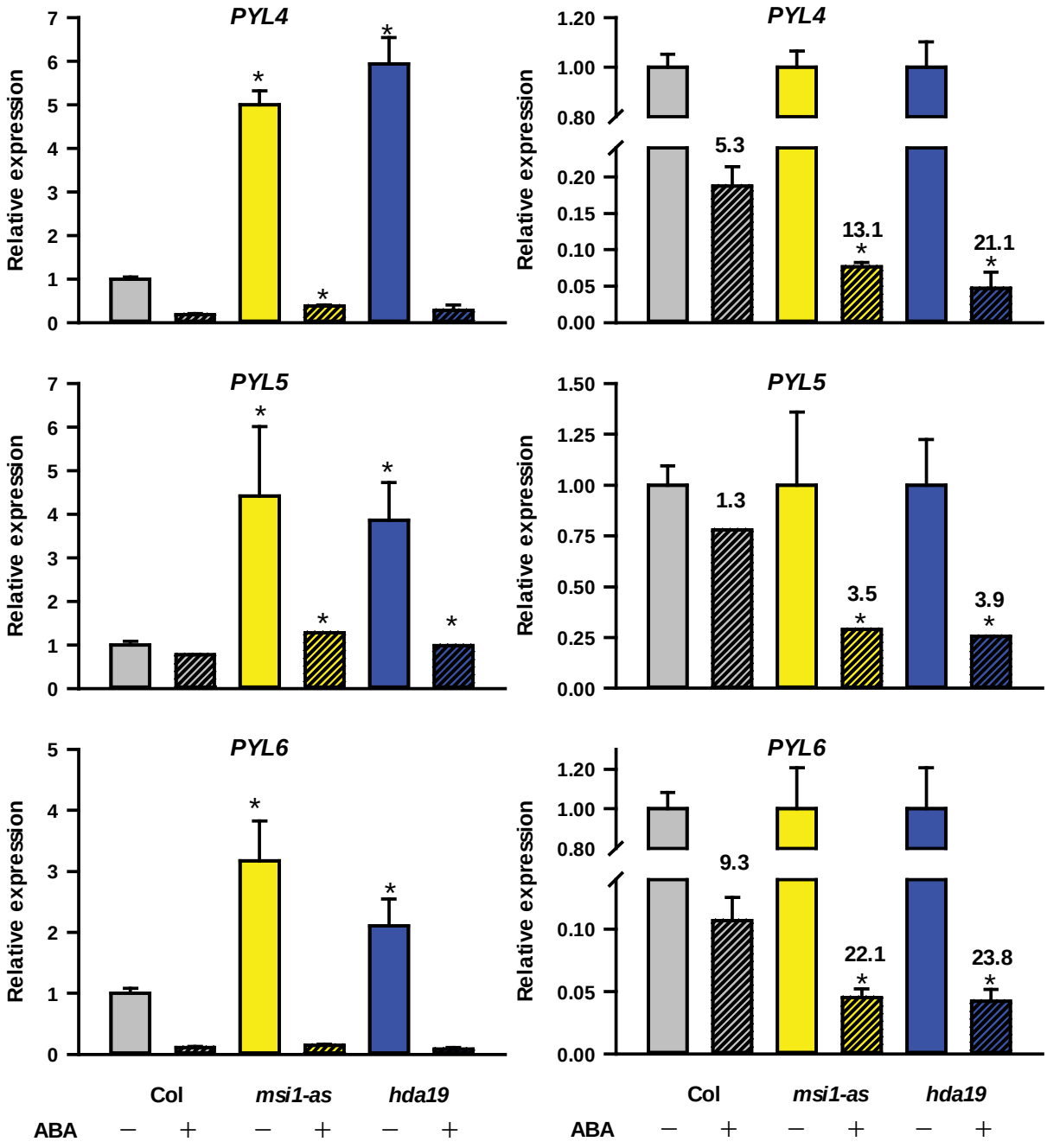
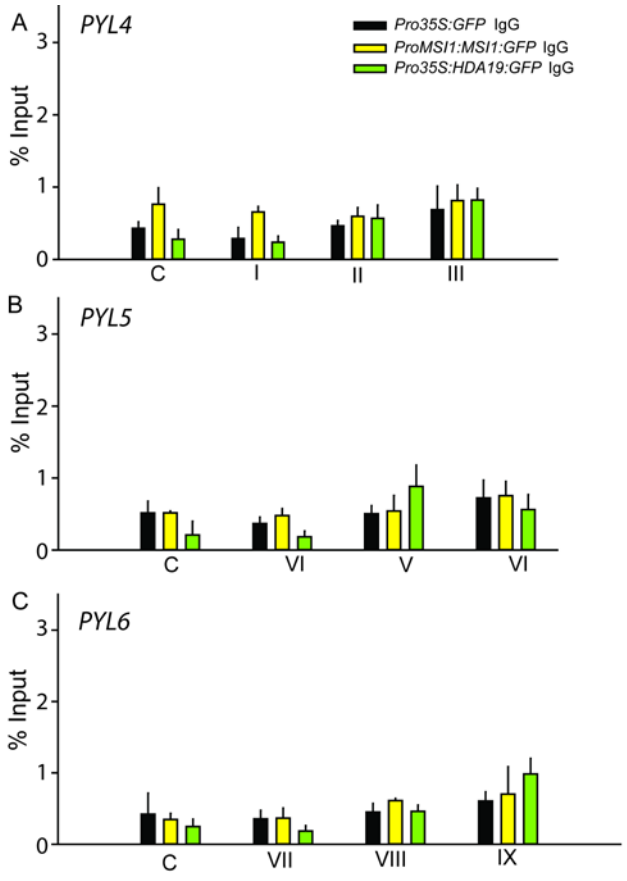


Supplemental Figure 1. Expression of *MSI1* and *HDA19* is strongly correlated. Transcript data for 79 developmental stages, organs and tissues were taken from Schmid et al., 2005. Each data point describes expression of *MSI1* and *HDA19* in one of the 79 samples.

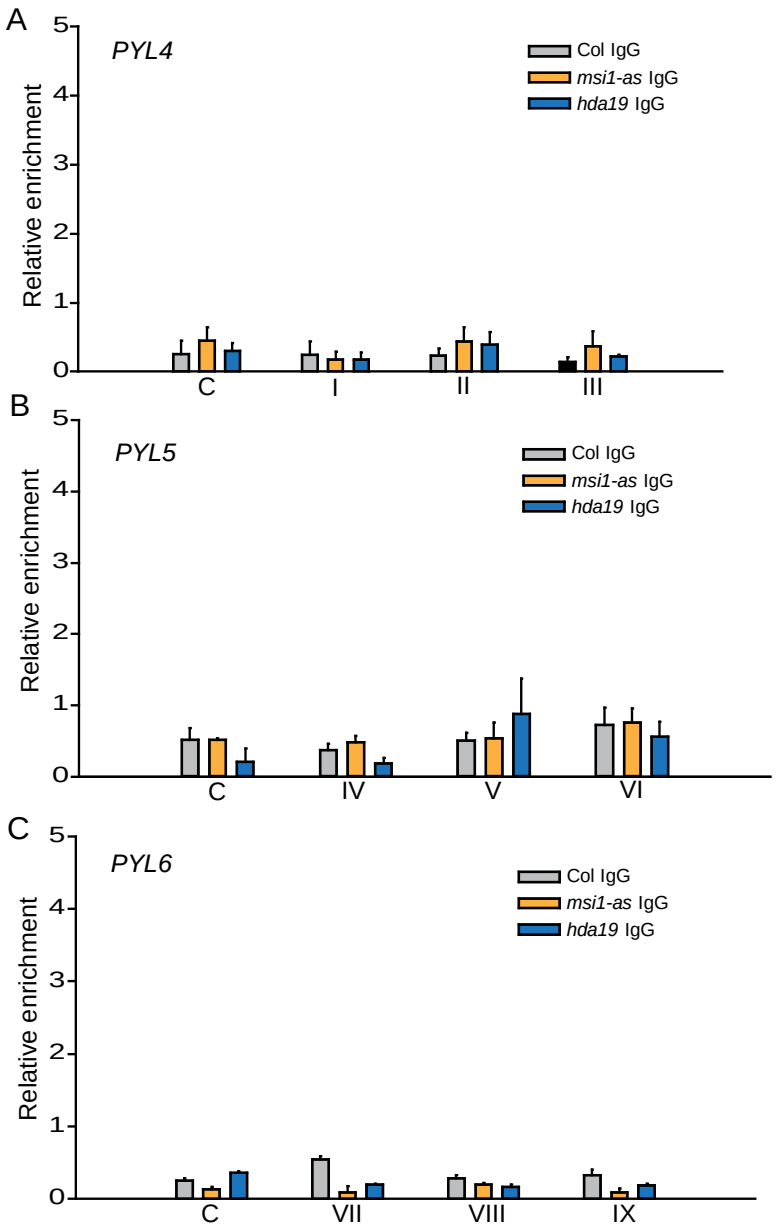
Schmid, M., Davison, T.S., Henz, S.R., Pape, U.J., Demar, M., Vingron, M., Scholkopf, B., Weigel, D. and Lohmann, J.U. (2005) A gene expression map of *Arabidopsis thaliana* development. Nat Genet 37: 501-506.



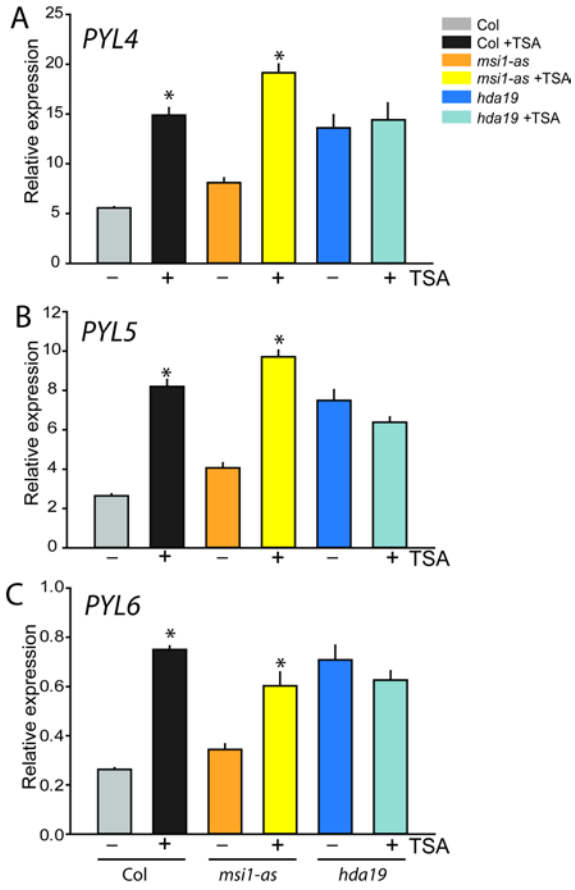
Supplemental Figure 2. Effect of MSI1 and HDA19 on the expression of the ABA-repressed genes *PYL4*, *PYL5* and *PYL6*. Seedlings were incubated for 24 h in 4 µM ABA. *PYL4, PYL5* and *PYL6* expression respectively in untreated (unshaded) as compared to ABA treated (shaded) wild-type (grey), *msi1-as* (yellow) and *hda19* (blue) seedlings is shown as means ± SE of three biological replicates. Left: Expression in untreated wild type Col was set to 1.0 to facilitate comparison between mutants and wild type. Right: Same data were replotted with expression in each untreated control set to 1.0 to facilitate comparisons of the ABA effect. Numbers on top of bars indicate fold repression as compared to the untreated samples. Asterisks indicate significant (p≤0.05) difference in repression to the wild type.



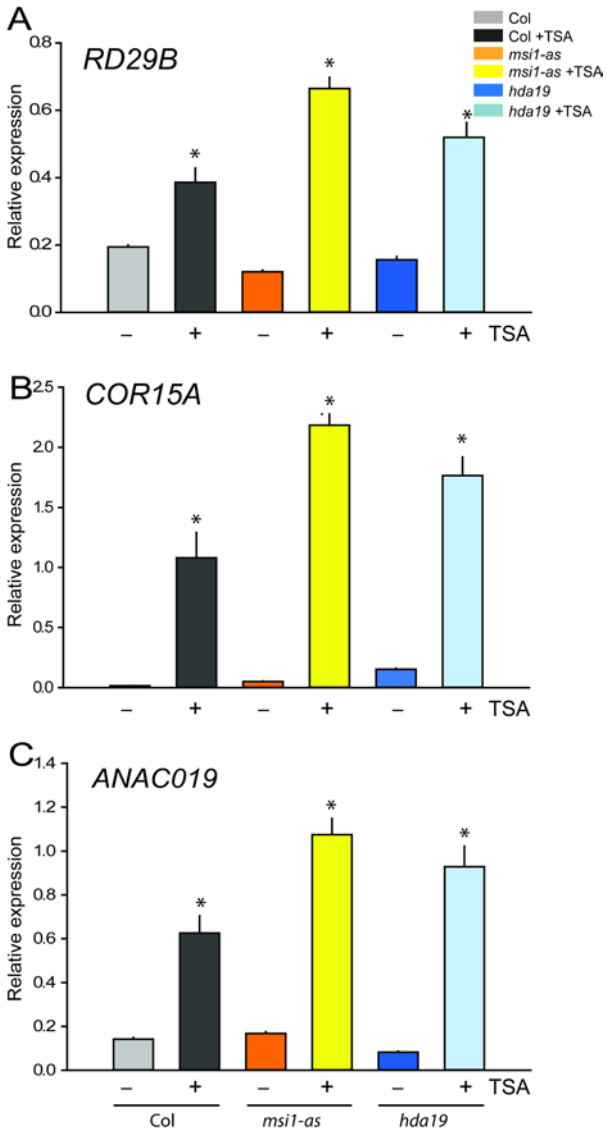
Supplemental Figure 3. IgG controls of anti-GFP ChIP. IgG controls are shown for *Pro35S:GFP* (black), *ProMSI1:MSI1:GFP* (yellow) and *Pro35S:HDA19:GFP* (green) at the *PYL4* (A), *PYL5* (B) and *PYL6* (C) loci, respectively. Graphs show the mean ± SE of three biological replicates.



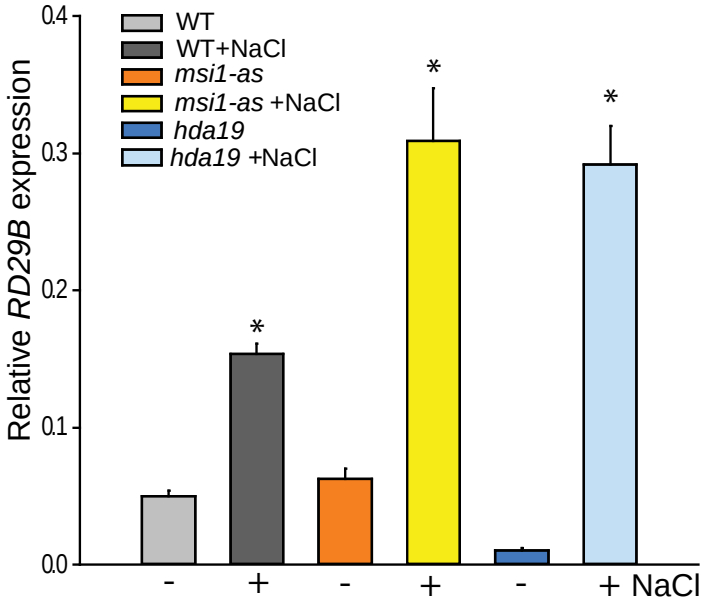
Supplemental Figure 4. IgG controls of anti-H3K9ac ChIP. IgG controls are shown for Col (grey), *msi1-as* (orange) and *hda19* (blue) at the *PYL4* (A), *PYL5* (B) and *PYL6* (C) loci, respectively. Graphs show the mean ± SE of three biological replicates.



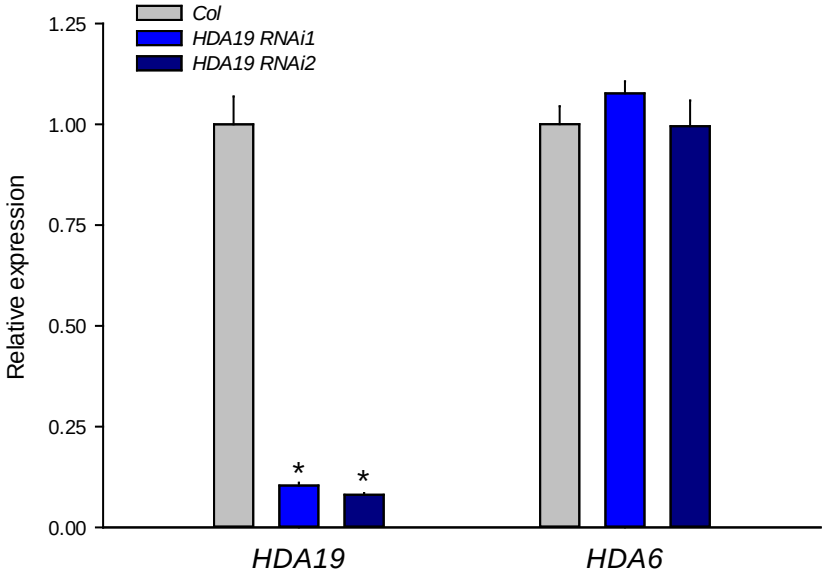
Supplemental Figure 5. Effect of TSA on the expression of ABA receptor genes. (A-C) *PYL4*, *PYL5* and *PYL6* expression in TSA treated wild-type (dark grey), *msi1-as* (yellow) and *hda19* (light blue) as compared to untreated wild-type (grey), *msi1-as* (orange) and *hda19* (blue) plants. Seven-day-old seedlings were hydroponically treated with 30 µM TSA for 24 h. Shown are means ± SE of three biological replicates. Asterisks indicate significant (p≤0.01) differences of TSA-treated to untreated samples.



Supplemental Figure 6. Effect of TSA on the expression of ABA-responsive genes. (A-C) *RD29B*, *COR15A* and *ANAC019* expression in TSA treated wild-type (dark grey), *msi1-as* (yellow) and *hda19* (light blue) as compared to untreated wild-type (grey), *msi1-as* (orange) and *hda19* (blue) plants. Seven-day-old seedlings were hydroponically treated with 30 µM TSA for 24 h. Shown are means ± SE of two biological replicates. Asterisks indicate significant (p≤0.01) differences of TSA-treated to untreated seedlings.



Supplemental Figure 7. Effect of salt on *RD29B* expression. Ten-day-old seedlings of wild type (grey), *msi1-as* (yellow) and *hda19* (blue) were hydroponically treated with 150 mM NaCl for 24 hours followed by RNA extraction and qPCR. Light colors represent untreated controls and dark colors represent treatments. Shown are means ± SE of two biological replicates. Asterisks indicate significant ($p \leq 0.01$) differences of salt-treated to untreated seedlings.



Supplemental Figure 8. Absence of off-target effect on *HDA6* in *HDA19 RNAi* lines. RNA was extracted from 10-day-old seedlings of wild type Col (grey), *HDA19 RNAi 1* (blue) and *HDA19 RNAi 2* (dark blue). Shown are means ± SE (n=3) of three technical replicates. Asterisks indicate significant ($p \leq 0.01$) differences to wild type Col. In contrast to the strong and significant reduction of *HDA19* levels, *HDA6* levels were not affected.

Supplemental Table 1. Sequences of primers used for ChIP-qPCR.

Symbol	Gene (position)	Forward primer	Reverse Primer
I	*PYL4* (-762)	TTGAAGATCATATCAAAGCA	ATTACCTGAGAGATTTGATG
II	*PYL4* (-188)	AAATCGAAAGGCACAGCC	GTGTATGGAGGAGAAGTATG
III	*PYL4* (+256)	GCTGTAGCGTCATCGGCGGA	CTCTCGGTGGAGCTAGCG
IV	*PYL5* (-918)	CCGGCGTAAGCTCTTTGATAAGGT	CACGTGCATGCACAGATGTTGA
V	*PYL5* (-156)	TTAAATTTCTCAAACAAAACCA	TATATTGCGATCGAGAGAGA
VI	*PYL5* (+134)	TTGCGATGCACCACACACACGA	ACTCAGGCGGCGCGTGGATCAT
VII	*PYL6* (-1015)	TAATCAACTTGAGCCTTTCG	CTGCTTAGTTTGATTTTCTT
VIII	*PYL6* (-196)	CGGTTGTCCACTTGGGATTTGTT	CGGGCCGGTCCTTGATATAAAGAA
IX	*PYL6* (+413)	TTGGGTCGGTGAGAGAGGTCA	CTGATGACGTGGCGATCATCGTCC
C	Intergenic	CCGTTCTTTACAACTAACAGTGGA	ACATTAGCACCGGACTTTCC

Supplemental Table 2. Sequences of gene-specific primers used for RT-qPCR.

Gene	Forward primer	Reverse Primer
RD29B	AGAAGGAATGGTGGGGAAAG	CAACTCACTTCCACCGGAAT
ANAC019	ACATCGGAAAAGCTCCTAAAGGT	ACCCAATCATCCAACTTAGTGCT
COR15A	CCTCAACGAGGCCACAAAGA	TCGCTTTCTCACCATCTGCT
PP2A	GTGCAGGCTACACTTTCGGA	GACTTGACGTGGAGCTGGAT
PYL4	CACCGGCTCTCTAACTACCG	CTCGGCTATTTTCGCAAGAG
PYL5	CGTGGTGGTGGAGTCTTACA	AGAGTTTCCTCCTCCGTGTTT
PYL6	GCATGAGTCGGAGGAGGAC	GACGTATGACTCAACGACACG
HDA6	TCGACCCAAGTCCTATGGAG	GTTGTTCCAGCAACGTGTTC
HDA19	CAAAGGACAAGGATGGACTGA	TCCCACTGGGTTTACTCCTG