

Supplementary Materials for

The ABA Receptor *PYL8* Promotes Lateral Root Growth by Enhancing *MYB77*-Dependent Transcription of Auxin-Responsive Genes

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Fig. S6. Sequence alignment of *MYB77* and its paralogs.

Fig. S7. *PYL8* enhances the abilities of *MYB44* and *MYB73* to activate *IAA19pro-LUC* expression in *abil-1* mutant protoplasts.

Table S1. Primers used for plasmid constructions.

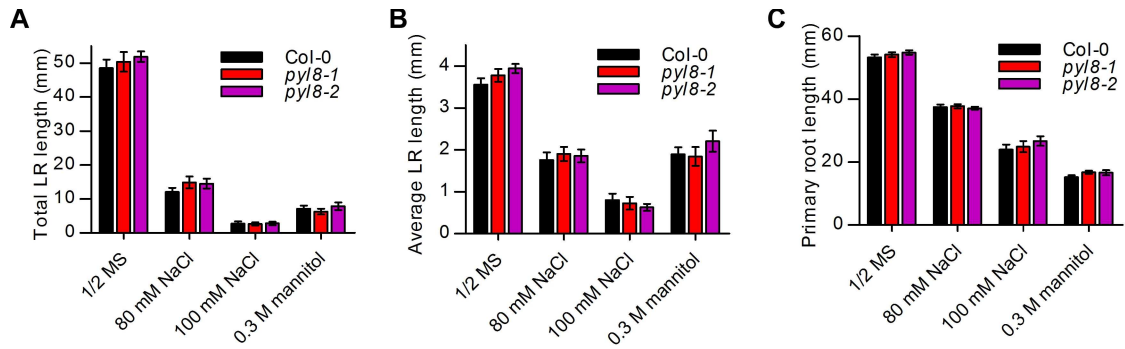


Fig. S1. *pyl8* mutants show no difference in root growth compared to the wild type when exposed to NaCl or mannitol stress. Lateral root length (A-B) and primary root length (C) of Col-0 and *pyl8* mutant seedlings at five dpt to media with or without NaCl or mannitol. $N \geq 8$ seedlings. Data are mean \pm S.E.M., $*p < 0.05$, Student's *t*-test.

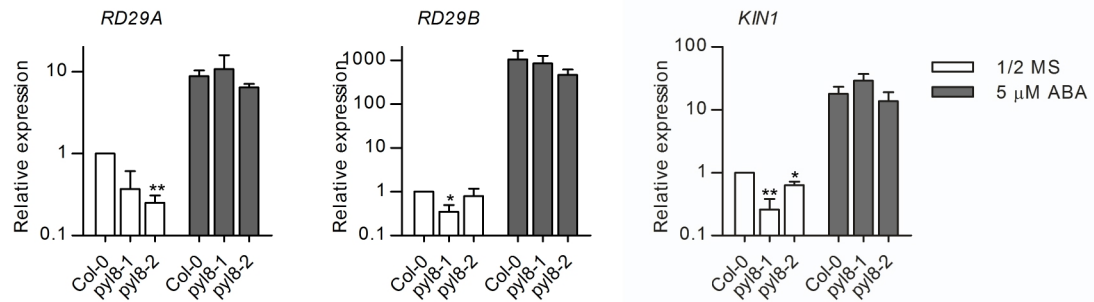


Fig. S2. Expression of stress-responsive genes in roots of *pyl8* mutant seedlings.

Quantitative RT-PCR was conducted on 3-day-old seedlings at 12 hour post transfer to media (1/2 MS, 1% sucrose) with or without 5 μM ABA. The expression levels of *RD29A*, *RD29B* and *KIN1* in Col-0 without ABA treatment were set as 1. N = 3 experiments. Data are mean ± S.E.M., * $p < 0.05$, ** $p < 0.01$, Student's *t*-test.

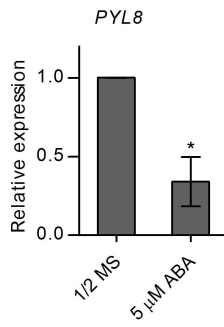


Fig. S3. Expression of *PYL8* in wild-type seedlings exposed to ABA. Quantitative RT-PCR was conducted on 3-day-old seedlings at 12 hour post transfer to media (1/2 MS, 1% sucrose) with or without 5 μM ABA. The expression level of *PYL8* in Col-0 without ABA treatment was set as 1. N = 3 experiments. Data are mean ± S.E.M., * $p < 0.05$, Student's *t*-test.

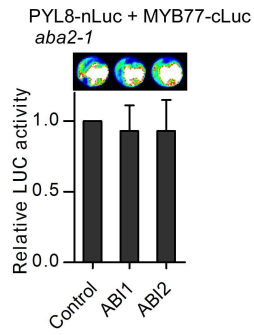


Fig. S4. The interaction between PYL8 and MYB77 is not reduced by overexpression of ABI1 or ABI2. PYL8-MYB77 interaction in LUC complementation assays in *aba2-1* mutant protoplasts with 5 μ M ABA. N = 6 experiments. Data are mean \pm S.E.M., * p <0.05, Student's *t*-test.

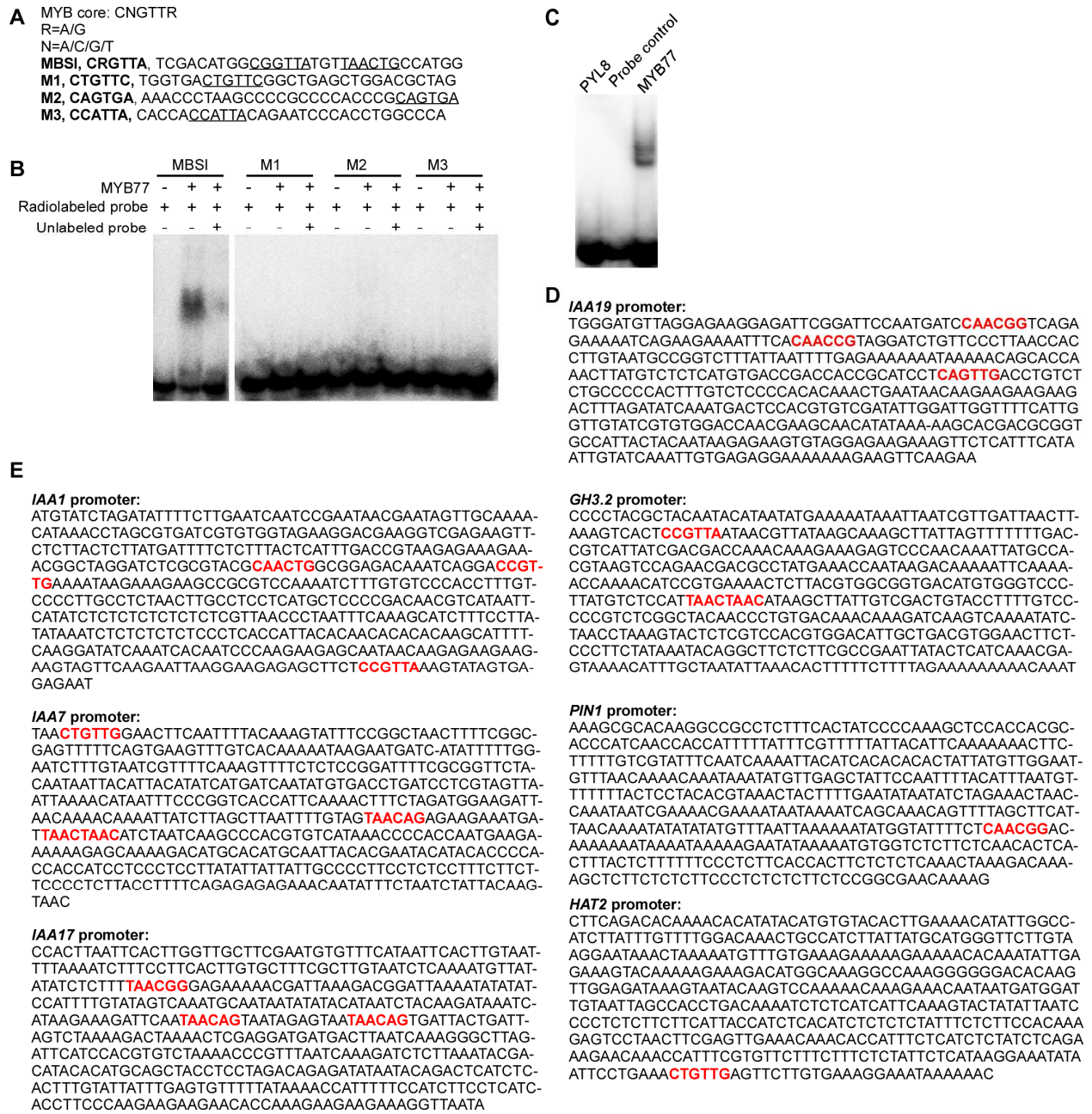


Fig. S5. The promoter region of auxin-regulated genes contains MBSI elements recognized by MYB77 and MYB44. (A) Oligonucleotides used in EMSA assay. Sequences of interest are underlined. (B) Binding between MYB77 and DNA oligonucleotides containing MBSI motif and mutated MBSI motif (M1-3) in EMSA assay. (C) Binding between MYB77 and MBSI motif-containing DNA oligonucleotides. (D) The 439-bp region of the translational start of *IAA19* is shown. MBSI elements are marked with red. (E) The 500-bp regions of the translational start of the indicated auxin-regulated genes are shown. MBSI and MBSII (GTTAGTTA) elements are marked with red.

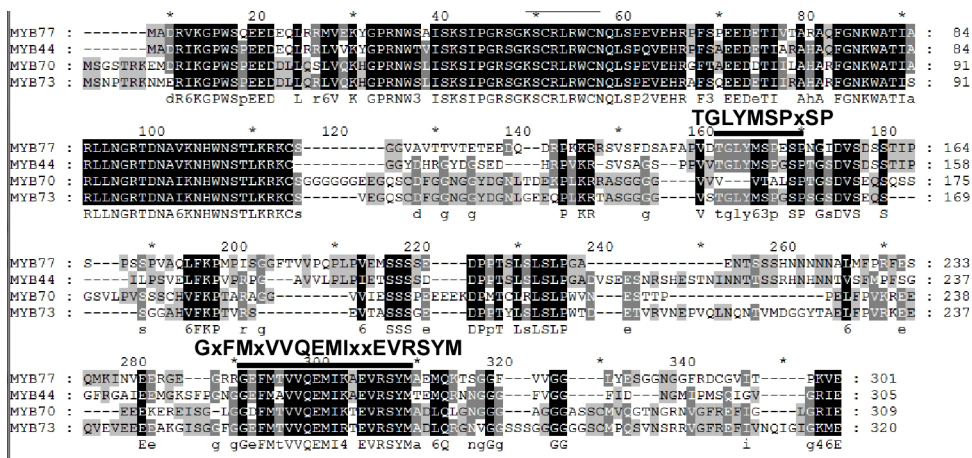


Fig. S6. Sequence alignment of MYB77 and its paralogs. MYB77, MYB44, MYB70 and MYB73 from *Arabidopsis* were aligned using ClustalX 2.0.5 with the default settings and were viewed using the GeneDoc software (<http://www.nrbc.org/gfx/genedoc/>). R2R3 MYB subgroup 22 contains two conserved motifs: TGLYMSPxSP and GxFMxVVQEMixxEVRSYM.

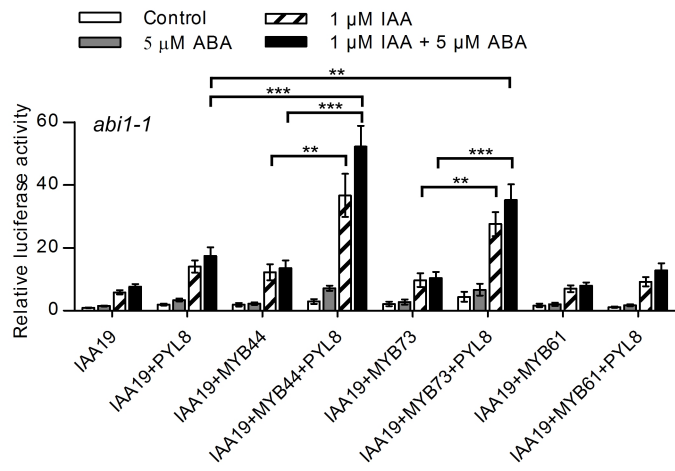


Fig. S7. PYL8 enhances the abilities of MYB44 and MYB73 to activate *IAA19pro-LUC* expression in *abi1-1* mutant protoplasts. *IAA19pro-LUC* expression in *abi1-1* mutant protoplasts co-transformed with the indicated combinations of *PYL8*, *MYB44*, *MYB73* and *IAA19pro-LUC* with varying concentration of ABA and IAA. N = 7 experiments. Data are mean \pm S.E.M., ** $p < 0.01$, *** $p < 0.001$, Student's *t*-test.

Table S1. Primers used for plasmid constructions.

Plasmids	Forward primers	Reverse primers
<i>IAA19pro-LUC</i>	<i>IAA19proF</i> : AGAGGATCCTGGGATGTTAGGAGAAGGAGATTCG	<i>IAA19proR</i> : CTTCCATGGTTCTTGAACCTCTTTTTTTCCTCTCAC
pHBT95-MYB44	CGGCTCCCTCTCCCCTTGCTCCGTGGATCC ATGGCTGATAGGATCAAAGGTCCAT	GTAGTCTGGAACGTCGTATGGGTAAGGCCT CTACTCGATTCTCCCAACTCCAATTTGAC
pHBT95-MYB73-HA	CGGCTCCCTCTCCCCTTGCTCCGTGGATCC ATGTCAAACCCGACCCGTAAG	GTAGTCTGGAACGTCGTATGGGTAAGGCCT CTCCATCTTCCCAATTCCG
pHBT95-MYB77	CGGCTCCCTCTCCCCTTGCTCCGTGGATCC ATGGCGGATCGTGTTAAAGG	GTAGTCTGGAACGTCGTATGGGTAAGGCCT CTACTCAACCTTAGGTGTTATTACTCC
pHBT95-MYB61-HA	CGGCTCCCTCTCCCCTTGCTCCGTGGATCC ATGGGGAGACATTCTTGCTGTTAC	GTAGTCTGGAACGTCGTATGGGTAAGGCCT AAGGGACTGACCAAAAAGAGACG
AD-MYB44	GTCATATGGCCATGGAGGCCAGTGAATTC ATGGCTGATAGGATCAAAGGTCCAT	ATTCATCTGCAGCTCGAGCTCGATGGATCC CTACTCGATTCTCCCAACTCCAATTTGAC
AD-MYB73	GTCATATGGCCATGGAGGCCAGTGAATTC ATGTCAAACCCGACCCGTAAG	ATTCATCTGCAGCTCGAGCTCGATGGATCC CTCCATCTTCCCAATTCCG
AD-MYB77	GTCATATGGCCATGGAGGCCAGTGAATTC ATGGCGGATCGTGTTAAAGG	ATTCATCTGCAGCTCGAGCTCGATGGATCC CTACTCAACCTTAGGTGTTATTACTCC
AD-MYB61	GTCATATGGCCATGGAGGCCAGTGAATTC ATGGGGAGACATTCTTGCTGTTAC	ATTCATCTGCAGCTCGAGCTCGATGGATCC CTAAAGGGACTGACCAAAAAGAGACG
6P1-MYB77	GAAGTTCTGTTCCAGGGGCCCTGGGATCC ATGGCGGATCGTGTTAAAGG	ATGCGGCCGCTCGAGTCGACCCGGGAATTC CTACTCAACCTTAGGTGTTATTACTCC
pET28a-PYL8	ATCGGATCC ATGGAAGCTAACGGGATTG	ATCGAATTC CTATAGTCTCGGGGTGAAG
pENTR-MYB77	CACCATGGCGGATCGTGTTAAAGG	CTCAACCTTAGGTGTTATTACTCC
cLUC-ABI1	CAGATCTCGTACGCGTCCCGGGCGGATCC ATGGAGGAAGTATCTCCGGC	TGTTTGAACGATCTGCAGTCTAGAGTCGACTTA TCAGTTCAAGGGTTTGCTCTTG