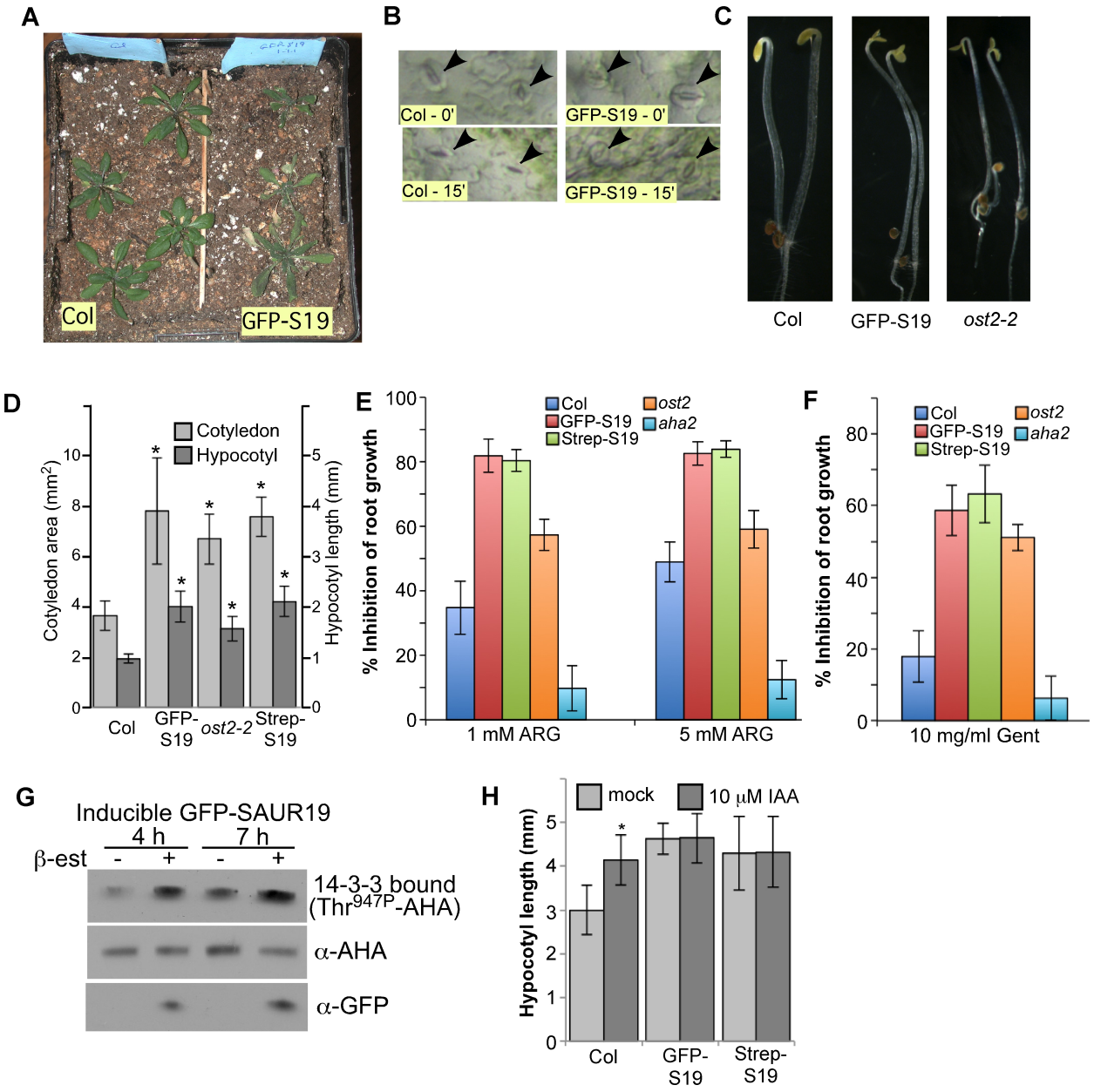
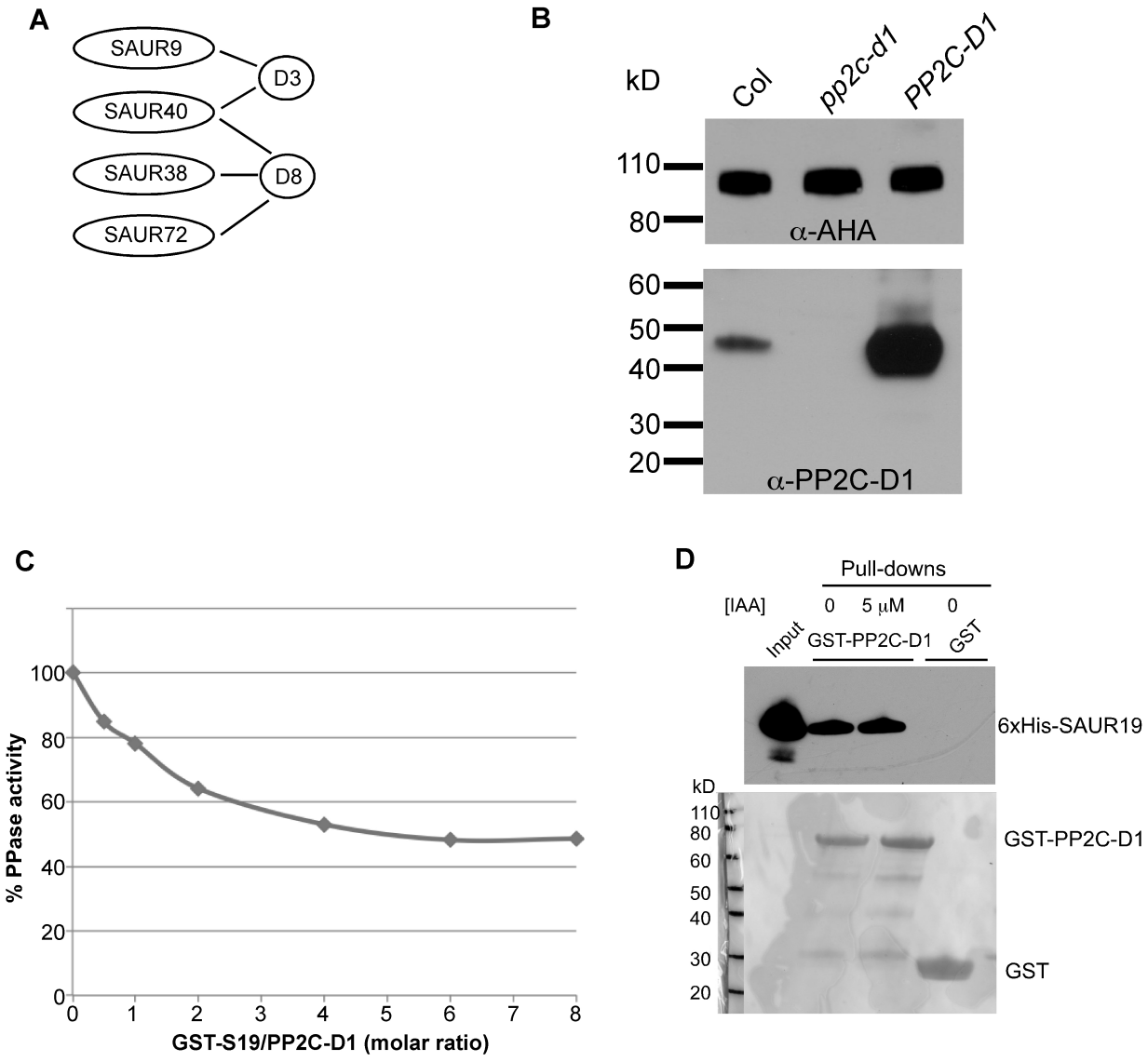
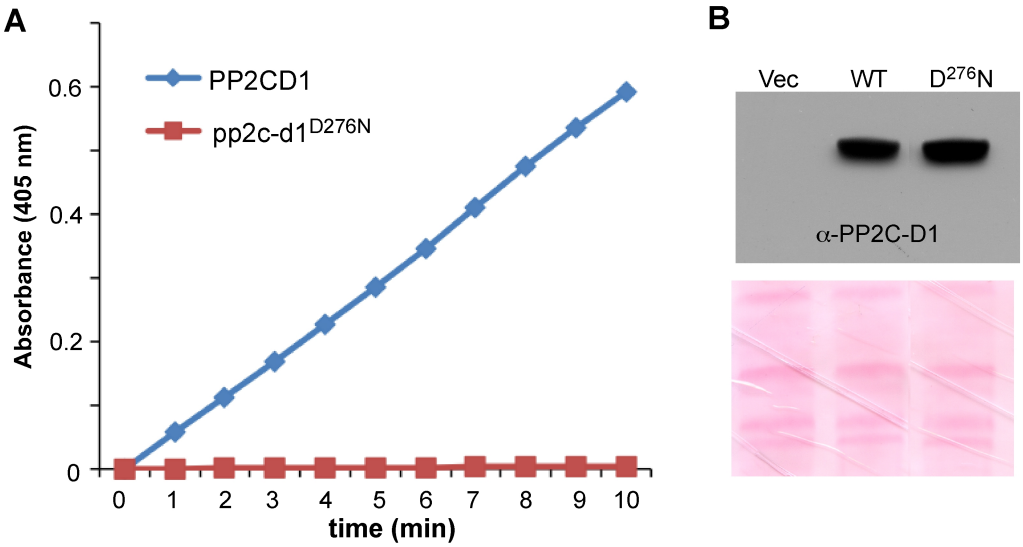


Supplemental Figure 1. Additional phenotypes of SAUR19 overexpression plants. **(A)** Three-week-old Col and GFP-SAUR19 plants photographed 10 days after cessation of watering. **(B)** Stomatal apertures (arrowheads) of Col and GFP-SAUR19 leaves immediately after excision from plant (top) or 15 min after excision (bottom). **(C)** Five-day-old etiolated seedlings. **(D)** Hypocotyl length and cotyledon area of 8 d.o. seedlings. Root growth on media containing arginine **(E)** or gentamicin **(F)**. Four-day-old seedlings were transferred from ATS plates to media containing supplements and grown an additional 4 days. Values indicate the mean inhibition of root growth (n=16) ± sd. **(G)** Five-day-old Col seedlings harboring an estrogen-inducible GFP-SAUR19 transgene were induced with 10 μM β-estradiol. AHA C-terminal phosphorylation status was then assessed by GST-14-3-3 far western blotting of microsomal extracts. **(H)** Three-day-old seedlings were transferred to mock or IAA supplemented media and

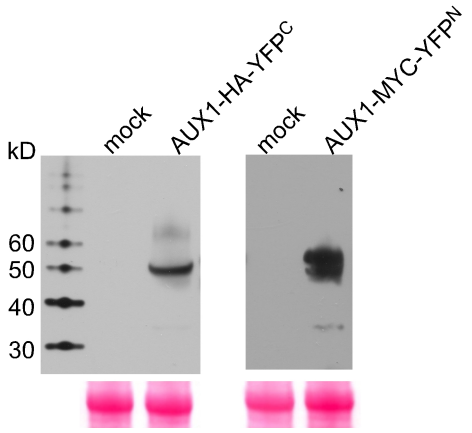
grown an additional 3 days. Seedlings were grown under yellow filters to slow IAA degradation. Values indicate the mean ($n \geq 12$) $\pm$ sd. Asterisk indicates significant effect of IAA versus mock-treated control as determined by one-way ANOVA; $P < 0.01$.



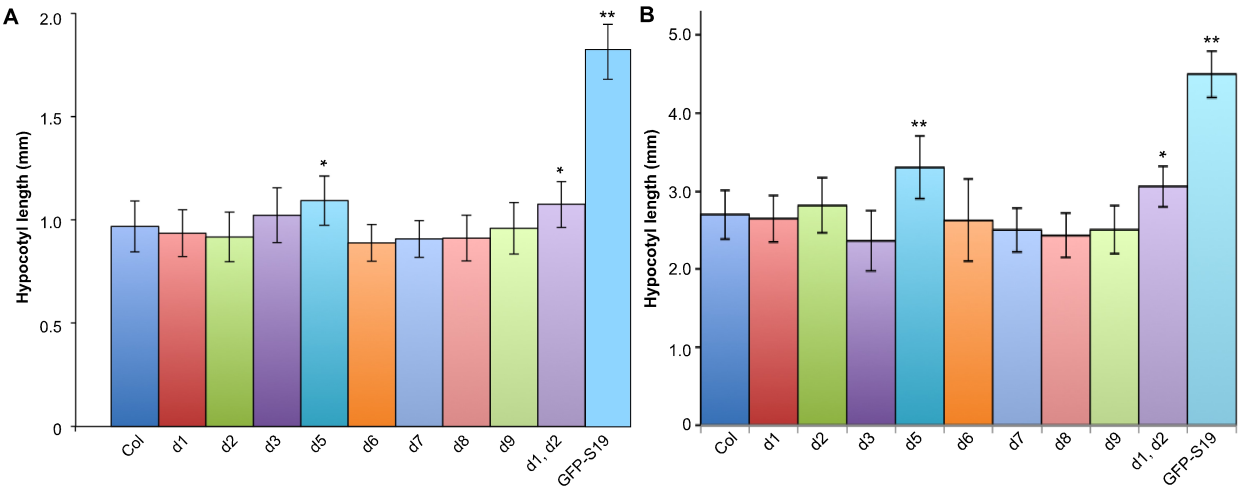
Supplemental Figure 2. Characterization of PP2C-D phosphatases. (A) SAUR-PP2C-D interactions obtained from the AI-1 Interactome database. **(B)** α-PP2C-D1 immunoblot of microsomal fractions. AHA is shown as a loading control. **(C)** Dose-response curve of PP2C-D1 inhibition by increasing concentrations of GST-SAUR19. **(D)** GST-PP2C-D1 or GST bait proteins bound to glutathione-agarose beads were incubated with 6xHis-SAUR19 ± 5 μM IAA for 1 h at 4ºC. Beads were collected by centrifugation, washed 3 times with 1 ml of buffer, and bound proteins were separated by SDS-PAGE. SAUR19 was detected by immunoblotting (top). Ponceau S-stained blot shows levels of the bait proteins (bottom).



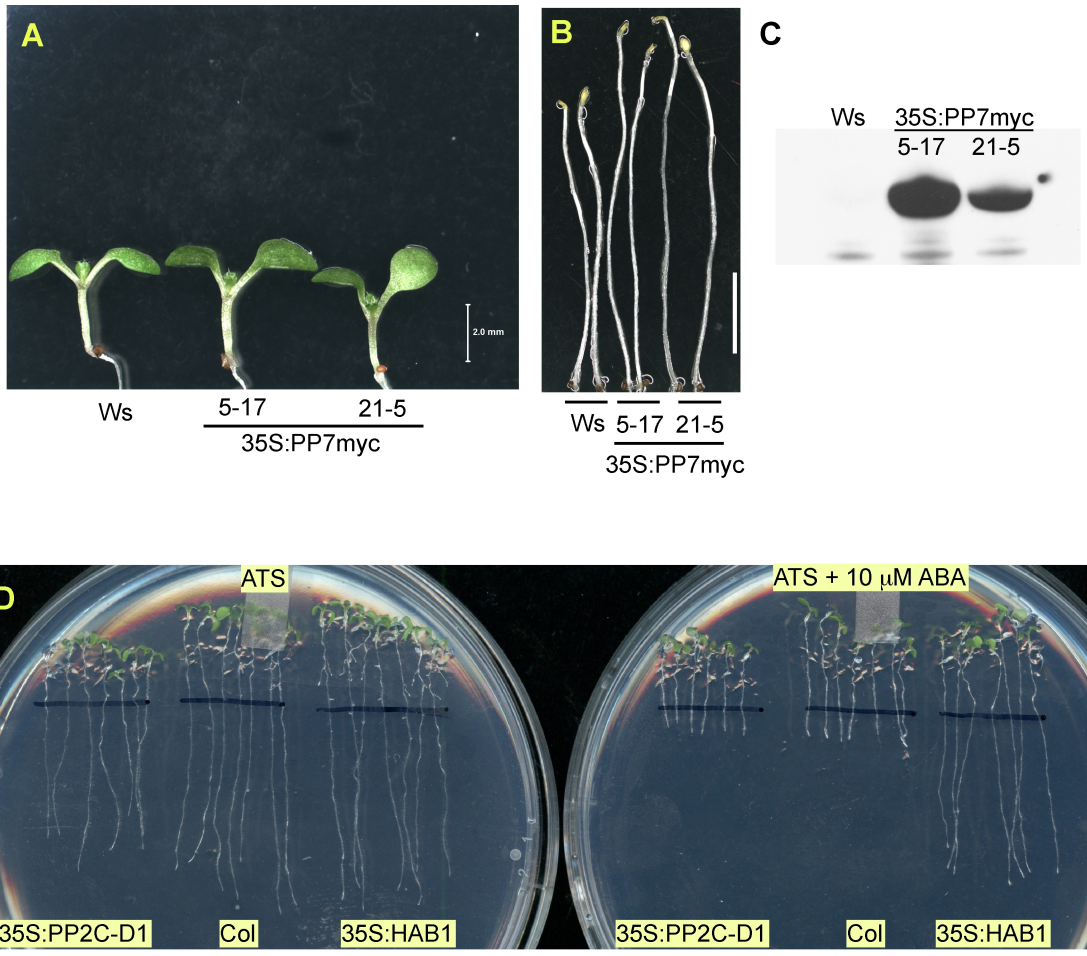
Supplemental Figure 3. The D276N mutation abolishes phosphatase activity of PP2C-D1. (A) pNPP phosphatase assays containing 0.5 μM recombinant GST-PP2C-D1 or GST-pp2c-d1^{D276N}. **(B)** PP2C-D1 immunoblot analysis of RS-72 yeast cells carrying the empty expression vector (vec) or PP2C-D1 expression constructs. The Ponceau S stained blot is shown below as a loading control.



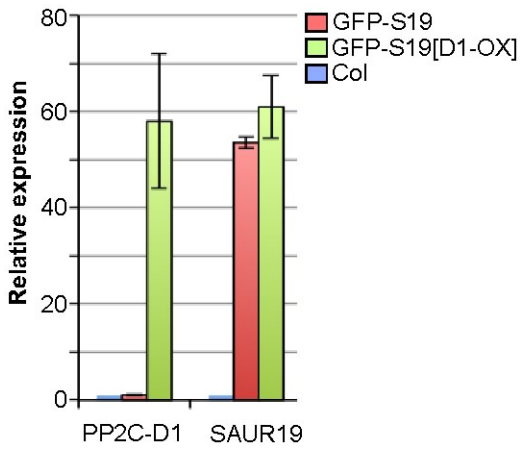
Supplemental Figure 4. Expression of AUX1 BiFC contructs in tobacco.
Microsomal extracts prepared from tobacco leaves infiltrated with AUX split YFP expression vectors or mock control were immunoblotted with HA or *c*-myc antibodies. Ponceau S staining of the large subunit of RuBisCo is shown as a loading control.



Supplemental Figure 5. Hypocotyl lengths of 7 d.o. *pp2c-d* mutants. Seedlings were grown under 65 (**A**) or 30 μE m^{-2} s^{-1} (**B**) Wc light; Mean (n ≥ 25) ± sd. Asterisks indicate significant difference from Col control (One-way ANOVA; *P < 0.05; **P < 0.01).



Supplemental Figure 6. Phosphatase overexpression controls. Seedlings expressing a 35S:*PP7myc* transgene do not exhibit short hypocotyls in the light **(A)** or dark **(B)**. Size bars = 2 mm (A) or 5 mm (B). **(C)** α-myc immunoblot of extracts prepared from the 35S:*PP7myc* seedlings shown in panel A. **(D)** 35S:*HAB1*, but not 35S:*PP2C-D1* confers resistance to ABA. 4 d.o. seedlings were transferred to ATS media ± 10 μM ABA and grown another 5 days. Black line indicates position of the root tips at the time of transfer.



Supplemental Figure 7. Quantitative RT-PCR analysis of GFP-*SAUR19* and *PP2C-D1* overexpression. Values represent the mean ± sd of 3 biological replicates with 7 d.o. seedlings.

Table 1. Primers used in this study.

gene	Primer sequence
ABI1	F: GGGGACAAGTTTGTACAAAAAAGCAGGCTG CATGGAGGAAGTATCTCCGGCGATCG R: GGGGACCACTTTGTACAAGAAAGCTGGGTAAGCTTA TCAGTTCAAGGGTTTGCTCTTGAG
PP2C-D1 At5g02760	F: GGGGACAAGTTTGTACAAAAAAGCAG GCTGCATGGTTAAACCCTGTTGGAGAATAG R: GGGGACCACTTTGTACAAGAAAGC TGGGTAAGCTTATCATGATGTTGAATGCATCGGG
PP2C-D5 At4g38520	F: GGGGACAAGTTTGTACAAAAAAGCAGGCTGCA TGCTATCTGGGTTGATGAATTTTC R: GGGGACCACTTTGTACAAGAAAGCTGGGTAAGC TTATCAGGAGGCGCCAGCAGCAGCAG
PP2C-D6 At3g51370	F: GGGGACAAGTTTGTACAAAAAAGCAGGCTGC ATGTTATCAACGTTAATG R: GGGGACCACTTTGTACAAGAAAGCTGGGTAAGCTTA TTAGATTTTCTTGGGGAATG
PP2C-D7 At5g66080	F: GGGGACAAGTTTGTACAAAAAAGCAGGCTGCATG TTATCCCTTTTCTTCAACTTTTTG R: GGGGACCACTTTGTACAAGAAAGCTGGGTAAGCTTA TTAAAGTTTCTTAGGTAAAGTG
PP2C-D9 At5g06750	F: GGGGACAAGTTTGTACAAAAAAGCAGG CTGCATGTTCTCCTGGTTAGC R: GGGGACCACTTTGTACAAGAAAGCTGGGTAA GCTTACTAAGAGAGGAAGATACTG
SAUR9 At4g36110	F: GGGGACAAGTTTGTACAAAAAAGCAGGCTGCATGGC GATAAAGAAGTCGAAC R:GGGGACCACTTTGTACAAGAAAGCTGGGTAAGCTTA TTATCTGAACATTGA GATGAG
SAUR19 At5g18010	F: GGGGACAAGTTTGTACAAAAAAGCAGGCTGC AGGATGGCTTTCGTGAGAAGTCTATTGG R: GGGGACCACTTTGTACAAGAAAGCTGGGTTCT AGATCATTGGAGCCGAGAAGTCAC
SAUR40 At1g79130	F: GGGGACAAGTTTGTACAAAAAAGCAGGCTGCA TGAAGCCTCTGATTCGAC R: GGGGACCACTTTGTACAAGAAAGCTGGGTAAG CTTACTACTCTGTAGA TACATCTTC
SAUR72 At3g12830	F: GGGGACAAGTTTGTACAAAAAAGCAGGCTGCATGAA GCAACTAATCCGTCGT

	R: GGGGACCACTTTGTACAAGAAAGCTGGGTAAGCTTA TCAAATAGTCCCGTCACCGA
pp2c-d T-DNA genotyping	d1: CACAAGATCCATAGGTGATGC/TGCCCTTGACACAGGAAGTG d2: GTATCGAGGTCTATAGGAGAC/CGCTGCCTCGTGAAGAGCCG d3: CAGATTGTGGTCTTGAAGCAC/GTGTTCACAATGTCAACAGC d5: CATCTGCGATGGGAAGCTAT/CAAACAGAGTGGGGTGTGTG d6: CGCTTTGACGGATGTGGAGG/GCTTGAACAACAGCCATGGAG d7: GAAAGCTTAGTTGTCTGTGTG/GCTGCCTCCTGCAGCGCAGC d8: CCCTGATGACTCACAAATCG/GACGGATTCCTGGAACATTGC d9: GGATGTTCTCCTGGTTAGCGAG/GATGATCAGAGATGTATCTAG
PPase cloning into pMP1612	D1; F: AAGCGGCCGCGAGAAGATGGTTAAACCCTGTTGGAGAATAG D2; R: AAGCGGCCGCTCATGATGTTGAATGCATCGGGTATCC D5; F: ataagaatGCGGCCGCATGCTATCTGGGTTGATGAATTTTCT D5; R: ataagaatGCGGCCGCTCAGGAGGCGCCAGCAGCAGCAG PP7; F: ataagaatGCGGCCGCATGGAAACTGTTCCACCATCTCC PP7; R: ataagaatGCGGCCGCTCAGCTATTTGGTTGTTCGTTATT At1g43900; F: ataagaatGCGGCCGCATGAAGAAAACTAGAAATGTTGC At1g43900; R: ataagaatGCGGCCGCTCAAGAAACCTCGAATCGTACAAC
qRT-PCR	PDF1.2-F: TGTTCTCTTTGCTGCTTTCGACGC PDF1.2-R: TGTGTGCTGGGAAGACATAGTTGC PR1-F: AGTATGGCTTCTCGTTCACA PR1-R: GGAGCTACGCAGAACAACTA SAUR19-F: GATTCTAAGCCGCTCCAC SAUR19-R: CCGAGAAGTCACATTGATG PP2CD1-F: GGGCAGATCTGAGAGAGGTG PP2CD1-R: CCGCACTAAGGATTGGCTTA PP2CD2-F: TCGTTGGGAACTCAAGGACT PP2CD2-R: AATGTCGTCTCACTTTCTTGTCA PP2CD3-F: CAAGGCCGTTCAGTTATCGT or AAAGTTTGGCGTGTCAAAGG PP2CD3-R: CCCTGAACTTTGCCAACAAT or GTCTCCGCACTCCTCTATCG PP2CD4-F: TGCAAGTATCGAATCTGTGAGAG PP2CD5-R: CCGAATGCCACGTTCTATCT PP2CD5-F: CGCGGATGATTCTGGACTAT PP2CD5-R: TCTGGCGAGTAAAAGGCATC

	PP2CD6-F: AACGGAGCATGAGATCCAAC PP2CD6-R: CGTGGAAATGTCTCCTCACA PP2CD7-F: CAATGTCTGGCGTGTTAAGG PP2CD7-R: CATGGAAATGCCTCCTGACT PP2CD8-F: GCCGTAGCTGAACGGTTATC PP2CD8-R: CCAGAGACCATCTGATGCAA PP2CD9-F: TGCTTGGTTCCATGGGTAGT PP2CD9-R: TTCTTCAGCGAGATGGAACC ACT7-F: GAGAAGATGACTCAGATC ACT7-R: ATCCTTCCTGATATCGAC
AHA2 Gateway	F: CACCATGTCGAGTCTCGAAGATATC R: GACAGTGTAGTGACTGGGAGTTTC
pp2c-d1^{D276N}	F: GTTTATAATTCTTGCTTCAaATGGGCTTTGGGAGCATC R: GATGCTCCCAAAGCCCATtTGAAGCAAGAATTATAAAC
AUX1 Gateway	F: CACCATGTCGGAAGGAGTAGAAGC R: AAGACGGTGGTGTAAAGCGGAG
amiD2/5/7/8/9	AMI-S: GATGATACCTGAATGATGCCCTTTCTCTCTTTTGTATTCC AMI-A: GAAAGGGCATCATTCAGGTATCATCAAAGAGAATCAATGA AMI-S*: GAAAAGGCATCATTCTGGTATCTTCACAGGTCGTGATATG AMI-A*: GAAGATACCAGAATGATGCCTTTTCTACATATATATTCCT