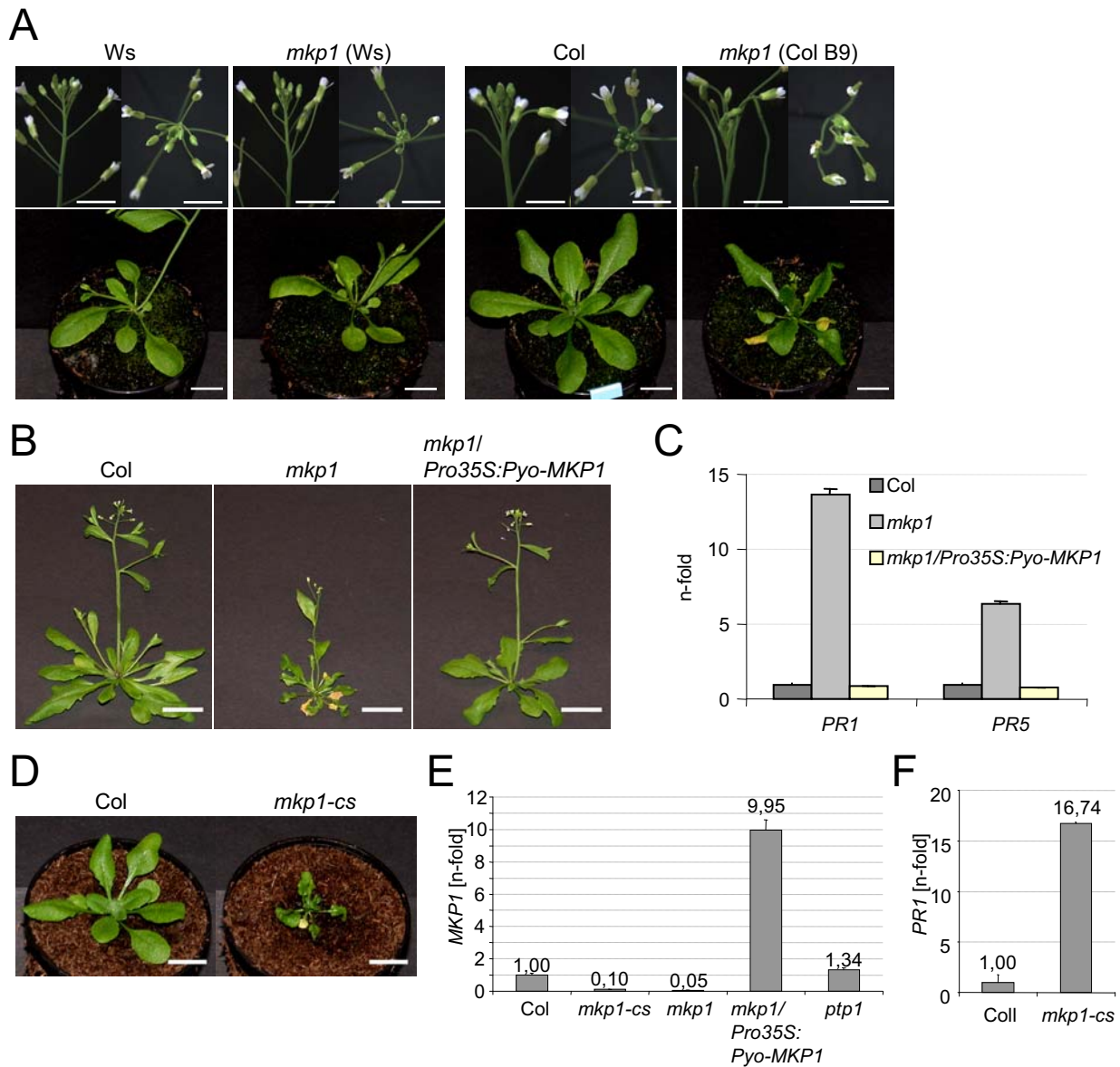


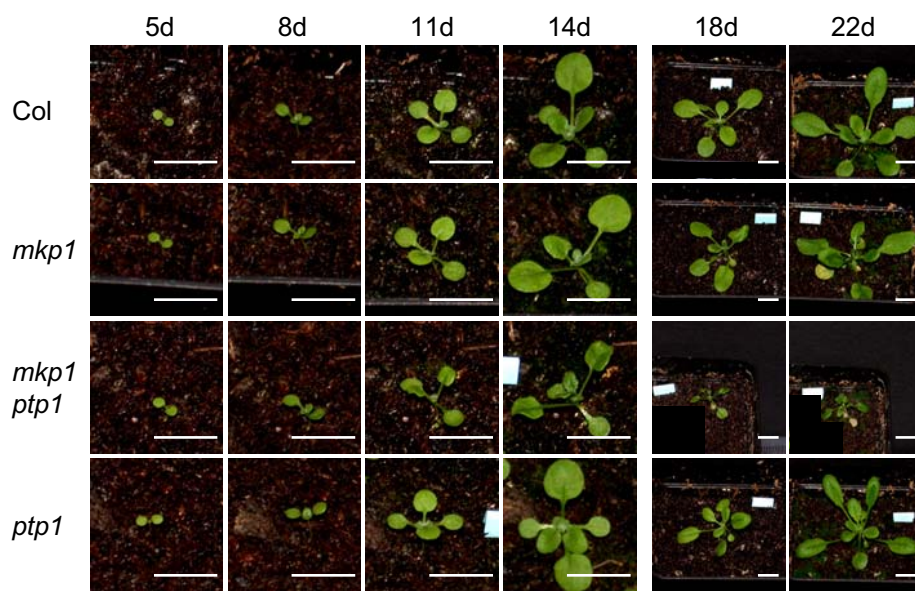
**Supplemental Figure 1**

- (A) The pROK2 T-DNA is inserted into exon 4 of *PTP1* (At1g71860) in the *ptp1-1* (SALK\_118658) mutant. The yellow blocks represent the exons and the connecting black lines the introns.
- (B) The T-DNA insertion is exactly between the indicated residues (green and yellow) and is associated with a 20-bp deletion (underlined). RB = right border of the T-DNA, LB = left border.
- (C) The *ptp1-1* mutant does not show any phenotype compared to Col wild type under standard growth conditions. Photographs of 22-d-old plants are shown. Bars = 1 cm.
- (D) RNA gel blot analysis shows absence of wild-type *PTP1* mRNA in the *ptp1-1* mutant. The blot was sequentially probed with *PTP1* and *PHS1* cDNA (loading control). Note that the larger transcript detectable in *ptp1-1* due to the T-DNA insertion cannot produce a functional *PTP1* protein.
- (E) Fresh weight of 20-d-old plants. The means  $\pm$  SE (n=47) are shown. The difference between Col and *mkp1*(Col) is statistically significant, as indicated by \*\*\* (Student's *t* test,  $P < 0.0001$ ). The difference between Col and *ptp1* is not significant (ns).



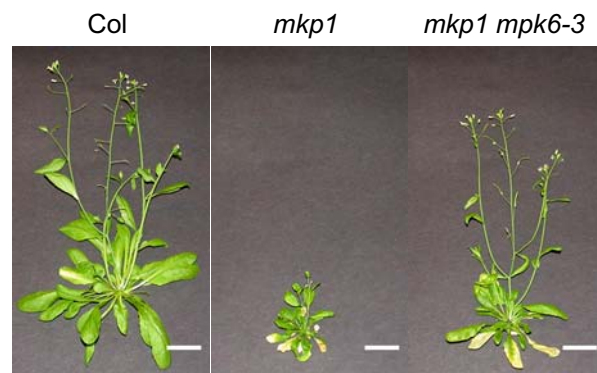
### Supplemental Figure 2

- (A) Growth of *mkp1*(Ws) is comparable to the Ws wild type under standard growth conditions. A comparison of *mkp1*(Col) to the Col wild type is shown as contrast. Photographs of inflorescences were taken of 40-d-old plants, of rosettes of 28-d-old plants. Bars = 0,5 cm (inflorescence) and 1cm (rosettes)
- (B) The *mkp1*(Col) growth phenotype is complemented by expression of a polyoma(Pyo)-tagged MKP1. Pictures of 33-d-old plants are shown. Bars = 2 cm.
- (C) The *PR*-gene misexpression phenotype of *mkp1*(Col) is complemented by expression of a polyoma(Pyo)-tagged MKP1. Quantitative RT-PCR data for *PR1* and *PR5* expression are shown. Error bars represent SD of technical triplicates.
- (D) An *MKP1*-co-suppression line (*mkp1-cs*) in the Col background shows aberrant growth phenotypes comparable to the *mkp1*(Col) T-DNA insertion line. Photographs of 22-d-old plants are shown. Bars = 1 cm.
- (E) Quantitative RT-PCR analysis of *MKP1* expression shows reduced *MKP1* mRNA levels in the *mkp1-cs* line, normal levels in *ptp1-1* and overexpression in the *mkp1/Pro35S:Pyo-MKP1* line. Error bars represent SD of three biological repetitions.
- (F) The *mkp1-cs* phenotype is associated with elevated *PR1* gene expression as determined by qRT-PCR. Error bars represent SD of three biological repetitions.
- (C, E, F) Samples from 22-d-old plants grown on soil under standard conditions.



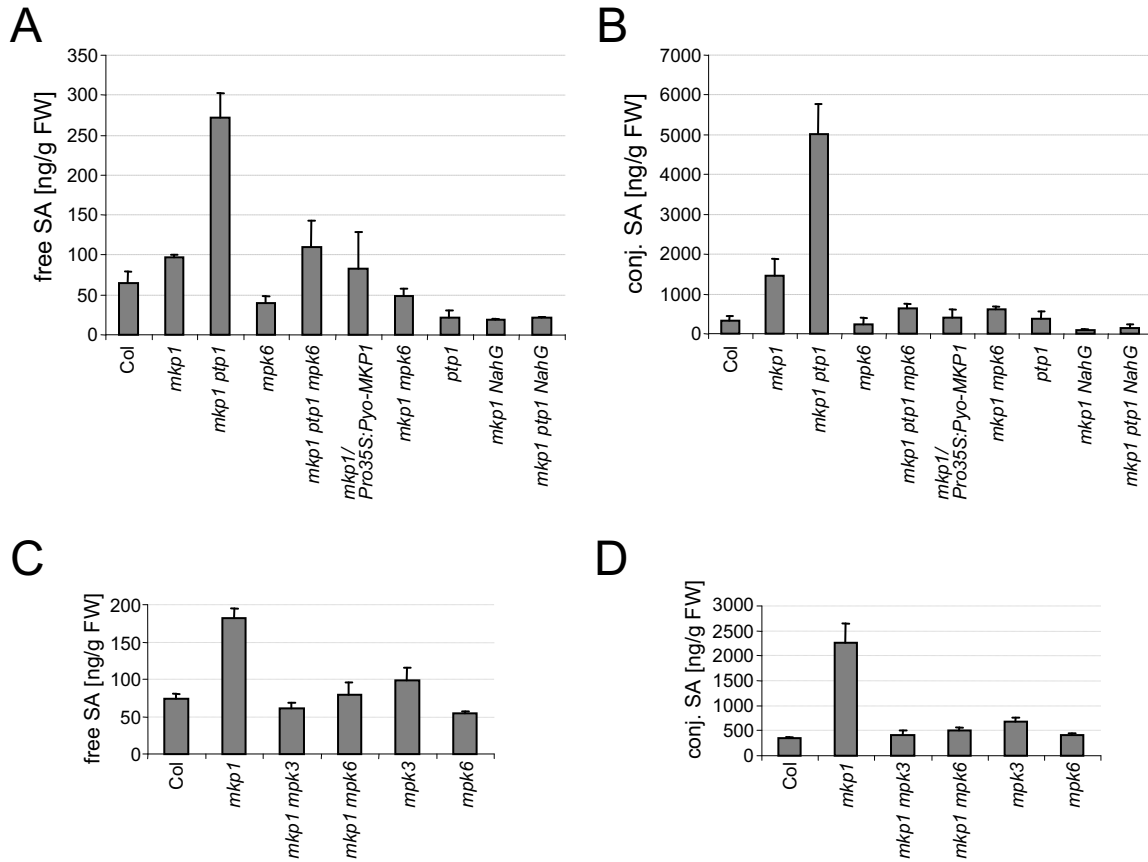
**Supplemental Figure 3**

Phenotypes of *mkp1*(Col) and *mkp1 ptp1* appear late in development. Photographs of plants at the indicated number of days after germination are shown. Bars = 1 cm.



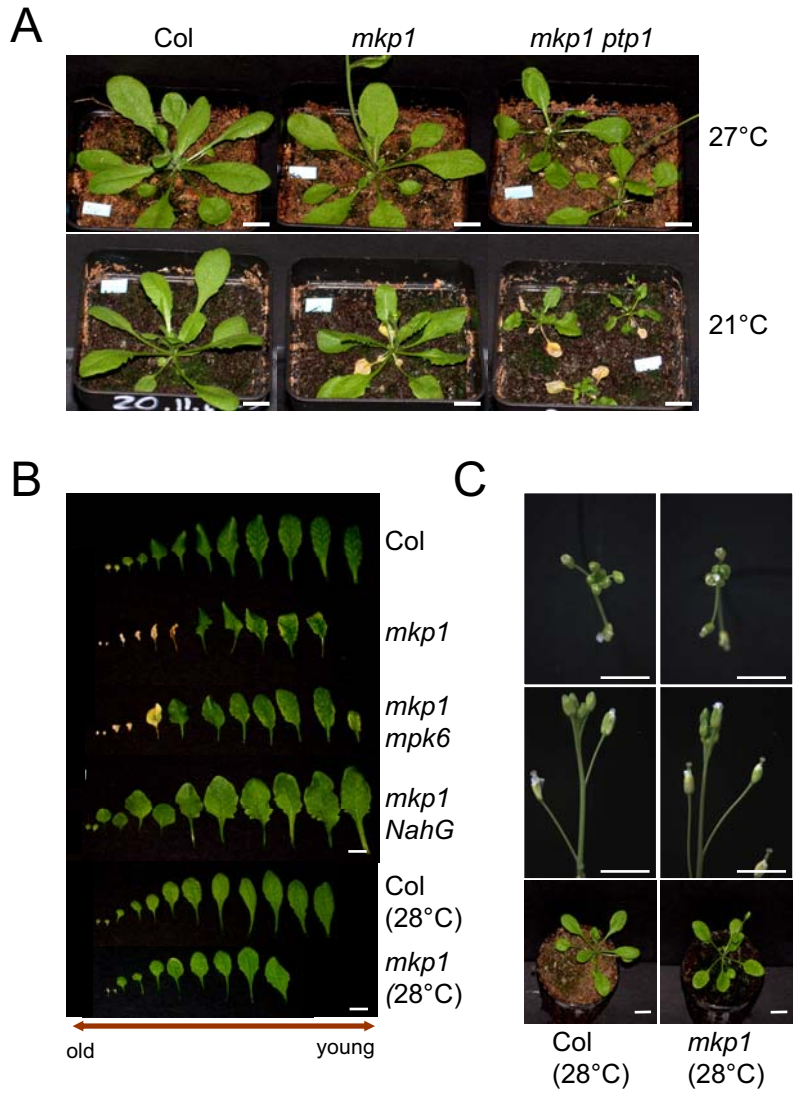
**Supplemental Figure 4**

Photographs of 40-d-old plants grown on soil under standard conditions are shown. Aberrant phenotypes of *mkp1*(Col) are partially suppressed by *mpk6-3*. Bars = 2 cm.



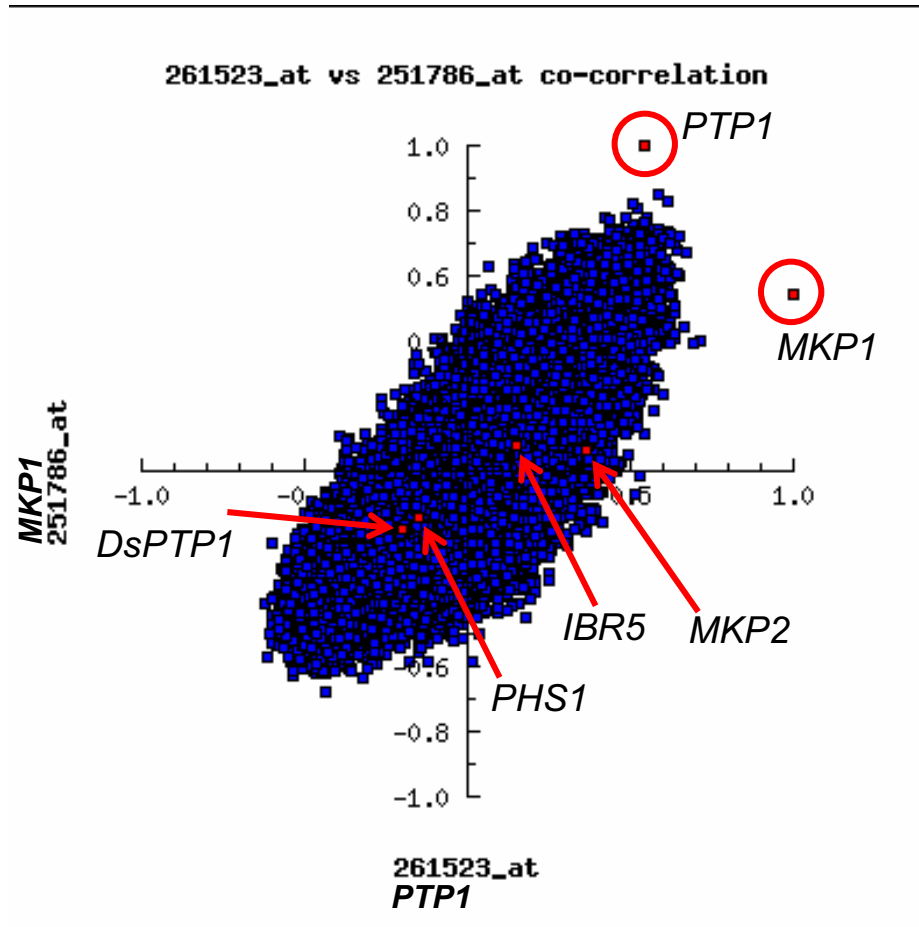
**Supplemental Figure 5**

Free (A, C) and conjugated (B, D) salicylic acid levels of 22-d-old soil-grown plants were measured by HPLC. (A, B) and (C, D) represent two different experiments. The average of three independent biological samples is shown for each genotype in each experiment. Error bars represent SD (n = 3).



**Supplemental Figure 6**

Growth phenotypes of *mkp1*(Col) and *mkp1 ptp1* are suppressed by elevated temperature, including the phenotypes of early senescence (**A**, **B**) and aberrant inflorescences (**C**). Photographs of 25-d-old plants are shown. Bars = 1 cm.



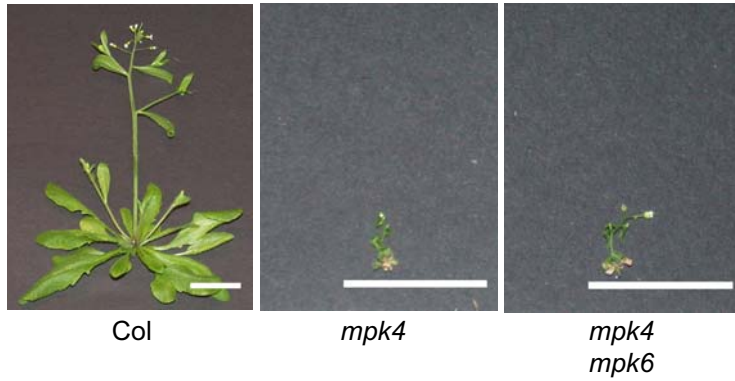
### Supplemental Figure 7

Co-correlation scatter plot according to the *Arabidopsis* Co-expression Tool (ACT). Pearson correlation coefficients are shown for *MKP1* and *PTP1* probes using 322 ATH1 arrays. The correlation  $r$ -values of each of 21891 genes with each of the two driver genes are plotted as blue squares. The values for the dual-specificity phosphatase genes are highlighted in red.

*MKP1* shows similar expression patterns with *PTP1*, giving a positive correlation against the other genes in the database. The two query genes always have correlation values of 1.0 with themselves. If they are strongly correlated with each other, they are located at the top right of the figure.

ACT: <http://www.arabidopsis.leeds.ac.uk/act/coexpanalyser.php#CO3>

Jen et al. (2006) *Plant J.* **46**: 336–348; Manfield et al. (2006) *Nucleic Acids Res.* **34**: W504–509.



**Supplemental Figure 8**

The *mpk6* mutation does not suppress the *mpk4* dwarf growth phenotype. Photographs of 22-d-old plants are shown. Bars = 2 cm.



**Supplemental Table 1: Primer sequences used for mutant genotyping.**  
The left-border-specific primer used to genotype SALK insertion lines is LBa1 (5'-TGGTTCACGTAGTGGGCC-3')

<b>eds1-22</b>	
S_071051_fw	5'-CTAACTCAGCTCTCTTGACG-3'
S_071051_rev	5'-TACGCTCAATGACCTTGGAG-3'
WT: S_071051_fw/S_071051_rev = 0.45 kb; S_071051_rev/LBa1 = none eds1-22: S_071051_fw/ S_071051_rev = none; S_071051_rev/LBa1 = 0.69 kb	
<b>mkp1</b>	
MKP1_fw	5'-ACAAGTCTATGGAAGAAGC-3'
MKP1_rev	5'-TGTCTTTCGCCACAGCATC-3'
pGKB5_GusRb1	5'-ACGCAGCACGATACGCTGG-3'
WT: MKP1_fw/MKP1_rev = 0.62 kb; MKP1_rev/pGKB5_GusRb1 = none mkp1: MKP1_fw/MKP1_rev = none; MKP1_rev/pGKB5_GusRb1 = 0.68 kb	
<b>mpk3-1</b>	
S_151594_fw	5'-CTTCTGTTGAACGCGAATTGCG-3'
S_151594_rev	5'-TCCGTTGATGCAAGTTGAGCC-3'
WT: S_151594_fw/S_151594_rev = 1.3 kb; S_151594_fw/LBa1 = none mpk3-1: S_151594_fw/S_151594_rev = none; S_151594_fw/LBa1 = 1.0 kb	
<b>mpk4</b>	
S_056245_fw	5'-TGACTGAATATGTTGTTACACG-3'
S_056245_rev	5'-ACTCACCAAAGCCGTACC-3'
WT: S_056245_fw/S_056245_rev = 1.0 kb; S_056245_rev/LBa1 = none mpk4: S_056245_fw/S_056245_rev = none; S_056245_rev/LBa1 = 0.66 kb	
<b>mpk6-2</b>	
S_073907_fw	5'-GATCTTTTCCATCTGCGTCAAG-3'
S_073907_rev	5'-CACTGTCGGGAAC TTATCAGTGA-3'
WT: S_073907_fw/S_073907_rev = 0.9 kb; S_073907_fw/LBa1 = none mpk6-2: S_073907_fw/S_073907_rev = none; S_073907_fw/LBa1 = 0.8 kb	
<b>NahG transgene</b>	
NahG_fw	5'-GAAAAACAATAAACTTGCTTGCG-3'
NahG_rev	5'-ACCTTCCAGCACATGACTACG-3'
WT: NahG_fw/NahG_rev = none NahG transgenic line: NahG_fw/NahG_rev = 0.52 kb	
<b>pad4-1</b>	
PAD4_fw	5'-TCGCATAAGACTAGCTAAGTTTTG-3'
PAD4_rev	5'-TAAGTCTCCATTGCGTCACTC-3'
pad4-1_fw	5'-TCGCATAAGACTAGCTAAGTTTTTA-3'
WT: PAD4_fw/PAD4_rev = 0.57 kb; pad4-1_fw/PAD4_rev = none pad4-1: PAD4_fw/PAD4_rev = none; pad4-1_fw/PAD4_rev = 0.57 kb	
<b>ptp1-1</b>	
S_118658_LP	5'-ACCTTTACCCTTTCTTCTCG-3'
S_118658_RP	5'-AAATAGTCCCCGCATTTAAC-3'
WT: S_118658_LP/S_118658_RP = 1.2 kb; S_118658_RP/LBa1 = none ptp1-1: S_118658_LP/S_118658_RP = none; S_118658_RP/LBa1 = 0.75 kb	
<b>snc1-11</b>	
S_047058_fw	5'-TCTGTTGCTTTAACCTTTGCTCC-3'
S_047058_rev	5'-TGGTGATTCCGATTTCTTCCAC-3'
WT: S_047058_fw/S_047058_rev = 0.64 kb; S_047058_rev/LBa1 = none snc1-11: S_047058_fw/S_047058_rev = none; S_047058_rev/LBa1 = 0.58 kb	

**Supplemental Table 2:** Primer sequences used for molecular cloning. *attB* recombination sites facilitating Gateway-based cloning are indicated in italic. Start ATG codons are indicated in blue, Stop codons in red.

<b>MKP1</b>	
attB1-MKP1	5' - GGGGACAAGTTTGTACAAAAAAGCAGGCTT <i>GATG</i> GTGGGAAGAGAGGATGCG-3'
attB2-MKP1	5' - GGGGACCACTTTGTACAAGAAAGCTGGGT <i>CGCTT</i> GCGGGTGGGT <i>GTTA</i> TAG-3'
attB2-MKP1 <sup>STOP</sup>	5' - GGGGACCACTTTGTACAAGAAAGCTGGGTCTAGCGCGCTCAGCAGTGC-3'
<b>PTP1</b>	
attB1-PTP1	5' - GGGGACAAGTTTGTACAAAAAAGCAGGCTT <i>GATG</i> GCGACCGGTAAAACC-3'
attB2-PTP1	5' - GGGGACCACTTTGTACAAGAAAGCTGGGT <i>CTTA</i> GGAACCTCGTTCCAGC-3'
attB2-PTP1 <sup>STOP</sup>	5' - GGGGACCACTTTGTACAAGAAAGCTGGGTCTGGAACCTCGTTCCAGCATTTG-3'
<b>MPK1</b>	
attB1-MPK1	5' - GGGGACAAGTTTGTACAAAAAAGCAGGCTT <i>GATG</i> GCGACTTTGGTTGATCCTC-3'
attB2-MPK1	5' - GGGGACCACTTTGTACAAGAAAGCTGGGT <i>CTCA</i> GAGCTCAGTGTTTAAGGTTG-3'
<b>MPK2</b>	
attB1-MPK2	5' - GGGGACAAGTTTGTACAAAAAAGCAGGCTT <i>GATG</i> GCGACTCCTGTTGATCC-3'
attB2-MPK2	5' - GGGGACCACTTTGTACAAGAAAGCTGGGT <i>CTCA</i> AAACTCAGAGACCTCATTGTTG-3'
<b>MPK3</b>	
attB1-MPK3	5' - GGGGACAAGTTTGTACAAAAAAGCAGGCTT <i>GATG</i> AACACCGGCGGTGGC-3'
attB2-MPK3	5' - GGGGACCACTTTGTACAAGAAAGCTGGGT <i>CCTA</i> ACCGTATGTTGGATTGAGTG-3'
<b>MPK4</b>	
attB1-MPK4	5' - GGGGACAAGTTTGTACAAAAAAGCAGGCTT <i>GATG</i> TCGGCGGAGAGTTGTTTC-3'
attB2-MPK4	5' - GGGGACCACTTTGTACAAGAAAGCTGGGT <i>CTCA</i> CACTGAGTCTTGGATTG-3'
<b>MPK6</b>	
attB1-MPK6	5' - GGGGACAAGTTTGTACAAAAAAGCAGGCTT <i>GATG</i> GACGGTGGTTCAGGTCAAC-3'
attB2-MPK6	5' - GGGGACCACTTTGTACAAGAAAGCTGGGT <i>CCTA</i> TTGCTGATATTCTGGATTGAAAG-3'