# Supporting Information

Cho *et al.* 10.1073/pnas.0805539105

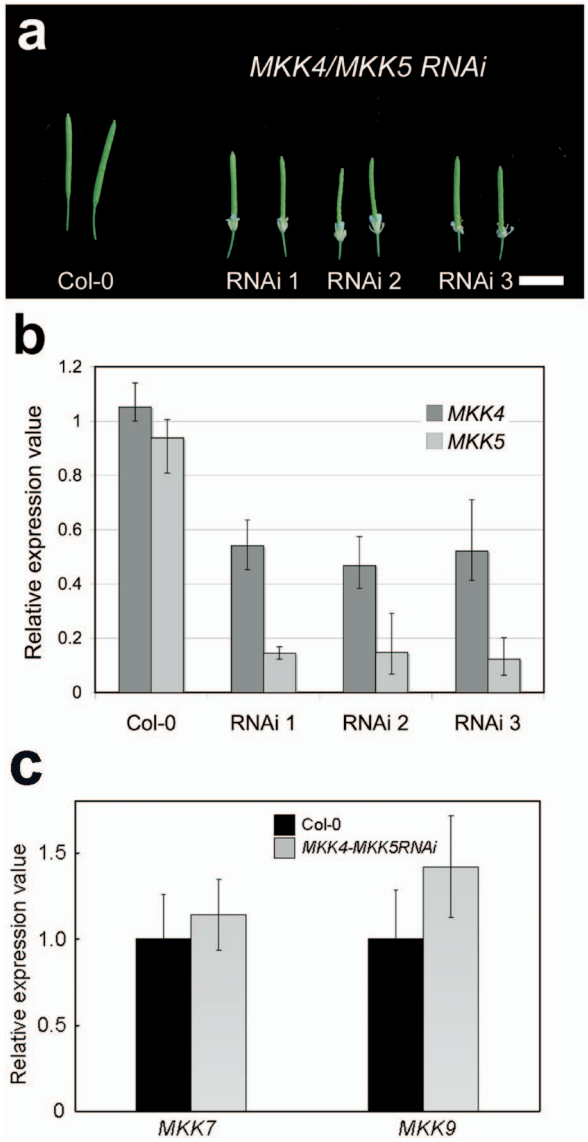


**Fig. S1.** *MKK4* and *MKK5* regulate the floral organ abscission. (*a*) Three independent lines of *MKK4-MKK5RNAi* transgenic plants show an abscission defective phenotype. (*b*) Expression of *MKK4* and *MKK5.* RNA was isolated from unopened flower bud clusters of Col-0 and *MKK4-MKK5RNAi* plants. Three biological replicas showed significantly reduced *MKK4* and *MKK5* mRNA accumulation from flowers of the *MKK4-MKK5RNAi* plants. Solid bars indicate the mean and error bars indicate the data ranges ($n = 3$). (*c*) Expression of *MKK7* and *MKK9* from flowers of Col-0 and *MKK4-MKK5RNAi* plants. Solid bars indicate the mean, and error bars indicate the data ranges ($n = 4$). (Scale bar: 1 cm.)

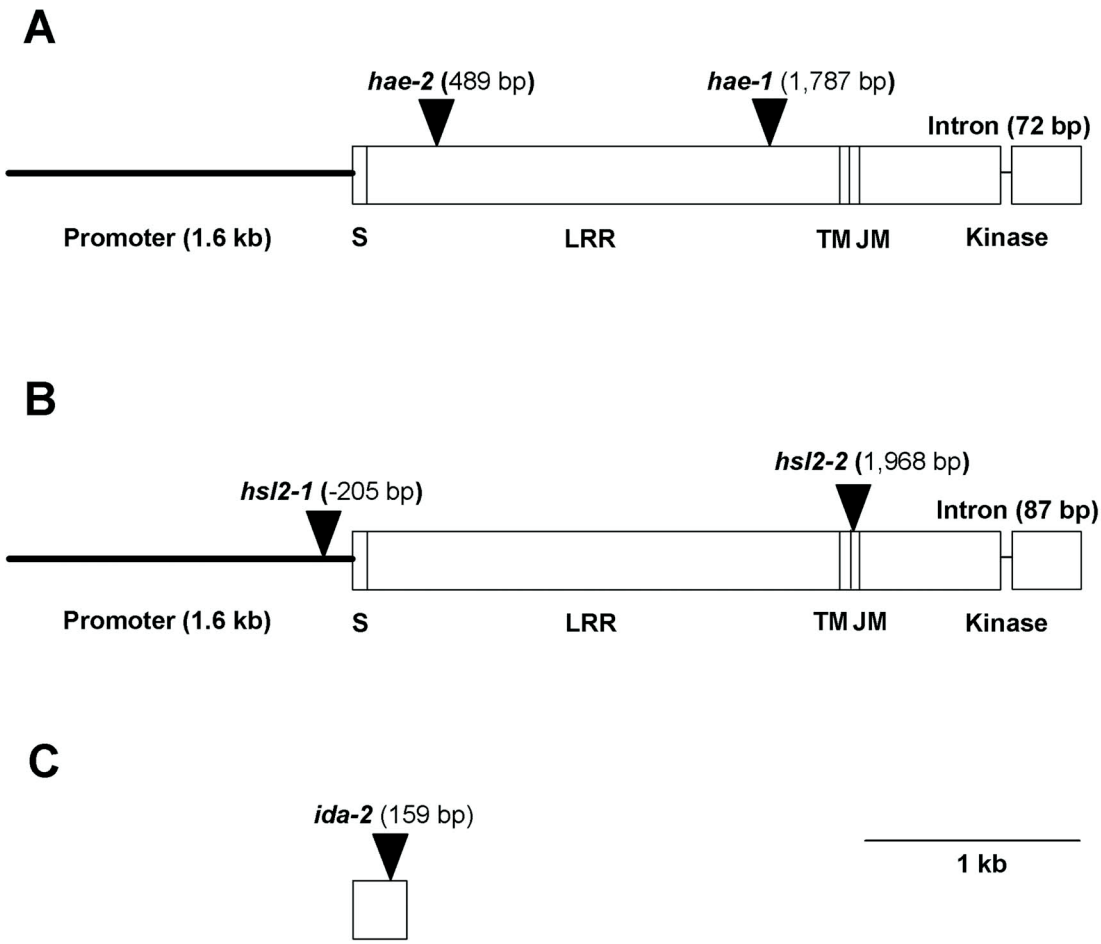


**Fig. S2.** T-DNA insertion alleles. (*A*) The *hae-1* T-DNA insertion (SALK_105975) is located at nucleotide 1787 from start codon. The *hae-2* T-DNA insertion (SALK_015074), is located at nucleotide 489 from start codon. The *hae-1* allele was used in this study. (*B*) The T-DNA of the *hsl2-1* allele (SALK_057117) is located at nucleotide −205, upstream of start codon. The T-DNA of *hsl2-2* (SALK_030520) is located at nucleotide 1968 from start codon. The *hsl2*-1 allele was used in this study. (*C*) *ida-2* (SALK_133209) has a T-DNA insertion 159 nucleotides from start codon. The bold line showed promoter region that used for GUS transcriptional fusion, and the thin line in the kinase domain indicates an intron. (*S*) signal peptide; LRR, leucine rich repeat; TM, transmembrane domain; JM, juxtamembrane region. (Scale bar: 1 kb.)

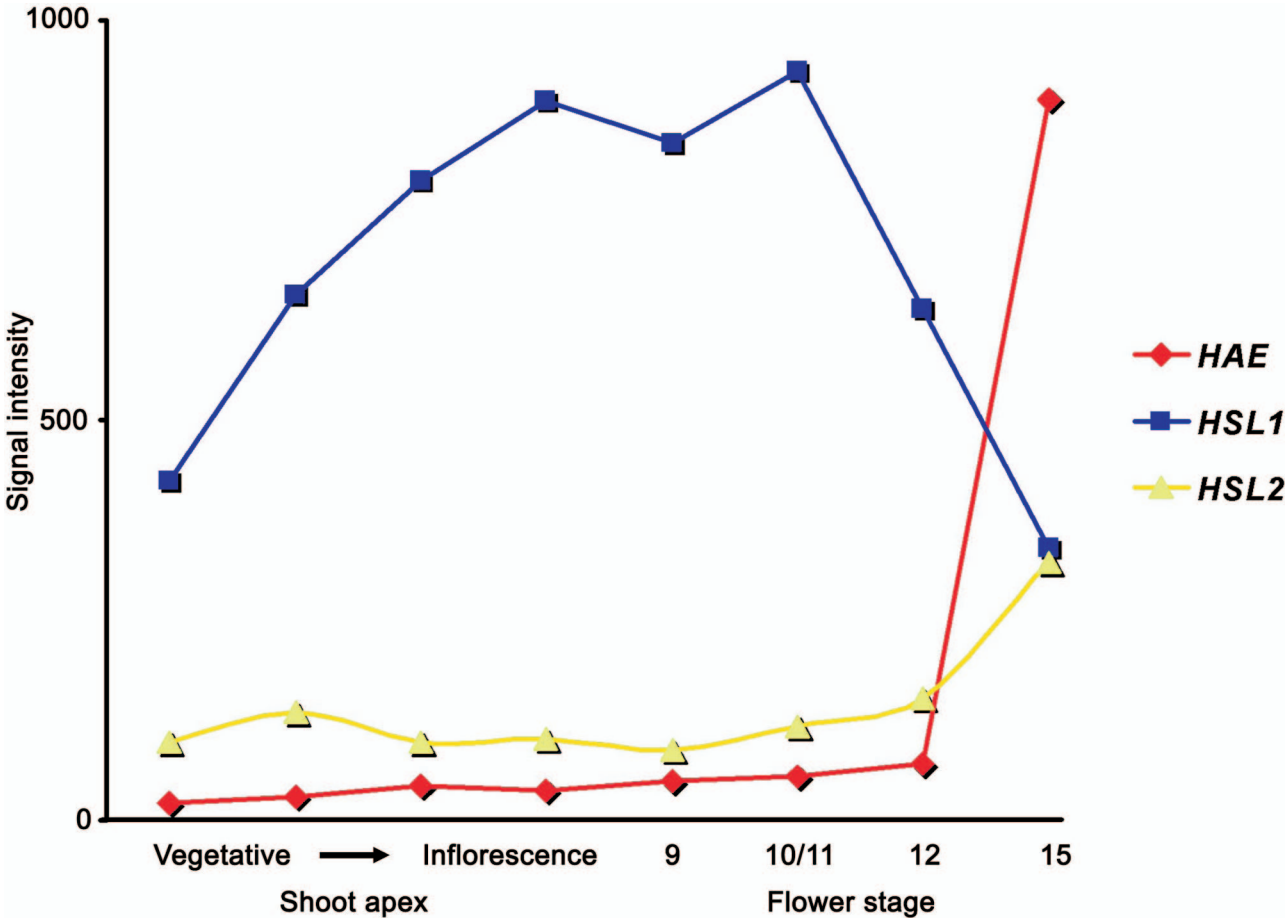


**Fig. S3.** Expression of *HAE, HSL1*, and *HSL2*. Expression pattern of *HAE*, *HSL1*, and *HSL2*. Publicly available microarray data were compiled using AtGenExpress (www.weigelworld.org/resources/microarray/AtGenExpress).

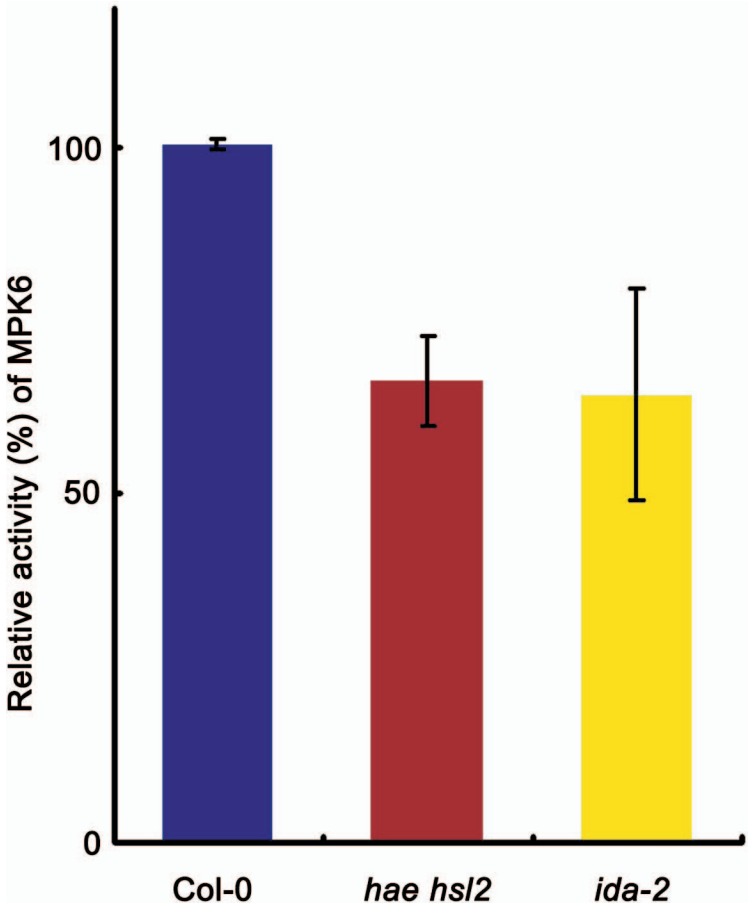


**Fig. S4.** MPK6 is activated in receptacle. Relative MPK6 activity from the receptacle of Col-0, *hae hsl2*, and *ida-2* plants. Biological replications ($n = 3$) show the reduced activity of MPK6 from receptacle of the mutants. Error bars indicate SE for the different mutants.

**Table S1. List of primers**

| Method used | | Primer | Sequence |
|---|---|---|---|
| Genotyping | 1 | hae-1-F | 5′-CAAACTGGGCTTATCCGACCCGG-3′ |
| | | hae-1-R | 5′-GTCCCCAACGTTTCAACCTCCGCTG-3′ |
| | 2 | hae-2-F | 5′-ATGGGAGAATCTGAATTACTTGAG-3′ |
| | | hae-2-R | 5′-CGAGAAGTGACAAGCGAGGC-3′ |
| | 3 | hsl2–1-F | 5′-CCCACTCGGAAGCTTACCATAGTCTG-3′ |
| | | hsl2–1-R | 5′-CGGGAATCACACCGGAGAAGTTGTTAGC-3′ |
| | 4 | hsl2–2-F | 5′-GTCTCGACGAACAGATTCTCCG-3′ |
| | | hsl2–2-R | 5′-TCCATTGCAAACTTAACAATGTCC-3′ |
| | 5 | ida-2-F | 5′-GTTCTTTGATCAGGAGAGAGCTTTG-3′ |
| | | ida-2-R | 5′-CTTCTCACGCAAAAGATAGAGTTGG-3′ |
| MPK6 | 1 | MPK6-F | 5′-TCTGAATTCGTCCGGTTACAGAGATCTCACAGA-3′ |
| | | MPK6-B | 5′-TCTCCCGGGCATGACCGGTAAAGATGAAAGCTT-3′ |
| mutagenesis | 2 | cMPK6-F | 5′-TCTCCCGGGATGGACGGTGGTTCAGGTCAACCG-3′ |
| | | cMPK6-Nosterminator-B | 5′-CTCTCTAGAAATTCCCGATCTAGTAACATAGAT-3′ |
| 35S::IDA | | IDAOE-F | 5′-ATGGCTCCGTGTCGTACGATG-3′ |
| | | IDAOE-R | 5′-TCAATGAGGAAGAGAGTTAACAAAAGAG-3′ |
| HAE::GUS | | GUS-HAE-F | 5′-CAGAAAGGATTAAACTAAAACTCTGTCACC-3′ |
| | | GUS-HAE-R | 5′-TTTTTTGGAAAAGGAATCGTTATTCTTC-3′ |
| HSL2::GUS | | GUS-HSL2-F | 5′-ACTTATATTGTGAAACAAAAAATTTGGTCC-3′ |
| | | GUS-HSL2-R | 5′-CGTGTTGGGAAGAGAGGTATGAAAC-3′ |
| qRT-PCR | 1 | QRT-MKK4-F | 5′-GAGGTTTCCTTTCCCTGTGA-3′ |
| | | QRT-MKK4-R | 5′-CTCTCTGCAAGCAACACGAG-3′ |
| | 2 | QRT-MKK5-F | 5′-CGTCGTCATATCGTTCATCG-3′ |
| | | QRT-MKK5-R | 5′-CATTGTTTGTGCCAAGATCC-3′ |
| | 3 | QRT-MKK7-F | 5′-GTTCGTAAACGCCGTCAAAT-3′ |
| | | QRT-MKK7-R | 5′-CTTCCTCTTCCGAGAACGTG-3′ |
| | 4 | QRT-MKK9-F | 5′-CAGTTGATGCGAGAGATGGA-3′ |
| | | QRT-MKK9-R | 5′-GCGAGTTTTTGCTCCGTTAC-3′ |
| | 5 | QRT-EF-1$\alpha$-F | 5′-TGAGCACGCTCTTCTTGCTTTCA-3′ |
| | | QRT-EF-1$\alpha$-R | 5′-GGTGGTGGCATCCATCTTGTTACA-3′ |

qRT-PCR, quantitative real-time PCR.