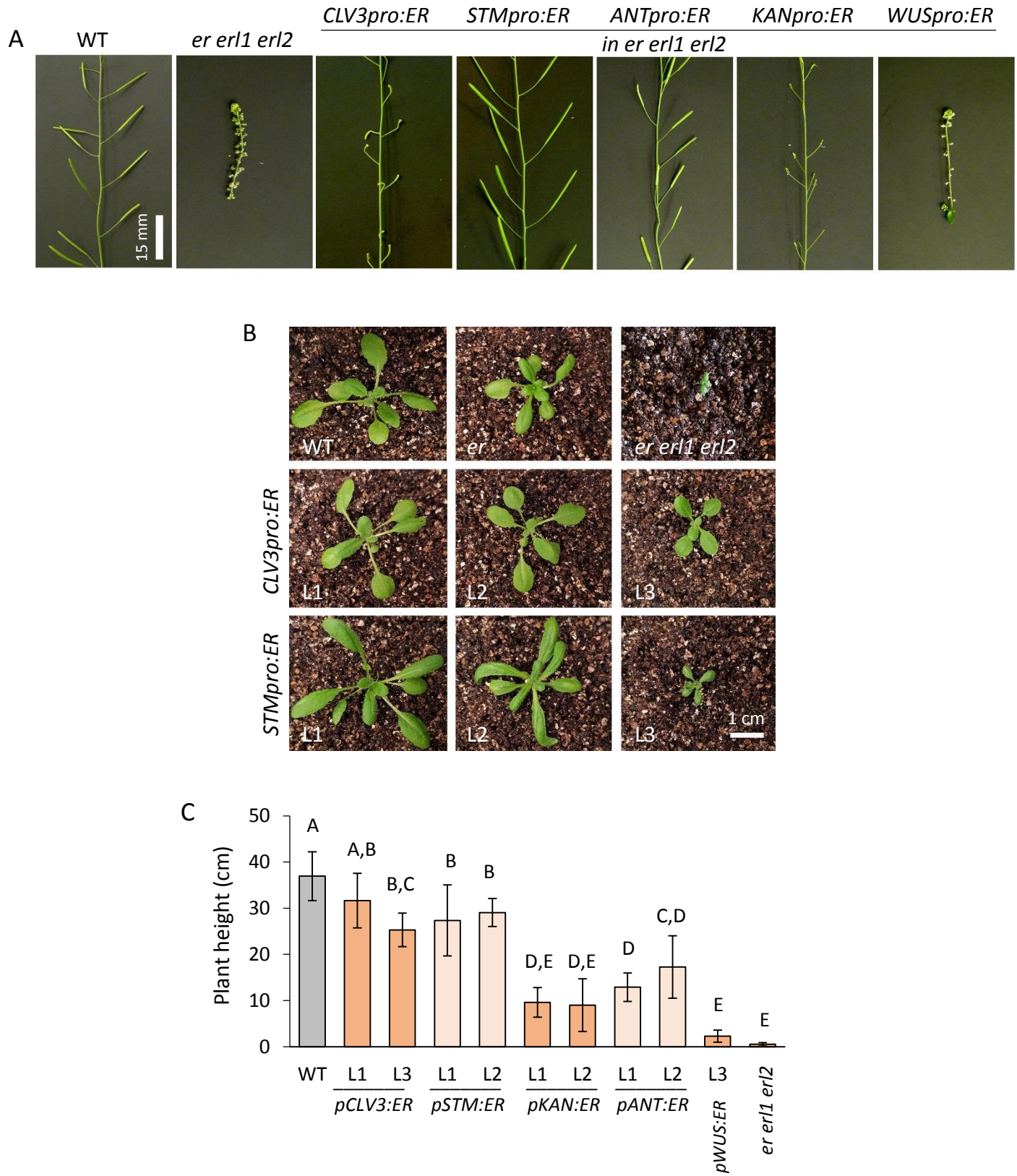
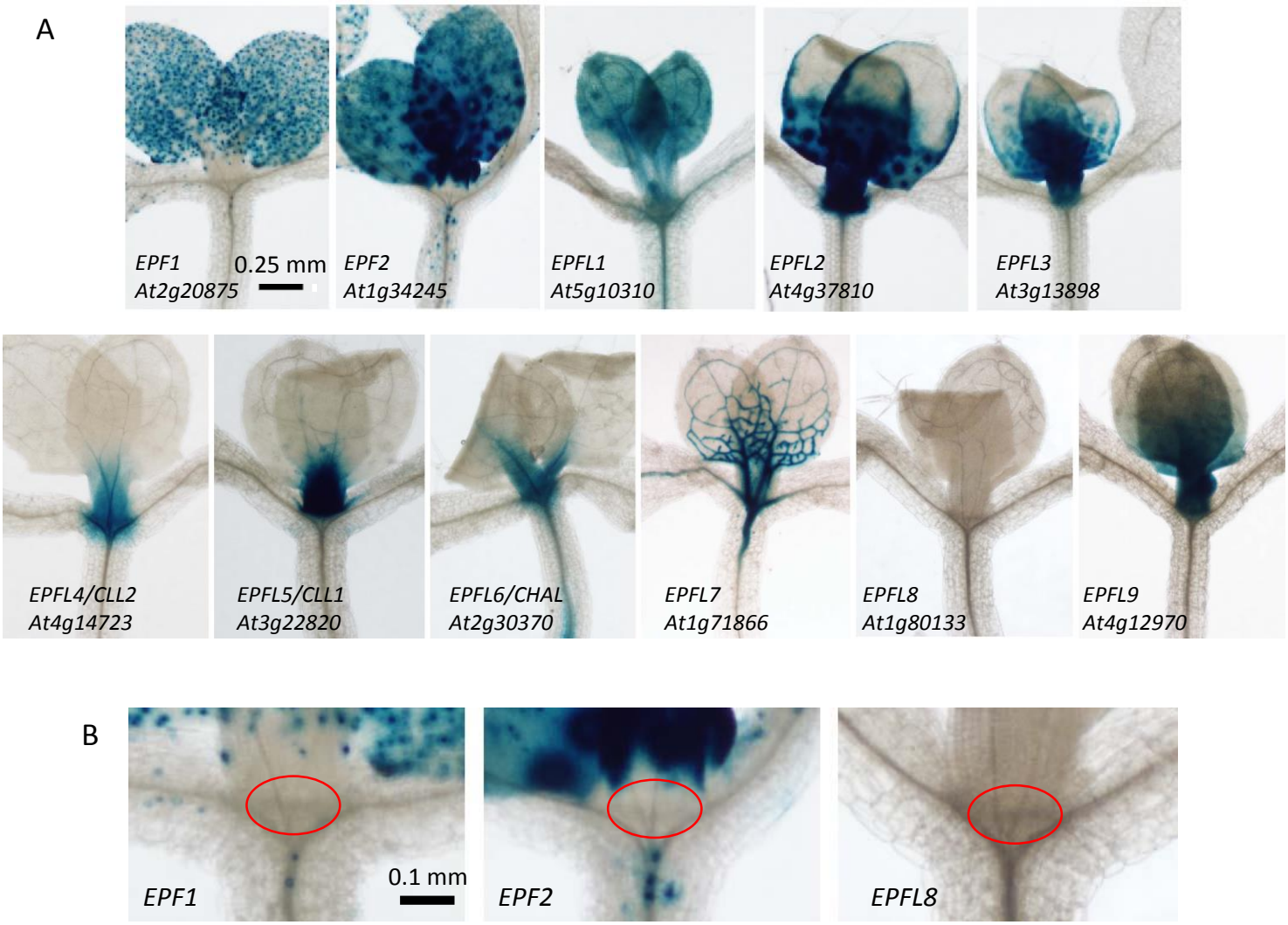
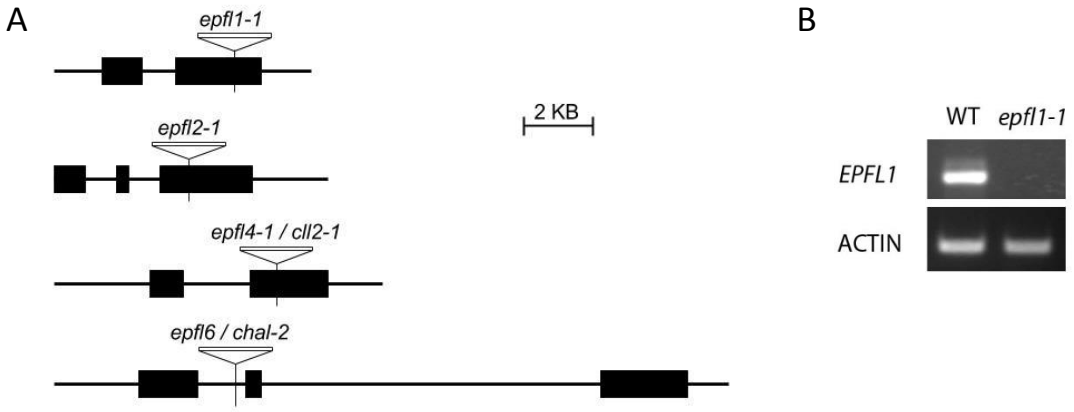


Supplemental Figure S1. The effect of *ERECTA* expression under different promoters on plant morphology. A. Expression of *ERECTA* under *STM* and *ANT* promoters rescues infertility of *er erl1 erl2*. B. twenty-days-old plants. C. The plant height was measured in five-weeks-old plants. N=5-16 for heights. Error bars represent SD. All images are under the same magnification in A and in B. Different letters indicate significant difference at $p < 0.05$, as determined by one-way ANOVA with Tukey's post-test. L1, L2, and L3 are independent transgenic lines. WT is wild-type.

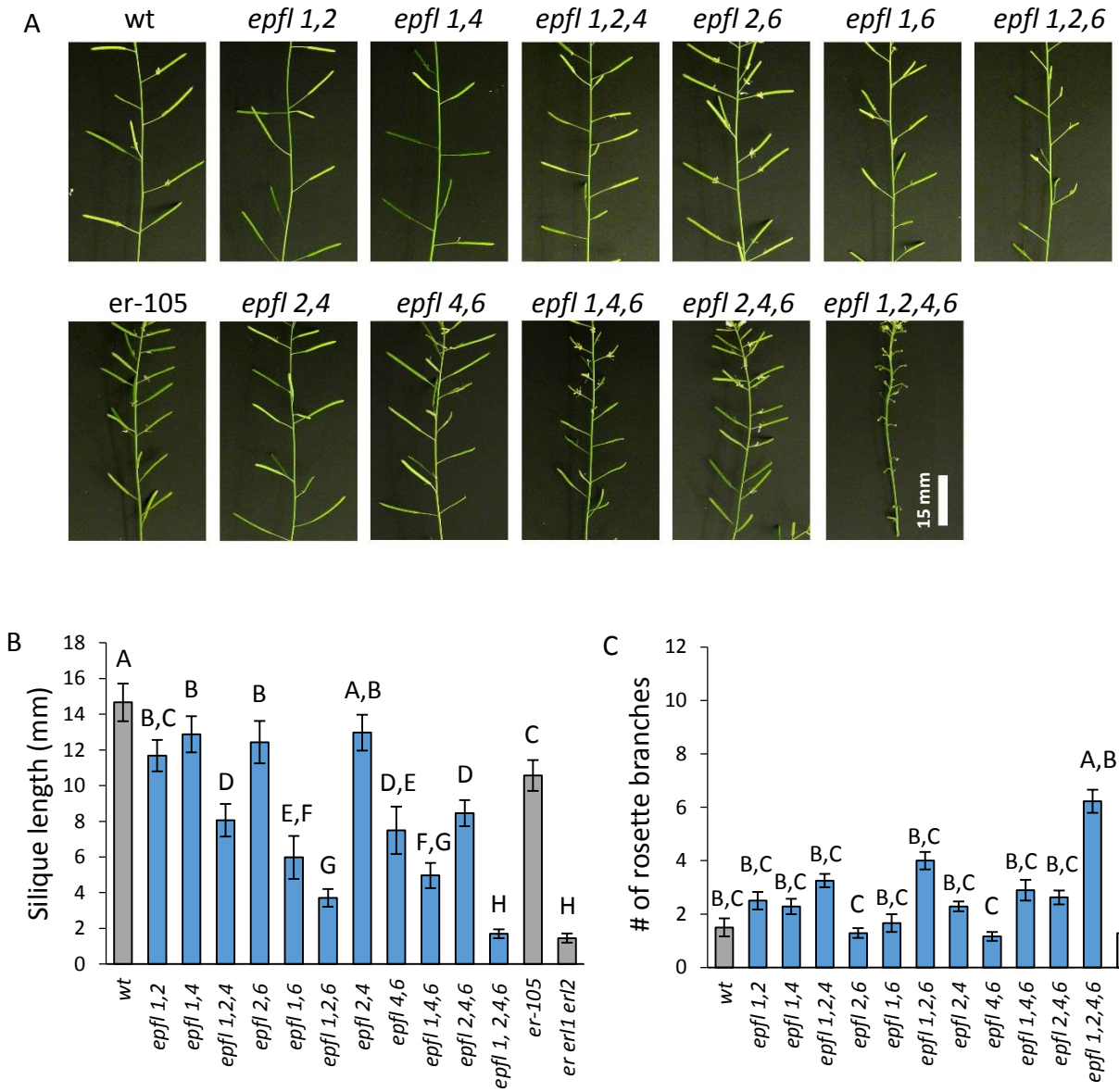


Supplemental Figure S2. The GUS reporter gene assay of the *EPF/EPFL* gene family. The assay demonstrates distinct patterns of expression in seedlings (A) and shows an absence of expression in the SAM for *EPF1*, *EPF2*, and *EPFL8* (B). Seedlings are 5 days post germination. In B are magnified images of the SAM region from seedlings depicted in A. In (B) the red ovals indicate location of the SAM. All images are under the same magnification in A and in B.

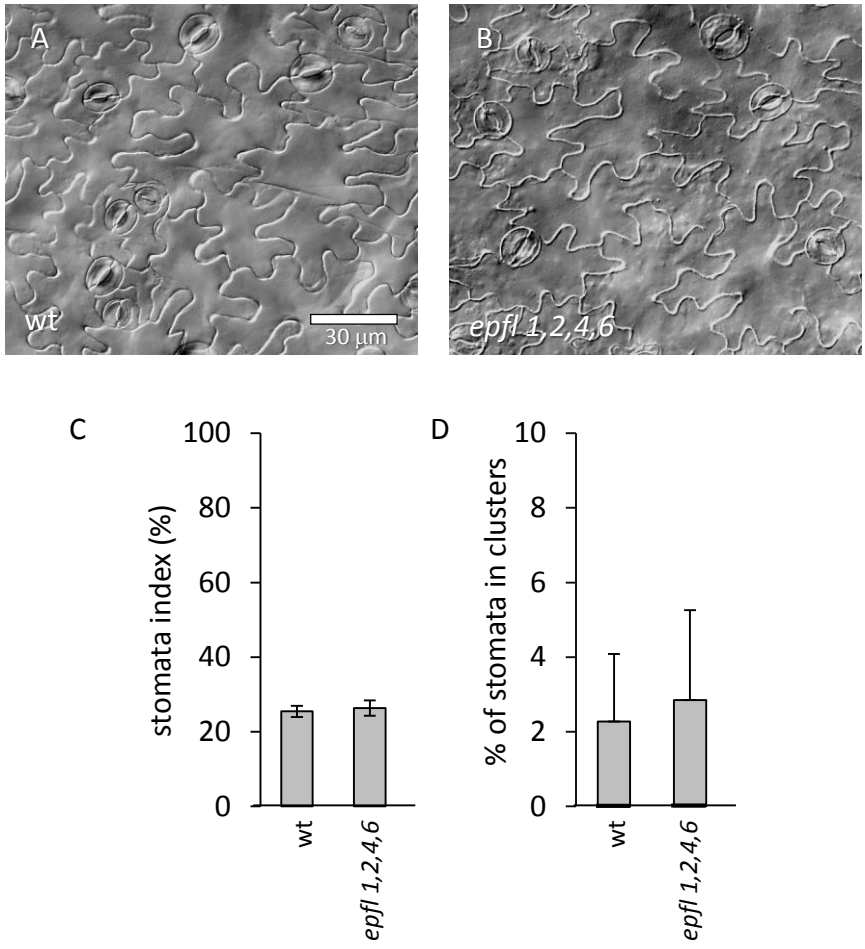


Supplemental Figure S3. *Epfl1-1* is a null mutant with a transposon insertion in the second exon.

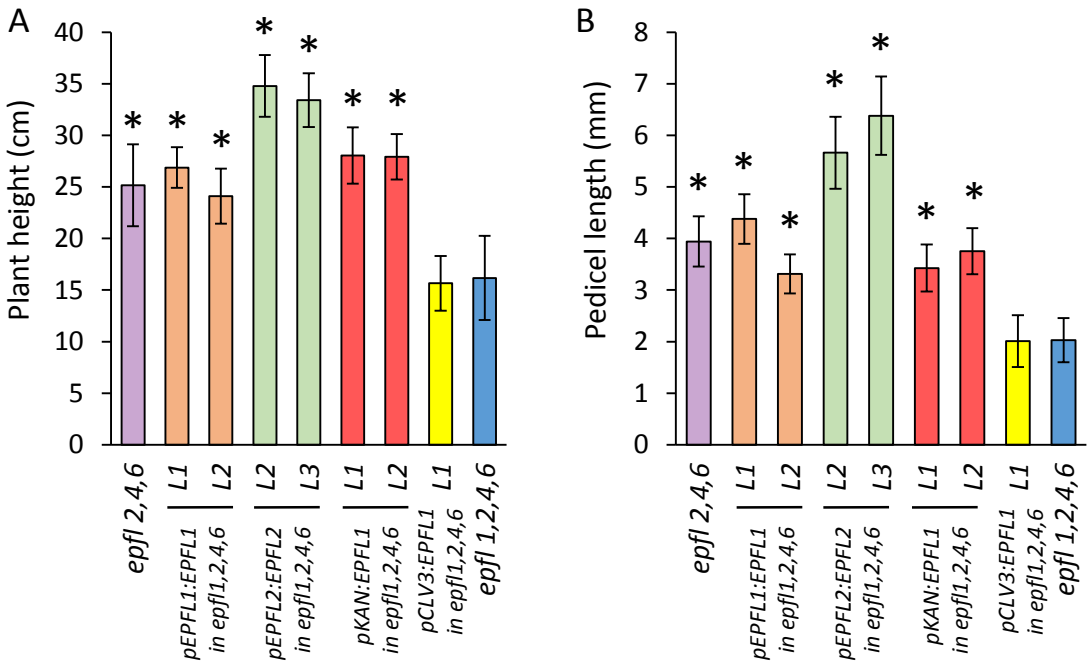
A. Schematic of the gene structure and insertion sites for mutants used in this study. Lines indicate introns or UTR regions, bars indicate exons, triangles indicate T-DNA insert position for *epfl4 and epfl6* or transposon site for *epfl1-1 and epfl2-1*. B. RT-PCR analysis of *epfl1-1*



Supplemental Figure S4. *EPFL1*, *EPFL2*, *EPFL4*, and *EPFL6* partially redundantly regulate flower development and apical dominance. (A) The wild type, *er-105* and *epfl* family mutant inflorescence stems. (B) Length of mature siliques on the main inflorescence stem (n=78-158; 7-8 measurements per stem). (C) The number of rosette branches is increased in some of *epfl* family mutants and in the *er erl1 erl2* mutant (n=6-9). B and C. Bars represent the average; Error bars represent SD. All images are under the same magnification in A. Different letters indicate significant difference at $p < 0.01$, as determined by one-way ANOVA with Tukey's post-test.



Supplemental Figure S5. The *epfl1,2,4,6* mutant does not exhibit obvious stomata patterning defects. A and B. Images are of the abaxial epidermis of cotyledons from 12-days-post-germination seedlings. Both images are under the same magnification. C and D. Epidermal phenotypes were analyzed on the abaxial side of 12-d-old cotyledons (n=10). (D) is the whisker and box plot. The median is indicated as a thick horizontal line and equals 0 in both wt and the mutant, upper quartiles are represented by the boxes, and the vertical lines designate the maximum.



Supplemental Figure S6. Expression of *EPFL1* under the endogenous and *KAN* promoters and *EPFL2* under endogenous promoter rescues elongation of stem and pedicels in the *epfl 1,2,4,6* mutant. Plant height (A) and pedicel length (B) were measured in mature 2-month-old plants in T3 or T4 generation in independent transgenic lines. N=13-20 for heights and n=48 for pedicel length. Error bars represent SD. Values significantly different from *epfl 1,2,4,6* are indicated by asterisks (P< 0.05 based on Student t-test).

Supplemental Table S1. Primers used for cloning.

WUS.PRO.FOR	CCGGATCCGTATGATCTCTGTTGTACTCAC
WUS.PRO.REV.	GGCTCCATGGGTGTTTGATTCG
KAN.PRO.FOR	AAGGATCCAAGACCAACACAAACAAATTACC
KAN.PRO.REV.	GGCCATGGAATTAAAGAAACCTTTCTCTTG
STM.PRO.FOR.V2	CCGGATCCTACAATTTCTCTAGCCTCCGTTTAATTT
STM.PRO.REV.V3.	ATATCTCTAAACAGAGCCATCTTCTCTTTCTCTCACTAG
ER.PSTM.OH.FOR	CTAGTGAGAGAAAGAGAAGATG GCTCTGTTTAGAGATAT
ER.1100.XBAL.REV.	ACATATGAAGTCTAGAAGCAGAATAACT
ANT.ER.OH.REV	ATATCTCTAAACAGAGCCATGGTTTCTTTTTTTGGTTTCT
ANT.PRO.FOR	CCGGATCCTATTATTGTGTTTCTCCTTTCTCT
ER.ANT.OH.FOR	AGAAACCAAAAAAAGAAACCATGGCTCTGTTTAGAGATAT
CLV3.PRO.FOR	CCGGATCC ATAAAATTAATCGAATTCCGG
CLV3.PRO.REV	ATATCTCTAAACAGAGCCATTTTTAGAGAGAAAG
ER.PCLV3.OH.FOR	CTTTCTCTCTAAAAATG GCTCTGTTTAGAGATAT
ER.TCLV3.OH.REV	AGCAACAAGAGATTAGGCTACTCACTGTTCTGAGAA
CLV3.TER.FOR	TTCTCAGAACAGTGAGTAG CCTAATCTCTTGTTGCT
CLV3.TER.REV	GG CTGCAGTCGAC ATTAAAAATAATACATTTATAATCAA
EPFL1-1	CACCTCTGTTCTCCCTGAGGAAA
EPFL1-2	TTTTGAGTTGGATTCAAGAATTACTACTATAA
ATTL1-T2.1	CCCCTTTTATAATGCCAACTTTGTACAAAAAAGCAGGCTAAGCTT
ATTL2-T2.1	GGGGTCTTATAATGCCAACTTTGTACAAGAAAGCTGGGTGGATCC
Q.EPF1-1	AAAAAAGCAGGCTAAGCTT ACGACGATGTCCTCTTTTGTC
Q.EPF1-2	AAGAAAGCTGGGTGGATCC GATATATTATCGCAAGTG
EPF2-2B	GTTTATAATCTTTTTTTTTAACAAGAAGAAAC
Q.EPF2-1	AAAAAAGCAGGCTAAGCTT TGGTCTAGAGAACAAGTGAAG
Q.EPF2-2	AAGAAAGCTGGGTGGATCC GTTTATAATCTTTTTTTTT
Q.EPFL2-1	AAAAAAGCAGGCTAAGCTT GACATTTGTAGTACAACC
Q.EPFL2-2	AAGAAAGCTGGGTGGATCC TTTCAGACACGAGATCGG
Q.EPFL3-1	AAAAAAGCAGGCTAAGCTT CGATTCATGGGTAGGTCCAT
Q.EPFL3-2	AAGAAAGCTGGGTGGATCC TTTCTATGATTCTTTTTACT
Q.EPFL4-1	AAAAAAGCAGGCTAAGCTTAGTAGTTCACCATTTTGGTTG
Q.EPFL4-2	AAGAAAGCTGGGTGGATCCTAGTCAAGAACCGGAGAGGA
Q.EPFL6-1	AAAAAAGCAGGCTAAGCTTACAGTGTGTCAGATCTTTGTA
Q.EPFL6-2	AAGAAAGCTGGGTGGATCCAATTACGAAACTTTCTGAAAAC
Q.EPFL7-1	AAAAAAGCAGGCTAAGCTT TAAAATTGGATAATTGTGGGG
Q.EPFL7-2	AAGAAAGCTGGGTGGATCC CTCTCTCTTTTCAAAGGCTT
Q.EPFL8-1	AAAAAAGCAGGCTAAGCTT TTTGGAGCTTCCCTTACAAGC
Q.EPFL8-2	AAGAAAGCTGGGTGGATCC ATCATCACAATTTTCTCAAA
Q.EPFL9-1	AAAAAAGCAGGCTAAGCTT CTTGGAATTCAGTCGTCTAAC
Q.EPFL9-2	AAGAAAGCTGGGTGGATCC TCTCTACTTCTTCTTCTTCT
EPFL1.US.BAM	ACGGATCCTTAAGTCATGGTTATATAC
EPFL1.DS.PST1.REV	ACATAGAACTGCAGTTCAAAATTTAAG
EPFL2.US.BAM	TTTGGATCCCTAAATCGCTCTAGAC
EPFL2.DS.PST1.REV	CACACTCTGCAGTTTTCTTTATG
EPFL1.NCO	ATCCAACTCAACCATGGTTGCTATATAC
EPFL1.CLV3.TER	CCACTTTTATAATCCTTAACCTAATCTCTTGTTG
CLV3.TER.EPFL1.REV	CAACAAGAGATTAGGTTAAGGATTATAAAAGTGG
CLV3.PRO.EPFL1	CTTTCTCTCTAAAAATGTTTGCTATATACAAATC
EPFL1.CLV3.PRO.REV	GATTTGTATATAGCAAACATTTTTAGAGAGAAAG

Supplemental Table S2 Primers used for genotyping *epfl1-1* and *epfl2-1*.

Primer name	sequence	purpose
3’ dSpm	TACGAATAAGAGCGTCCA TTTTAGAGTGA	Genotyping *epfl1-1*
epfl1.74	ATCCTTTCTTCAACCTATCCAACCTCCT	
epfl1.436.rev	TTAAGGATTATAAAAGTGGCCATTGCA	
epfl2.1	ATGGTGTGGAGCAGCAACATGTCAAGC	Genotyping *epfl2-1*
epfl2.540.rev	TCAAGGGTTGTAGATAGAGTTACCA	
GUS.43.rc	GTTTTTTGATTTCACGGG	

Supplemental Table S3 Primers used for RT-PCR

Primer name	sequence	Annealing temperature
Act2-1	GCCATCCAAGCTGTTCTCTC	51.9°C
Act2-2	GCTCGTAGTCAACAGCAACAA	
qPCR ERF	TGAATGTGGCCAACAATGATCTGG	61.9 °C
qPCR ERR	TTTTGAAATGCTCGGGGTATAGTGC	
epfl1.1	ATGTTTGCTATATACAAATCAACCCTTCTTC	52 °C
epfl1.436.rev	TTAAGGATTATAAAAGTGGCCATTGCA	