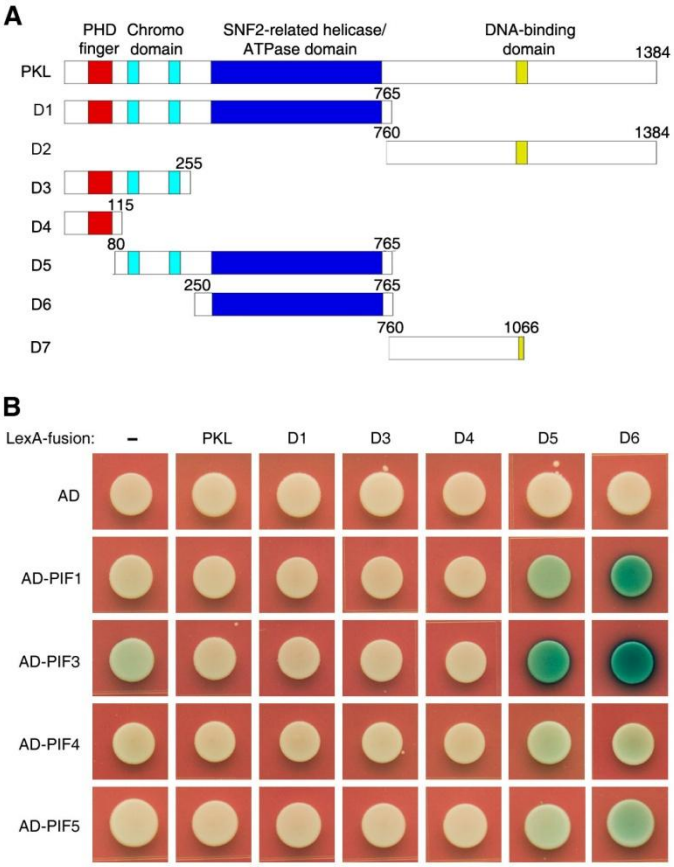
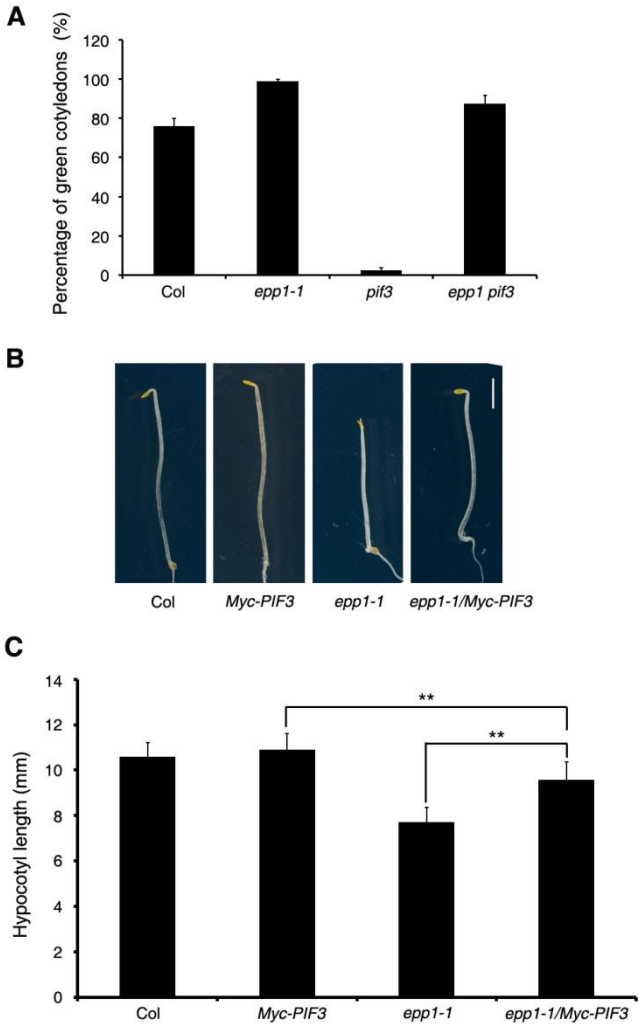
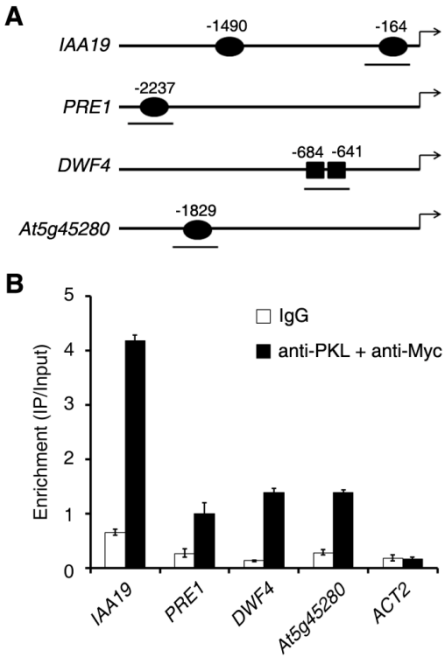


Supplemental Figure 1. Yeast two-hybrid assay showing the interaction between PKL and PIFs.

(A) Diagram of the domain structures of PKL and various PKL truncations (Jing et al., 2013). **(B)** Yeast two-hybrid analysis of AD-fused PIF1, 3, 4, or 5 and the indicated LexA-BD-tagged PKL fragments.

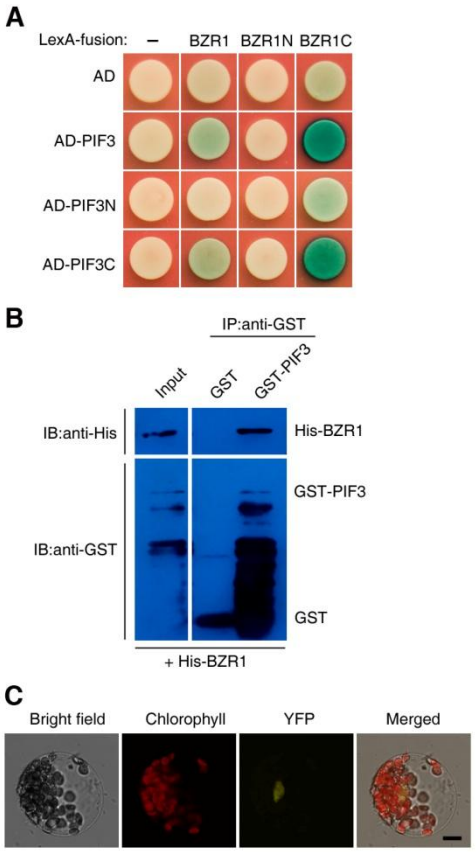


Supplemental Figure 2. Phenotypes of *epp1 pif3* and *epp1/Myc-PIF3* plants.
(A) Seedling greening phenotypes of *epp1*, *pif3*, and *epp1 pif3* mutants and the Col wild type. Six-day-old etiolated seedlings were exposed to white light (60 μmol/m^2/s) for 1 d, and greening rate was determined by counting the percentage of dark-green cotyledons from 50 to 80 seedlings. **(B)** The skotomorphogenic phenotype of wild-type and *epp1* plants and *epp1* plants transformed with *Pro35S:Myc-PIF3* grown in the dark for 5 d. Bar = 2 mm. **(C)** Hypocotyl length of the seedlings shown in (A). Data represent the mean ± SD of at least 20 seedlings. Asterisks indicate significant difference at $P < 0.01$ using Student's *t*-test.



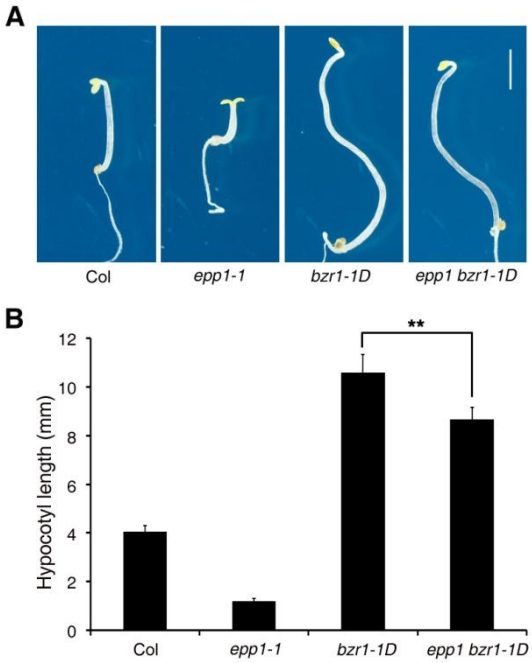
Supplemental Figure 3. PIF3 and PKL bind to the promoters of cell elongation-related genes.

(A) Promoter diagrams of four cell elongation-related genes. Arrows indicate the translation start sites of the genes. Ovals indicate the G-box (CACGTG) motif and squares denote the core sequence of the BZR1-binding site (CGTG). The positions of these motifs are labeled. The approximate regions for ChIP-qPCR are lined below the motifs. **(B)** ChIP-qPCR assay showing relative enrichment of the promoter fragments of several cell elongation-related genes pulled down sequentially by PKL and MYC antibodies in *Pro35S:Myc-PIF3* transgenic plants. Seedlings were grown in the dark for 5 d. Data represent the mean ± SD of biological triplicates. Amplification of *ACT2* serves as a negative control.



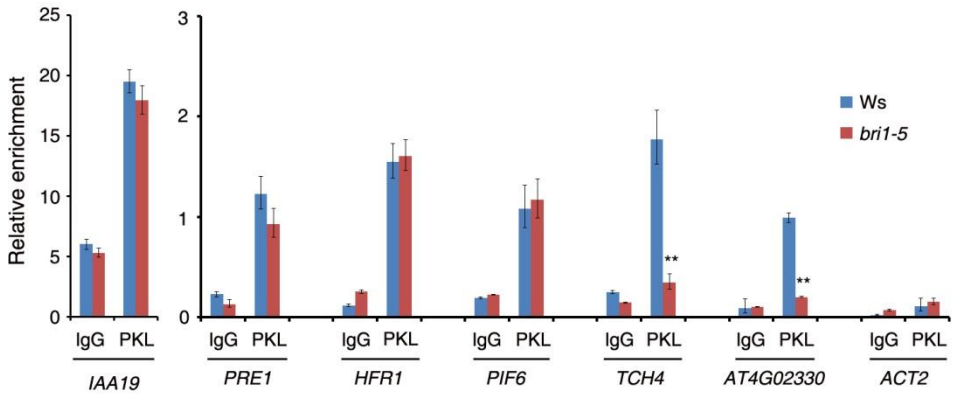
Supplemental Figure 4. PIF3 interacts with BZR1.

(A) A yeast two-hybrid assay between PIF3 and BZR1. The full-length, N- or C-termini of PIF3 and BZR1 were fused to the AD domain or LexA BD domain, respectively. PIF3N, amino acid (aa) 1-285 ; PIF3C, aa 286-524, containing the bHLH domain; BZR1N, aa 1-109, containing the DNA binding domain; and BZR1C, aa 110-336. **(B)** Pull-down assay between recombinant His-BZR1 and GST-PIF3 or GST alone. IB, immunoblot; IP, immunoprecipitation. **(C)** BiFC assay showing that YFP^N-PIF3 and BZR1-YFP^C interact in the nucleus. Bar = 5 μm.

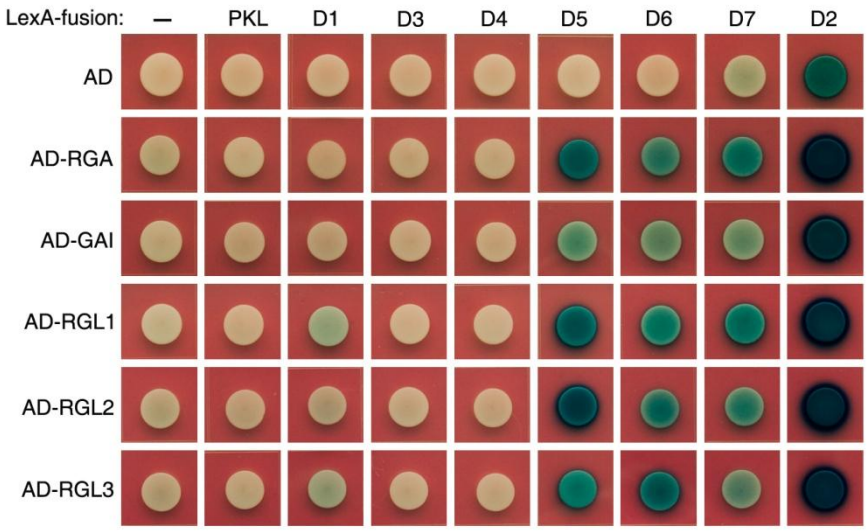


Supplemental Figure 5. Phenotype of *epp1/bzr1-1D* plants.

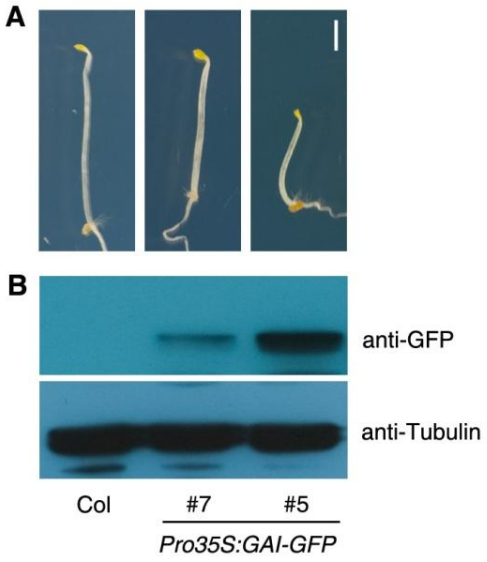
(A) Seedling morphology of *epp1*, *bzr1-1D,* and *epp1 bzr1-1D* mutants and the Col wild type. Plants were grown in MS medium containing 1 μM PCZ in darkness for 5 d. Bar = 2 mm. **(B)** Hypocotyl length of seedlings as shown in (A). Data represent the mean ± SD of at least 20 seedlings. Asterisks indicate significant difference at P < 0.01 using Student's *t*-test.



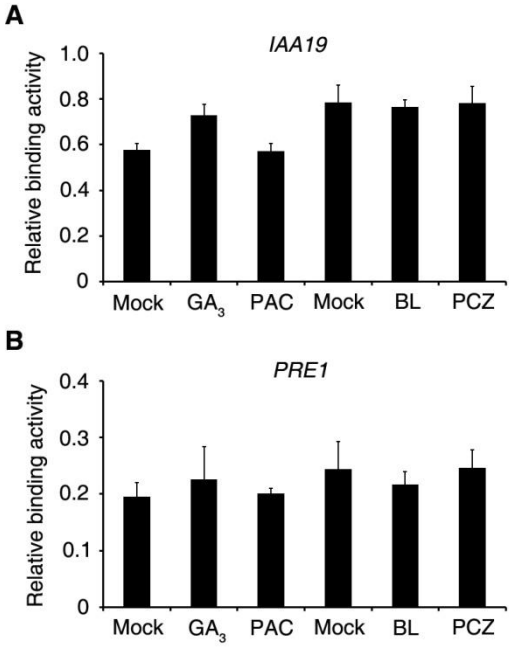
Supplemental Figure 6. ChIP-qPCR assay in the wild type and *bri1-5* mutant.
Ws wild type and *bri1-5* seedlings were grown in darkness for 5 d. After precipitation with PKL antibody or IgG control, the genomic fragments of various target genes were amplified by PCR. *ACT2* serves as a negative control. Data represent the mean ± SD of three biological replicates. Asterisks indicate significant difference from the wild type at $P < 0.01$ using Student's *t*-test.



Supplemental Figure 7. Interaction between PKL and DELLA proteins in yeast.
Yeast two-hybrid assay between PKL and DELLAs. RGA, GAI, RGL1, RGL2 and RGL3 were fused with the activation domain, whereas different fragments of PKL were tagged with the LexA DNA-binding domain.



Supplemental Figure 8. Characterization of *Pro35S:GAI-GFP* transgenic plants.
(A) Short hypocotyl phenotype of *GAI* overexpression plants (*Pro35S:GAI-GFP*) grown in the dark for 5 d. Two representative lines are shown and line #5 was used for further analysis. Bar = 2 mm. **(B)** Immunoblot using GFP antibody showed the expression level of the GAI-GFP fusion protein in the transgenic lines. Immunoblot with tubulin antibody served as an equal loading control.



Supplemental Figure 9. Relative binding activity of PKL to the downstream genes.

A ChIP assay was performed as described in Figure 6C and 6D. After immunoprecipitation, the protein-DNA samples were equally divided. One set of samples was used for quantifying the amount of *IAA19* **(A)** and *PRE1* **(B)** promoter fragments by qPCR, and another one was immunoblotted with the PKL antibody. Relative binding activity is expressed as amount of DNA/ amount of PKL protein after ChIP. Data represent the mean ± SD of three technical replicates.

Supplemental Table 1. List of primers used in this study.

Gene AGI code	Oligo name	Sequence (5'-3')	Purpose
PKL/EPP1 AT2G25170	EPP1/2/3-F	CAATTGATGAGTAGTTTGGTGGAGAG	Cloning of PKL and its fragments
	EPP1-R	GGTACCTCGAGGCTAGCTCAATCAACGACCATGTTCTTTG	
	EPP1-D1-R	CTCGAGCTTTGATCCATACCTGATGATGTCA	
	EPP1-D2-F	CAATTGATGATCAGGTATGGATCAAAGGAGC	
	EPP1-D3-R	CTCGAGTCAATTTCTTTTATGGTCAACATCT	
	EPP1-D4-R	CTCGAGTCATTCACTAGATTTTGTAGGACGC	
	EPP1-D5-F	CAATTGATGCTTAAAGATGCTTCCGTGGAAA	
	EPP1-D6-F	CAATTGATGGTTGACCATAAAAGAAATCCCA	
	EPP1-D7-R	CTCGAGTCATCCACTTCTCAGTCCGGGGAATC	
	EPP1-Q-F	GAGCGAATTGATGGAAAGGT	qRT-PCR
	EPP1-Q-R	TTCCTAAGCCACCAGCTCTT	
	epp1-1-F	CACAGTGGGAGTGAGCTTTATTG	Genotyping of *epp1-1*
	epp1-1-R	TTCAGCAATGTTCTCCTCTCCCT	
PIF1 AT2G20180	PIF1-F	GGTACCGAATTCATGCATCATTTTGTCCCTGAC	Cloning for yeast two-hybrid assays
	PIF1-R	GTCGACACCTGTTGTGTGGTTTCCGT	
	PIF1-Fc	GGTACCGAATTCATGCAAGCACGTGTATCAACAAC	
	PIF1-Rn	GTCGACTTTTGTTTCCTCGCTACGGGA	
PIF3 AT1G09530	PIF3-F	GGTACCGAATTCATGCCTCTGTTTGAGCTTTTC	
	PIF3-R	CTCGAGCGACGATCCACAAAACTGATC	
PIF4 AT2G43010	PIF4-F	GAATTCATGGAACACCAAGGTTGGAG	
	PIF4-R	GTCGACGTGGTCCAAACGAGAACCGTC	
PIF5	PIF5-F	GAATTCATGGAACAAGTGTTTGCTG	

AT3G59060	PIF5-R	CTCGAGGCCTATTTTACCCATATGAAG	
RGA AT2G01570	RGA-MfeI-F RGA-SalI-R	CAATTGATGAAGAGAGATCATCACCAATTC GTCGACGTACGCCGCCGTCGAGAGTTTC	
	RGA-BamHI-F RGA-NotI-R	GGATCCATGAAGAGAGATCATCACCAATTC GCGGCCGCGTACGCCGCCGTCGAGAGTTTC	Recombinant protein expression
GAI AT1G14920	GAI-EcoRI-F GAI-SalI-R	GAATTCATGAAGAGAGATCATCATCATC GTCGACATTGGTGGAGAGTTTCCAAG	Cloning for yeast two-hybrid assays
	GAI-BamHI-F GAI-NotI-R	GGATCCATGAAGAGAGATCATCATCATC GCGGCCGCATTGGTGGAGAGTTTCCAAG	Recombinant protein expression
BZR1 AT1G75080	BZR1-F BZR1-R BZR1C-F BZR1N-R	GAATTCATGACTTCGGATGGAGCTACATCGAC GTCGACACCACGAGCCTTCCCATTTCCAAG GGATCCGAATTCTCACAGAACCAGAGCCCTC GCGGCCGCGTCGACTGAATATGGAGTTACTCGAG	Cloning for yeast two-hybrid assays
RGL1 AT1G66350	RGL1-F RGL1-R	CAATTGATGAAGAGAGAGCACAACC GTCGACTTCCACACGATTGATTCGC	Cloning for yeast two-hybrid assays
RGL2 AT3G03450	RGL2-F RGL2-R	CAATTGATGAAGAGAGGATACGGAG GTCGACGGCGAGTTTCCACGCCGAGG	
RGL3 AT5G17490	RGL3-F RGL3-R	CAATTGATGAAACGAAGCCATCAAG GTCGACCCGCCGCAACTCCGCCGCTAG	
GFP	GFP-F GFP-R	TCTAGAGATCTGAATTCGGATCCCTCGAGATGGGTAAAGGA GAACTTTTCACTGGGATG AGGCCTACTAGTTTAGATAGATCTGTATAGTTCATCCATGCC	pVIP-N-GFP construction
IAA19 AT3G15540	IAA19-Q-F IAA19-Q-R	TTTCATCTGGTGGTGACGCT CATACCCTAACCCCACTTTCG	RT-qPCR
DWF4 AT3G50660	DWF4-Q-F DWF4-Q-R	TCCCTAGTGGGTGGAAAGTGT CGCTCCGTTGTTTTGCTGTT	

PRE1 AT5G39860	PRE1-Q-F PRE1-Q-R	GTTCTGATAAGGCATCAGCCTCG GTTCTGATAAGGCATCAGCCTCG	
AT5G45280	AT5G45280-Q-F AT5G45280-Q-R	CTCAGCTTCAAACCGTTCAA AAAGAACCAATCTCCAACCG	
AT2G43050	AT2G43050-Q-F AT2G43050-Q-R	GTTCGATCCCATCCACGACT TTTCTTGAAGGCTCTGCTCACA	
UBQ1 AT3G52590	UBQ-F UBQ-R	TTCCTTGATGATGCTTGCTC TTGACAGCTCTTGGGTGAAG	
IAA19 AT3G15540	IAA19-I2-F IAA19-I2-R	ATCTGTTCCCTTAACCACCTTGT AAACCAATCCAATATCGACACG	ChIP-qPCR
PRE1 AT5G39860	PRE1-CHIP-F PRE1-CHIP-R	GAGGGATAATGAGGGATTTCG CTATGTCACGTGTCACCACCATGTC	
TCH4 AT5G57560	TCH4-CHIP-F TCH4-CHIP-R	CGTGATTTCCAAAGCCAATA GCGGTTCGTATAGAGGAAGG	
HFR1 AT1G02340	HFR1-CHIP-F HFR1-CHIP-R	GTCGCTCGCTAAGACACCAAC ACGTGATGCCCTCGTGATGGAC	
PIF6 AT3G62090	PIF6-CHIP-F PIF6-CHIP-R	GTCTAATACACTGCATACGGGT GATAGGACCTACAAGGTGTTTG	
AT4G02330	AT4G02330-CHIP-F AT4G02330-CHIP-R	TTTGGGATCTAAGAATGAGACTACA TTGATCCGATCCATAATTGTTT	
DWF4 AT3G50660	DWF4-CHIP-F DWF4-CHIP-R	GGGTTTGACTGTCCAGTTCGGTAAT ACCCTTAGGATATGGGAAAAGGGTG	
AT5G45280	AT5G45280-CHIP-F AT5G45280-CHIP-R	AACTTGATTCGGTGCATTTG GTCCATATCAATTCGGCTCA	
ACT2 AT3G18780	ACT2-CHIP-F ACT2-CHIP-R	TCTGGATCTACTTTATTTGCTG TACACAAACTTCATCTAACCTT	