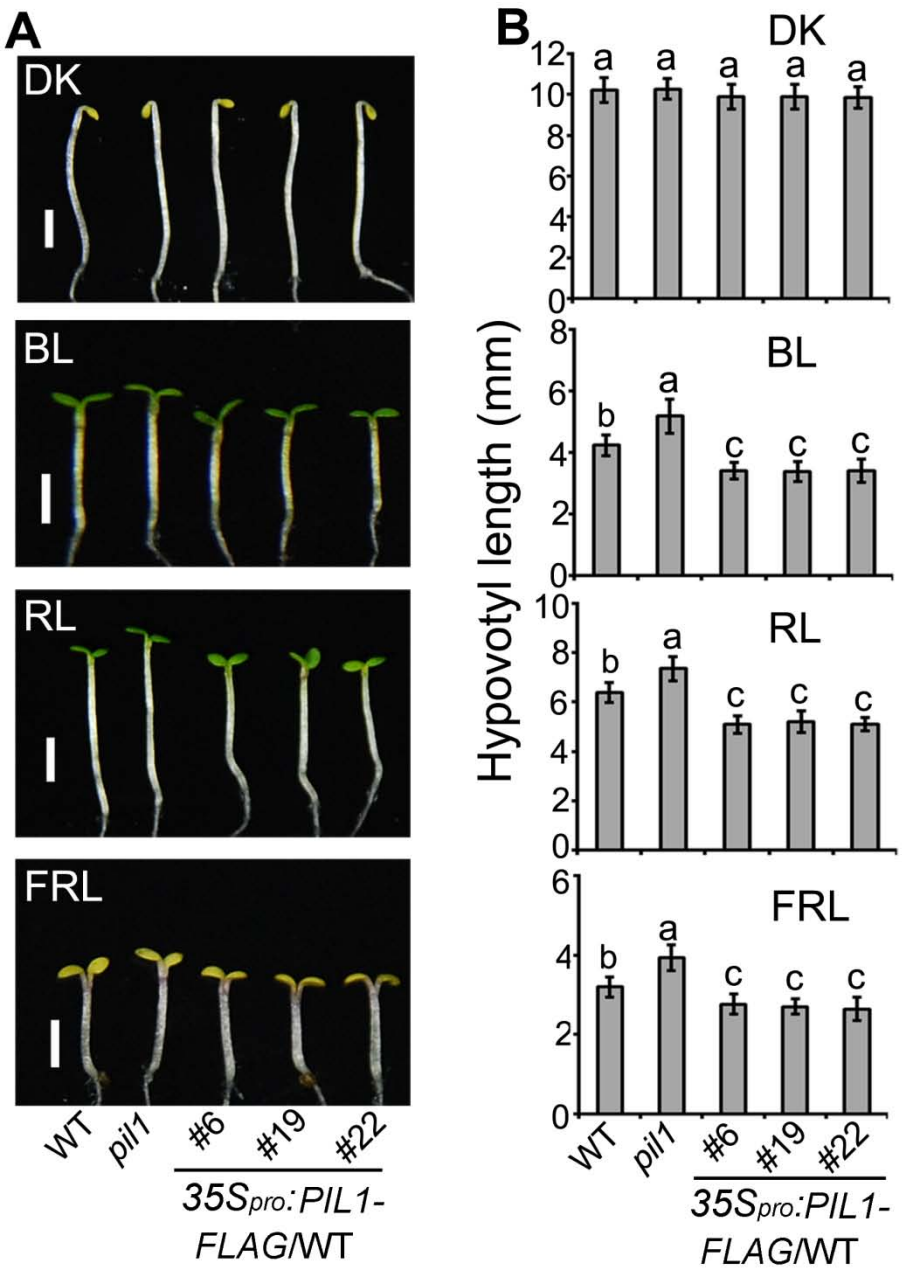
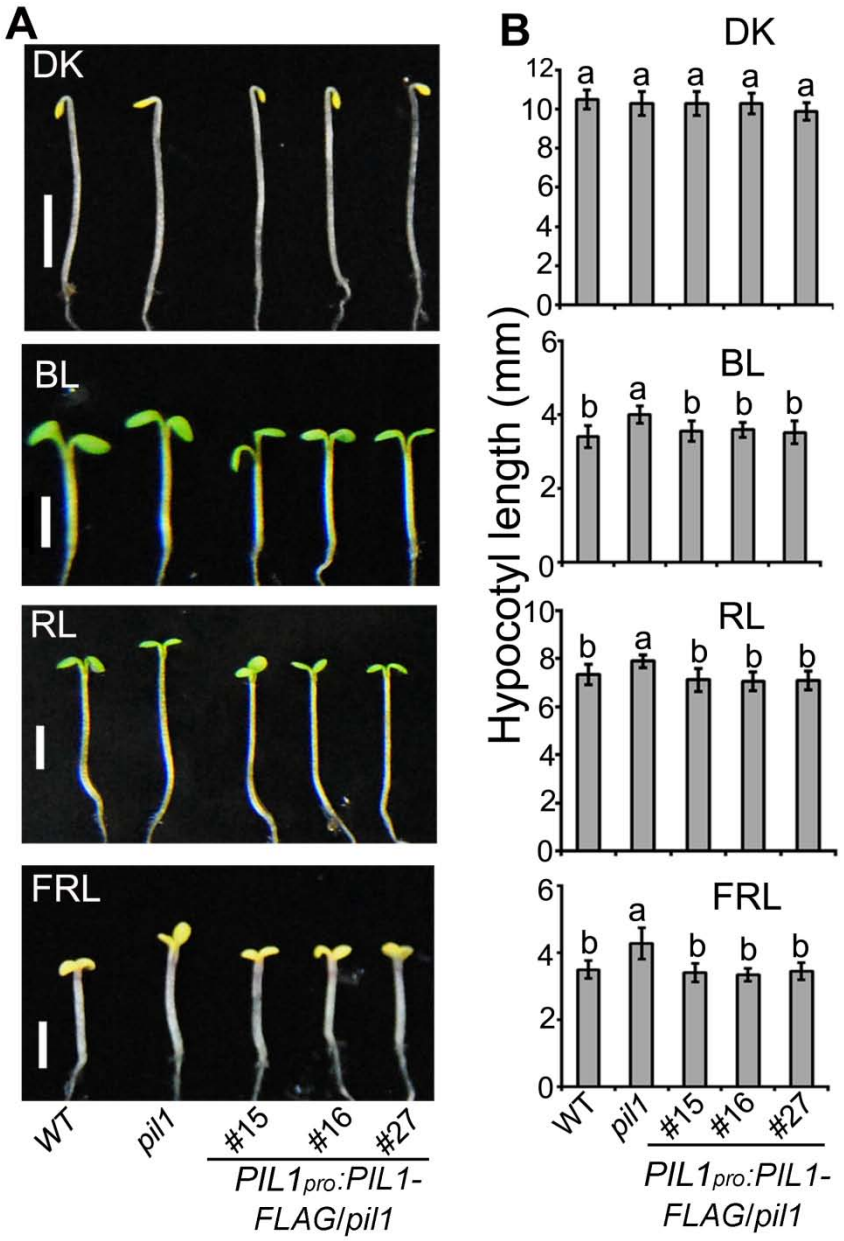
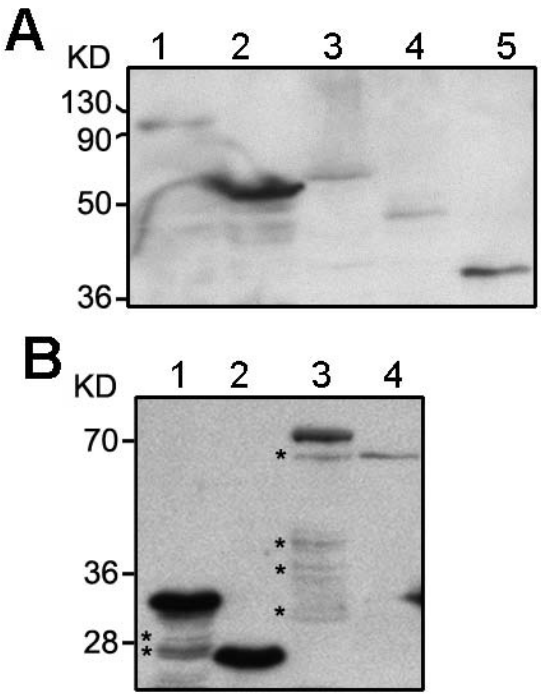


Supplemental Figure 1. Transgenic *35S$_{pro}$:PIL1-FLAG* Plants Display Inhibited Hypocotyl Elongation Phenotypes under Light Conditions. **(A)** Photograph of representative seedlings of indicated genotypes. Seedlings were grown under continuous indicated conditions for 4 d. Bars, 2 mm. DK, darkness; BL, blue light; RL, red light; FRL, far-red light. #6, #19 and #22, three independent lines of *35S$_{pro}$:PIL1-FLAG*/WT transgenic plants. **(B)** Quantification of hypocotyl lengths of the seedlings shown in (**A**). Error bars represent ± SD (n = 30). The letters "a" to "c" indicate statistically significant differences between means for hypocotyl lengths of indicated genotypes determined by Tukey's LSD test ($P \leq 0.01$).

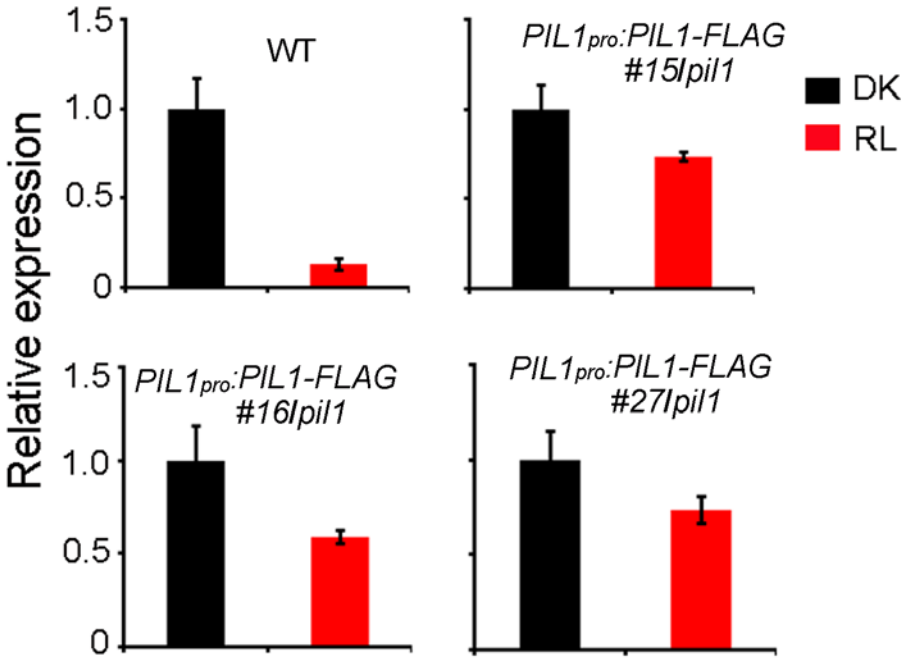


Supplemental Figure 2. Expression of *PIL1-FLAG* under the Control of the *PIL1* Native Promoter in the *pil1* Mutant Rescues the Elongated Hypocotyl Phenotype.

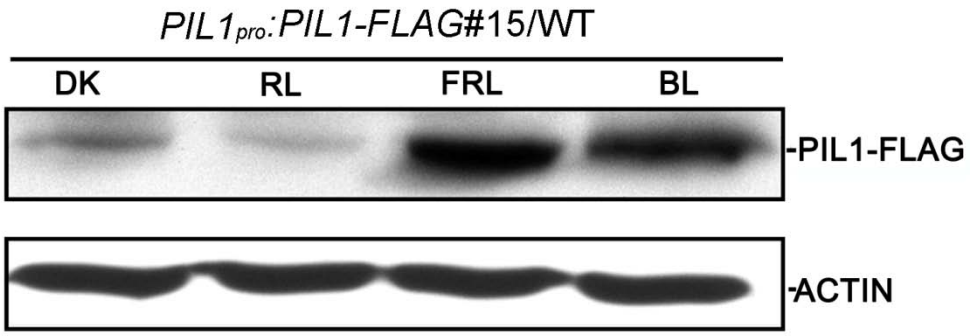
(A) Photograph of representative seedlings of indicated the genotypes. Seedlings grown under continuous indicated conditions for 4 d. Bars, 2 mm. DK, darkness; BL, blue light; RL, red light; FRL, far-red light. #15, #26 and #27, three independent lines of *PIL1*$_{pro}$*:PIL1-FLAG/pil1* transgenic plants. **(B)** Quantification of hypocotyl lengths of the seedlings shown in **(A)**. Error bars represent ± SD (n = 30). The letters "a" and "b" indicate statistically significant differences between means for hypocotyl length of indicated genotypes determined by Tukey's LSD test ($P \leq 0.01$).



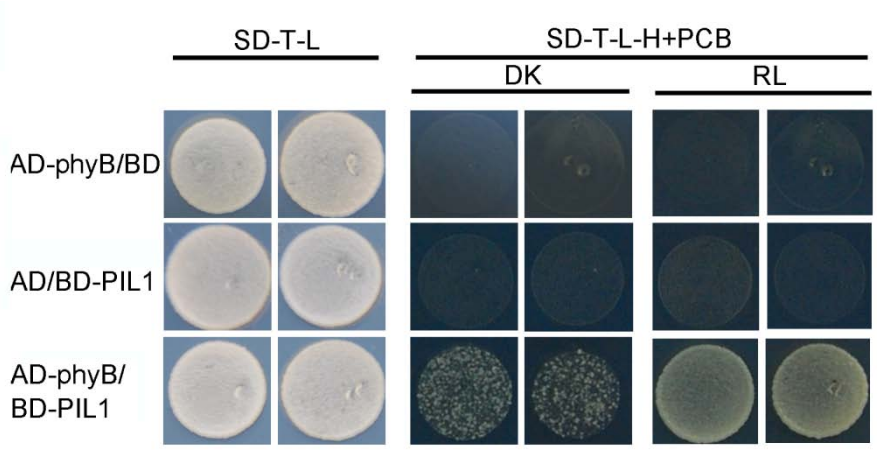
Supplemental Figure 3. Immunoblot Analysis of the Protein Levels of COP1 and PIL1 Fragments in Yeast Cells. (**A**) and (**B**) Total protein extracted from transformed yeast cells was subjected to immunoblot analysis with anti-LexA (**A**) and anti-HA (**B**) antibodies, respectively. Yeast cells expressing the indicated combination of constructs are numbered as (**A**) 1, COP1/PIL1; 2, COP1△283-675/PIL1; 3, COP1△1-282/PIL1; 4, COP1△1-386/PIL1; 5, COP1△1-282△387-675/PIL1; and (**B**) 1, COP1/PIL1△1-283; 2, AD/BD; 3, COP1/PIL1; 4, COP1/PIL1△283-416. Asterisks denote degraded protein.



Supplemental Figure 4. qRT-PCR Analysis Showing the Expression of *PIL1* in *PIL1$_{pro}$:PIL1-FLAG/pil1* Seedlings. The seedlings were grown in darkness for 4 d (DK), and then transferred to red light for 60 min (RL). Expression levels were normalized to an internal *ACTIN2* control and presented relative to the seedlings grown in darkness set at unity. Error bars represent ± SD (n = 3). WT represents wild type; #15, #16, and #27 represent three independent lines of *PIL1$_{pro}$:PIL1-FLAG/pil1* transgenic plants.

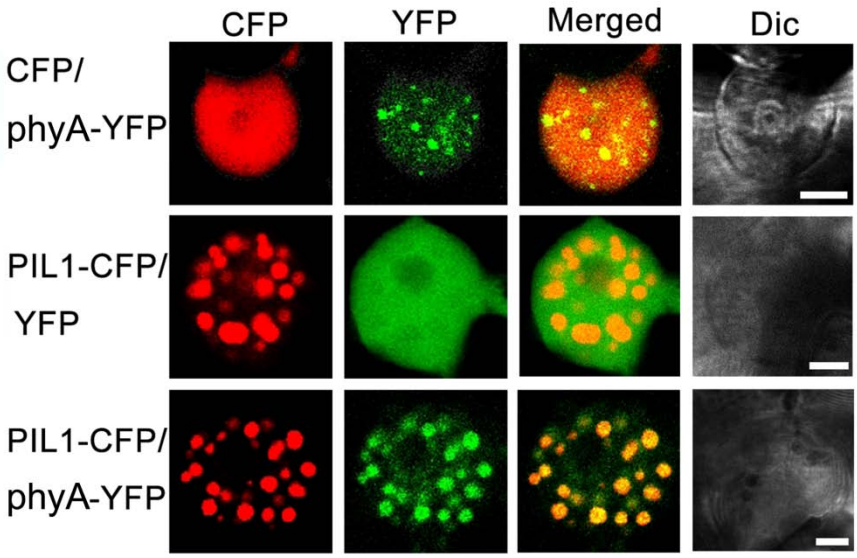


Supplemental Figure 5. Immunoblot Analysis Showing PIL1-FLAG Accumulation in *PIL1*$_{pro}$*:PIL1-FLAG*#15*/pil1* Seedlings. Total protein from *PIL1*$_{pro}$*:PIL1-FLAG*#15*/pil1* seedlings grown in continuous darkness (DK) and the indicated light conditions for 4 d were subjected to immunoblot analysis with anti-FLAG and anti-ACTIN antibodies. RL, red light; FRL, far-red light; BL, blue light.

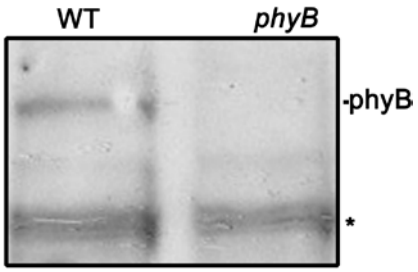


Supplemental Figure 6. PIL1 Preferentially Interacts with the Pfr Form of phyB.

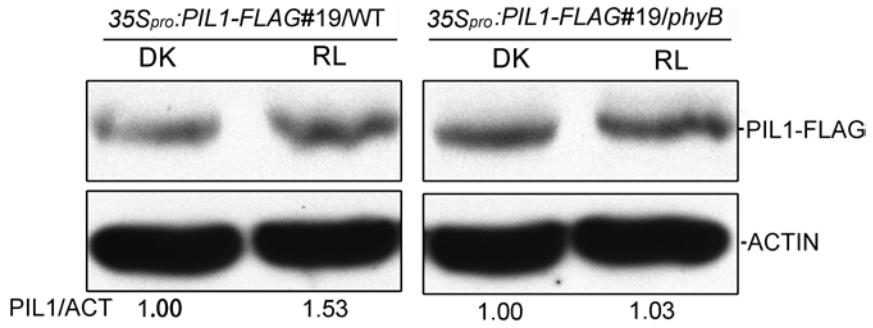
Yeast cells coexpressing the constructs of indicated combinations, were grown on nonselective (SD-T-L) or selective media with 25 μM PCB (SD-T-L-H+PCB) in continuous red light (RL= 3 μmol/s·m^2) or darkness (DK) for 6 d.



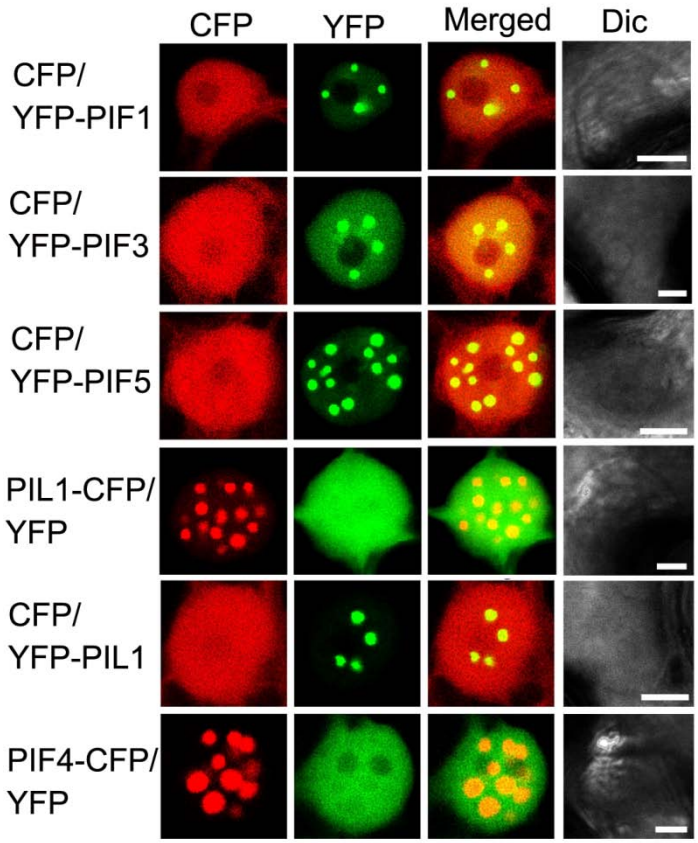
Supplemental Figure 7. PIL1 and phyA Localize Together to NBs in Tobacco Cells. Dic, differential interference contrast. Bars, 5 μm.



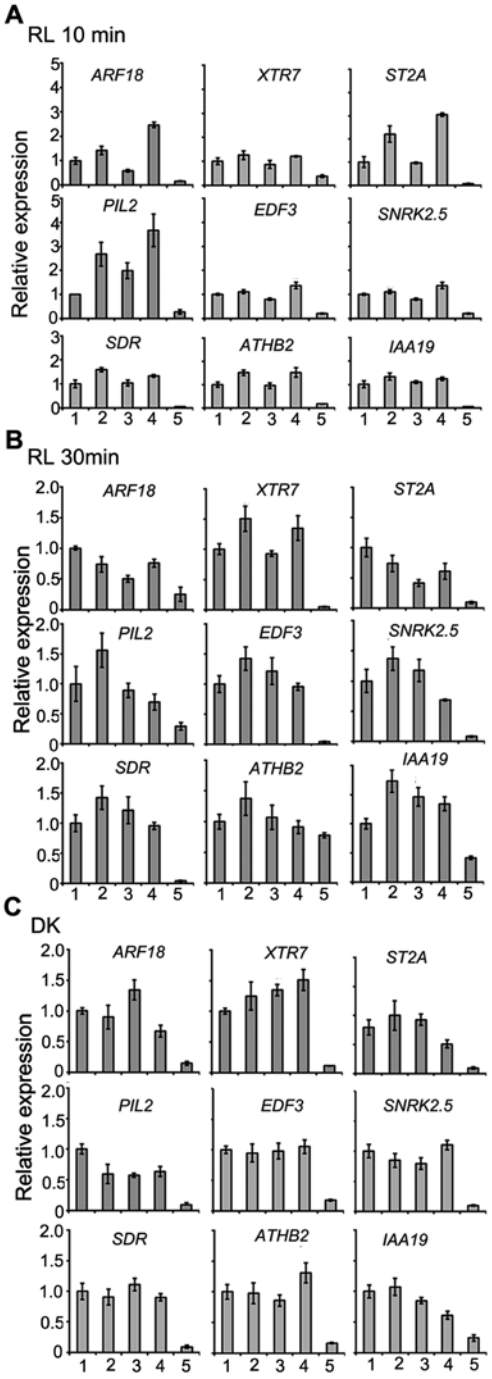
Supplemental Figure 8. Immunoblot Analysis Showing Specificity of Anti-phyB Antibody. phyB is detected in WT and *phyB* by immunoblotting used anti-phyB antibody. The asterisks show non-specific bands.



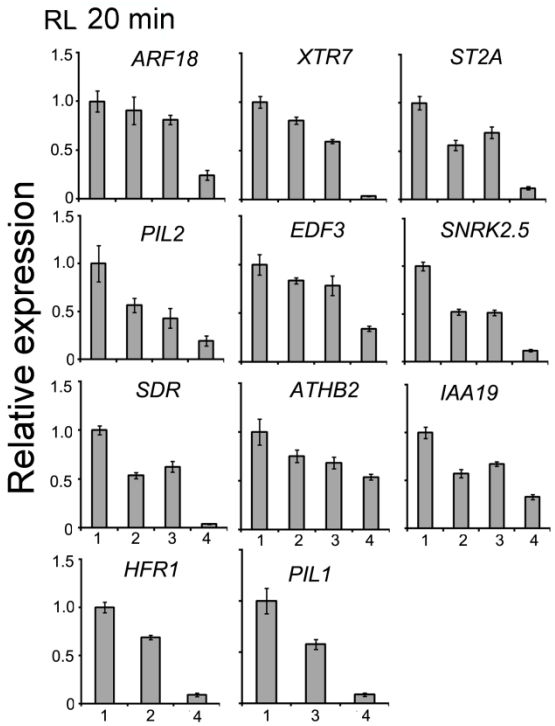
Supplemental Figure 9. PIL1 Accumulation is Promoted by phyB in Continuous Red Light Conditions. Total protein from *35S$_{pro}$:PIL1-FLAG*#19/WT and *35S$_{pro}$:PIL1-FLAG*#19/*phyB* seedlings grown in continuous darkness (DK) and red light (RL) for 4 d was subjected to immunoblot analysis with anti-FLAG and anti-ACTIN antibodies. PIL1/ACT indicates the band intensities of PIL1-FLAG normalized to ACTIN and is presented relative to that in darkness set at unity.



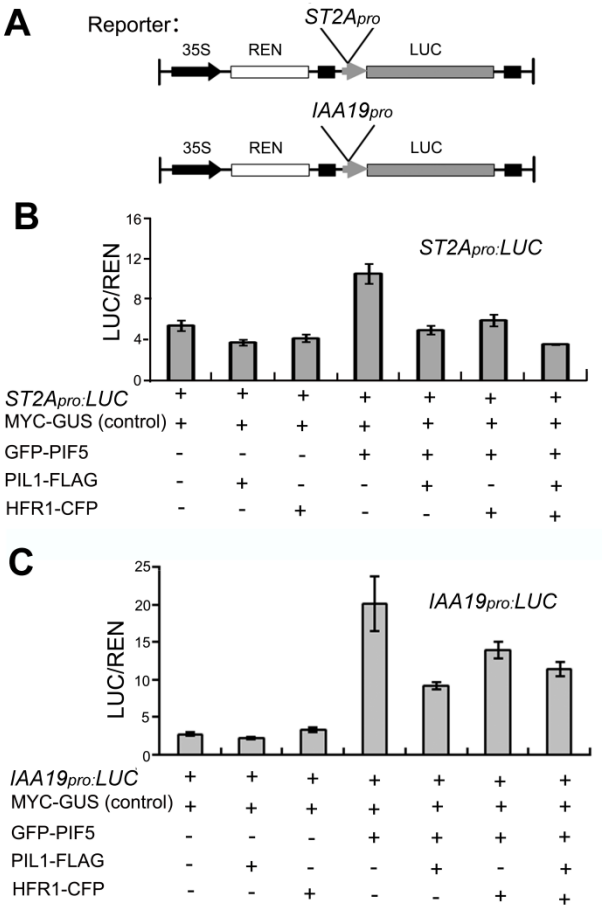
Supplemental Figure 10. Negative Controls Showing No Colocalization of CFP with YFP-PIF1, YFP-PIF3, YFP-PIF5, or YFP-PIL1, and YFP with PIL1-CFP or PIF4-CFP in Vivo. Dic, differential interference contrast. Bars, 5 μm.



Supplemental Figure 11. qRT-PCR Analysis Showing the Expression of PIF Direct-Target Genes in Multiple Genotypes. (A), **(B)** and **(C)** Expression levels were determined by qRT-PCR, normalized to an internal *ACTIN2* control and presented relative to the wild type set at unity. 1, Wild type; 2, *hfr1*; 3, *pil1*; 4, *pil1 hfr1*; 5, *pifq.* Data represent the mean of biological triplicates ± SD (n = 3). The seedlings were grown in darkness for 3 d **(C)**, and then exposed to red light for 10 min **(A)**, 30 min **(B)**, respectively.



Supplemental Figure 12. Expression of PIF Direct-Target Genes is Suppressed in Transgenic Plants Overexpressing *PIL1* and *HFR1*. Expression levels were determined by qRT-PCR, normalized to an internal *ACTIN2* control and presented relative to the wild type set at unity. 1, WT; 2, *35S$_{pro}$:PIL1-FLAG*#19/WT; 3, *35S$_{pro}$:GFP-HFR1*/*hfr1*; 4, *pifq*. Data are represented as the mean of biological triplicates ± SD (n = 3). The seedlings were grown in darkness for 3 d and exposed to red light for 20 min.



Supplemental Figure 13. PIL1 and HFR1 Suppress *ST2A* and *IAA19* Expression in the Dual-Luciferase Assay. (A) Schematic presentation of the reporter construct expressing *LUC* under the control of *ST2A* and *IAA19* promoters ($ST2A_{pro}$ and $IAA19_{pro}$), respectively. **(B)** and (**C**) Tobacco leaves were infiltrated with the strains harboring the $ST2A_{pro}$*:LUC* (**B**) or $IAA19_{pro}$*:LUC* (**C**) reporter and effectors in the indicated combinations. The values represent the ratio of LUC activities to REN activities (LUC/REN). Error bars represent ± SD (n = 3).

Supplemental Table 1. List of Vectors and Primers Used in This Work.

Assays	Destination products	Template	Primer name	Primer sequence
Yeast two-hybrid	pB42AD-PIL1	PIL1	PIL1F1	5’-GCCGGATCCATGGAAGCAAAACCCT
			PIL1R1	TAGCATCA-3’ 5’-GGACTAGTTTAGTTTGGCGAGCGATAATAACT-3’
	pB42AD-PIL1△284-416		PIL1F1	
			PIL849R1	5’-GGACTAGTCTGAACTTGAAGTTGAAGGG TCCG-3’
	pB42AD-PIL1△1-283		PIL1 850F1	5’-GCCGGATCCATGATGAGTATGGGAAATGGA TTA-3’
			PIL1R1	
	pBrige-PIL1		PIL1F2	5’-GCCGGATCCGGATGGAAGCAAAACC
			PIL1R2	CTTAGCATCA-3’ 5’-GGGGTCGACTTAGTTTGGCGAGCGATAATAACT-3’
	pBrige-PIL1△APB	PIL1	PIL1F2	
			PIL181R1	5’-TCTTTGGTCTTTTTAATTTTGGTTTAATGT TTGA-3’
			PIL1 139F1	5’-AAAATTAAAAAGACCAAAGAACAACGGTTCTTTT-3’
			PIL1R2	
	LexA-COP1	COP1	COP1F1	5’-CGGAATTCATGGAAGAGATTTCGAC
			COP1R1	GGATCCG-3’
	LexA-COP1△283-675		COP1F1	5’-CCCCTCGAGTCACGCAGCGAGTACCAGAACTTT-3’
			COP1N 282R	
			COP1C T1F	5’-CCCCTCGAGTCACGAATCTGACCCACTCAGCGCATC-3’
	COP1△283-675		COP1R1	
			COP1C T2F	5’-CGGAATTCCAAAGTTTGAATCAGTCAACTGTC-3’
			COP1R1	
			COP1C	

	LexA-COP1△1-282		T2F	5’-CGGAATTCGCCACTGCTGGTGTTTCTAGATGT-3’
			COP1R1	
			COP1C	
			T1F	
	LexA-COP1△1-386		COP1C T3R	5’-CGGAATTCGCCACTGCTGGTGTTTCTAGATGT-3’
			HFR1F1	
			HFR1R1	
	LexA-△1-282△387-675		PIF5F1	
			PIF5R1	5’-CCCCTCGAGAAACAGCTCATCATCACGATCAAA-3’
	LexA-HFR1	HFR1	phyBF1	5’-CGGAATTCATGTCGAATAATCAAGCTTTCATG-3’
			phyBR1	5’-CCCCTCGAGTCATAGTCTTCTCATCGCATGGGA-3
	pGADT7-PIF5	PIF5		5’-CGGAATTCATGGAACAAGTGTTTGCTGATTGG-3’
				5’-CCCCTCGAGTCAGCCTATTTTACCCATATGAAGA-3’
	pGADT7-phyB	phyB		5’-GGCCAATTGATGGTTTCCGGAGTCGGGGGTAGT-3’
				5’-CCCCCCGGGCTAATATGGCATCATCAGCATCAT-3’
Colocalization	pHB-CFP	CFP	CFPF1	5’-GGACTAGTATGGTGAGCAAGGGCGA
			CFPR2	GGAGCTG-3’
				5’-CGG
				AGCTCTTACTTGTACAGCTCGTCCATGC
				C-3’
	pHB-PIL1-CFP	PIL1	PIL1F1	
			PIL1R3	5’-GGACTAGTGTTTGGCGAGCGATAATA
				ACTAAA-3’

	pEarleyGate104-PIL1		PIL1attr1	5’-CACCATGGAAGCAAAACCCTTAGCATCA-3’
			PIL1attr2	5’-TTAGTTTGGCGAGCGATAATAACT-3’
	pEarleyGate104-COP1	COP1	COP1attr1	5’-CACCATGGAAGAGATTTCGACGGATCCG-3’
			COP1attr2	5’-TCACGCAGCGAGTACCAGAACTTT-3’
	pHB-PIF4-CFP	PIF4	PIF4infusionF	5’-TCCTGCAGCCCGGGGGATCCAATGGAACACCAAGGTTGGAGTTTT-3’
			PIF4infusionR	5’-GCCCTTGCTCACCATACTAGTGTGGTCCAAACGAGAACCGTCGGT-3’
	pEarleyGate101-HFR1	HFR1	HFR1attr1	5’-CACCATGTCGAATAATCAAGCTTTCATG-3’
			HFR1attr2	5’-TAGTCTT CTCATCGCATGGGAAGA-3’
	pEarleyGate101-phyB	phyB	phyBattr1	5’-CACCATGGTTTCCGGAGTCGGGGGTAGT-3’
			phyBattr2	5’-ATATGGCATCATCAGCATCATGTC-3’
	pEarleyGate104-PIF1	PIF1	PIF1attr1	5’-CACCATGGATCCTCAGCAGCAACCTTCT-3’
			PIF1attr2	5’-TTAACCTGTTGTGTGGTTTCCGTG-3’
	pEarleyGate104-PIF3		PIF3attr1	5’-CACCATGCCTCTGTTTGAGCTTTTCAGG-3’
			PIF3attr2	5’-TCACGACGATCCACAAAACTGATC-3’

	pEarleyGate104-PIF5	PIF5	PIF5attr1	
			PIF5attr2	5’-CACCATGGAACAAGTGTTTGCTGATTGG-3’
	pHB-YFP	YFP	YFPF1	5’-GCCTATTTTACCCATATGAAGACT-3’
			YFPR1	5’-CCCAAAGCTTATGGTGAGCAAGGGCGAGGAGCTG-3’
				5’-CGGAGCTCTTACTTGTACAGCTCGTCCATGCC-3’
BiFC	pXY104-PIL1	PIL1	PIL1F1	
			PIL1R4	5’-GTCGACGTTTGGCGAGCGATAATAACTAAA-3’
	pXY106-PIL1		PIL1F1	
			PIL1R5	5’GGGGTCGACTTAGTTTGGCGAGCGATAAT-3’
	pXY106-PIL1△APB	PIL1△APB	PIL1F1	
			PIL1R4	
	pXY106-HFR1	HFR1	HFR1F2	5’-GCCGGATCCATGTCGAATAATCAAGCTTTCATG-3’
			HFR1R2	
			PIF1F1	5’-GGACTAGTTAGTCTTCTCATCGCATGGGAAGA-3’
	pXY106-PIF1	PIF1	PIF1R1	5’-GCTTCTAGAATGGAACAAGTGTTTGCTGATTGG-3’
			PIF3F1	5’-GGGGTCGACGCCTATTTTACCCATATGAAGACT-3’
	pXY106-PI	PIF3	PIF3R1	5’-GCCGGATCCATGCCTCTGTTTGAGC

	F3			TTTTCAGG-3’
			PIF4F1	5’-GGGGTCGACTCACGACGATCCACAA AACTGATC-3’
	pXY106-PIF4	PIF4	PIF4R2	5’-GCTTCTAGAATGGAACACCAAGGTT GGAGTTTT-3’
			PIF5F2	5’-GGGGTCGACCTAGTGGTCCAAACGA GAACCGTC-3’
	pXY104-PIF5	PIF5	PIF5R2	5’-GCCGGATCCATGGAACAAGTGTTTG CTGATTGG-3’
			phyBF2	5’-GGGGTCGACGCCTATTTTACCCATA TGAAGA-3’
			phyBR2	
	pXY104-phyB	phyB		5’-CCCCCGGGGGATGGTTTCCGGAGTC GGGGGTAGT-3’
				5’-GCTTCTAGAACTACCCCCGACTCCG GAAACCAT-3’
Dual-LUC	PGreen_0800-*PIL1*$_{pro}$-LUC	*PIL1*$_{pro}$	*PIL1*$_{pro}$F1	5’-GCCGGATCCCGTATTCGTATAGAAT AGTTTATT-3’
			PIL1$_{pro}$R1	5’-GCTTCTAGATGAAGTAAACTGAACA AAGCTTTC-3’
	PGreen_0800-*IAA19*$_{pro}$-LUC	*IAA19*$_{pro}$	*IAA19*$_{pro}$F1	5’-GCCGGATCCGAGTTCTAAATTTTGA CTTAACTA-3’
			IAA19$_{pro}$R1	5’-GCTTCTAGATTCTTGAACTTCTTTTT TTCCTCT-3’
	PGreen_0800-*ST2A*$_{pro}$-LUC	*ST2A*$_{pro}$	*ST2A*$_{pro}$F1	5’-GCCGGATCCTAAAGATTAAGAAAAA GGATAAAC-3’
			ST2A$_{pro}$R1	5’-GCTTCTAGATGTTTTTTTTGTTATAG ATATAT-3’
	pHB-HFR1	HFR1	HFR1F2	

	-CFP	GFP	HFR1R3	
			GFPF1	5’-GGACTAGTTCTTCTCATCGCATGGGAAGA-3’
	pBs-GFP-PIF5		GFPR1	5’-CCCCTCGAGATGGTGAGCAAGGGCGAGGAGCTG-3’
		PIF5		
			PIF5F2	5’-CCCAAAGCTTTTACTTGTACAGCTCGTCCATGCC-3’
			PIF5R3	
		MYC		
			MYCF1	5’-GGACTAGTTCAGCCTATTTTACCCATATGAAGA-3’
	pKL71-MYC-GUS		MYCR1	5’-CCCCTCGAGCGGTATCGATTTAAAGCTATGGA-3’
			GUSF1	
		GUS		5’-CGG
			GUSR1	AGCTCCCCCGGGCTGCAGGAATTCAAGT-3’
				5’-CGGAGCTCATGTTACGTCCTGTAGAAACCCCA-3’
				GCTTCTAGATCATTGTTTGCCTCCCTGCTGCGG-3’
Transformation	pCAMBIA 1300-NOS	NOS	NOSF1	5’-GCCGGATCCGAATTCCATGGGCCCACTAGTTCGTTCAAACATTTGGCAATAAAG-3’
			NOSR1	
	pCAMBIA 1300-*pPIL1*-NOS	$PIL1_{pro}$	$PIL1_{pro}$F2	5’-GGCCAATTGGCTGTCGAGGGGGGATCAATTCCC-3’
			$PIL1_{pro}$R2	5’-GCTTCTAGACGTATTCGTATAGAATAGTTTATT-3’
		PIL1		5’GCCGGATCCTGAAGTAAACTGAACAAAGCTTTC-3’
	pBS-PIL1-FLA		PIL1F1	
			PIL1R2	

	G pCAMBIA 1300-*pPIL1* -PIL1FLAG -NOS pBS-PIL1-GFP	pBS-PIL 1-FLAG GFP PIL1	PIL1F1 pBSR1 GFPF2 GFPR2 PIL1F3 PIL1R6	5’-GCTTCTAGATAAAGGGAACAAAAG CTGGAGCTC-3’ 5’-GCCGGATCCATGGTGAGCAAGGGCG AGGAGCTG-3’ 5’-GGACTAGTTTACTTGTACAGCTCGTC CATGCC-3’ 5’-GGGGTCGACATGGAAGCAAAACCCT TAGCATCA-3’ 5’-GCCGGATCCGTTTGGCGAGCGATAAT AACTAAA-3’

Supplemental Methods

Supplemental Method 1. Growth Conditions

Seeds were sown on Murashige and Skoog (MS) medium and were cold treated for 3 d at 4 °C. After exposure to white light for 12 h to stimulate germination, plates with seeds were transferred to appropriate light conditions for 3 to 4 d at 22 °C. Blue, red, and far-red light were supplied by LED light sources, with irradiance fluence rates of: 15 μmol/m^2/s, 8 μmol/m^2/s, and 2 μmol/m^2/s, respectively, unless otherwise indicated. Light intensity was measured with an ILT1400-A radiometric photometer (ILT). For MG132 and DMSO treatments, seedlings were first grown on solid MS medium for 4 d, and then transferred to liquid MS medium containing MG132 (50 μM, dissolved in DMSO) or 0.5% DMSO under the indicated light conditions.

Supplemental Method 2. Plasmid Construction

PCR-amplified fragments encoding GFP and full-length PIL1 without terminator were ligated into *Bam*HI-*Spe*I and *Xho*I-*Bam*HI sites of pBluescript SKt (abbreviated as pBS), respectively, resulting in pBS-PIL1-GFP, and fragment encoding full-length PIL1 without terminator cloned into the *Bam*HI-*Spe*I sites of pBS-3×FLAG (Liu et al., 2008), resulting in pBS-PIL1-FLAG. Fragments encoding PIL1-GFP and PIL1-3×FLAG, were excised by *Sal*I-*Sac*I and cloned into the plant expression vector pKYL71 (Schardl et al., 1987) to generate pKYL71-PIL1-GFP and pKYL71-PIL1-3×FLAG, respectively.

To make constructs expressing BD-PIL1△APB and nYFP-PIL1△APB, the fragment encoding PIL1△APB (PIL1 lacking 28-46 amino acid) was obtained by overlapping PCR with primers listed in Supplemental Table 1 online, excised by *Bam*HI- *Sal*I or *Bam*HI-*Spe*I, and cloned into the pBbrige (Clontech) and pXY106 vectors, respectively, to generate BD-PIL1△APB and nYFP-PIL1△APB. To make constructs for the Dual-LUC assay, PCR-amplified fragments encoding GFP without terminator and full-length PIF5 were cloned into *Xho*I-*Hind*III and *Bam*HI -*Spe*I sites of pBS, respectively, resulting in pBS-GFP-PIF5. Fragment encoding GFP-PIF5, was

excised by *Xho*I-*Sac*I and cloned into pKYL71 to generate pKYL71-GFP-PIF5. Fragment encoding 6×MYC and full-length GUS were cloned into *Xho*I-*Sac*I and *Sac*I-*Xba*I sites of pKYL71, respectively, resulting in pKYL71-MYC-GUS. All of the constructs used were confirmed by DNA sequencing. Other constructs were generated through PCR and subsequent cloning into the corresponding vectors listed in Supplemental Table 1 online. All the primers used in the study are also listed in Supplemental Table 1 online.

Supplemental Method 3. Construction of Double, Triple, and Quintuple Mutants

To generate *pil1 hfr1* double mutants, *pil1-2* was crossed with *hfr1-201*. F2 seeds were plated and then grown on soil to the adult stage. PCR was used to confirm the double mutants. For the construction of the *cop1 pil1*, *cop1 hfr1* and *cop1 pil1 hfr1* mutants, we firstly crossed *cop1-4* with *pil1-2* and *hfr1-201* respectively. F2 seeds were plated and grown under darkness for 3 d. The seedlings with short hypocotyls and expanded cotyledons were chosen and grown on soil and the double mutants were confirmed by PCR. Then we crossed *cop1 pil1* with *cop1 hfr1*, and identified the *cop1 pil1 hfr1* triple mutant in F2. For the construction of the *pil1 pifq* quintuple mutant, *pifq* was crossed with *pil1-2*. F2 seeds were plated and grown under blue light for 4 d, and the seedlings with taller hypocotyls were chosen and grown on soil, and the seedlings containing homozygous *pil1-2* mutations were confirmed by PCR. The F3 seeds were plated and grown under blue light for 4 d, and seedlings with shorter hypocotyls were identified. The final confirmation of the *pil1 pifq* quintuple mutant was performed by PCR. All the primers used in PCR were described previously (Soh, 2000; Yamashino et al., 2003; Huq et al., 2004; Monte et al., 2004; Khanna et al., 2007; Leivar et al., 2008).

Supplemental Method 4. Hypocotyl Length Measurements

Thirty seedlings grown for 4 d under the indicated light conditions were photographed and the resulting digital photographs were subjected to measurements of hypocotyl lengths using ImageJ software (http://rsbweb.nih.gov/ij/).

Supplemental Method 5. Fluorescence Microscopy

Root cells of the 4-d-old *35S$_{pro}$:PIL1-GFP*#5/WT and *35S$_{pro}$:PIL1-GFP*#5/*cop1* seedlings grown on MS medium under different treatments were analyzed using a confocal microscope with GFP filter sets. All fluorescence images were taken with identical exposure.

Supplemental Method 6. Antibodies

Rabbits were vaccinated with synthesized peptide (CVPRKRPLSTASGSG) to generate anti-phyB antiserum. The anti-phyB antibody was further purified from the antiserum using protein A. The anti-ACTIN, -HA, and -LexA antibodies were purchased from Abmart Inc. and Merck Inc.

Supplemental Method 7. Yeast Protein Extraction

All yeast cells were harvested when OD600 was at 0.4~0.6. Equal amounts of yeast cells for each sample were calculated from OD600. The total yeast protein was extracted using A Yeast Protein Extraction kit according to the manufacture's manual (CWbiotech Inc. Cat#CW0890).

Supplemental Method 8. qRT-PCR

Total RNA (500 ng) was reverse-transcribed using the PrimeScript RT Reagent Kit (Takara). Amplification was carried out with SYBR Premix Ex Taq II (Takara). Real-time PCR was performed in a CFX96 Real time system (Bio-Rad). The thermal profile for real-time PCR was 95 °C for 2 min, followed by 40 cycles of 95 °C for 15 s and 60 °C for 30 s. The expression of PIF direct-target genes was normalized against the expression of the endogenous control gene *ACTIN2*. All experiments were performed with three independent biological replicates in three technical repetitions each. The RT-PCR primers were described previously (Zhang et al., 2013).

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