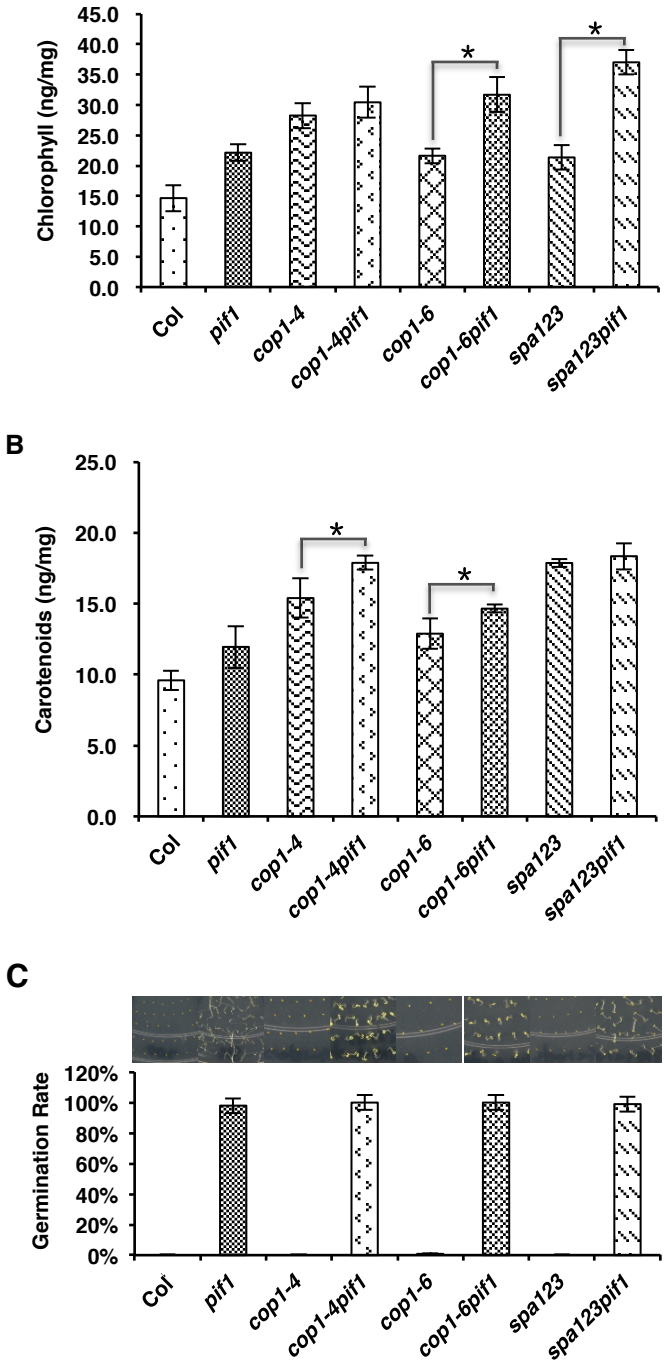
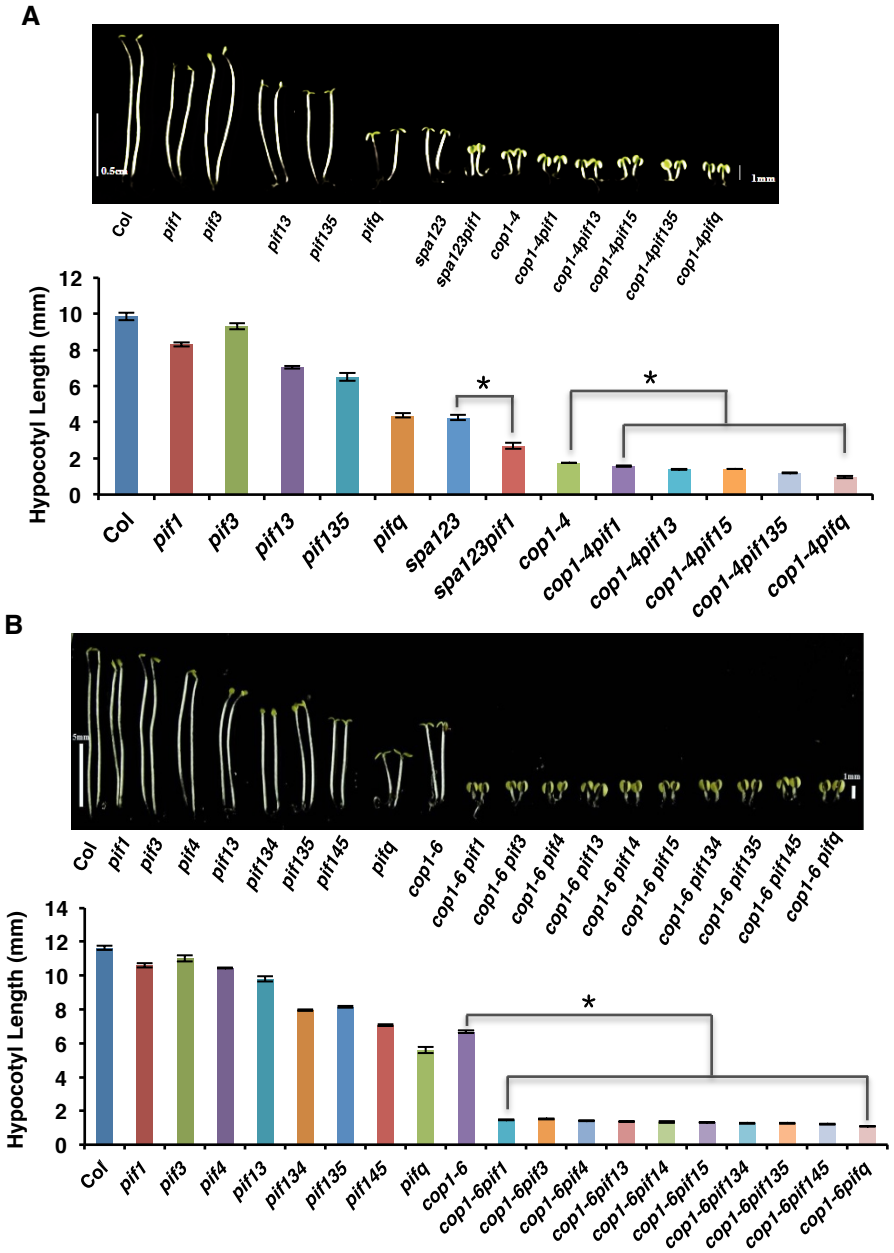


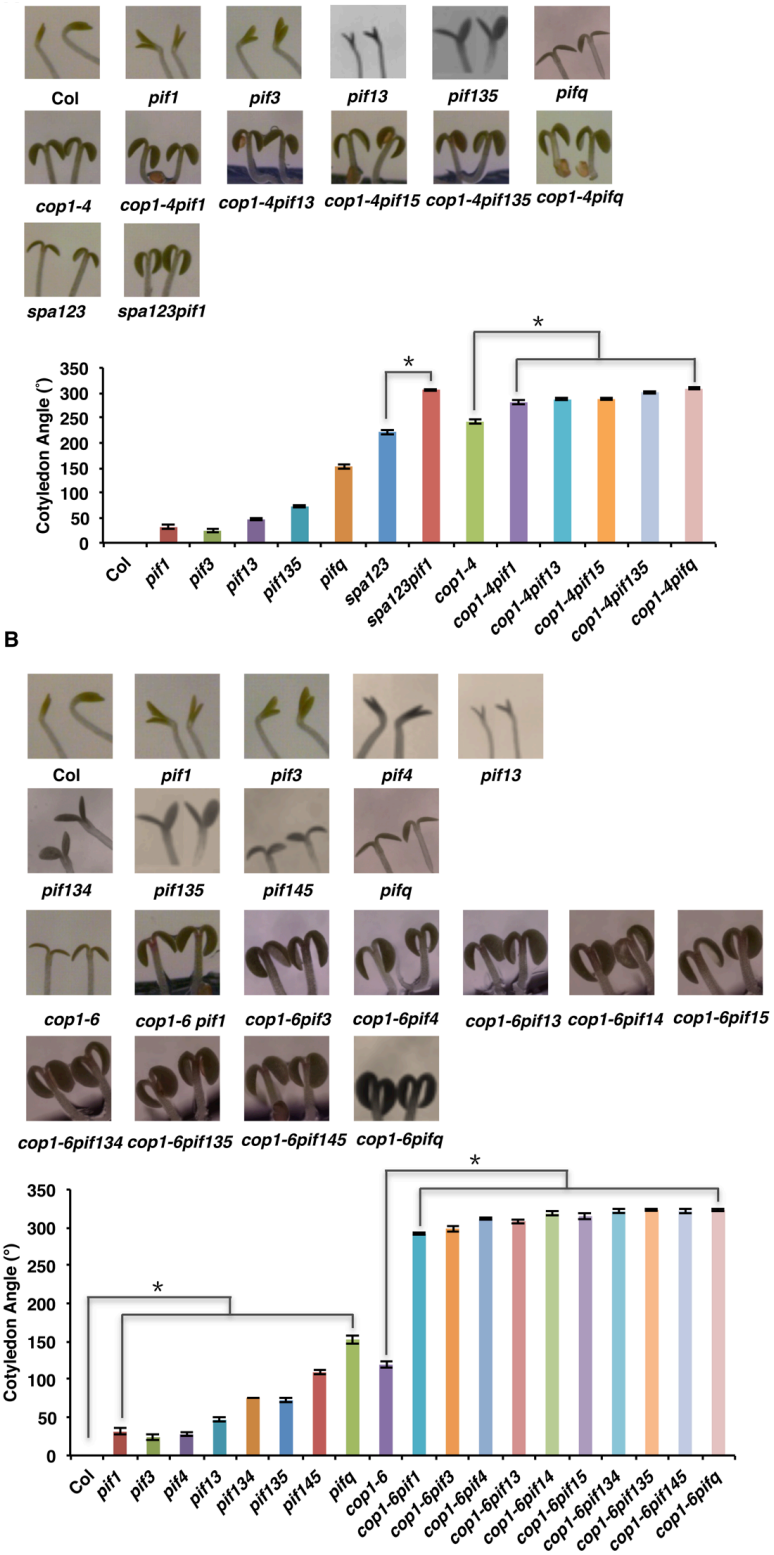
Supplementary Figure S1: *pif1* enhances the accumulation of chlorophyll and carotenoid in the *cop1* and *spa123* backgrounds in the dark.

(A, B) Bar graphs show the concentration of chlorophyll (A) and carotenoids (B) for various *pif1* combinations with *cop1-4, cop1-6* and *spa123* mutants. Seedlings were grown in the dark for 4 days and then exposed to white light for 5 hours before extraction of chlorophylls and carotenoids. *, indicates significant difference ($p<0.05$). Error bars indicate standard deviation. (C) The seed germination phenotype of *pif1* is not affected by *cop1-4, cop1-6* and *spa123* mutants. (Top) Photographs show the germinated and nongerminated seeds of various genotypes. (Bottom) Bar graph shows the percent of seeds germinated for various genotypes as indicated.



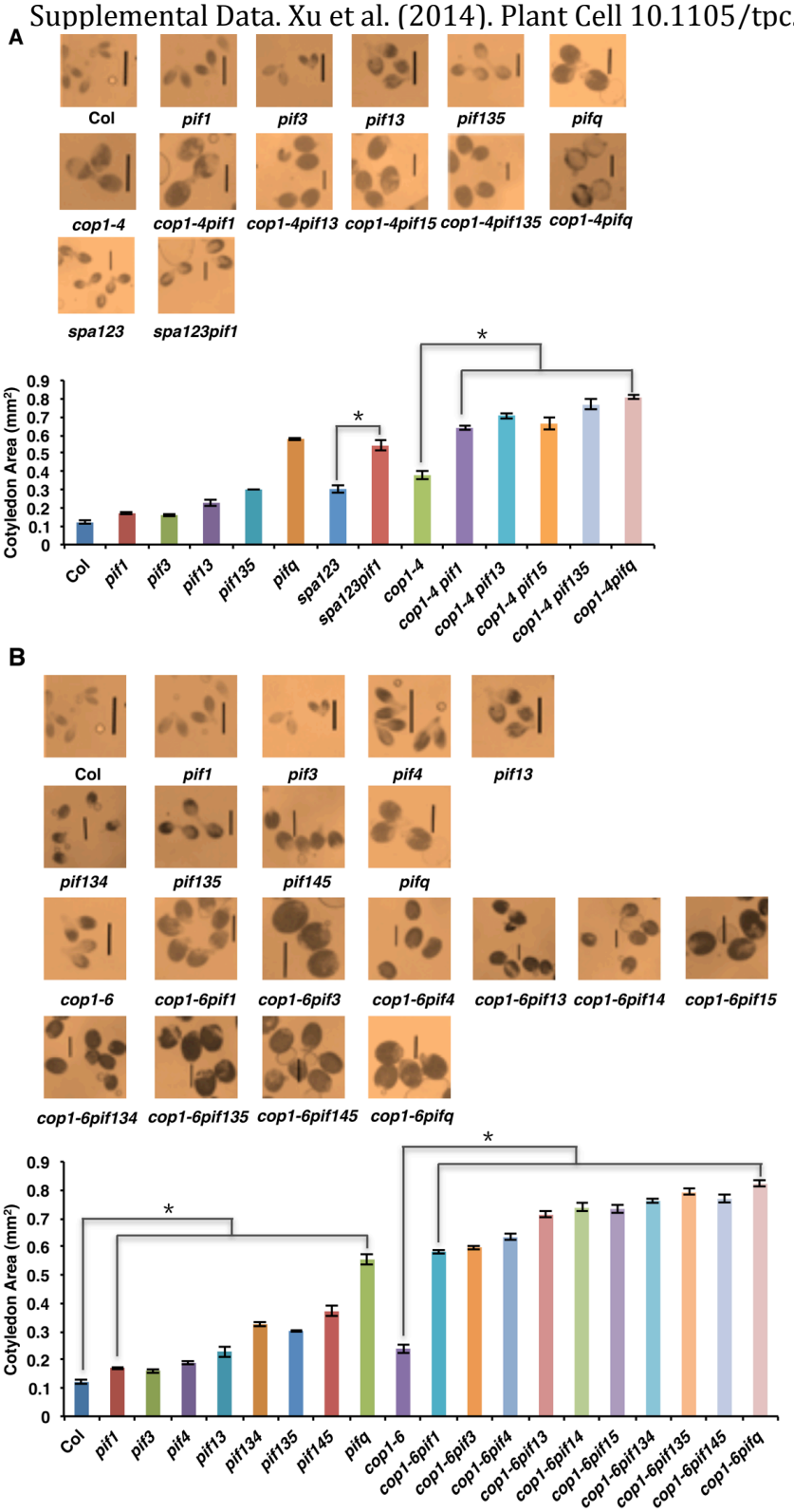
Supplementary Figure S2: *pif*s enhance the photomorphogenic development synergistically with *cop1* and *spa123* in the dark.

(A) (Top) Photographs of seedlings of wild type (Col-0), *cop1-4*, *spa123*, and various *pif* combinations with and without *cop1-4* and *spa123*. (Bottom) Bar graph shows the hypocotyl lengths of dark-grown seedlings of various genotypes as indicated. Seeds of various genotypes were grown on MS medium without sucrose for 5 days in the dark. Error bars indicate standard deviation. ***,** indicates significant difference ($p<0.05$). (B) (Top) Photographs of seedlings of wild type (Col-0), *cop1-6*, and various *pif* combinations with and without *cop1-6.* (Bottom) Bar graph shows the hypocotyl lengths of 5-day-old dark-grown seedlings of various genotypes as indicated. Error bars indicate standard deviation. ***,** indicates significant difference ($p<0.05$).



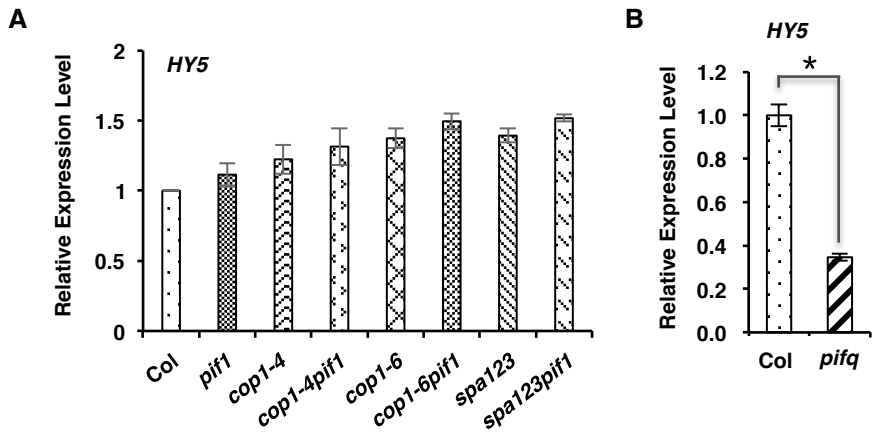
Supplementary Figure S3: *pif*s increase the cotyledon angle of dark-grown seedlings synergistically with *cop1* and *spa123*.

(A) (Top) Photographs of cotyledon angles of dark-grown seedlings of wild type (Col-0), *cop1-4*, *spa123*, and various *pif* combinations with and without *cop1-4* and *spa123*. (Bottom) Bar graph shows the cotyledon angles of dark-grown seedlings of various genotypes as indicated. Error bars indicate standard deviation. ***,** indicates significant difference ($p<0.05$). (B) (Top) Photographs of cotyledon angles of dark-grown seedlings of wild type (Col-0), *cop1-6*, and various *pif* combinations with and without *cop1-6*. (Bottom) Bar graph shows the cotyledon angles of dark-grown seedlings of various genotypes as indicated. Seeds of various genotypes were grown on MS medium without sucrose for 5 days in the dark. Error bars indicate standard deviation. ***,** indicates significant difference ($p<0.05$).

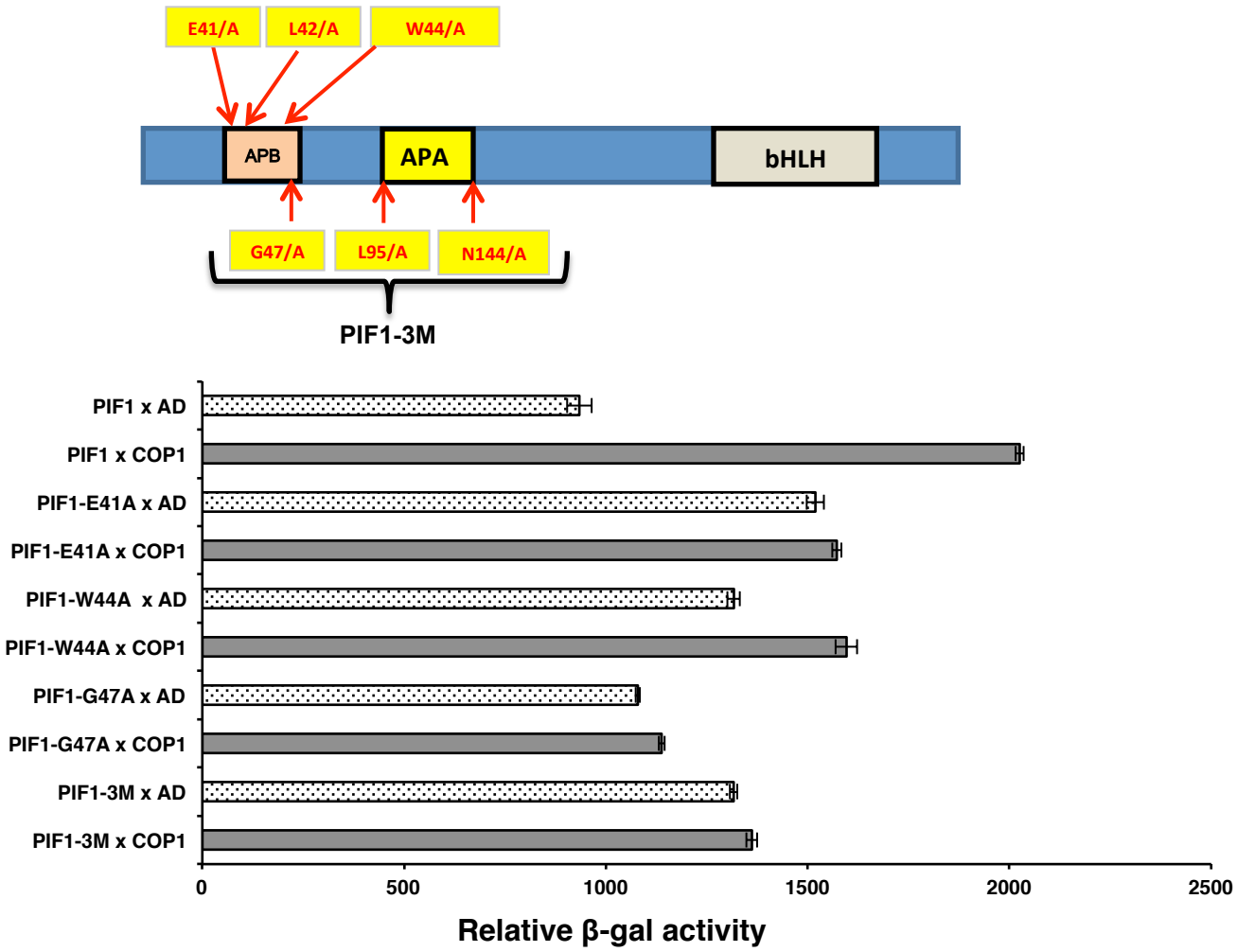


Supplementary Figure S4: *pif*s increase the cotyledon area of dark-grown seedlings synergistically with *cop1* and *spa123*.

(A) (Top) Photographs of cotyledon areas of dark-grown seedlings of wild type (Col-0), *cop1-4*, *spa123*, and various *pif* combinations with and without *cop1-4* and *spa123*. Bar = 1 mm. (Bottom) Bar graph shows the cotyledon areas of dark-grown seedlings of various genotypes as indicated. Error bars indicate standard deviation. ***,** indicates significant difference ($p<0.05$). (B) (Top) Photographs of cotyledon areas of dark-grown seedlings of wild type (Col-0), *cop1-6*, and various *pif* combinations with and without *cop1-6.* Bar = 1 mm. (Bottom) Bar graph shows the cotyledon areas of dark-grown seedlings of various genotypes as indicated. Seeds of various genotypes were grown on MS medium without sucrose for 5 days in the dark. Error bars indicate standard deviation. ***,** indicates significant difference ($p<0.05$).

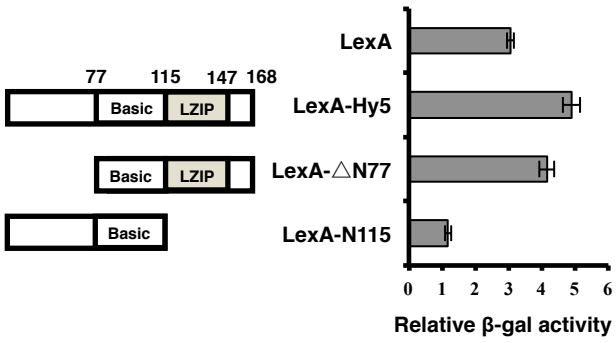


Supplementary Figure S5: *HY5* mRNA level in various mutants compared to wild type. (A) Bar graph showing the *HY5* mRNA levels in the indicated mutants indicated. *HY5* mRNA level was determined using qRT-PCR assays. Total RNA was extracted from 4-day-old dark-grown seedlings as described above. (B) Bar graph shows the *HY5* mRNA level in the wild type (Col-0) and *pifq* based on RNAseq data as described (Zhang et al., 2013). Error bars indicate standard deviation. ***,** indicates significant difference ($p<0.05$).



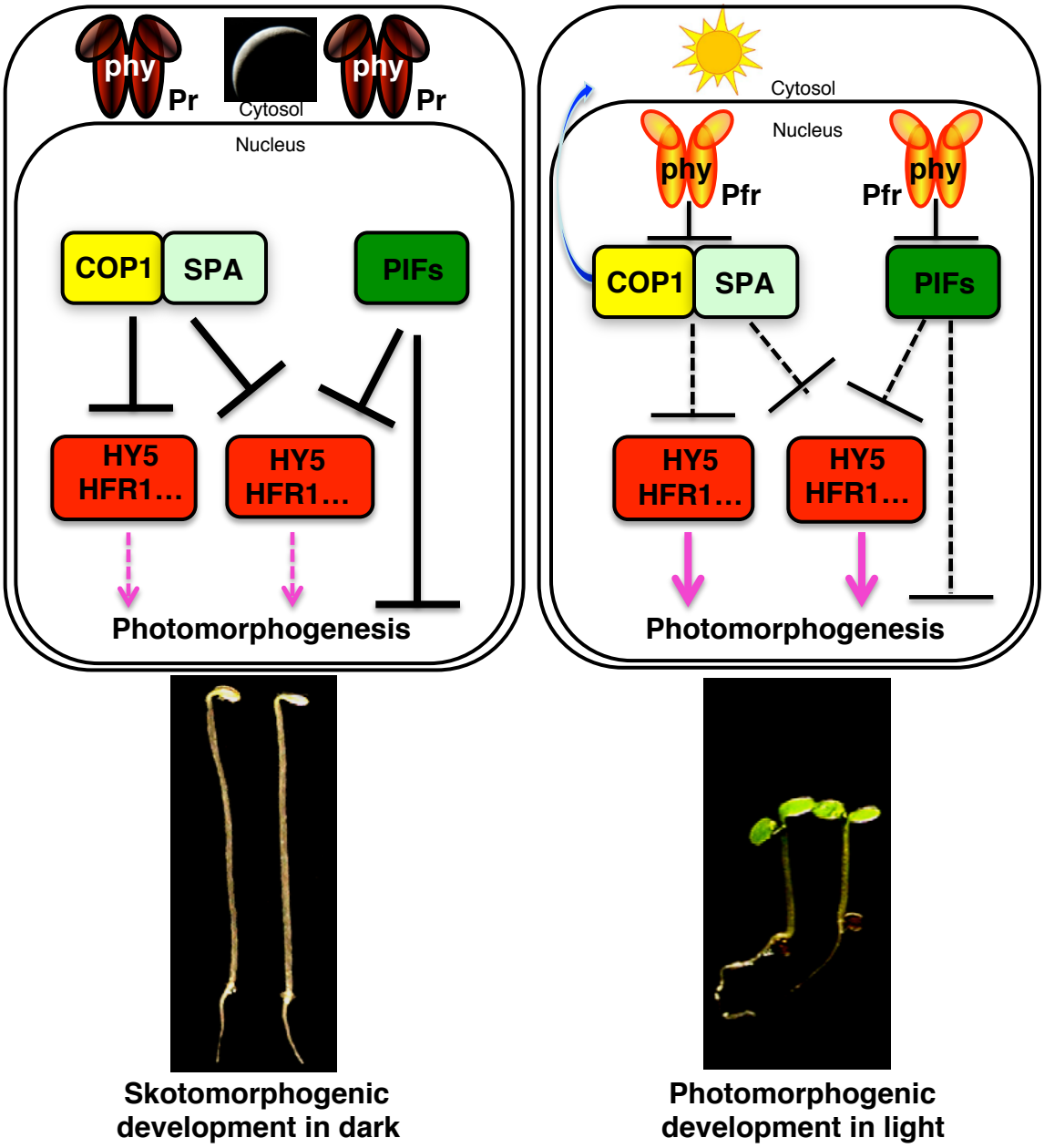
Supplementary Figure S6: The APB domain of PIF1 is necessary for interaction with the full-length COP1 in yeast two-hybrid assays.

(Top) Schematic diagram of PIF1 structure showing the position of APB, APA and bHLH domains. The point mutations in the APB and APA domains involved in phytochrome interaction are shown. (Bottom) The bar graph shows the β-galactosidase activities of various PIF1 wild type and point mutant versions with full-length AD-COP1. Error bars indicate standard deviation (n=3).



Supplementary Figure S7: PIF1 interacts with the bZIP domain of HY5 in yeast two-hybrid assays.

Left panel shows the full-length and various deletion fragments of LexA-HY5 fusion constructs. The basic and the Leucine zipper (LZIP) of HY5 are as indicated. Right panel shows the corresponding β-galactosidase activities with full-length AD-PIF1. Error bars indicate standard deviation (n=3).



Supplementary Figure S8: Model showing how PIFs and COP1-SPA proteins function synergistically as well as independently to repress photomorphogenesis in the dark. (Left) phys are localized to the cytosol as an inactive Pr form, while PIFs and COP1/SPA proteins are constitutively localized to the nucleus in the dark. PIFs repress photomorphogenesis by transcriptional repression of light-regulated genes. COP1/SPA proteins independently repress photomorphogenesis by targeting the positively acting transcription factors (e.g., HY5/HFR1/ LAF1 and others) for Ub/26S proteasome-mediated degradation. In addition, PIFs and COP1/ SPA proteins also promote synergistic degradation of positively acting factors to repress photomorphogenesis in the dark. (Right) Light signals induce photo-conversion of the Pr form to the active Pfr form and thereby promote nuclear translocation of phys. Within the nucleus, the Pfr forms of phys interact with PIFs and induce phosphorylation, ubiquitylation and 26S proteasome-mediated degradation. In response to light, COP1/SPA complexes are also inactivated by phys in an unknown mechanism and/or by nuclear exclusion of COP1 under prolonged light (indicated by blue arrow) (Subramanian et al., 2004), thereby stabilizing the positively acting transcription factors. The light-induced degradation of PIFs as well as inactivation/nuclear exclusion of COP1 relieve the negative regulation to promote photomorphogenesis.

Supplemental Table 1

Supplementary Table 1: Primer sequences used in experiments described in the text

Gene	Forward	Reverse
For qRT-PCR		
CAB3	GAGCTCAAGAACGGAAGATTGGC	CCGGGAACAAAGTTGGTTGC
RBCS1A	ACCTTCTCCGCAACAAGTGG	GAAGCTTGGTGGCTTGTAGG
RBCL	TCGGTG GAGGAACTTT AGGC	TGCAAGATCACGTCCCTCAT
Fed A	CTTCATTCATCCGTCGTTCC	AGGGTAAGCAGCACAAGTGA
HY5	GCTGCAAGCTCTTTACCATC	TCCGACAGCTTCTCCTCCAAACTC
PP2A	TATCGGATGACGATTCTTCGTGCAG	GCTTGGTCGACTATCGGAATGAGAG
For cloning		
PIF1	cgaGAATTCatgcatcattttgtccctgac	tgaGTCGACttaacctgttgtgtggtttccgtg
PIF1-N55	ctgGAATTCatgcatcattttgtccctgac	ctgGTCGACtctctggttttgaacaacaac
PIF1-N150	ctgGAATTCatgcatcattttgtccctgac	ctgGTCGACcagcctcgagaaattcatgaa
PIF1-C328	ctgGAATTCagaggggattttaataacgg	ctgGTCGACttaacctgttgtgtggtttcc
PIF1 pENTR	CACCatgcatcattttgtccctgacttcg	acctgttgtgtggtttccgtg
COP1 pENTR	CACCatggaagagatttcgacggatcc	cgcagcgagtaccagaactttgatgg

References:

Subramanian, C., Kim, B.H., Lyssenko, N.N., Xu, X., Johnson, C.H., and von Arnim, A.G. (2004). The Arabidopsis repressor of light signaling, COP1, is regulated by nuclear exclusion: mutational analysis by bioluminescence resonance energy transfer. Proc Natl Acad Sci USA. **101,** 6798-6802.