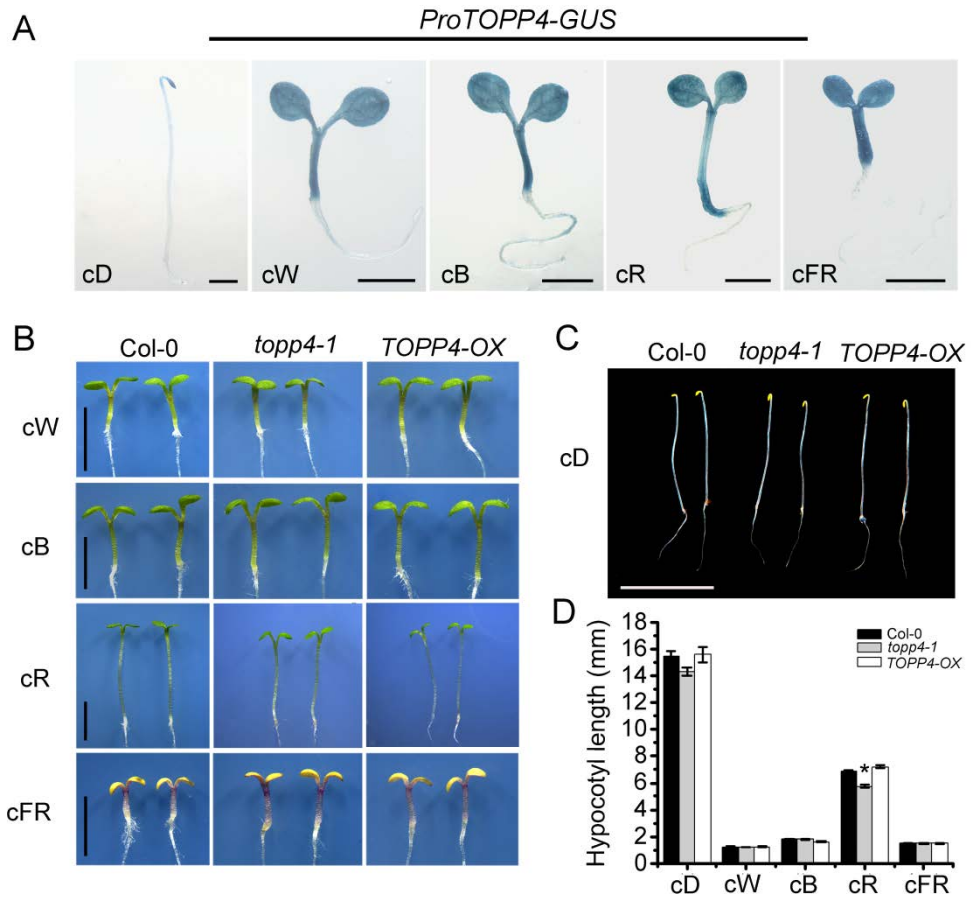
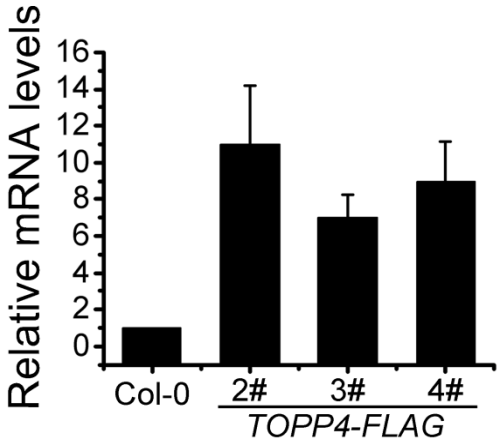
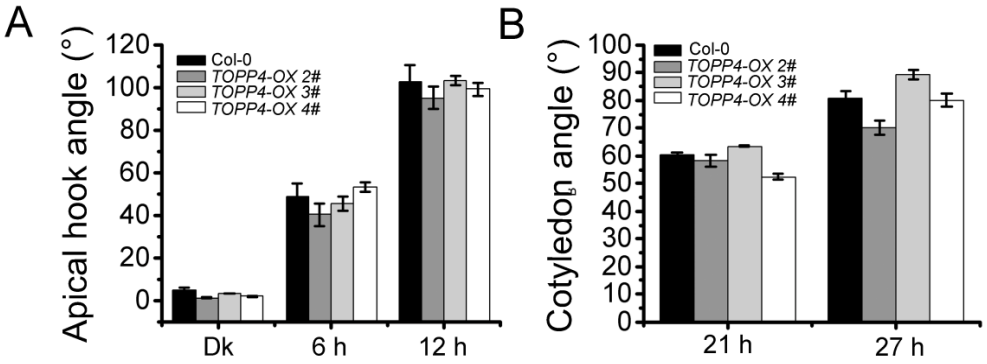


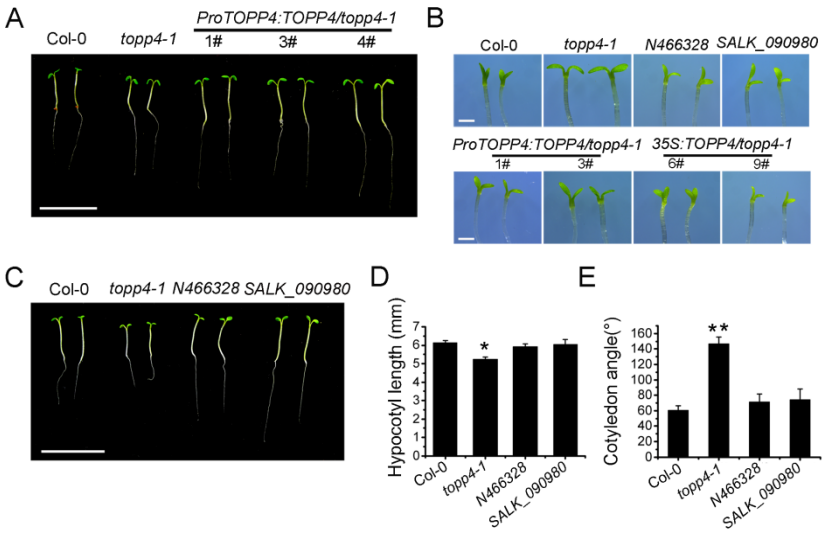
Supplemental Figure S1. Analysis of *TOPP4* expression and photoresponses of *topp4-1* mutant and *TOPP4* overexpression seedlings under different light conditions. (A) Histochemical assay of *ProTOPP4-GUS* expression in Col-0 grown for 4 days under continuous dark (cD), white (cW) (100 μmol m^{-2} s^{-1}), blue (cB) (42 μmol m^{-2} s^{-1}), red (cR) (56 μmol m^{-2} s^{-1}), and far-red (cFR) (2 μmol m^{-2} s^{-1}). Scale bars = 1 mm. (B) The phenotypic analysis of 5-d-old seedlings of wild type *Arabidopsis* (Col-0), *topp4-1*, and *TOPP4-OX* under various light conditions as in (A). Three independent analyses were performed and displayed the same phenotypes. Scale bars = 3 mm. (C) The phenotypic analysis of 5-d-old seedlings as in (B) under continuous dark (cD). Scale bar = 1 cm. (D) Quantitative analysis of the hypocotyl length of seedlings as in (B) under various light conditions. Error bars indicate SE. Statistical significance was determined by Tukey's LSD test (*P < 0.05). The hypocotyl lengths of approx. 60 seedlings were measured.



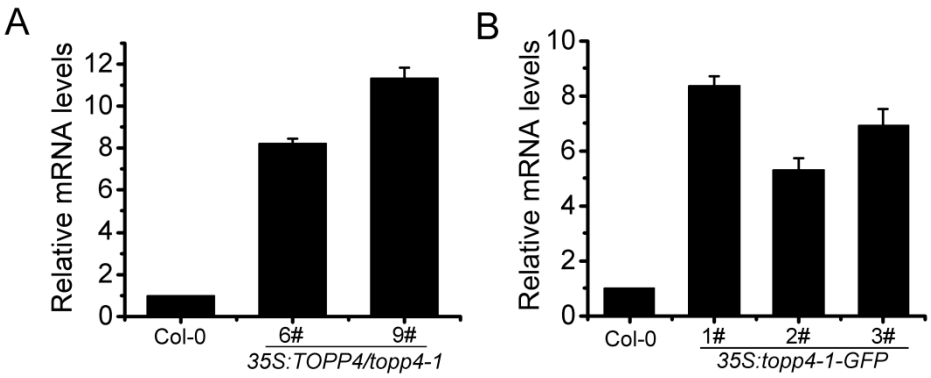
Supplemental Figure S2. The expression levels of *TOPP4* in *TOPP4-FLAG* overexpression seedlings. Real-Time PCR analysis of *TOPP4* expression in 5 d *TOPP4-FLAG* 2#, 3#, 4# seedlings under red light. PP2A was used as a reference gene.



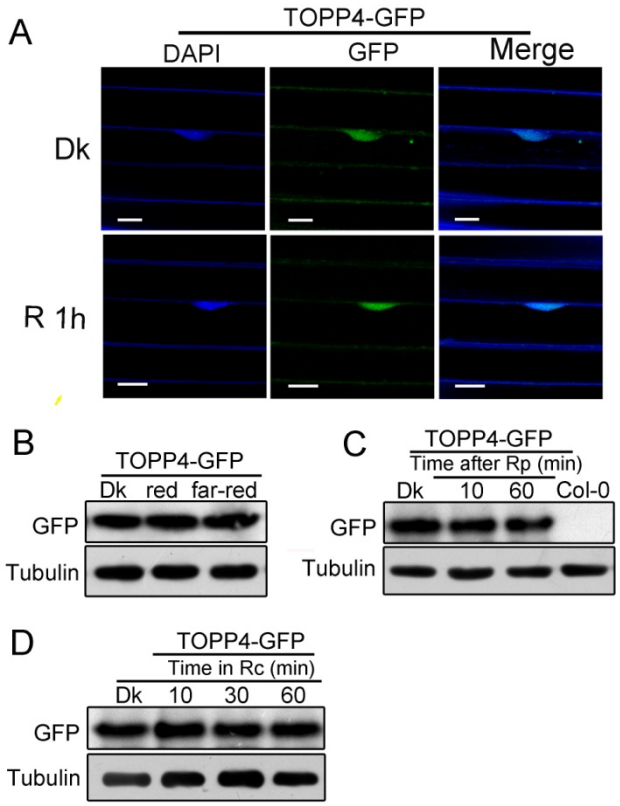
Supplemental Figure S3. Quantitative analysis of the apical hook angle and cotyledon angle of *TOPP4-OX* seedlings under red light. (A) Quantification of apical hook angle of *TOPP4-OX* lines 2#, 3#, 4#. Seedlings were grown in the dark (Dk) for 4 d, and subsequently transferred to red light for 6 h and 12 h as indicated. (B) Quantification of cotyledon angle of *TOPP4-OX* lines 2#, 3#, 4#. Seedlings were grown in the dark (Dk) for 4 d, and subsequently transferred to red light for 21 h and 27 h as indicated. In (A) and (B), error bars represent SE (n=50).



Supplemental Figure S4. Overexpression of *TOPP4* in the *topp4-1* mutant rescues its cotyledon opening defects. (A) Photographs of 5-d-old seedlings of the indicated genotypes grown under red light condition. Scale bar = 1 cm. (B) The phenotype of cotyledon angle of the indicated genotypes grown in the dark for 4 d, and subsequently transferred to red light for 21 h. Scale bars = 1 mm. (C) Photographs of seedlings of the indicated genotypes grown under red light for 5 d. Scale bar = 1 cm. (D) Quantification of hypocotyl lengths (average of 50 seedlings) of 5-d-old Col-0, *topp4-1*, *N466328*, and *SALK_090980* seedlings grown under red light condition. (E) Quantification of cotyledon angle of Col-0, *topp4-1*, *N466328*, and *SALK_090980* seedlings grown as in (B), n=50. In (D) and (E), error bars indicate SE. Statistical significance was determined by Tukey's LSD test (*P < 0.05; **P < 0.01).

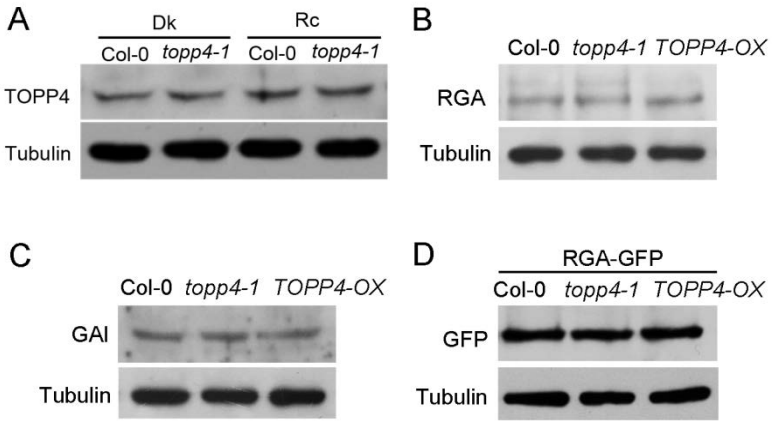


Supplemental Figure S5. Quantification of *TOPP4/topp4-1* expression levels in *35S:TOPP4* and *35S:topp4-1-GFP* seedlings. (A) Expression of *TOPP4* was determined by quantitative PCR in *35S:TOPP4/topp4-1* 6#, 9# seedlings grown for 5 days under red light. PP2A was used as a reference gene. (B) Expression of *topp4-1* in *35S:topp4-1-GFP* 1#, 2#, 3# seedlings grown as in (A). PP2A was used as a reference gene.

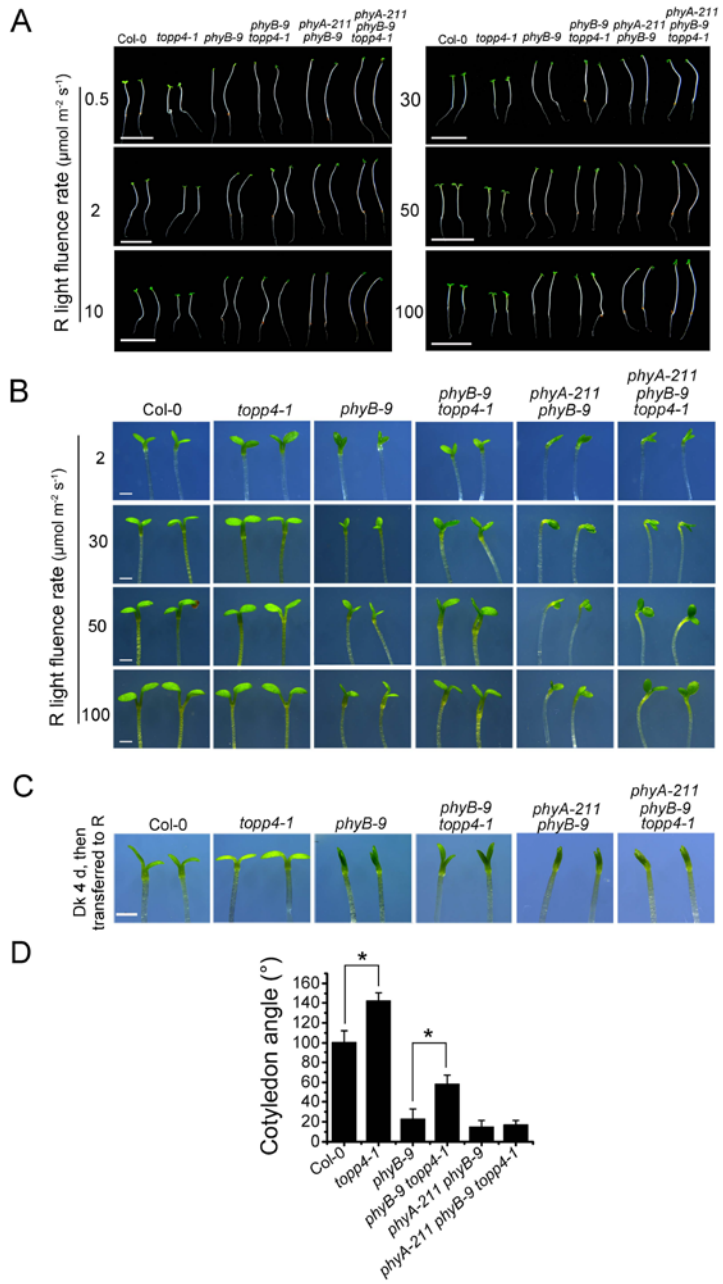


Supplemental Figure S6. The localization and accumulation of TOPP4 are not affected by red light. (A) Epifluorescent imaging of GFP fluorescence in

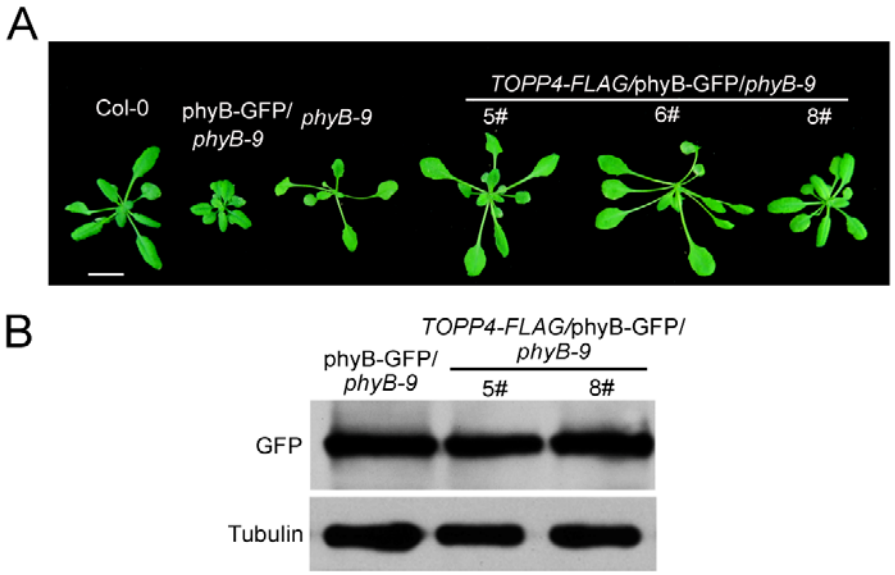
hypocotyl-cell of transgenic seedlings expressing TOPP4-GFP. Seedlings were grown for 4 days in darkness and then either maintained in the dark (Dk) or treated with 1 h red light (R). Scale bars = 10 μm. (B) Western blot analysis of TOPP4 protein levels in 4-d-old TOPP4-GFP seedlings under continuous red and far-red light. Tubulin was used as a loading control. (C) Western blot analysis of TOPP4 protein levels in 4-d-old TOPP4-GFP seedlings grown in darkness (Dk) after exposed to a saturating Rp (7500 μmol m^{-2} in 33 s), followed by return to darkness for the indicated time before extraction. (D) Western blot analysis of TOPP4 protein levels in 4-d-old dark-grown TOPP4-GFP seedlings after exposure10-, 30-, and 60-min red light.



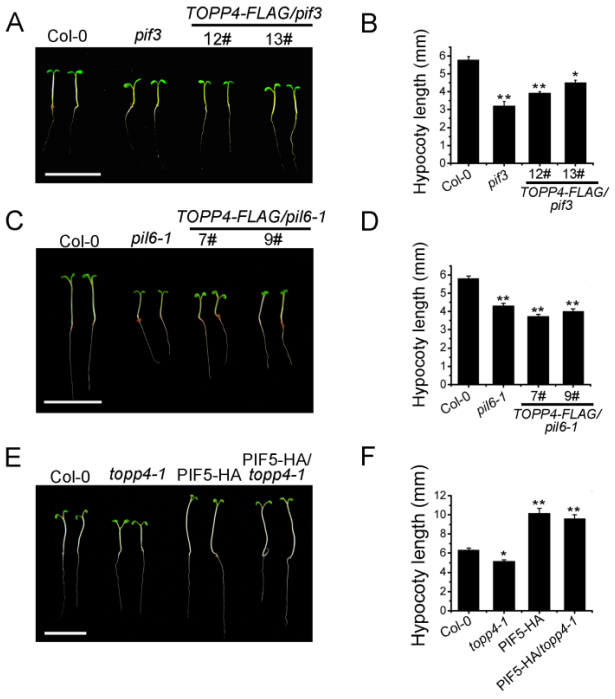
Supplemental Figure S7. The accumulation of TOPP4 is not altered in *topp4-1* mutant and DELLA proteins are not affected by mutation or overexpression of *TOPP4* in *Arabidopsis* seedlings under red light. (A) Immunoblot analysis of 5-d-old Col-0, *topp4-1* under continuous dark (Dk) or red light (Rc) by anti-TOPP4. (B) and (C) Immunoblot analysis of 5-d-old Col-0, *topp4-1*, *TOPP4-OX* grown under continuous red light by anti-GAI and anti-RGA antibody. (D) Immunoblot analysis of RGA-GFP (by anti-GFP antibody) in 5-d-old Col-0, *topp4-1*, and *TOPP4-OX* *Arabidopsis* seedlings grown under continuous red light.



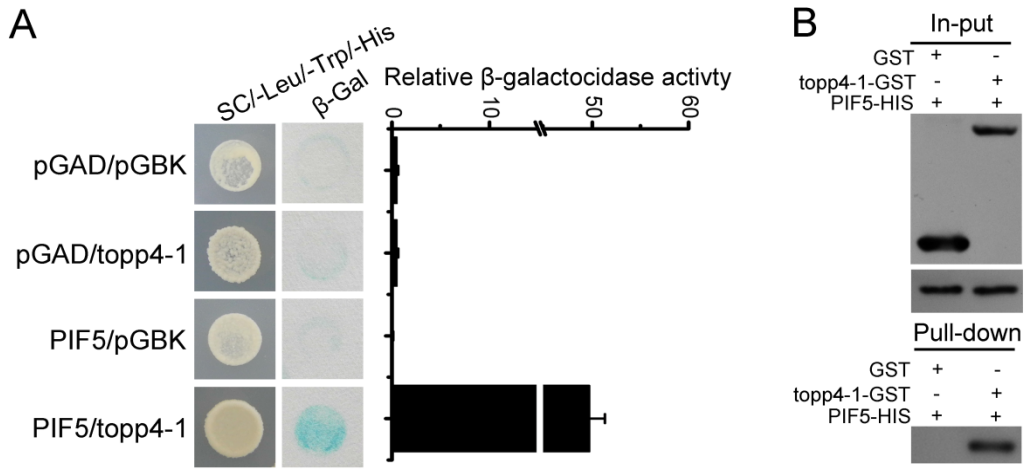
Supplemental Figure S8. The *topp4-1* mutation could partly recover the closed cotyledon angle of *phyB-9* and *phyA-211 phyB-9*. (A) Phenotypes of 5-d-old seedlings grown under various red (R) light fluence rate. Scale bar =1 cm. (B) Cotyledon opening angle of 5-day-old seedlings grown under 2, 30, 50, and 100 μmol m^{-2} s^{-1} red light. Scale bar =1 mm. (C) Photographs of cotyledon angles of 4 d dark-grown seedlings treated with red light for 32 h. Scale bar = 1 mm. (D) Quantification of cotyledon angles of seedlings shown in (C). Error bars represent SE (n=50). Statistical significance was determined by Tukey's LSD test (*P < 0.05; **P < 0.01).



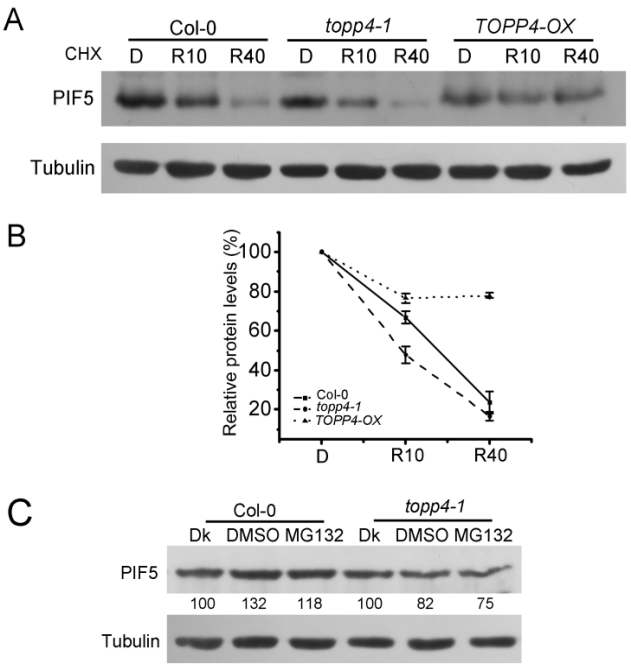
Supplemental Figure S9. Overexpression of *TOPP4* in phyB-GFP seedlings has no notable effect on phyB protein Levels. (A) The phenotypes of *TOPP4-FLAG/*phyB-GFP*/phyB-9* plants. Plants were grown under long-day conditions for 26 d. Scale bar=1 cm. (B) Western blot analysis of phyB protein levels in 5-d-old seedlings grown under continuous 8 μmol m^{-2} s^{-1} red light by anti-GFP. Tubulin was used as a loading control.



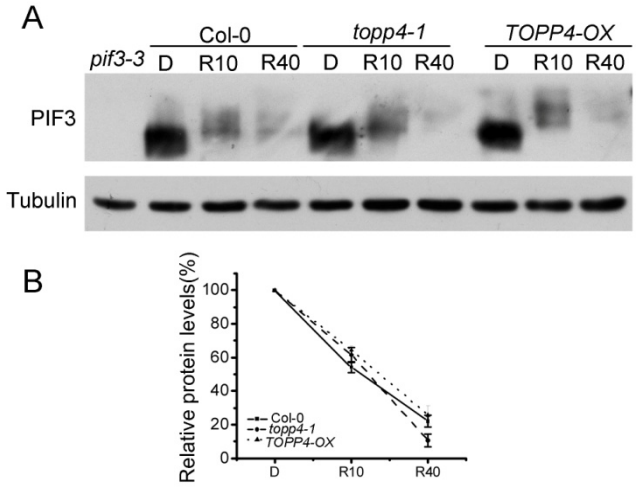
Supplemental Figure S10. *PIF* is genetically epistatic to *TOPP4*. (A) and (B) Hypocotyl lengths of seedlings of Col-0, *pif3*, *35S:TOPP4/pif3* 12#, 13# grown under red light for 5 d. Scale bar = 1 cm. (C) and (D) Hypocotyl lengths of seedlings of Col-0, *pil6-1*, *TOPP4-FLAG/pil6-1* 7#, 9# grown under red light for 5 d. Scale bar = 1 cm. (E) and (F) Hypocotyl lengths of seedlings of Col-0, *topp4-1*, PIF5-HA, PIF5-HA/*topp4-1* grown under red light for 5 d. Scale bar = 1 cm. In (B), (D), and (F), error bars represent SE, which were analyzed based on more than 50 seedlings. Asterisks indicate significant differences (*P < 0.05; **P < 0.01), as determined by Tukey's LSD test.



Supplemental Figure S11. topp4-1 interacts with PIF5. (A) Yeast two-hybrid assays showing that topp4-1 interacts with PIF5. The panel shows the corresponding β-galactosidase activities. (B) Pull-down assays using GST-topp4-1 and GST pull down PIF5-HIS. PIF5 was detected by western blots using anti-HIS.



Supplemental Figure S12. TOPP4 regulates PIF5 stability after translation in response to red light, and the PIF5 proteins are not degraded in *topp4-1* in the absence of light. (A) and (B) 4-d-old dark-grown seedlings were pretreated with 50 μM CHX for 30 min, and seedlings were kept in CHX application and exposed to a saturating Rp (7500 μmol m^{-2} in 33 s), followed by return to darkness for the indicated time before extraction (R10 indicates 10 min from initial Rp; R40 indicates 40 min from initial Rp) and subjected to western-blot analysis using anti-PIF5 or anti-tubulin antibody (A) and quantified using Image J software (B). Quantitative data are shown as mean SE, n = 3. (C) 4-d-old dark-grown (Dk) Col-0 and *topp4-1* seedlings were treated with MG132 or DMSO for 4 h before extraction and subjected to immunoblot analysis using anti-PIF5 or anti-tubulin antibodies, and quantified using Image J software. Quantitative data are shown as mean SE, n = 3.



Supplemental Figure S13. The dephosphorlation and stability of PIF3 could not be affected by TOPP4. (A) and (B) Dark-grown seedlings Col-0, *topp4-1*, *TOPP4-OX* were exposed to a Rp (7500 μmol m^{-2} in 33 s), followed by return to darkness for the indicated time before extraction (R10 indicates 10 min from initial Rp; R40 indicates 40 min from initial Rp). Protein samples were separated on a 6.5% SDS-PAGE gel and subjected to western-blot analysis using anti-PIF3 or anti-tubulin antibody (A), and quantitative data (B) are shown as mean SE, n = 3. *pif3-3* as a negative control.

Supplemental Table S1. List of primers used for Real-Time PCR analyses.

Genes	**Forward Primers**	**Reverse Primers**
TOPP4	AATCTGTGGTGACATACATGG	ACTCTGTTTGCCTCTGTCCA
CAB2	TCGCAAGGAACCGTGAGCTA	AGCCTTGAACCAAACTGCCT
CHS	ACGCTTGCCTTCTATCTGCC	GTCGAATAGACCTGTCCAGCAC
RBCS	CCTAGACCCTCCGATCACTC	GGTTTGGTCTAGTGCTTTGG
PP2A	TATCGGATGACGATTCTTCGTGCAG	GCTTGGTCGACTATCGGAATGAGAG
CCA1	CCTTTTACAAACACCGGCTCT	AATCGGGAGGCCAAAATGA

	T	
SIGE	CTCGCTCTCGACGATGTGCTC	CATCAAGGCCTTGACTTCATG
PIL1	AAATTGCTCTCAGCCATTCGTGG	TTCTAAGTTTGAGGCGGACGCAG
ATHB2	TCACAGTACTCTCAATCCGAAGC	CCGTAAGAACTCGCAGTCTAC
HFR1	ATTGGCCATTACCACCGTTTAC	TGAGGAGAAGAAGCTGGTGATG
AT5G02580	CATCCATTTGGTGCATCATTTG	CACTCTTCTTTGCCCATGTTGA