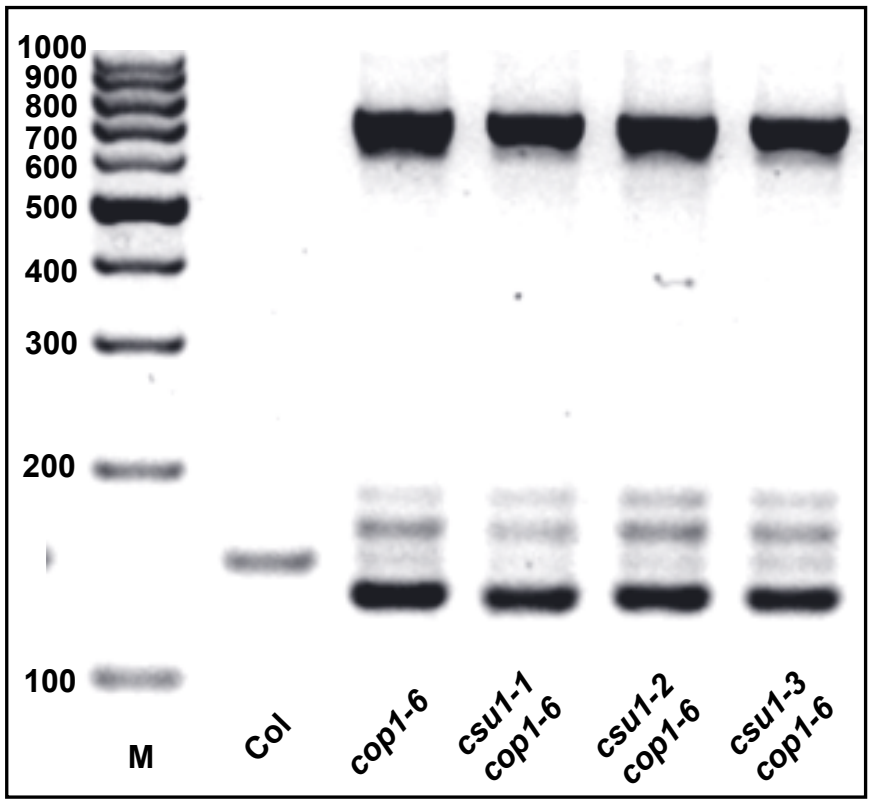
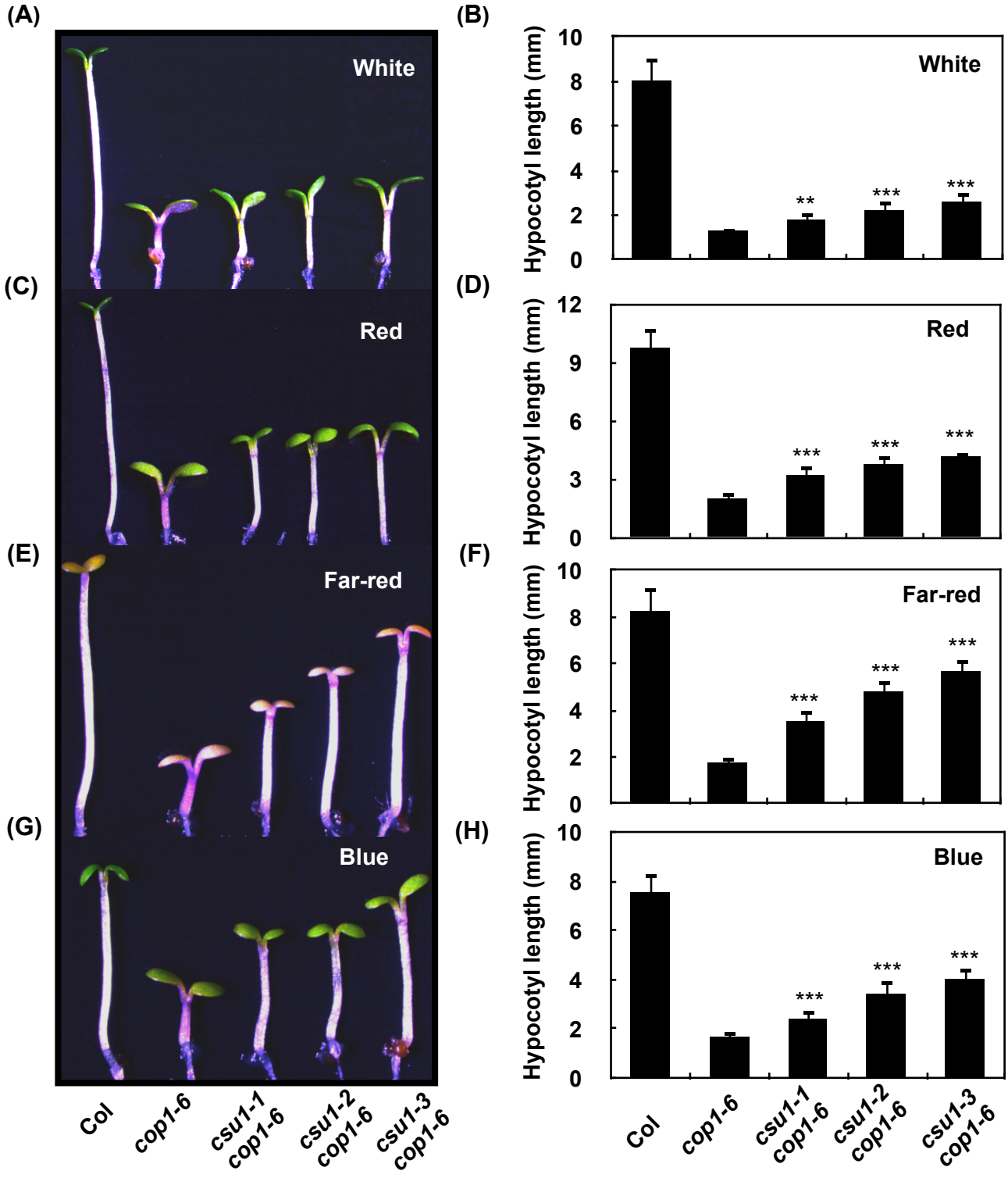
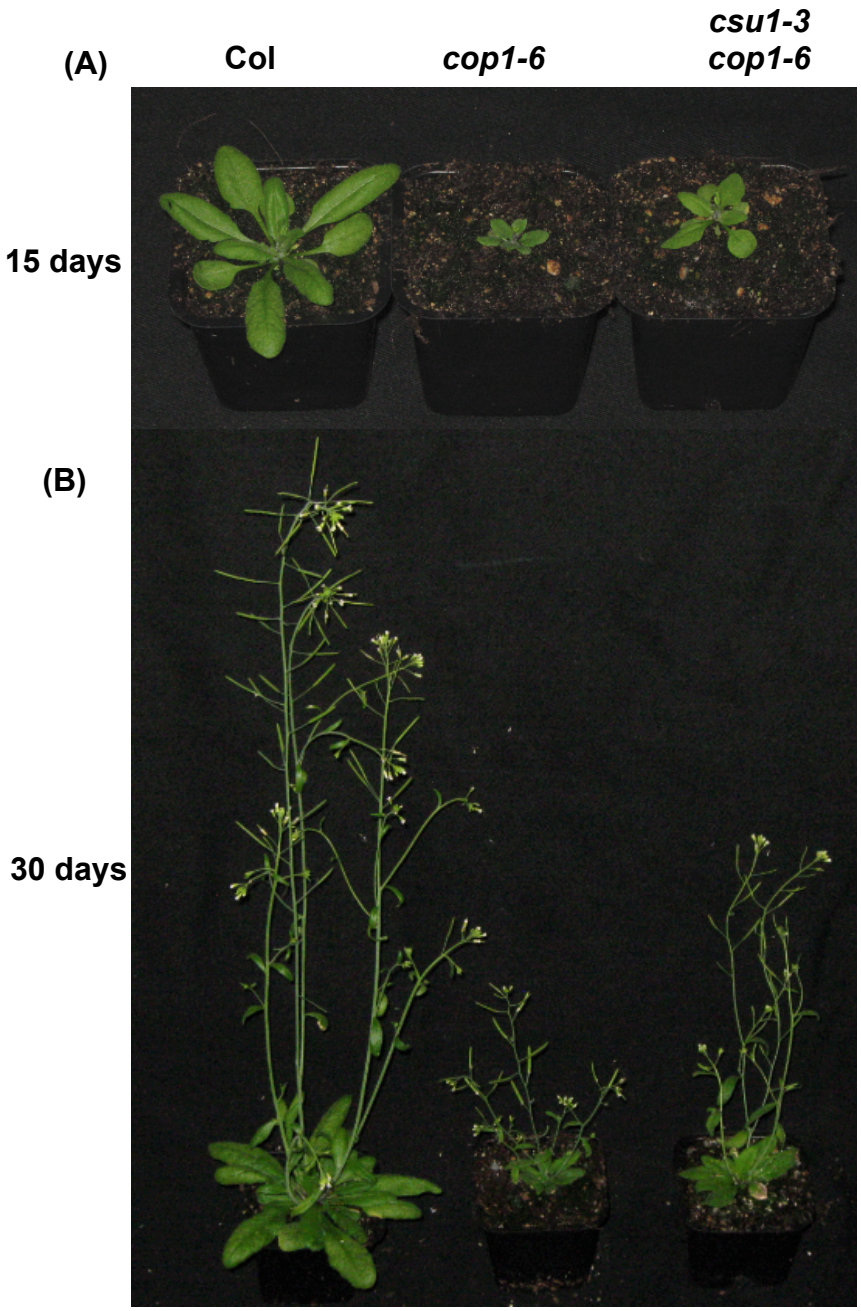


Supplemental Figure 1. *csu1* has no effect on the splicing pattern of *COP1-6* mRNA. The *cop1-6* mutation led to four cryptically spliced products at intron 4. PCR products generated from wild-type (WT), *cop1-6* and *csu1 cop1-6* mutant seedings using primers corresponding to the adjacent exons were examined on a 4% agarose gel. M, molecular size markers in base pairs.



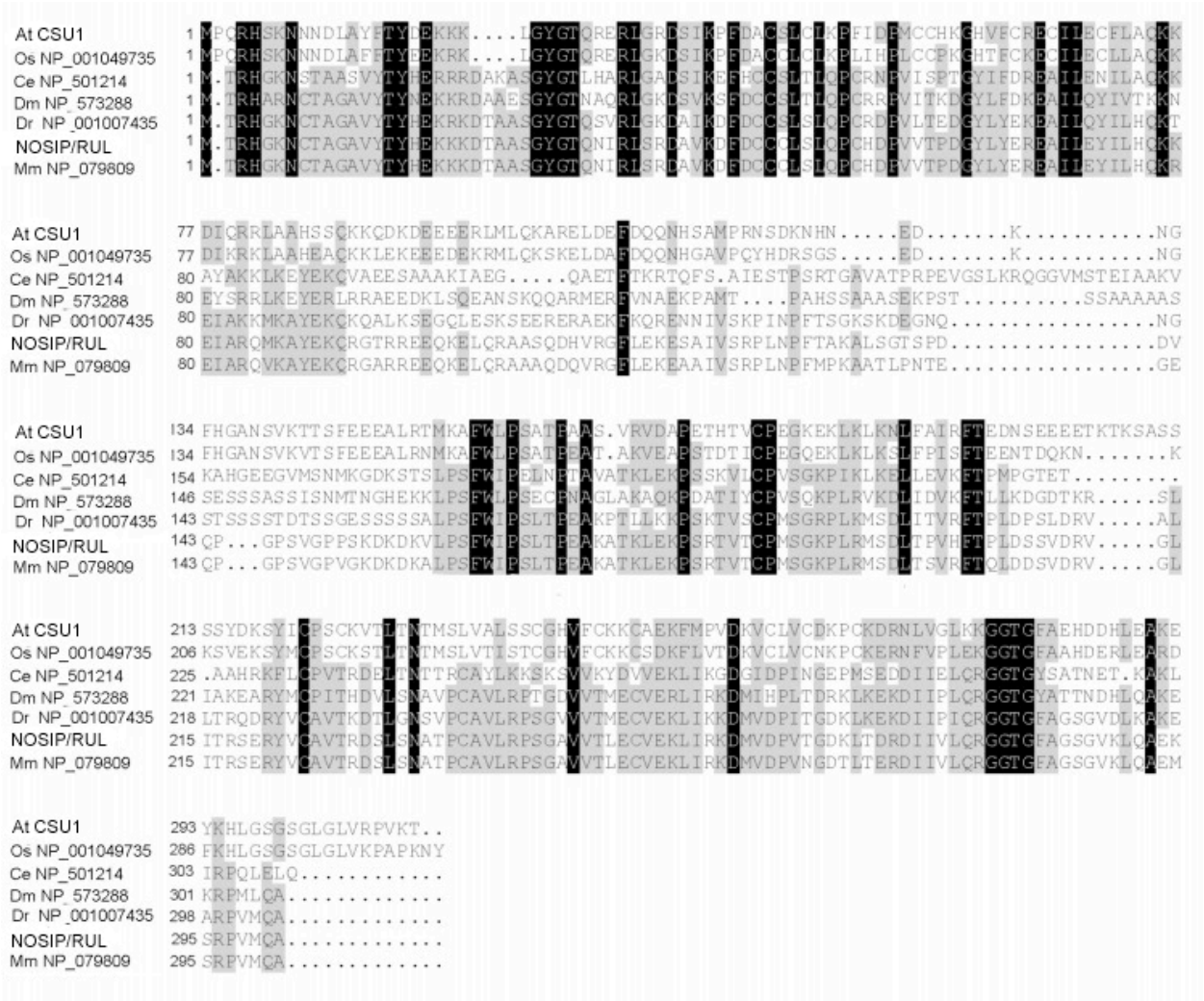
Supplemental Figure 2. *csu1* partially supresses the *cop1* in the light.

Hypocotyl phenotypes and lengths of 5-d-old wild-type, *cop1-6*, and *csu1 cop1-6* mutant seedlings grown under white (A and B), red (C and D) far-red (E and F), blue (G and H) light conditions. Error bars represent SE (n≥20). **P < 0.01 and ***P < 0.001 (Student's *t* test) for the differences between *csu1 cop1-6* and the *cop1-6* mutants.

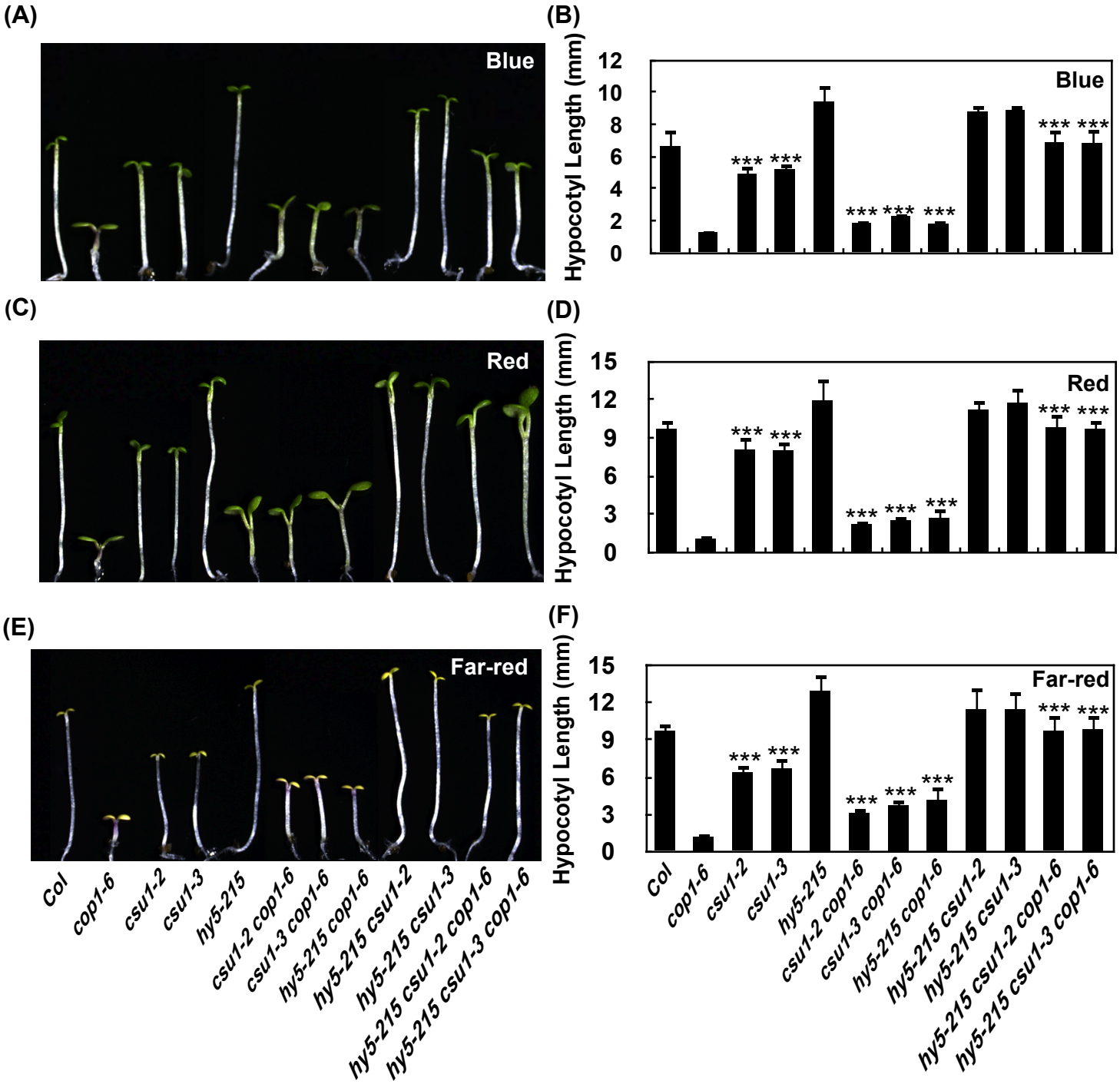


Supplemental Figure 3. The morphology of adult wild-type and mutant plants.

Plants were grown for 15 (A) or 30 (B) days in soil under long day conditions (16h Light /8h dark).

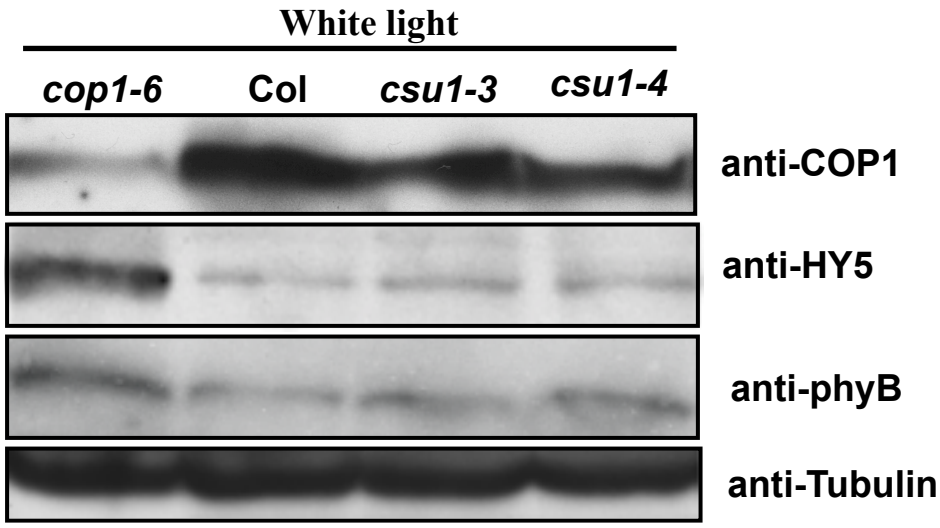


Supplemental Figure 4. Alignment of CSU1 with its homologs from other species. *Oryza sativa* (NP_001049735), *Caenorhabditis elegans* (NP_501214), *Drosophila melanogaster* (NP_573288), *Danio rerio* (NP_001007435), *Mus musculus* (NP_079809), and *Homo sapiens* (NP_057037). Black boxes are identical residues; dots indicate gaps.

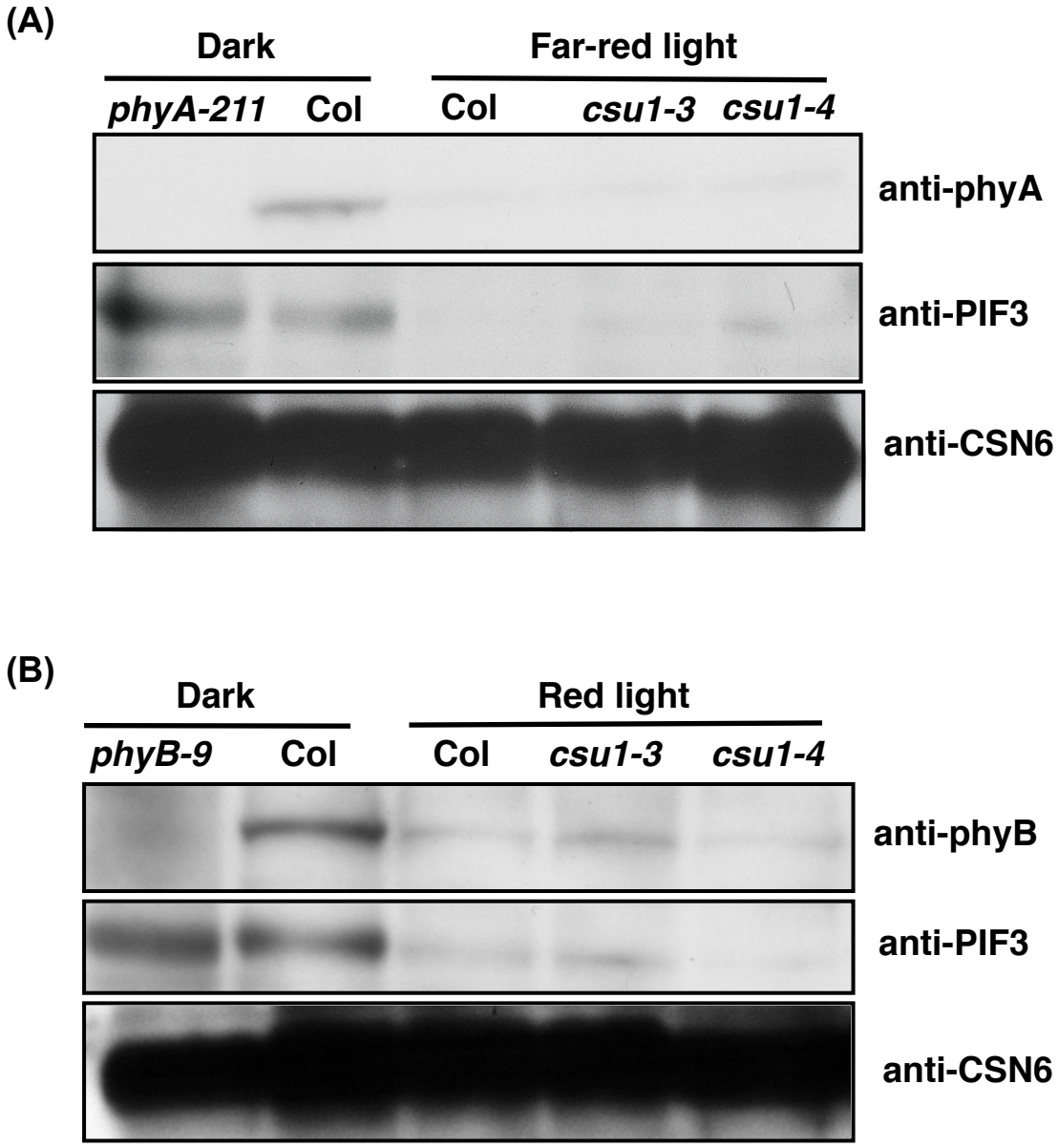


Supplemental Figure 5. *csu1* and *hy5* co-suppress *cop1* in B, R and FR light.

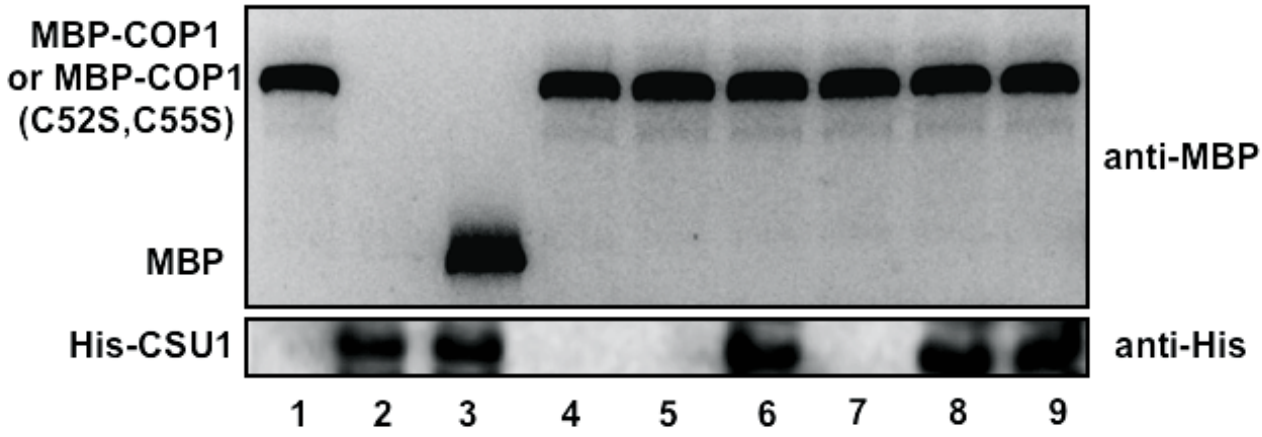
Hypocotyl length and phenotypes of 5-d-old wild-type, *cop1-6*, *csu1*, *hy5-215, csu1 cop1-6, hy5-215 csu1*, and *hy5-215 csu1 cop1-6* mutant seedlings grown under blue (5 μmol m^{-2} s^{-1}) (A and B), red (20 μmol m^{-2} s^{-1}) (C and D), and far-red (1 μmol m^{-2} s^{-1}) (E and F) light conditions. Error bars represent SE (n≥20). ***P < 0.001 (Student's *t* test) for the differences between WT and the *csu1* , *csu1 cop1-6* and *cop1-6*, or *hy5-215 csu1 cop1-6* and *csu1 cop1-6* seedings, respectively.



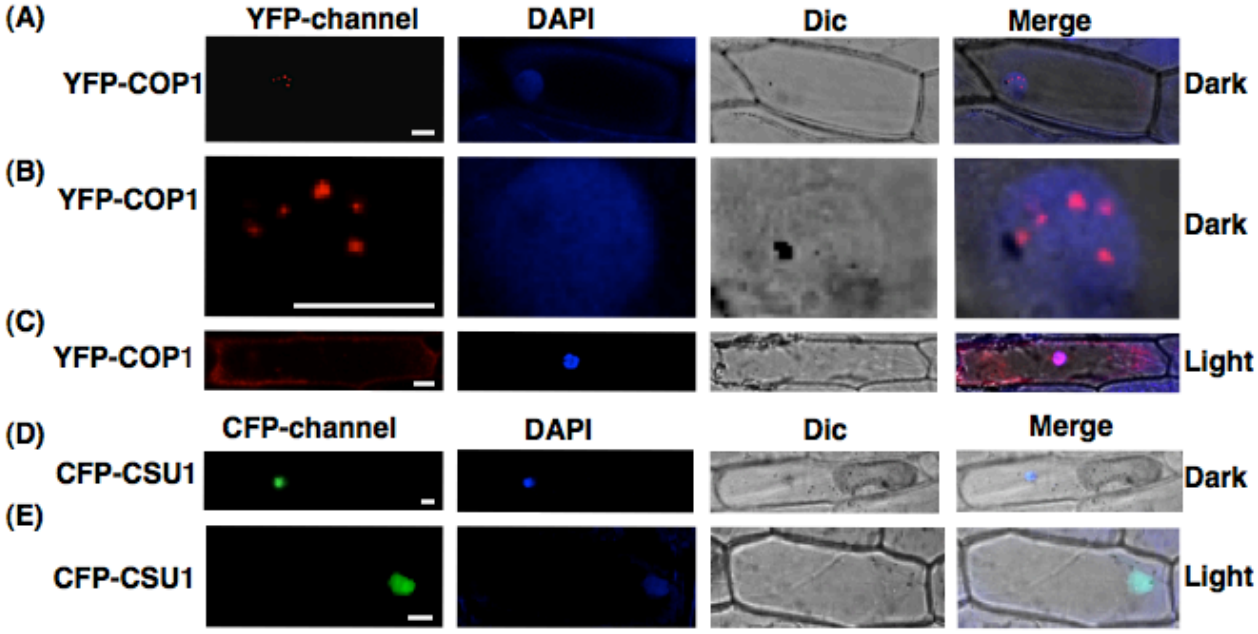
Supplemental Figure 6. COP1 protein levels in the white light-grown *csu1* mutant seedlings. COP1, HY5, and phyB protein levels in *cop1-6*, *csu1*, and Col grown under white light. Plant total protein were extracted from 5-day-old continuous white light grown seedlings. Tubulin levels were used as loading controls.



Supplemental Figure 7. phyA , phyB and PIF3 protein levels in the far-red or red light-grown *csu1* mutant seedlings. (A) PHYA, and PIF3 protein levels in *csu1*, and Col grown in the far-red. (B) phyB, and PIF3 protein levels in *csu1*, and Col grown under red light. Plant total protein were extracted from 5-day-old continuous far-red or red light grown seedlings. Dark-grown *phyA-211*, *phyB-9* and Col were used as negative or positive controls, respectively. CSN6 levels were used as loading controls.



Supplemental Figure 8. 5% input used *in vitro* ubiquitination assays. Related to Figure 8A. 25 ng of MBP or MBP-COP1 and 10 ng of 6×His-CSU1 (1% input) were loaded onto a 10% SDS-PAGE gel and immunoblotted by antibodies against MBP or His.



Supplemental Figure 9.CSU1 localizes to nucleus both in the dark and light.

Onion epidermal cells were bombarded with YFP-COP1 plasmids with a helium gun incubated in the dark for 24 hours (Dark) (A) or in the dark for 12 hours, then treated with white light for 12 hours (Light) (C). (B) are closeups of the nuclei as shown in (A). Onion epidermal cells were bombarded with CFP-CSU1 plasmids with a helium gun, then incubated in the dark for 24 hours (Dark) (D) or in the dark for 12 hours, then treated with white light for 12 hours (Light) (E). YFP channel, YFP channel image; CFP channel, CFP channel image; DAPI, 4',6-diamidino-2-phenylindole staining image; Dic, differential interference contrast in light microscope mode; Merge, merged image between DAPI and YFP or CFP. The scale bar in all panels represents 50 μm.

Supplemental Table 1: List of Primers Used in This Study.

Primer name	Primer sequences (5'→3') (Note: The underlined nucleotides indicate the restriction sites for cloning.)	
Genotyping		
CSU1LP	CCTCTTCGCTGTTGTCTTCTG	
CSU1RP	TTGTTCTCTCTGCTTGAAGCC	
SALK_LBb1.3	ATTTTGCCGATTTCGGAAC	
Quantitative Real-time RT-PCR		
CSU1-real(F)	CCATAAGGGTCATGTCTTTTGC	
CSU1-real(R)	CTTGCTTCTTTTGAGACGAATG	
PP2A(F)	TATCGGATGACGATTCTTCGTGCAG	
PP2A(R)	GCTTGGTCGACTATCGGAATGAGAG	
RT-PCR		
CSU1-rt(F)	CCTTTGATGCTTGTTCTCTCTG	
CSU1-rt(R)	CCTCCTTTCTTTAACCCAACC	
UBQ10(F)	GATCTTTGCCGGAAAACAATTGGAGGATGGT	
UBQ10(R)	CGACTTGTCATTAGAAAGAAAGAGATAACAGG	
Splicing test		
cop1-6-S(F)	GTCAACTGTCTCAATGGCTAGAAA	
cop1-6-S(R)	CTATAGCCTTCCCTCCGTACTACA	
Protein expression		**Plasmid Constructs**
CSU1-NdeI(F)	GGGAATTCCATATGATGCCGCAAAGACACTCGAA	*pET28b-CSU1*
CSU1-XhoI(R)	CCGCTCGAG TTATCATGTCTTAACCGGCCTCAC	
Colocalization assay		*pAM-PAT-35SS-CFP-CSU1*
CSU1-NdeI(F)	GGGAATTCCATATGATGCCGCAAAGACACTCGAA	
CSU1-XhoI(R)	CCGCTCGAG TTATCATGTCTTAACCGGCCTCAC	
Complementation test		
CSU1-KpnI(F)	CGGGGTACCTCAGATGTGTATAGCTTTGGAGTG	*pFP100-CSU1*
CSU1-PstI(R)	AAAACTGCAGTTATCATGTCTTAACCGGCCTCAC	