Supplementary Materials

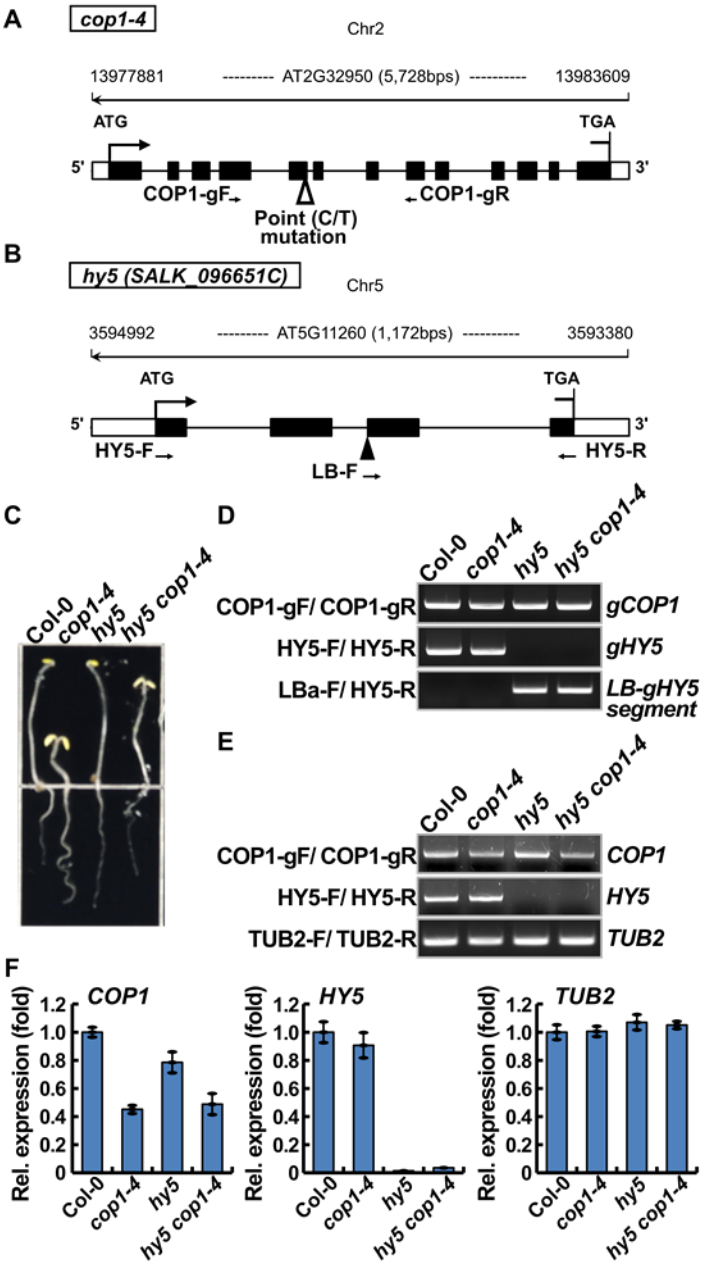

Figure S1. Identification of *cop1-4*, *hy5*, and *hy5 cop1-4* mutants. (**a, b**) Schematic representations of the predicted gene structures of *HY5* (**a**) and *COP1* (**b**). Black elbow arrows represent the start codon (ATG). Filled boxes and horizontal black lines indicate exons and introns, respectively. Blank boxes at either end of the genes represent 5′ and 3′ untranslated regions (UTRs). The position of T-DNA insertion in *hy5* and that of the point mutation in *cop1-4* are indicated by black and white arrowheads, respectively. Black arrows represent the binding sites of primers used for genotyping. (**c–f**) Confirmation of *cop1-4*, *hy5* and *hy5 cop1-4* mutant lines by phenotypes of 5-day-dark-grown plants (**c**), genomic DNA-based PCR (**d**), semi-quantitative reverse transcription PCR (sqRT-PCR), (**d**) and quantitative real-time PCR (qRT-PCR) (**f**). (**f**) Expression analysis of *COP1*, *HY5*, and *TUB2* (control) genes in 2-week-old WT (Col-0), *cop1-4*, *hy5*, and *hy5 cop1-4* plants by qRT-PCR. Data represent mean ± standard error of mean (SEM).

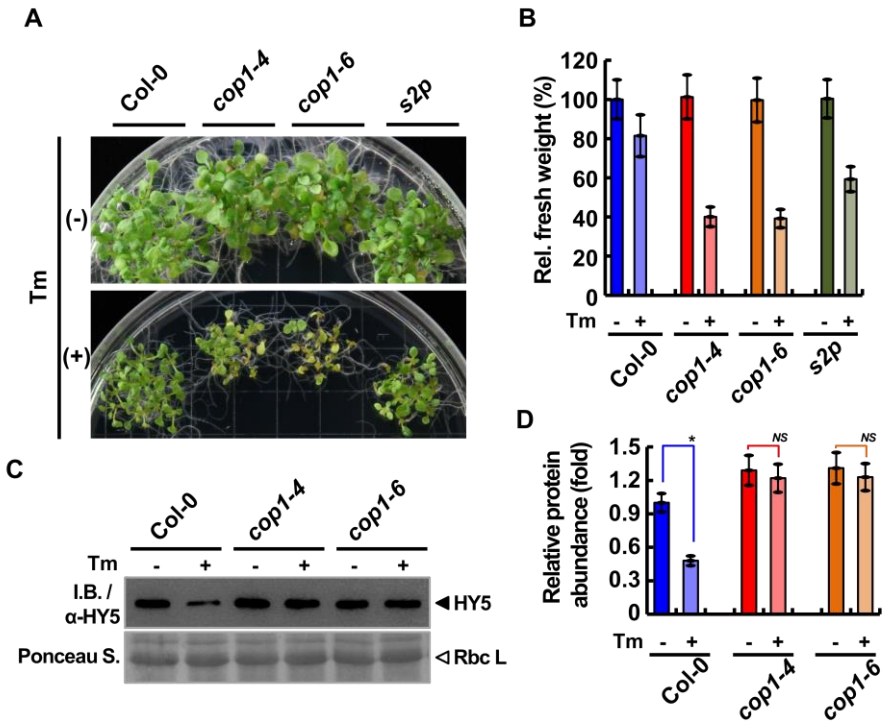

Figure S2. Confirmation of the role of COP1 in ER stress response using the *cop1-6* mutant. (**a**) Phenotypes of 2-week-old WT (Col-0), *cop1-4*, *cop1-6*, and *s2p* seedlings grown on Murashige and Skoog (MS) medium supplemented with (+) or without (-) 10 ng/mL tunicamycin (Tm). (**b**) Relative fresh weight of plants treated with Tm, as indicated in (**a**). Data represent mean ± SD (n = 3). (**c**) Comparison of Tm-induced changes in the amount of HY5 protein in WT (Col-0), *cop1-4*, and *cop1-6* seedlings. Total proteins extracted from 10-day-old seedlings before (-) or after (+) 6 h treatment with 5 μg/mL Tm were subjected to immunoblotting analysis with anti-HY5 antibody. (**d**) Quantification of the relative abundance of HY5 protein in (c) compared with that in the control condition (Col-0, -).

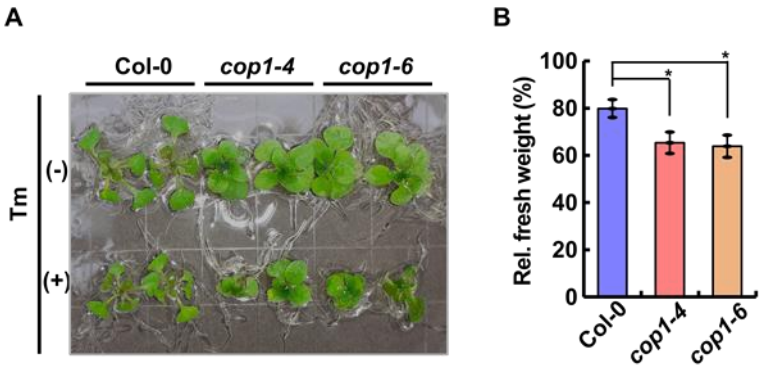

Figure S3. Comparison of growth of WT (Col-0) and *cop1* mutant plants after treatment of 5 μg/mL Tm for 6 h. 10-day-old WT, *cop1-4*, and *cop1-6* plantlets were treated 5 μg/mL Tm for 6 h, and allowed to recover on MS plates. (**a**) Plants were analyzed for phenotypic differences 5 days post treatment. (**b**) Relative fresh weight of plants treated with Tm (+) compared to the Tm-untreated plants (-), as indicated in (**a**). Data represent mean ± SD (n = 3).

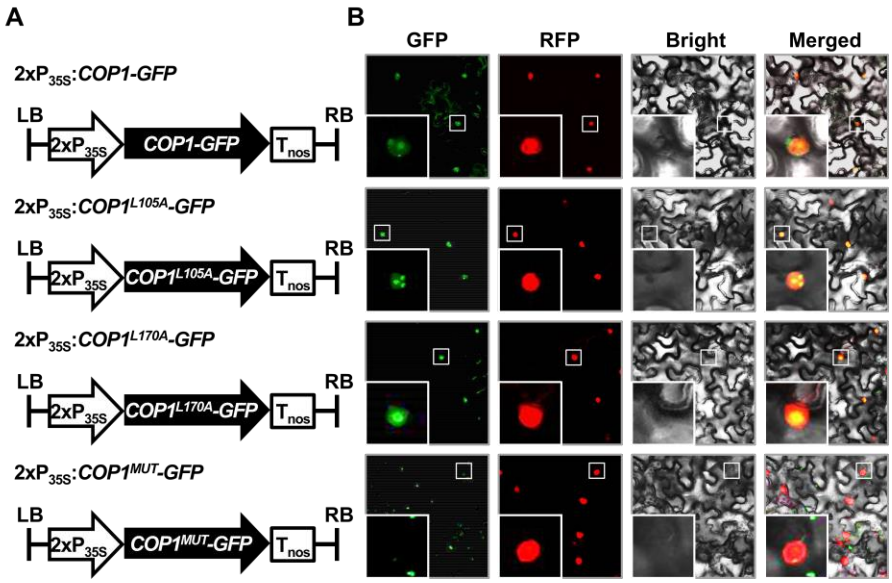

Figure S4. Subcellular localization analysis of WT and mutant COP1 proteins. (**a**) Schematic representations of constructs containing diverse *COP1* alleles. P_{35S} and T_{NOS} represent the cauliflower mosaic virus (CaMV) *35S* promoter, and *nopaline synthase* (*NOS*) terminator, respectively. (**b**) Subcellular localization analysis of green fluorescent protein (GFP)-fused diverse COP1 proteins in *Agrobacterium*-infiltrated tobacco leaves. Tobacco leaves were infiltrated with *Agrobacteria* harboring diverse *COP1* allele constructs depicted in (**a**). At 2 days post-infiltration, the localization of GFP-fused diverse COP1 proteins was observed under a confocal microscope. Green color indicates GFP-fused diverse COP1 proteins, whereas red color indicates NLS-RFP (nucleus marker). Inset images represent f-fold magnification of the small squares outlined with white lines in the GFP panel.

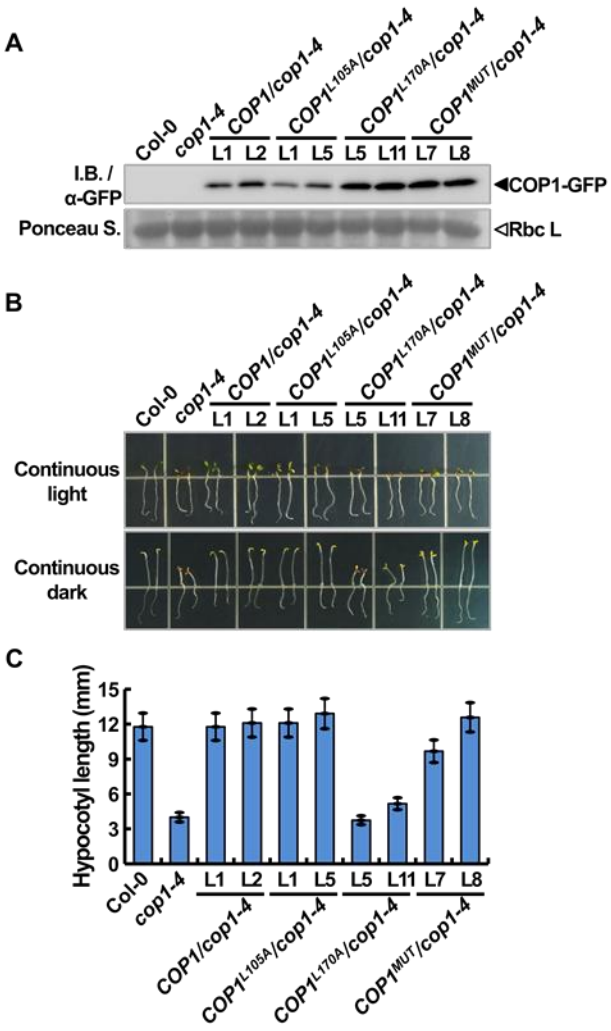

Figure S5. Selection of *cop1-4* complementation lines expressing *COP1*, *COP1*^{L105A}, *COP1*^{L170A}, and *COP1*^{MUT}. (**a**) Detection of GFP-fused COP1 proteins in selected *cop1-4* complementation lines transformed with *COP1*, *COP1*^{L105A}, *COP1*^{L170A}, and *COP1*^{MUT} constructs. Total proteins extracted from 2-week-old seedlings of the WT (Col-0), *cop1-4* mutant, and selected *cop1-4* complementation lines were subjected to immunoblotting analysis using anti-GFP antibody. (**b**) Photographs of seedlings of different genotypes grown for 5 days under either continuous light or continuous dark conditions. (**c**) Hypocotyl lengths of seedlings grown under continuous dark. Data represent mean ± SD (n = 3).

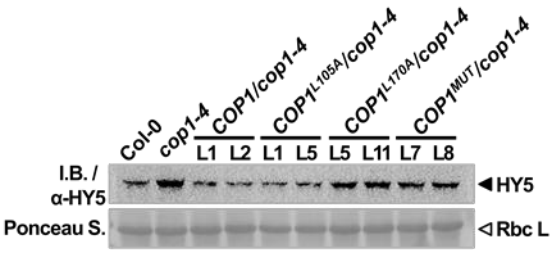

Figure S6. Comparison the amount of HY5 protein in Tm-treated seedlings of WT (Col-0), *cop1-4*, and various *cop1-4* complementation lines. Total proteins extracted from 10-day-old seedlings after 6 h treatment with 5 μg/mL Tm were subjected to immunoblotting analysis with anti-HY5 antibody.

Table S1. List of primers used in this study.

Gene	AGI code	Primer name	Sequence (5'-3')	Purpose
COP1	AT2G32950	COP1 qF	GAGGCAGGAAGCAAGTGTGA	qRT-PCR
		COP1 qR	CGACCGCAATGTAGTTGCTT	
HY5	AT5G11260	HY5 qF	CACTACAGCCGGTATGCAAG	
		HY5 qR	CGATCCTAAACCAAACCCTTC	
TUB2	AT5G62690	TUB2 qF	AAACTCACTACCCCCAGCTTTG	
		TUB2 qR	CACCAGACATAGTAGCAGAAATCAAGT	
ACT2	AT3G18780	ACT2 qF	TGATGCACTTGTGTGTGACAA	
		ACT2 qR	GGGACTAAAACGCAAAACGA	
UBQ1	At3g52590	UBQ1 qF	TTCCTTGATGATGCTTGCTC	
		UBQ1 qR	TTGACAGCTCTTGGGTGAAG	
UBQ10	AT4G05320	UBQ10 qF	AGATCCAGGACAAGGAGGTATTC	
		UBQ10 qR	CGCAGGACCAAGTGAAGAGTAG	
BIP3	AT1G09080	BIP3 CHIP-1F	GATTTAATGTCACGTGTCTGCTTGT	ChIP
		BIP3 CHIP-1R	TTGGCGCGCTCCTTACTT	
		BIP3 CHIP-2F	CAAAATAACCCATTAAGCTTACGTG	
		BIP3 CHIP-2R	CTCGGTAGAGTGTCCTCTCCAAT	
TA3 retrotransposon	AT1G37110	TA3 FW	CTGCGTGGAAGTCTGTCAAA	
		TA3 RW	CTATGCCACAGGGCAGTTTT	
18s rRNA	AT3G41768	18s rRNA qF	GGGCATTCGTATTTCATAGT	
		18s rRNA qR	CGTTCTTGATTAATGAAAAC	
COP1	AT2G32950	COP1 gF	CTCTCATGGGCTACCAAAGA	Geno-typing
		COP1 gR	TACATCCCACACTGTTACTA	
HY5	AT5G11260	HY5-F	ATGCAGGAACAAGCGACTAG	
		HY5-R	TCAAAGGCTTGCATCAGCAT	
TUB2	AT5G62690	TUB-F	CCAACAACGTGAAATCGACA	
		TUB-R	TCTTGGTATTGCTGGTACTC	
Lba-T-DNA		LB-F	TGGTTCACGTAGTGGGCCATCG	
COP1	AT2G32950	COP1 F	ATGGAAGAGATTTCGACGGAT	Cloning
		COP1 R	TCACGCAGCGAGTACCAGAAC	
		COP1 attB1 F*	*AAAAAGCAGGCCAT*ATGGAAGAGATTTCGACG	
		COP1 attB2 R*	*AGAAAGCTGGGT*TCACGCAGCGAGTACCAG	
attB		attB1*	*GGGGACAAGTTTGTACAAAAAAGCAGGCCAT*	
		attB2*	*GGGGACCACTTTGTACAAGAAAGCTGGGT*	
P_{BIP3}:*LUC* (Reporter construct)	AT1G09080	LUC(P_{BIP3})-F	CGAAAAATGGAAGACGCCAAAAACATAAAG	
		LUC(T_{35S})-R	CTCGAGATCTGGATTTTAGTACTGGATTTT	
		P_{BIP3}-F	AGCTGGAGCTCGCATTCACTACAATTACAT	
		P_{BIP3}-R	CGTCTTCCATTTTTCGTTGTTGAGAACTCT	
		P_{BIP3}-FE	CTAAAGGGAACAAAAGCTGGAGCTCGCATT	
		LUC(T_{35S})-RE	CCGGGCCCCCCCTCGAGATCTGGATTTTAG	
COP1	AT2G32950	COP1(L105A) F	GCGGCCGATAAGGCAGCGAAGAAAACTTCAGCT	Site-directed mutation
		COP1(L105A) R	TTCGCTGCCTTATCGGCCGCGAAATTAGGGTAA	
		COP1(L170A) F	GCTGCGGACTTTGCGCATTGTGCAAGGAAGCAA	
		COP1(L170A) R	GCACAATGCGCAAAGTCCGCAGCTATCTGCATG	
		COP1(MUT1) F	TCTCAATGGCTAGTAAGACACGGATTCATGCTC	
		COP1(MUT1) R	GAGCATGAATCCGTGTCTTACTAGCCATTGAGA	
		COP1(MUT2) F	ATGTTACCTCCAAACGCGGAGTCAGTTGGCAGA	
		COP1(MUT2) R	TCTGCCAACTGACTCCGCGTTTGGAGGTAACAT	

• attB1 and attB2 sites (*) are italicized.