Fig. S1.

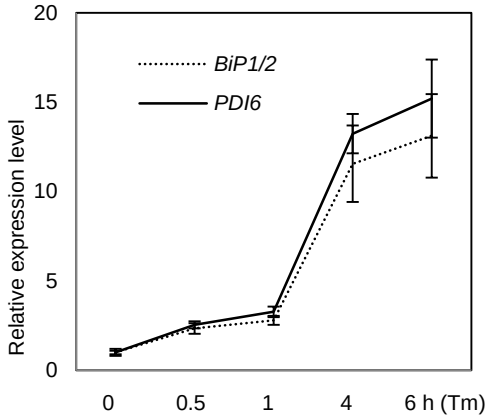

Fig. S1. Tunicamycin induces activation of UPR target genes.
RT-qPCR analyses of *BiP1/2* and *PDI6* transcripts in ten-day-old Col-0 Arabidopsis seedlings after treatment with 5 μg/ml Tm for 0.5, 1, 4, or 6 h. Error bars represent standard error of the mean (SEM) from three independent biological replicates.

Fig. S2.

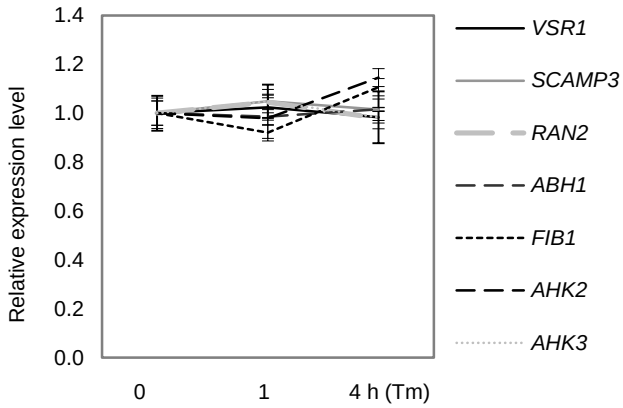

Fig. S2. The transcripts of genes encoding ER-localized and nuclear proteins remain unchanged during Tm treatment.
RT-qPCR analyses of *VSR1*, *SCAMP3*, *RAN2*, *ABH1*, *FIB1*, *AHK2*, and *AHK3* transcripts in ten-day-old Col-0 Arabidopsis seedlings after treatment with 5 μg/ml Tm for 0, 1, or 4 h. Error bars represent standard error of the mean (SEM) from three independent biological replicates. No statistical differences were observed between the expression levels of individual genes in the time course.

Fig. S3.

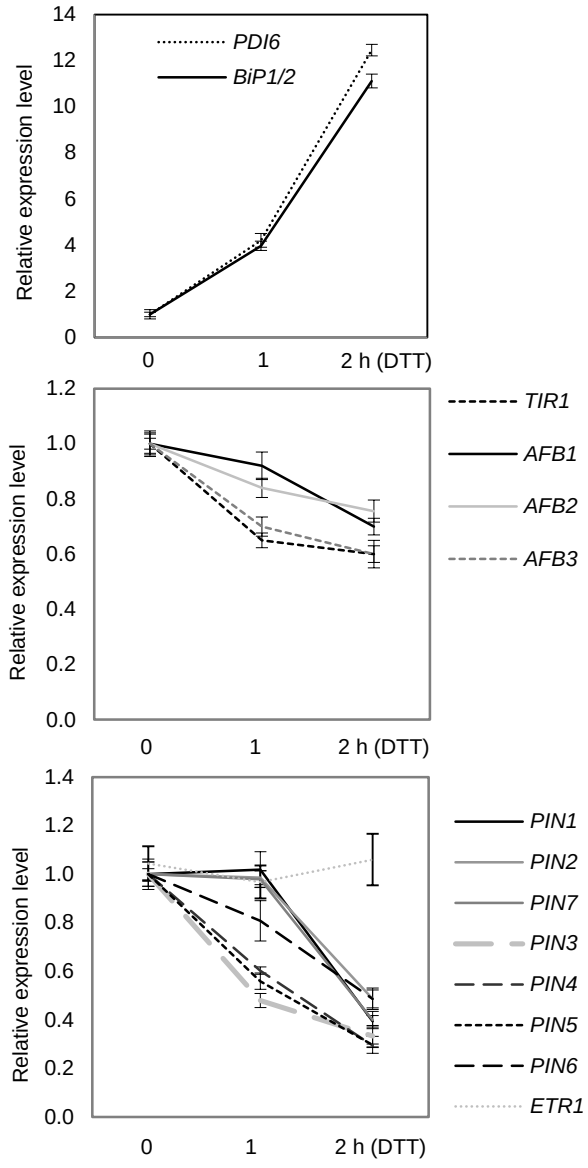

Fig. S3. DTT transcriptionally activates UPR target genes and down-regulates auxin regulators.
RT-qPCR analyses of *BiP1/2*, *PDI6*, *TIR1*, *AFB1*, *AFB2*, *AFB3,* and *PIN* family transcripts in ten-day-old Col-0 Arabidopsis seedlings after treatment with 2mM DTT for 0, 1, or 2 h. Error bars represent standard error of the mean (SEM) from three independent biological replicates.

Fig. S4.

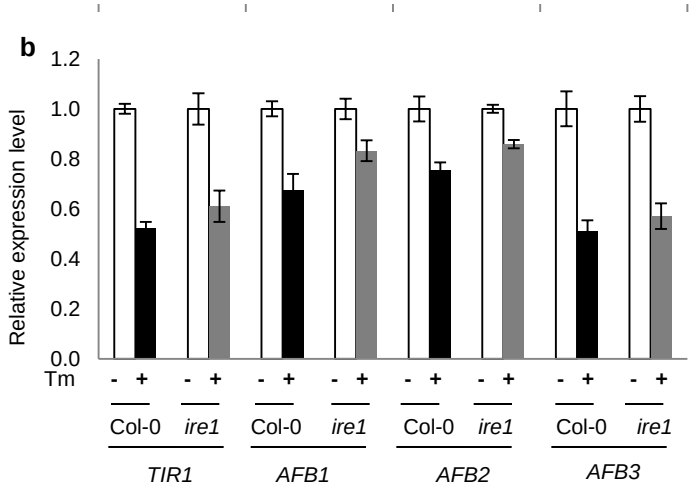

Fig. S4 IRE1 plays fine-tuning roles in ER stress-induced down-regulation of TIR1/AFBs.

RT-qPCR analyses of *TIR1*, *AFB1*, *AFB2*, and *AFB3* expression in ten-day-old wild type Col-0 and *atire1a atire1b* (*ire1*) Arabidopsis seedlings after treatment with 5 μg/ml Tm for 4 h. Error bars represent SEM from three independent biological replicates.

Fig. S5.

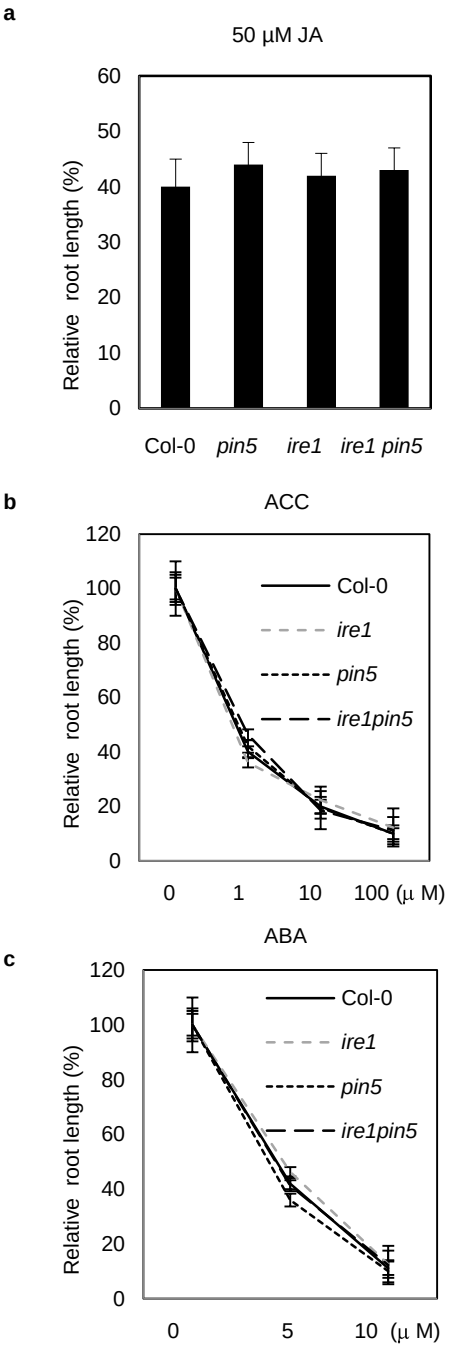

Fig. S5 *ire1* and *ire1 pin5* display comparable sensitivity to JA, ACC, and ABA.

(a-c) Relative primary root length of ten-day-old Col-0, *pin5*, *ire1*, and *ire1 pin5* eedlings grown in the presence of 50 μM JA (a) or 1, 10, 100 μM ACC (b), or 5, 10 μM ABA (c) compared to those grown in the absence of the chemicals. Error bars represent standard error of the mean (SEM), n > 30.

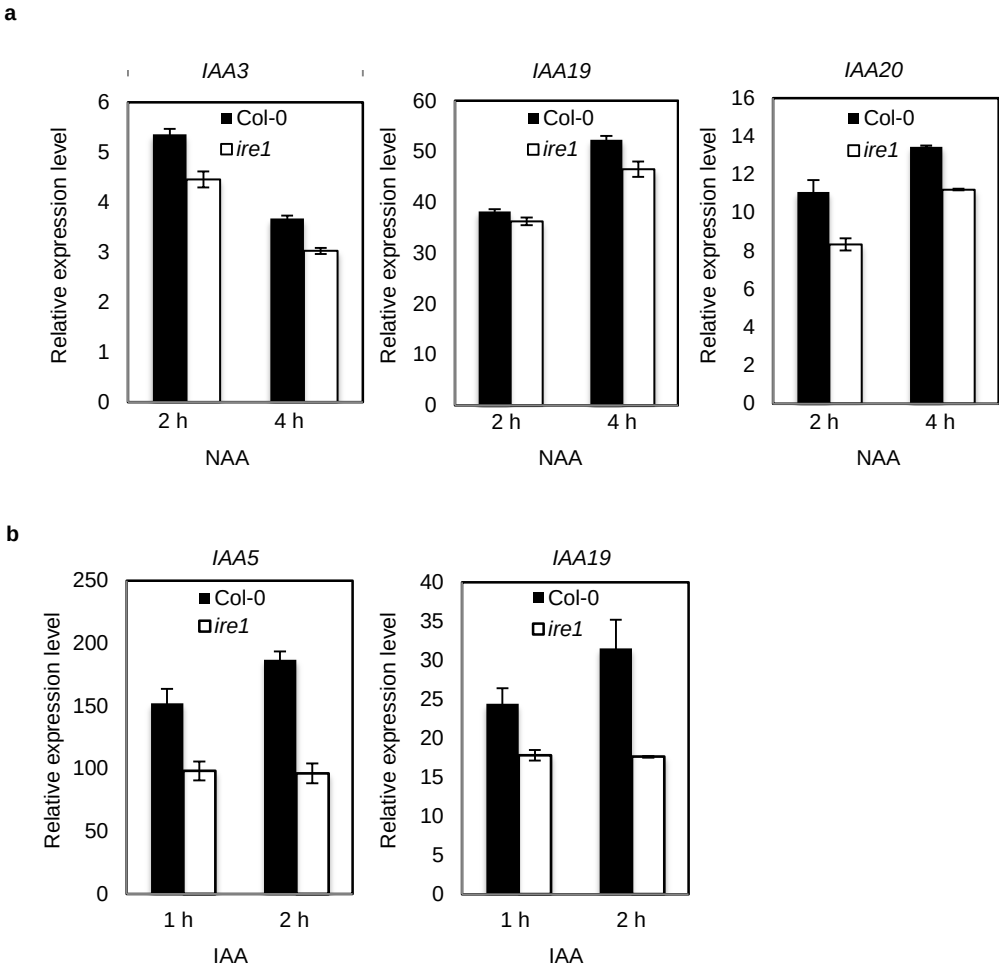

Fig. S6. *ire1* displays reduced activation of auxin-responsive genes upon NAA and IAA treatment.

(a) RT-qPCR analysis of *IAA3*, *IAA19,* and *IAA20* expression in ten-day-old Col-0 and *ire1* seedlings after a 2- or 4-h treatment with 10 μM NAA. *P*-values are relative to Col-0: *IAA3* ($P < 0.00098$), *IAA19* ($P < 0.00479$), and *IAA20* ($P < 0.00036$).

(b) RT-qPCR analyses of *IAA5* and *IAA19* in ten-day-old Col-0 and *ire1* seedlings after a 1- or 2-h treatment with 10 μM IAA. *P*-values are relative to Col-0: *IAA5* ($P < 0.00086$) and *IAA19* ($P < 0.00112$).

Fig. S7.

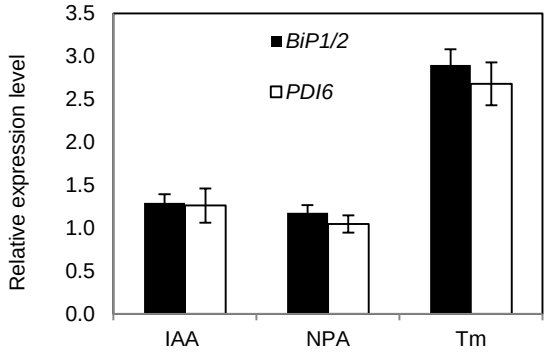

Figure. S7. The UPR target genes were not altered under IAA or NPA treatment. (a) RT-qPCR analyses of *BiP1/2* and *PDI6* in ten-day-old Col-0 relative to DMSO or EtOH mock control after a 1-h treatment with 10 μM IAA, 50 μM NPA, or 5 μg/ml Tm. Error bars represent standard error of the mean (SEM) from three independent biological replicates.

Fig. S8.

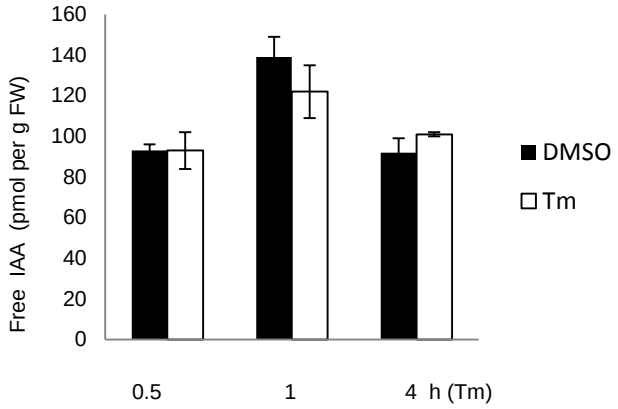

Fig. S8. The free auxin level is unchanged under ER stress.
Free IAA measurement in the roots of ten-day-old Col-0 after treatment with 5 μg/ml Tm or DMSO for 0.5, 1, or 4 h. Error bars represent SEM from three independent biological replicates.

Fig. S9.

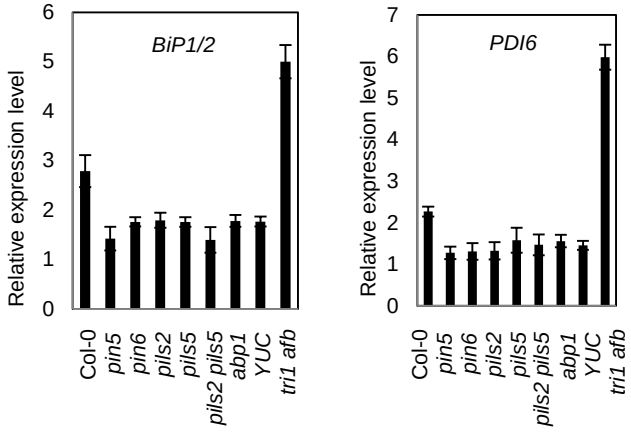

Figure. S9. Mutants impaired in auxin intracellular transport display a defective UPR phenotype.

RT-qPCR analyses of *BiP1/2* and *PDI6* in ten-day-old Col-0, *pin5-5* (*pin5*), *pin6-4* (*pin6*), *pils2-2* (*pils2*), *pils5-2* (*pils5*), *pils2-2 pils5-2* (*pils2 pils5*), *abp1-5* (*abp1)*, *YUC*, and *tir1 afb1 afb2 afb3* (*tir1 afb*) relative to DMSO mock control after a 1-h treatment with 5 μg/ml Tm. Error bars represent standard error of the mean (SEM) from three independent biological replicates. *P*-values are relative to Col-0: *pin5* (*P* = 0.00113), *pin6* (*P* = 0.00185), *pils2* (*P* = 0.00175), *pils5* (*P* = 0.00218), *pils2 pils5* (*P* = 0.00095), *abp1* (*P* = 0.00215), *YUC* (*P* = 0.00204), *tir1 afb* (*P* = 0.00012).

Fig. S10.

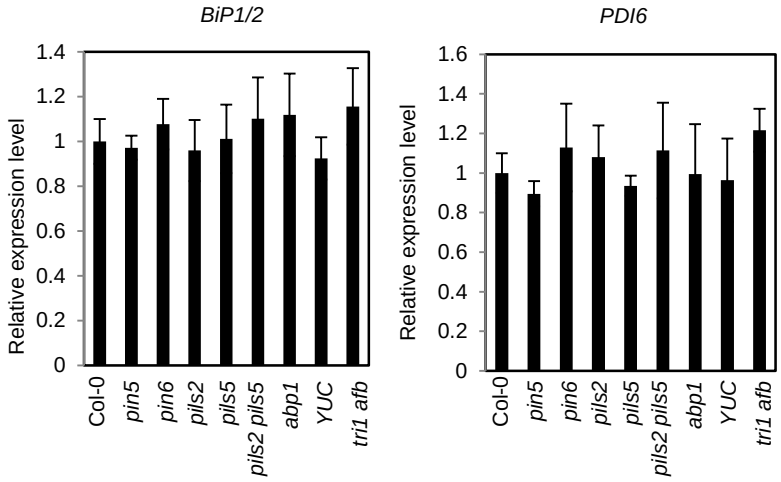

Fig. S10. Mutants impaired in intracellular auxin transport display comparable expression levels of UPR genes.

RT-qPCR analyses of *BiP1/2* and *PDI6* in ten-day-old Col-0, *pin5-5* (*pin5*), *pin6-4* (*pin6*), *pils2-2* (*pils2*), *pils5-2* (*pils5*), *pils2-2 pils5-2* (*pils2 pils5*), *abp1-5* (*abp1)*, *YUC*, and *tir1 afb1 afb2 afb3* (*tir1 afb*) seedlings without Tm treatment. Error bars represent standard error of the mean (SEM) from three independent biological replicates.

Fig. S11.

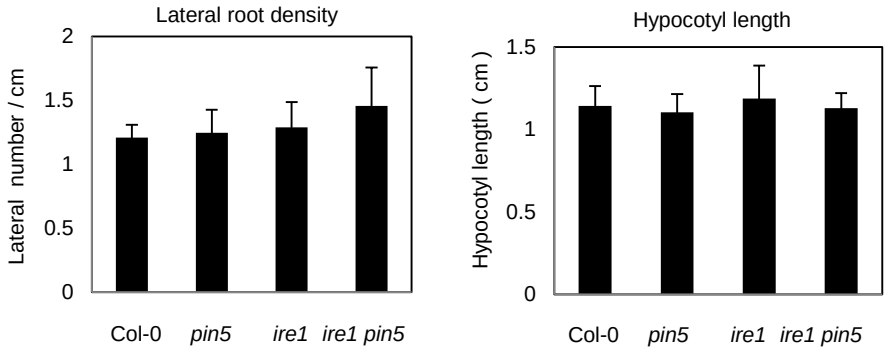

Fig. S11 *ire1* and *ire1 pin5* display normal root density and hypocotyl elongation.
(a)Lateral root density of ten-day-old Col-0, *pin5*, *ire1*, and *ire1 pin5*,seedlings. Lateral root density is calculated as the number of lateral roots per cm of primary root Error bars represent standard error of the mean (SEM), n > 30.
(b)Quantification of the hypocotyl length of five-day-old Col-0, *pin5*, *ire1*, and *ire1 pin5* seedlings grown under dark condition. Error bars represent standard error of the mean (SEM), n > 30.