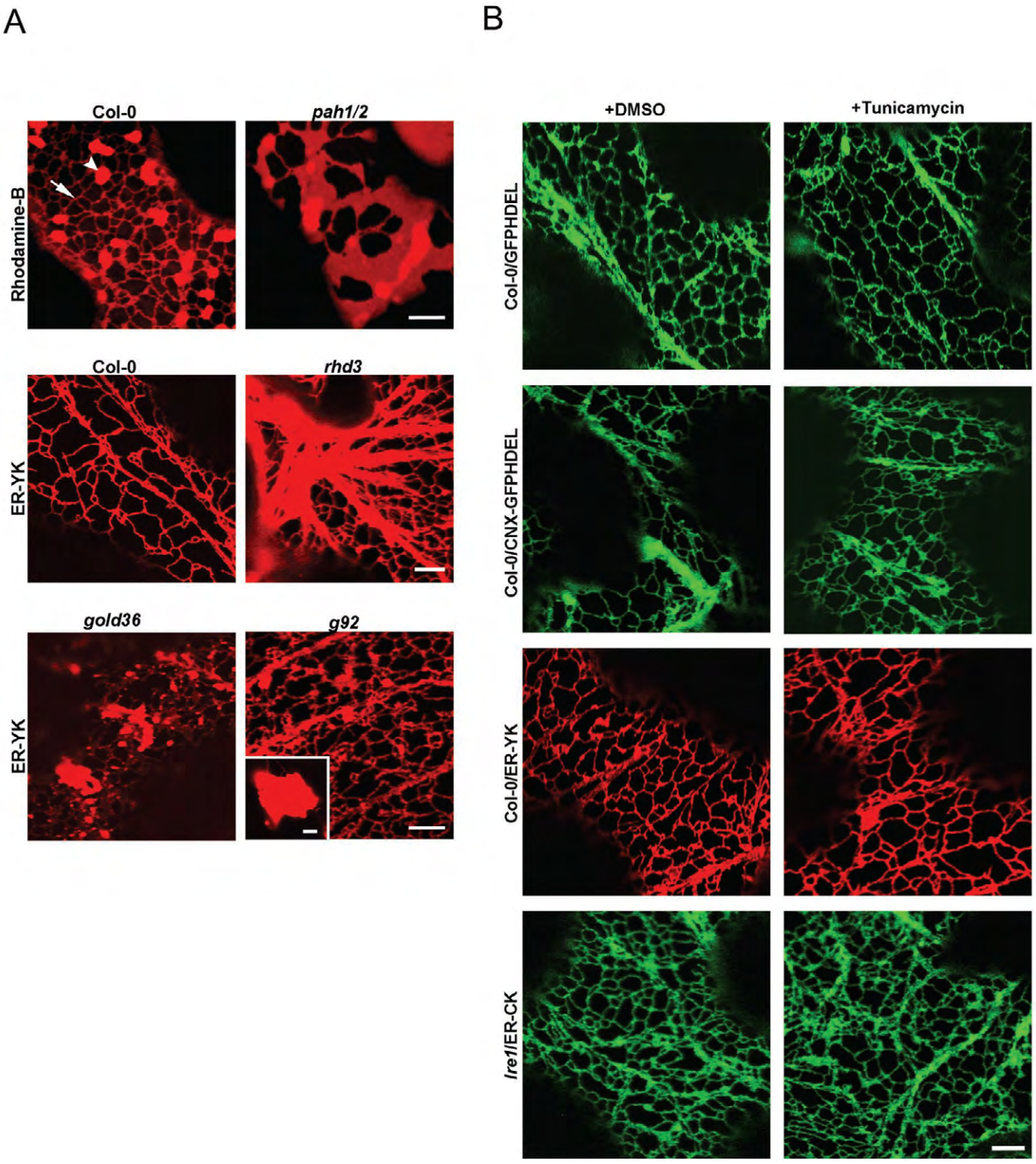

Fig. S1. ER phenotypes of Arabidopsis mutants with either defective ER structure or UPR signaling.

(**A**) Representative images of 12-day-old cotyledon epidermal cells with the following genotypes: wild type, *pah1/2*, *gold36*, *rhd3* and *g92*, either stained with Rhodamine-B (top panel) or expressing the ER lumen marker (ER-YK). Note that Rhodamine-B stains the ER network (arrows) and Golgi stacks (arrowheads). Inset indicates the inner region of the cell. (**B**) Col-0 or *ire1* expressing the ER marker GFP-HDEL (lumenal marker) or calnexin-GFP (CNX-GFP; membrane marker) in control conditions (DMSO) and Tm (0.5 µg/ml) treatment for 1 day. No obvious differences were noted in the morphology of the ER in response to the treatment and in the two backgrounds. Scale bars= 5 mm.

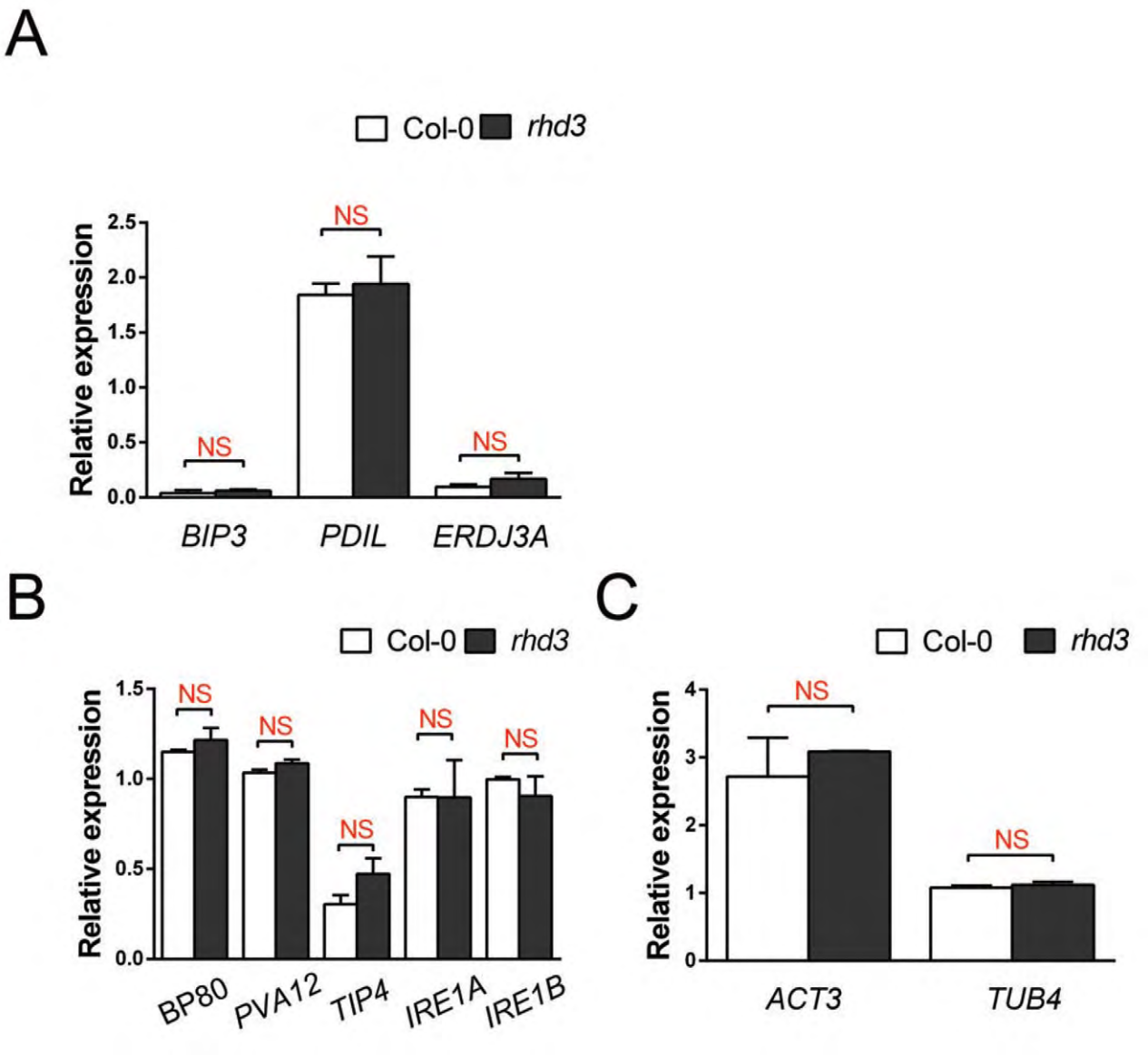

Fig. S2. Loss of RHD3 does not affect the basal levels of the UPR and the genes encoding secretory and cytosolic proteins in conditions of ER stress

(**A**) qRT-PCR of UPR indicators. cDNA was synthesized using 14-day-old seedlings exposed to medium containing DMSO, which serves as ER stress treatment control, for 1 day. The experiment shows that the basal levels of UPR indicators in wild type and *rhd3* are low and similar. (**B, C**) Transcriptional levels of secretory proteins such as the prevacuolar sorting receptor, BP80, the ER associated VAMP-like protein, PVA12, and the tonoplast intrinsic protein, TIP4, and AtIRE1 isoforms IRE1A, IRE1B, as well as cytosolic proteins actin (ACT3) and tubulin (TUB4). Error bars represent SE among three replicates. (NS, not significant).

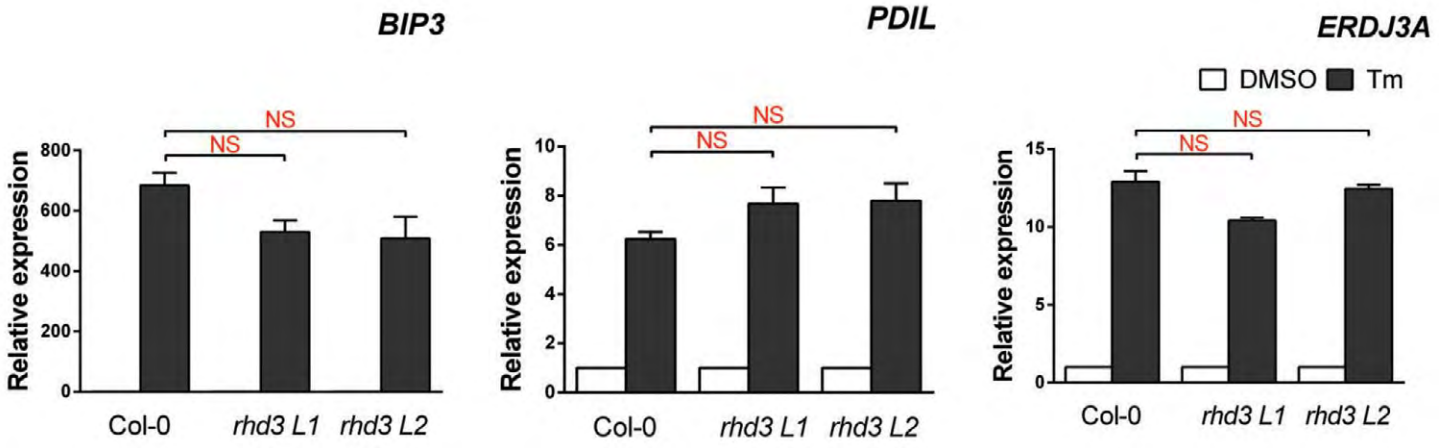

Fig. S3. The compromised UPR induction phenotype is specific to the loss of RHD3

qRT-PCR of UPR indicators in wild type and *RHD3*-like mutants. cDNA was synthesized using 14-day-old seedlings treated with Tm (0.5 µg/ml) for 1 day. Values are presented relative to indicated DMSO control, which was set to 1. Error bars represent SE of three replicates. No significant differences were found from the corresponding controls (mutant versus wild type under treatment). (NS, not significant).

Supplemental Table 1. Loci numbers and primers .

Primer name	AGI number	Sequence	Purpose
UBQ10 For	At4g05320	5'-GGCCTTGTATAATCCCTGATGAATAAG-3'	For amplifying endogenous transcript of UBQ10 by qRT-PCR
UBQ10 Rev	At4g05320	5'-AAAGAGATAACAGGAACGGAAACATAGT-3'	For amplifying endogenous transcript of UBQ10 by qRT-PCR
BIP3 For	At1g09080	5'-CGAAACGTCTGATTGGAAGAA-3'	For amplifying endogenous transcript of BIP3 by qRT-PCR
BIP3 Rev	At1g09080	5'-GGCTTCCCATCTTTGTTCAC-3'	For amplifying endogenous transcript of BIP3 by qRT-PCR
PDIL For	At1g21750	5'-AAGTGGTCCTGCTTCTGTTGAA-3'	For amplifying endogenous transcript of PDIL by qRT-PCR
PDIL Rev	At1g21750	5'- TTGAACAGCCTCACTGCAGGT-3'	For amplifying endogenous transcript of PDIL by qRT-PCR
ERdj3A for	At3g08970	5'-GTGAAAGCGAAGAGCGTTGAT-3'	For amplifying endogenous transcript of ERDJ3A by qRT-PCR
ERdj3A Rev	At3g08970	5'-TCACGCTGCTTTGCATCCT-3'	For amplifying endogenous transcript of ERDJ3A by qRT-PCR
IRE1a_FWD	At2g17520	5'-GCTTCAGACCTCATATCCCG-3'	For amplifying endogenous transcript of IRE1A by qRT-PCR
IRE1a_REV	At2g17520	5'- AGCATCACGAAGGAAAGACAG-3'	For amplifying endogenous transcript of IRE1A by qRT-PCR
IRE1b_FWD	At5g24360	5'-GGTGGGATGAGAAACTGGATAG-3'	For amplifying endogenous transcript of IRE1B by qRT-PCR
IRE1b_REV	At5g24360	5'-AGTTTGTTCCGTATGACCCG-3'	For amplifying endogenous transcript of IRE1B by qRT-PCR
bZIP60s_FWD	At1g42990	5'-GGAGACGATGATGCTGTGGCT-3'	For amplifying endogenous transcript of sBZIP60 by qRT-PCR
bZIP60s_REV	At1g42990	5'- CAGGGAACCCAACAGCAGACT -3'	For amplifying endogenous transcript of sBZIP60 by qRT-PCR
BP80 For1	At3g52850	5'- GCTCTTTCCGGTGGTGATATG -3'	For amplifying endogenous transcript of BP80 by qRT-PCR
BP80 Rev1	At3g52850	5'- CAGGATGTGGAACCGACTCA -3'	For amplifying endogenous transcript of BP80 by qRT-PCR
PVA12 For1	At2g45140	5'-CAAGGTTAAGACGACGAATCCAA-3'	For amplifying endogenous transcript of PVA12 by qRT-PCR
PVA12 Rev1	At2g45140	5'-TCTGGGATGAACAACACCAGTATT-3'	For amplifying endogenous transcript of PVA12 by qRT-PCR
At Tip4;1 For2	At2g25810	5'-GGACTCGCCGGTTTCATCTA-3'	For amplifying endogenous transcript of TIP4 by qRT-PCR
At Tip4;1 Rev2	At2g25810	5'-GTCAGCGACTGGGACATGTG-3'	For amplifying endogenous transcript of TIP4 by qRT-PCR
At Actin3 For2	At3g53750	5'-CAGGCCCGTCGATTGTTC-3'	For amplifying endogenous transcript of Actin3 by qRT-PCR
At Actin3 Rev2	At3g53750	5'-TCCGGAAGCAGACTTAACTTCAA-3'	For amplifying endogenous transcript of Actin3 by qRT-PCR
At Tub4 For2	At5g44340	5'-TGGATCCCAAACAACGTCAA-3'	For amplifying endogenous transcript of TUB4 by qRT-PCR
At Tub4 Rev2	At5g44340	5'-GCCATTTTCAAACCCTTTGGT-3'	For amplifying endogenous transcript of TUB4 by qRT-PCR
G92/Sec24A	At3g07100	n.a.	n.a.
Gold36	At1g54030	n.a.	n.a.
Pah1	At3g09560	n.a.	n.a.
Pah2	At5g42870	n.a.	n.a.
RHD3	At3g13870	n.a.	n.a.
RHD3-L1	At5g45160	n.a.	n.a.
RHD3-L2	At1g72960	n.a.	n.a.