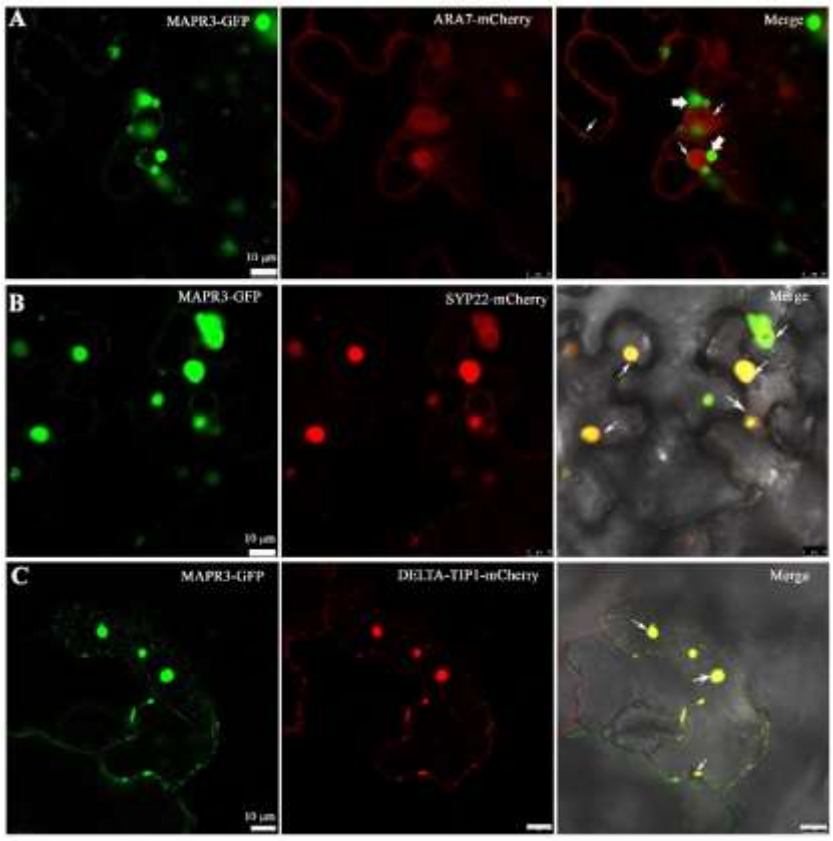
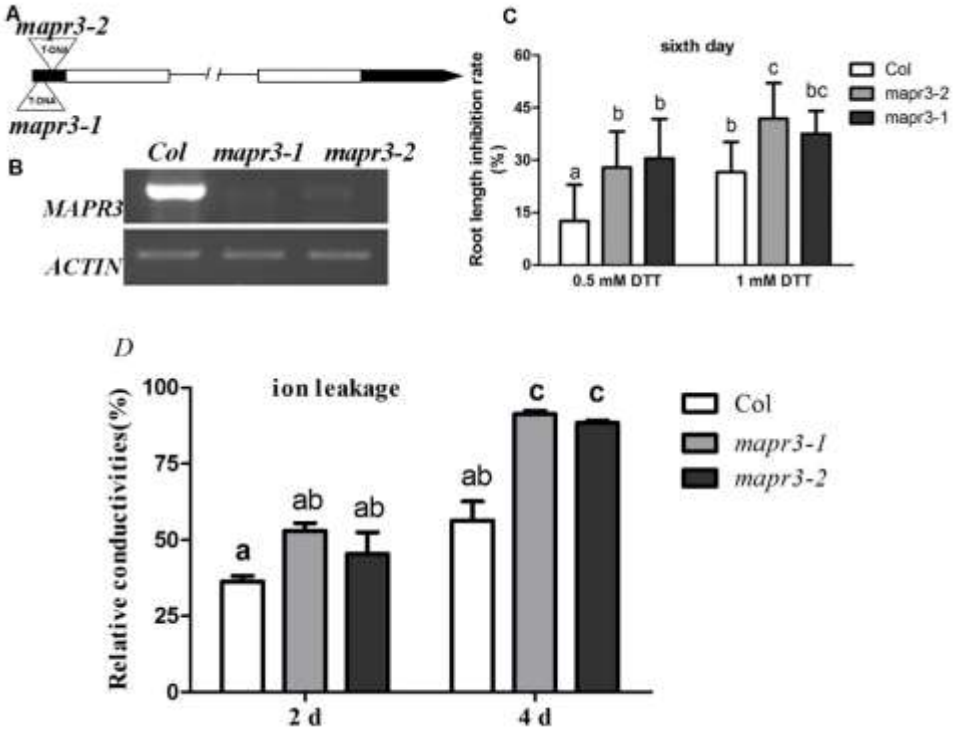
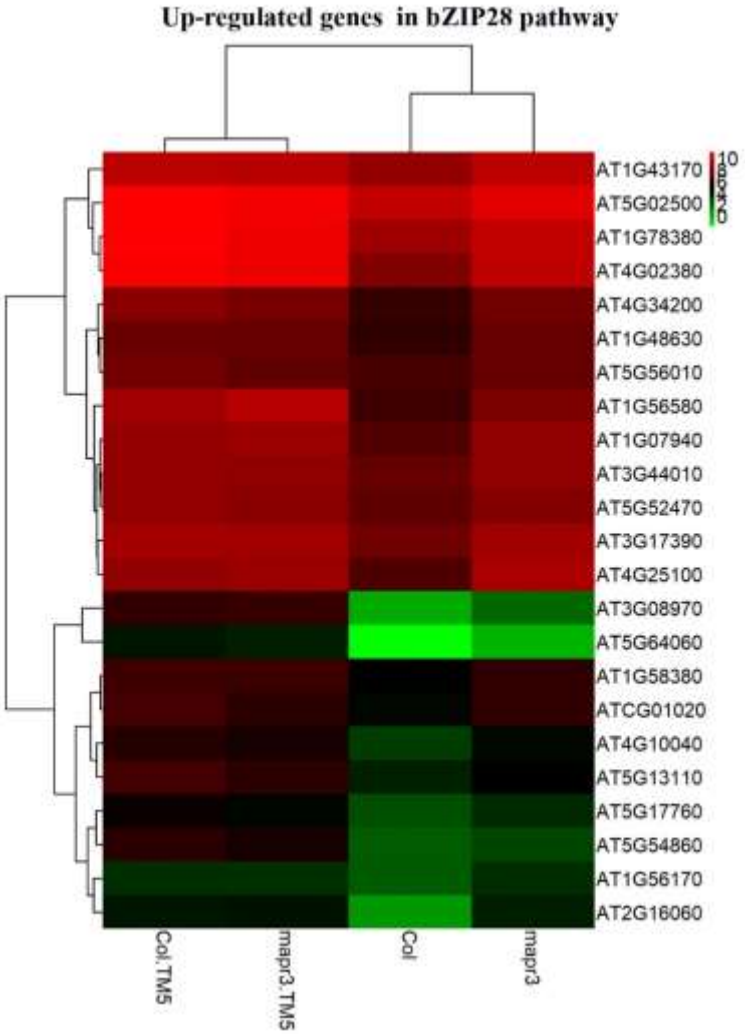


Supplementary Fig. S1 The endosome marker ARA7-mCherry or SYP22-mCherry and vacuolar marker DELTA-TIP1-mCherry marker proteins could be found in the puncta structure of 35S:: MAPR3-GFP when they are co-expressed.

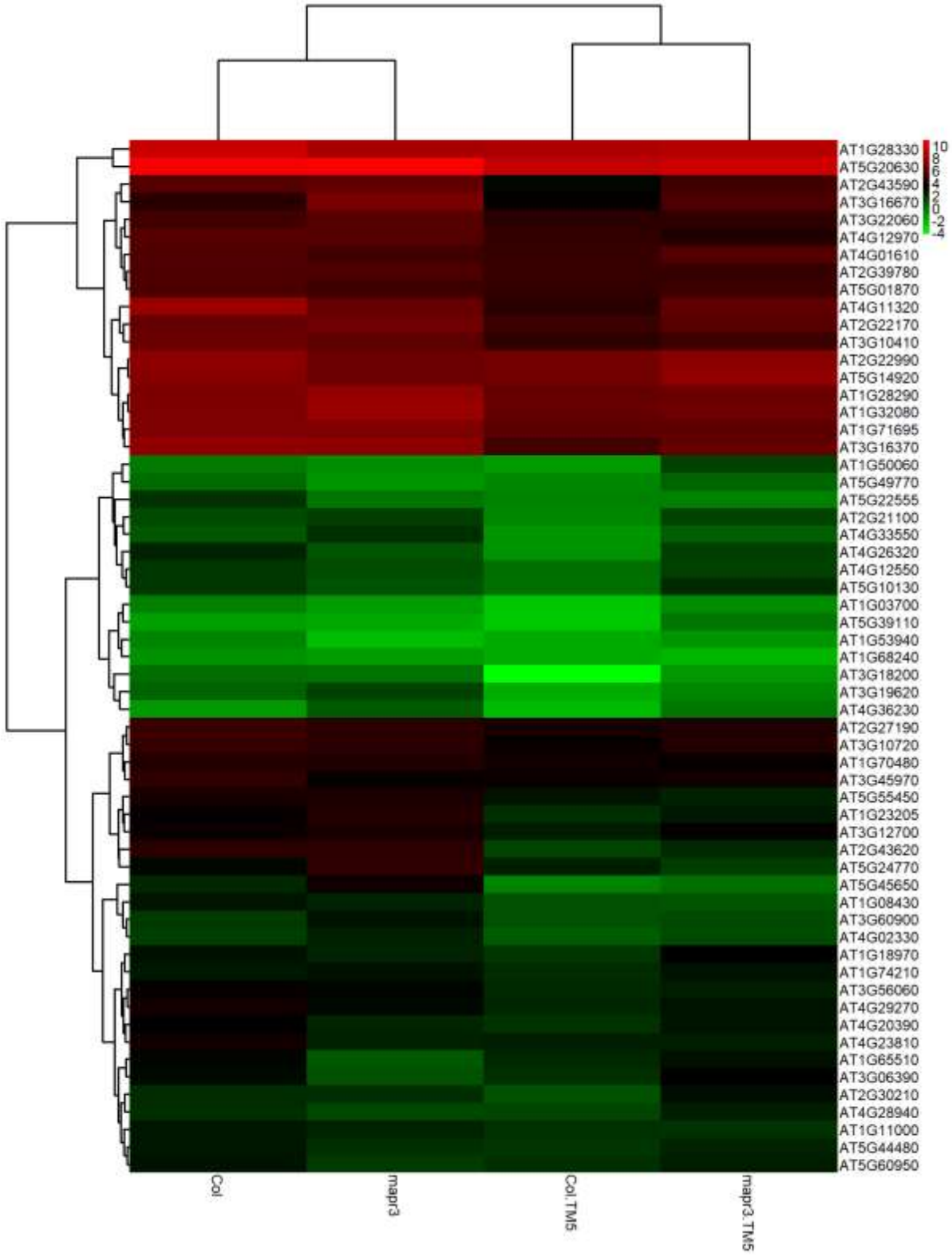


Supplementary Fig. S2 MAPR3 transcripts level in mutants and the sensitivity of the mutants to ER stress assayed. (A) Schematic representation of T-DNA insertion sites in *mapr3-1* and *mapr3-2*. White and black boxes indicate coding sequences and untranslated regions, respectively. T-DNA insertion site of *mapr3* is located in the promoter of the gene. **(B)** Expression levels of *MPAR3* in the WT, *mapr3-1* and *mapr3-2* were determined by RT-PCR using total RNA isolated from 2-week-old seedlings. **(C)** The root inhibition rate of 6-d old seedlings cultured on the medium containing 0, 0.5 and 1 mmol L^{-1} DTT. Error bars represent SD of more than 80 samples each lines. **(D)** The sterile 7 d-old seedlings of Col, *mapr3-1* and *mapr3-2* were vacuum infiltrated with 0.15 μg mL^{-1}TM for 30 m and the relative conductivity was determined at different times post treatment. Data are expressed as the mean ±SD. Different letters indicate significant differences between different plants.

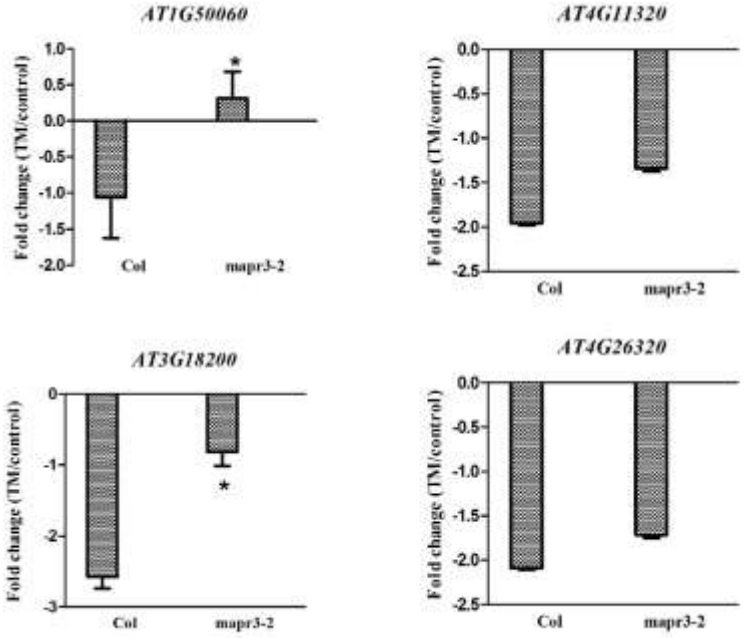
(student test, *p<0.05, n = 5).



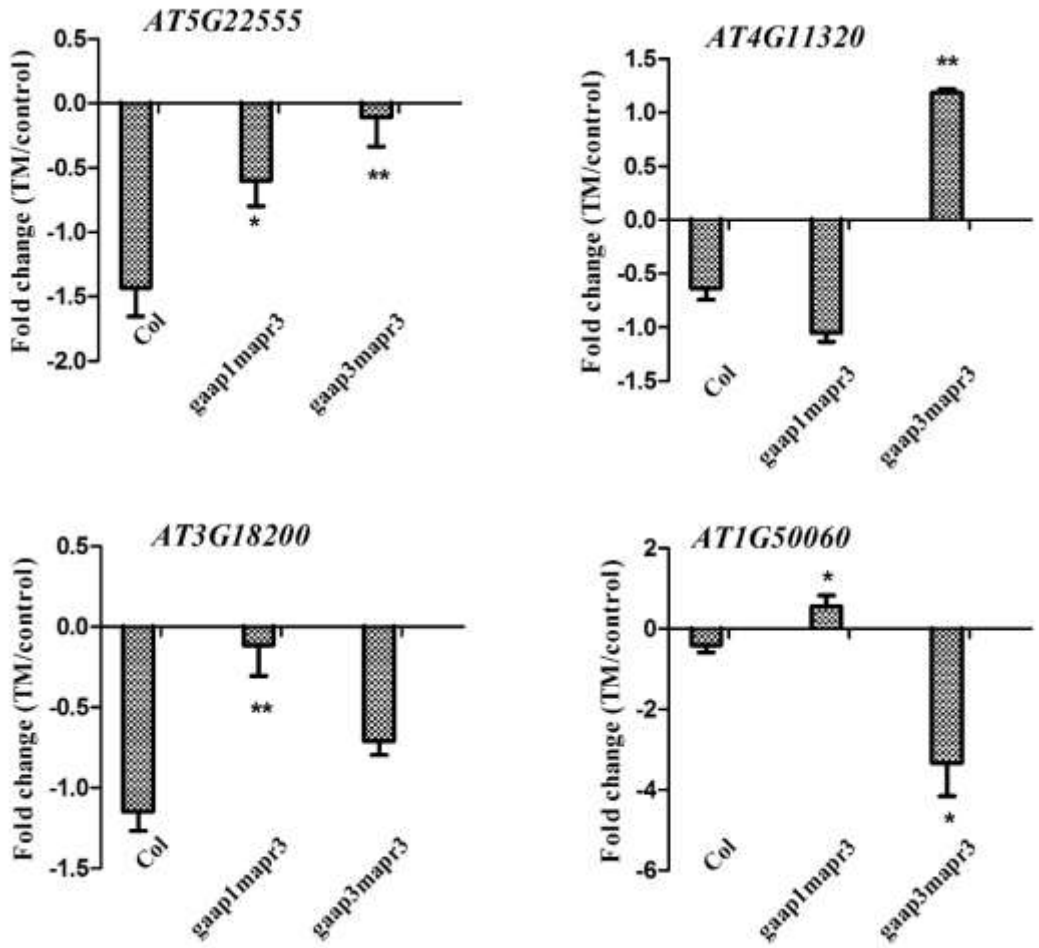
Supplementary Fig.S3 The heatmap showing levels of transcript abundance of bZIP28 pathway genes in Col and *mapr3* mutant under control and 5 μg mL^{-1} TM treatment for 5h. The significantly lower up-regulated genes by TM treatment in *mapr3* compared than in Col were showed.



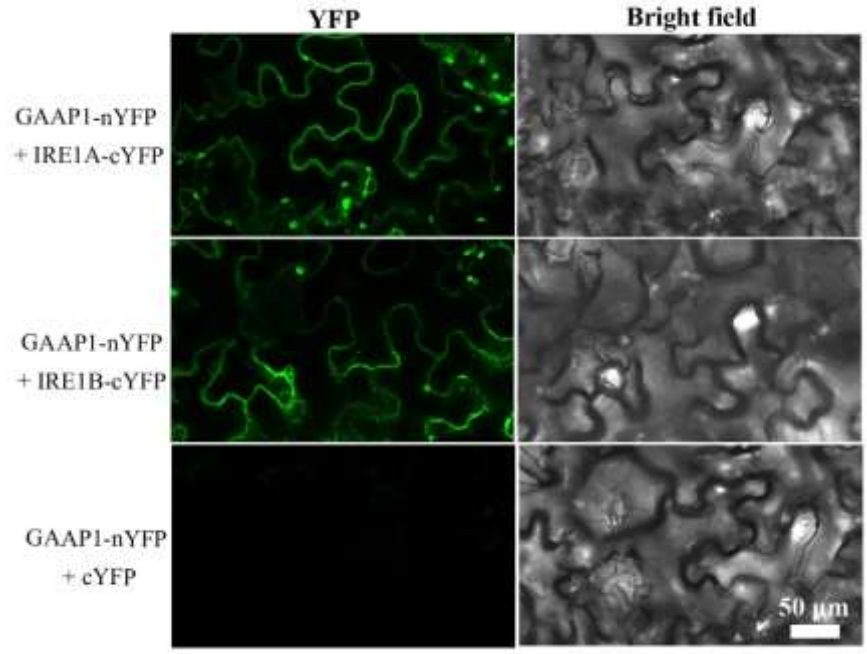
Supplementary Fig.S4 The heat map showing levels of transcript abundance of RIDD genes of Col (fold change of Log_2 FC <-0.5) and *mapr3* mutant under control and 5 μg mL^{-1} TM treatment for 5h.



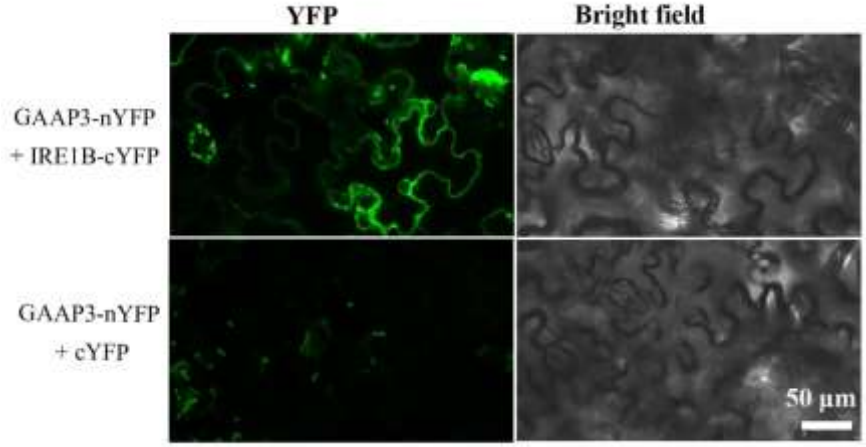
Supplementary Fig.S5 Quantitative reverse transcription polymerase chain reaction (qRT-PCR) analysis of RIDD genes in 10-d-old *mapr3* and *Col* plants at 5 h after 5 μg mL^{-1} TM treatment or mock treatment. The fold change (FC) of treatment and control of each gene was transformed as Log2 FC. Error bars represent SE of two independent biological experiments with 3 technical replicates. *Statistical differences between mutant and Col (student's t-test, *$P < 0.05$, **$P < 0.01$).



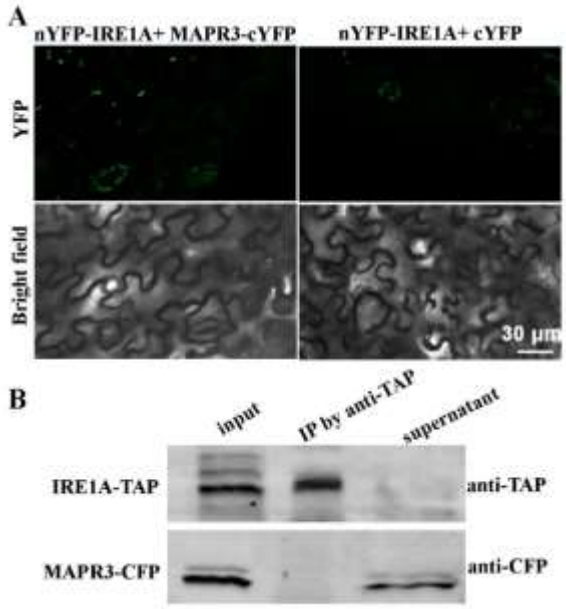
Supplementary Fig.S6 Quantitative reverse transcription polymerase chain reaction (qRT-PCR) analysis of RIDD genes in 7-d-old *gaap1 mapr3* and *gaap3 mapr3* plants at 5 h after 1 μg mL^{-1} TM treatment or mock treatment. The relative gene expression was the expression level of each gene in different genotype plants normalized to the level in the wild-type control, both of which were normalized to the expression of ACTIN8. And the fold change (FC) of treatment and control of each gene was transformed as Log2 FC. Error bars represent SE of two independent biological experiments with 3 technical replicates. *Statistical differences between mutant and Col (student's t-test, *$P < 0.05$, **$P < 0.01$).



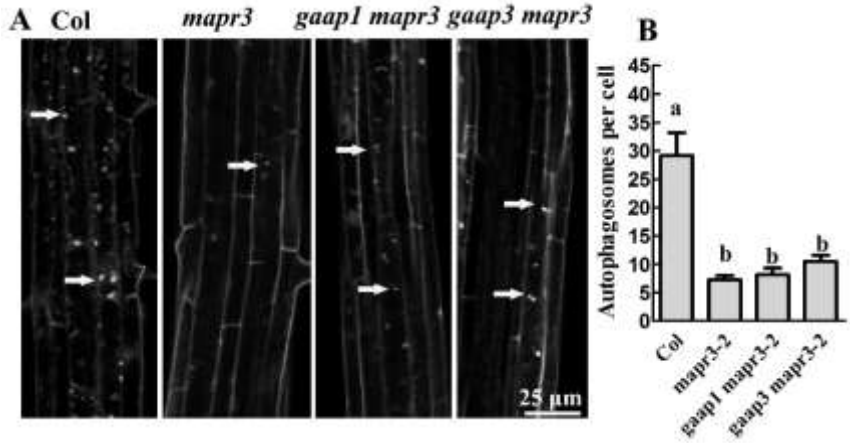
Supplementary Fig. S7 GAAP1 interacted with IRE1A/IRE1B by BIFC assay. YFP fluorescence was observed when nYFP-GAAP1 and IRE1A-cYFP (or IRE1B-cYFP), nYFP-GAAP1 and cYFP were co-expressed in the tobacco leaf cell.



Supplementary Fig. S8 GAAP3 interacted with IRE1B by BIFC assay. YFP fluorescence was observed when nYFP-GAAP3 and IRE1B-cYFP, nYFP-GAAP3 and cYFP were co-expressed in the tobacco leaf cell.



Supplementary Fig. S9 MAPR3 did not associate with IRE1A showed by BiFC assay (A) and co-immunoprecipitation assay (B).



Supplementary Fig. S10 Mutations in MAPR3 and/or GAAP1/GAAP3 impaired the autophagy induced by ER stress in the presence of concA. (A) Five-day-old seedlings of wild-type Col, *mapr3-2*, *gaap1mapr3* or *gaap3 mapr3* were transferred to MS liquid medium supplemented with 4 mM DTT with 1 μM concA for 10 h, followed by MDC staining. Then, roots were observed using confocal microscopy. Arrows indicate autophagosomes. (B) The average number of autophagosomes per cortical cell in root mature region was counted after DTT treatment. Data are average values ± SD calculated from two independent experiments. For each experiment, over 10 seedlings were used for the calculation for each genotype. Different lower case letters indicate significant differences ($P < 0.05$ by two-way ANOVA and Tukey's range).