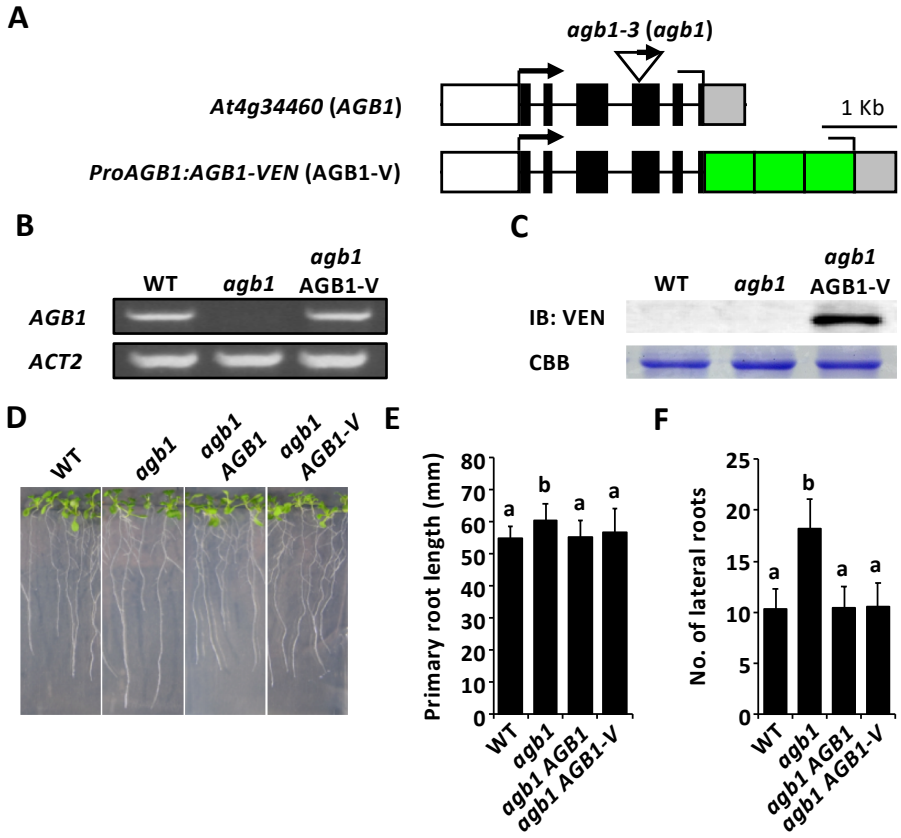
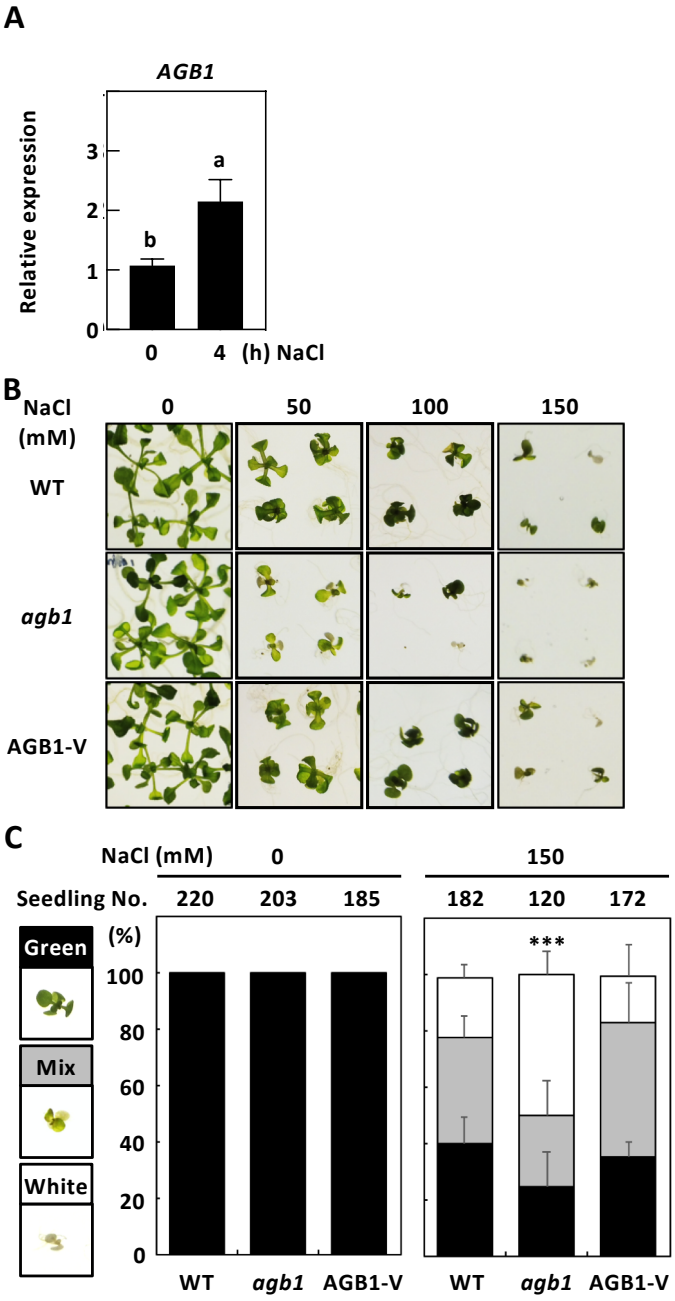
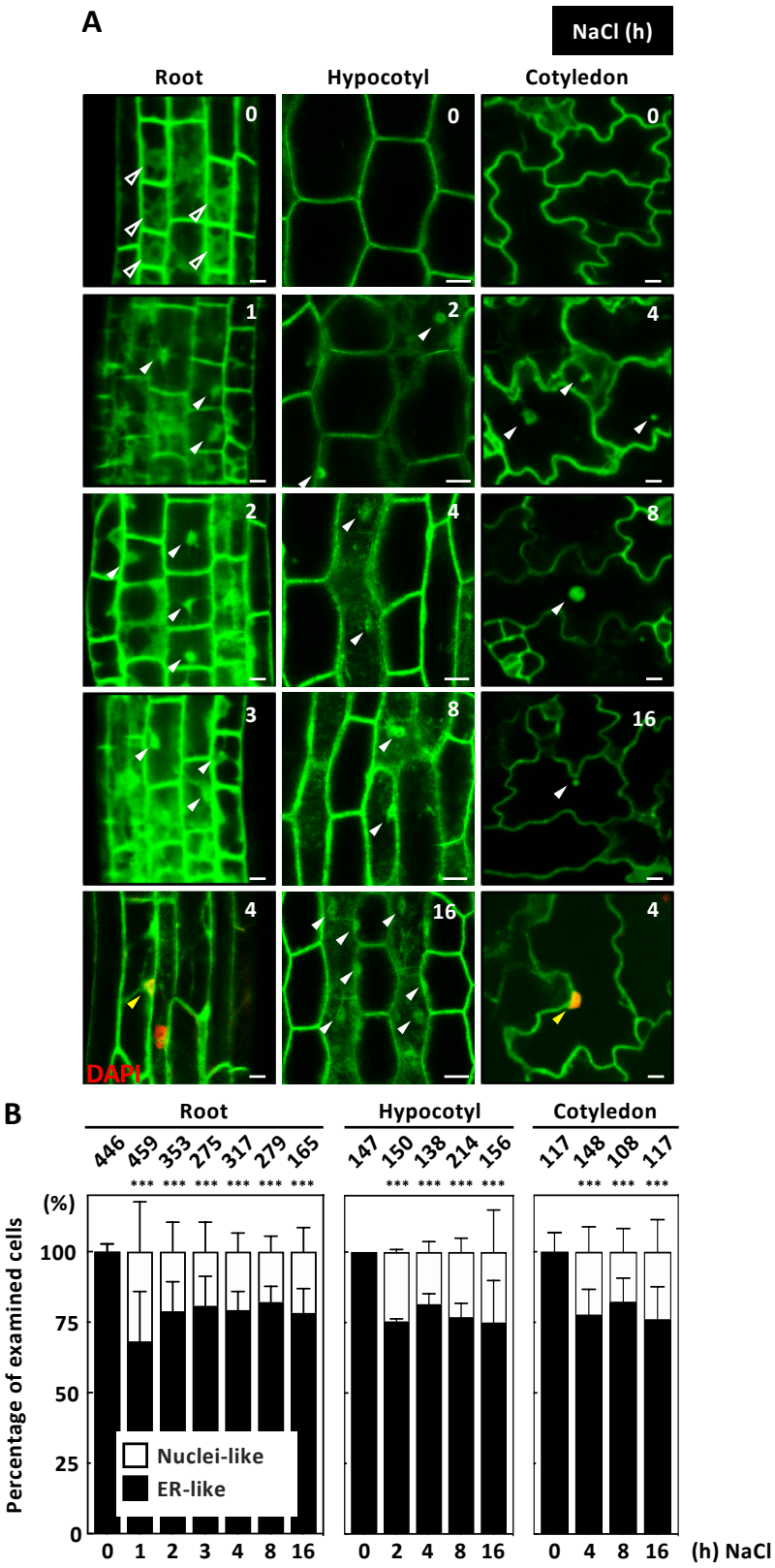


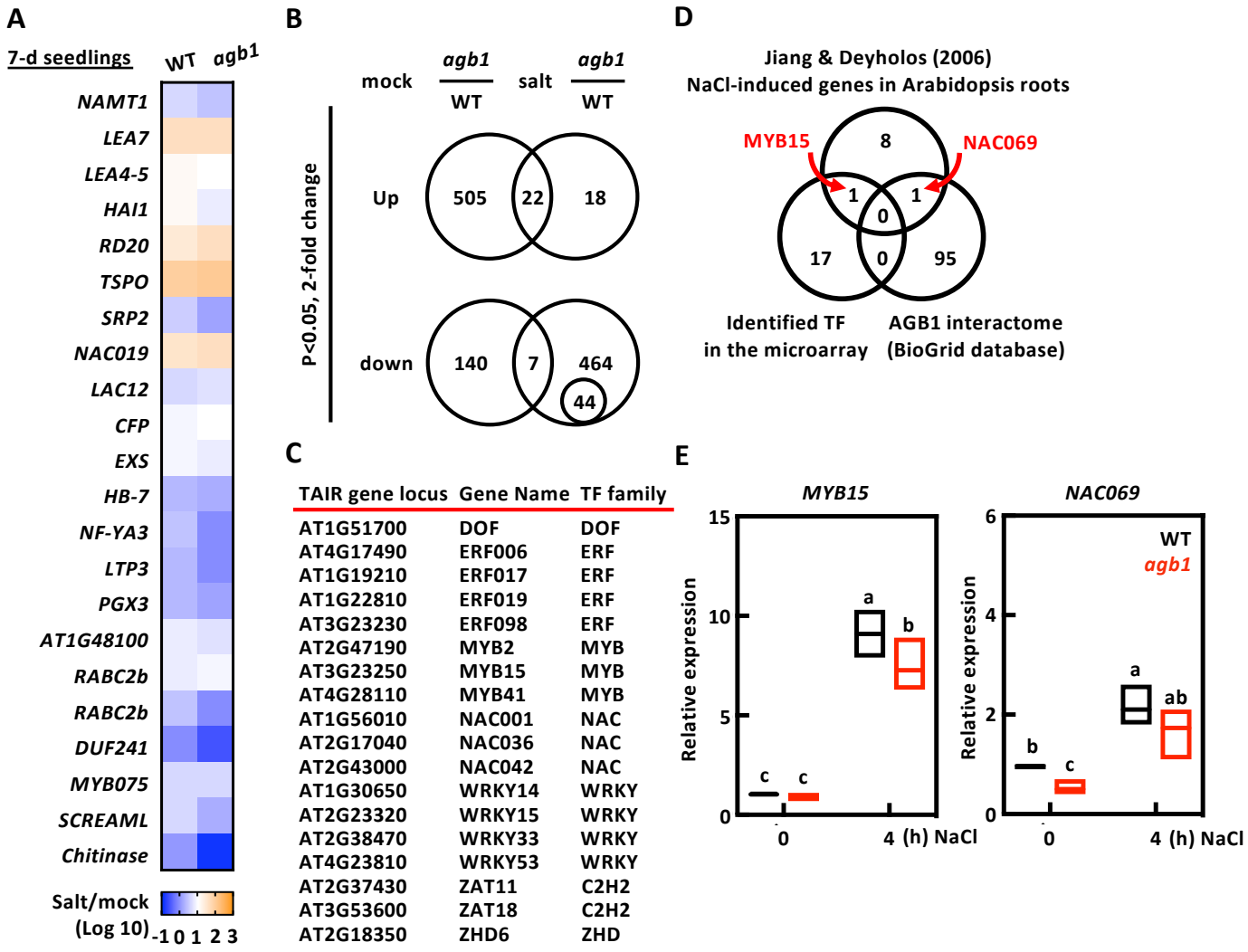
Supplemental Figure 1. AGB1 genomic DNA fragment with Venus tag complements *agb1* defects.
(**A**) The gene structure of the *AGB1* gene (*At4g34460.1*) and its mutant *(agb1-3*, *agb1)* generated by T-DNA insertion. White box as the promoter, black boxes as six exons, black line as five introns, gray box as 3'UTR and green boxes as triplicate Venus. (**B**) RT-PCR analysis for the wild type (WT), *agb1-3* (*agb1*), *agb1* AGB1-V. *ACTIN2* (*ACT2*) was used as positive control. (**C**) Immunoblot analysis of AGB1-V proteins. CBB staining as the loading control. (**D**) Representative images of vertical growth of 14-day WT, *agb1*, *agb1 pAGB1:AGB1* (*agb1* AGB1) and *agb1 pAGB1:AGB1-Venus* (*agb1* AGB1-V) seedlings on ½ MS agar plates. The root phenotype including primary root length (**E**) and lateral root number (**F**) were shown as bar chart.



Supplemental Figure 2. AGB1-V is biological functioned for seedling fitness under high salinity.
(**A**) RT-qPCR analysis of 7-day-old WT seedlings with 0 or 4 h of 150 mM NaCl treatment. The *AGB1* expressions were normalized to *ACTIN2* and average *AGB1* expression level under normal condition was set as 1. Data were mean ± SD of three biological replicates. Data with different letters represent significant differences [one-way ANOVA at $P < 0.05$]. (**B**) Representative images of 14-day-old WT, *agb1* mutant, and *agb1 pAGB1:AGB1-Venus* (AGB1-V) transgenic plants were grown on ½ MS containing NaCl with indicated concentration to induce salt stress. The morphological phenotypes were classified into healthy (Green, black box), at least one albino leaf (Mix, gray box) and all albino leaves (White , white box) groups and analyzed for their salt tolerance. Number of seedlings belong different groups were shown above each bar. Error bar, Mean + SD. Asterisk indicated the statistically differences comparing to WT. ***, $P<0.05$.

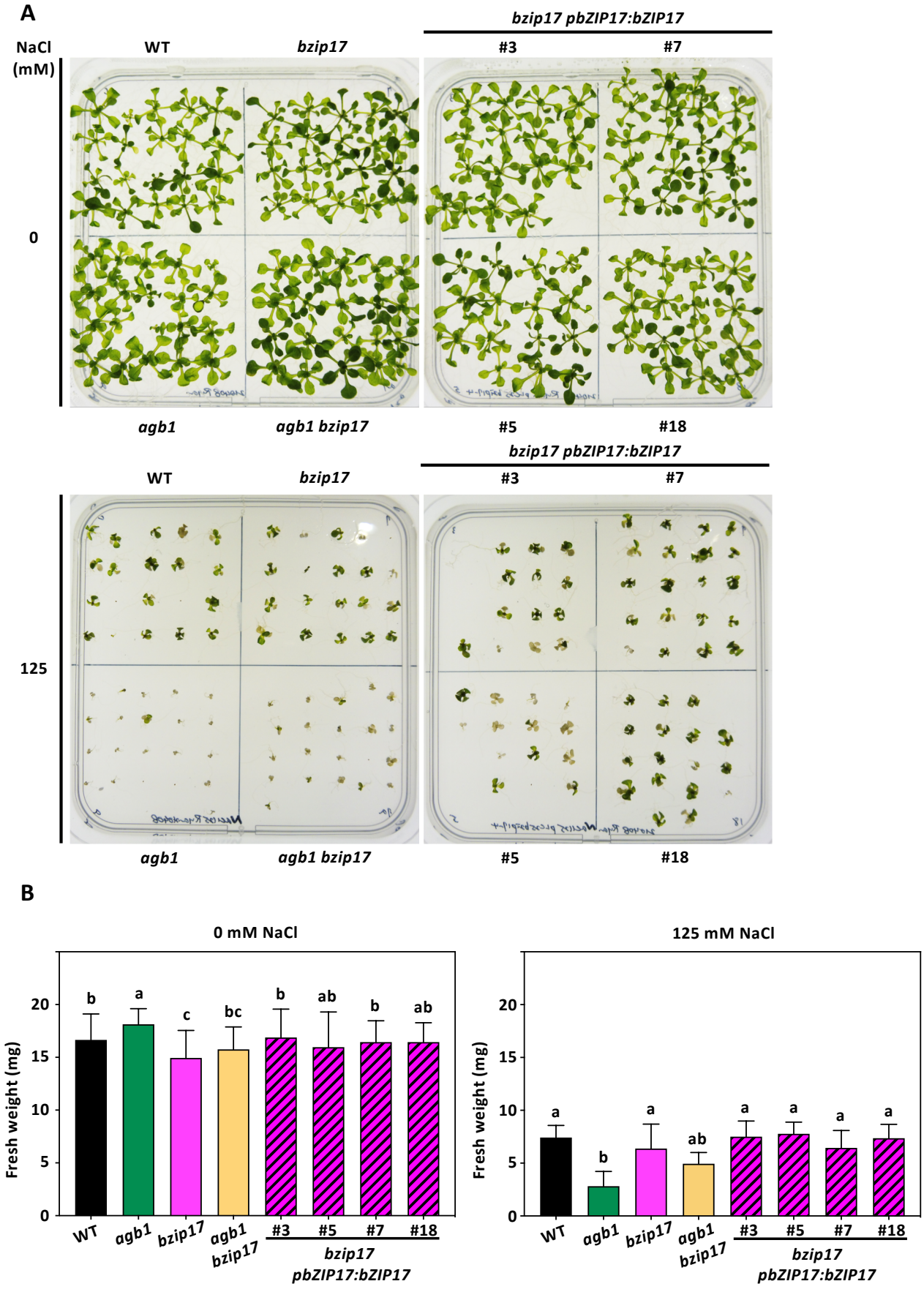


Supplemental Figure 3. Nuclei localization of AGB1-V was induced by salt stress in whole seedling. (**A**) Representative images of root, stem and leaf epidermis of pAGB1:AGB1-VENUS (AGB1-VEN) in a stable transgenic complementation plant in the absence (½ MS medium, 0 h) or presence of 150 mM NaCl as indicated time for salt stress induction. Solid arrow heads indicated the ER-like AGB1 localization while the empty white arrow heads indicated the nuclei localization of AGB1. The nulcei localization of AGB1 was confirmed by DAPI staining (red). The ratio of different subcellular localization of AGB1-VEN were quantified as shown in (**B**). Scale bars equal to 10 μm. (**B**) Quantification analysis of subcellular localization of AGB1 in root, hypocotyl and cotyledon of 7-day-old AGB1-VEN plant. Each value represents the means ± SD of the percentage of mRFP-bZIP17 localization (ten seedlings) for at three independent experiments per time point. The total numbers of examined epidermal cells for corresponding tissue were shown at the top of each bar. The epidermal cells expressed nuclei-like mRFP-bZIP17 were classified into to white group, while the ER-like mRFP-bZIP17 were classed into black group. ***, $P < 0.001$.



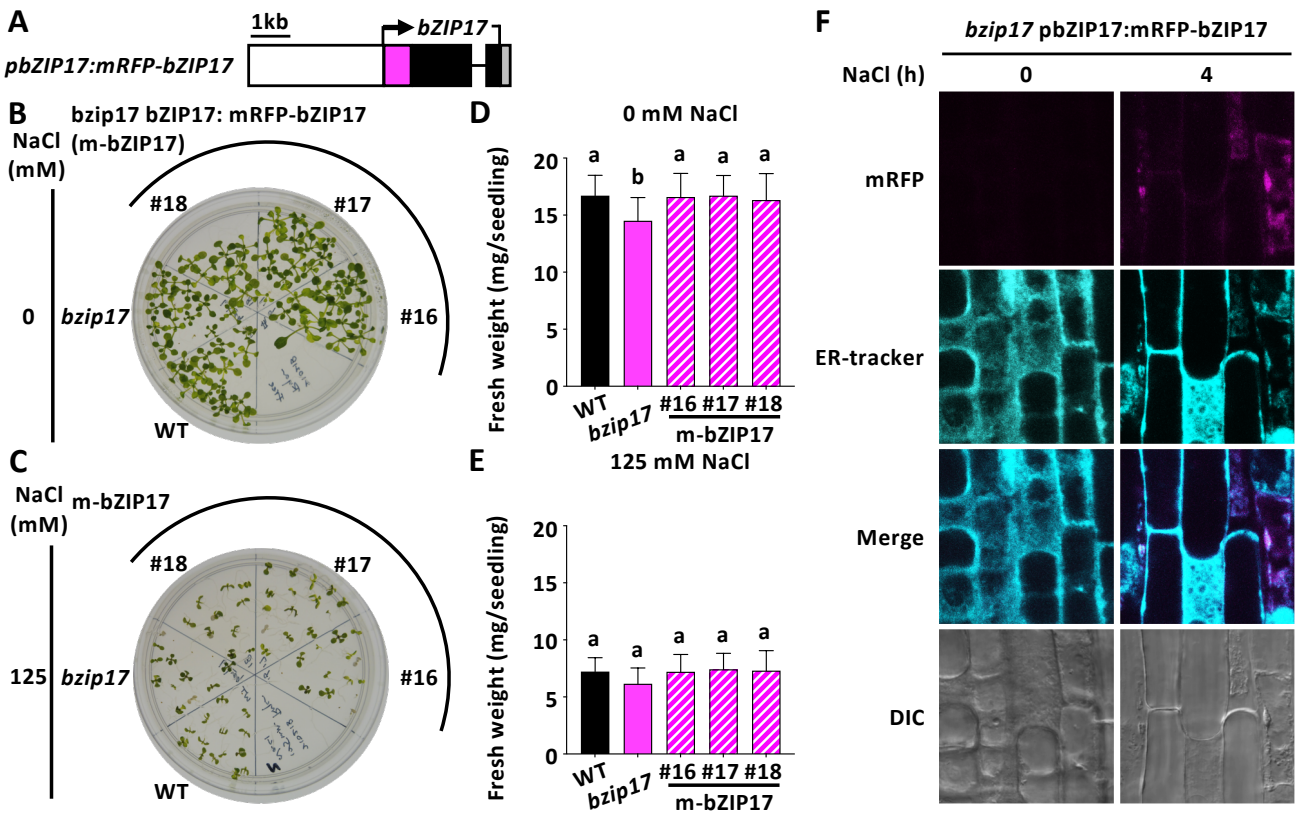
Supplemental Figure 4. Schematic representation of AGB1-mediated salinity response through bZIP17 signaling in Arabidopsis roots.

(**A**) Twenty two bZIP17-mediated salt stress responsive genes were selected from Liu *et al*., (2007) and their expressions under salt stress in 7-day-old WT or *agb1-3* (*agb1*) mutant were shown as heatmap. Whole seedlings were collected after 0 (control) or 4 hours (salt) of 150 mM NaCl treatment for microarray analysis. The Log10 values indicated the means of the ratio of the representative transcripts under salt stress (4-h) comparing the mock condition in WT or *agb1* mutant from three independent replicates. (**B**) The AGB1-regulated salt responsive genes were identified by intersection of *agb1*/WT between control and salt condition. The up- or down-differential expression genes (DEG) were selected by two-fold differences (*P*<0.05 threshold for total genes in parentheses). (**C**) The salt stress responsive transcription factors from the down-DEG group of the *agb1*/WT under salt condition. (**D**) Venn diagram of selected ten genes from microarray and confirmed by RT-qPCR in Jiang & Deyholos (2006), identified 18 TFs with lower salt stress induction in *agb1* seedlings in our study (**C**), and 96 AGB1 interactors reported in the BioGrid database (https://thebiogrid.org). The overlap genes *MYB15* and *NAC069* were highlighted in red. (**E**) RT-qPCR analysis of 7-day-old WT (black) and *agb1* (red) seedlings with 0 or 4 h of 150 mM NaCl treatment. The *MYB15* (left) and *NAC069* (right) expressions were normalized to *ACTIN2* and average of each gene expression level under normal condition was set as 1. Data were mean ± SD of three biological replicates. Data with different letters represent significant differences [one-way ANOVA at P < 0.05].



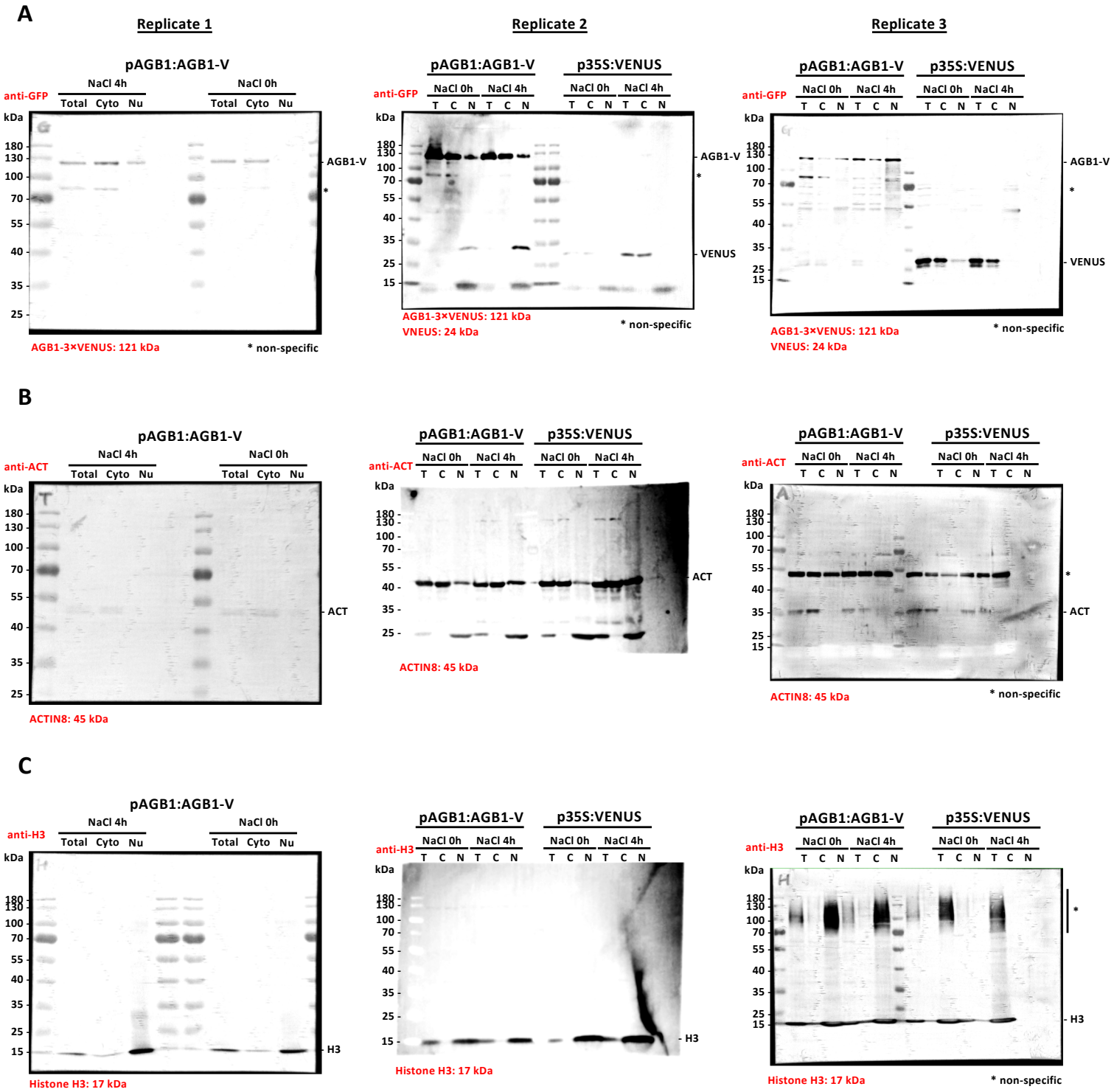
Supplemental Figure 5. Additional bZIP17 genomic DNA complementation lines are biological functioned for seedling growth.

Representative images (**A**) of 14-day-old WT, *agb1*, *bzip17*, *agb1 bzip17* mutants, and *bzip17* pbZIP17:bZIP17 complementation lines were grown on ½ MS containing NaCl with indicated concentration to induce salt stress. (**B**) Representative plots for fresh weight of 14-day-old seedlings grown on 0 (left) or 125 mM NaCl (right) were measured individually with three biological experiments (n=20) and shown as mean+SD. Data with different letters represent significant differences [one-way ANOVA at $P < 0.05$].



Supplemental Figure 6. Salinity tolerance and subcellular localization of transgenic mRFP-bZIP17 plants.

(**A**) The gene structure of the genomic *bZIP17* fragment with N-terminal fusion of mRFP reporter after ATG start codon. White box as the promoter, black boxes as two exons, black line as intron, gray box as 3'UTR and pink box as mRFP reporter. Representative images (**B**, **C**) of 14-day-old *WT*, *bzip17* mutants, and *bzip17 pbZIP17:mRFP-bZIP17* (m-bZIP17) complementation lines #16, #17, #18 were grown on ½ MS containing NaCl with indicated concentration to induce salt stress. (**D**, **E**) Representative chart for fresh weight of 14-day-old seedlings grown on 0 (up) or 125 mM NaCl (down) were measured individually with three biological experiments (n=15) and shown as mean+SD. Data with different letters represent significant differences [one-way ANOVA at $P < 0.05$]. (**F**) Subcellular localization of mRFP-bZIP17 in root of 7-day-old m-bZIP17 plants. Fluorescence of mRFP-bZIP17 (pink) and staining of the endoplasmic reticulum by ER-tracker in the treatment of 150 mM NaCl for 0 or 4 hours. Co-localization signals of mRFP-bZIP17 and staining dye were shown in the merge images as purple colors in the bottom panel. Differential interference contrast (DIC) images to show cellular structures. Scale bars equal to 10 μm.



Supplemental Figure 7. Original images of immunoblot anti-GFP, anti-ACT8 and anti-Histone H3.
The original images of immunoblots against GFP (for VENUS, **A**), ACTIN8 for cytosolic fractions (**B**) and Histone H3 (**C**) for nuclear fractions with replicates using 7-d *pAGB1:AGB1-V agb1-3* and *p35S:VENUS* seedlings after 0- or 4-h of 150 mM NaCl treatment. Three replicates showed full length membranes, with membrane edges visible. The third replicate was used to prepare images showed in Fig. 2C. The size of anti-GFP blot was showed without crop further to cover both AGB1-V (121 kDa) and VENUS (24 kDa). For both anti-ACT8 and anti-H3 blots, the images were cropped from original one as displayed here.