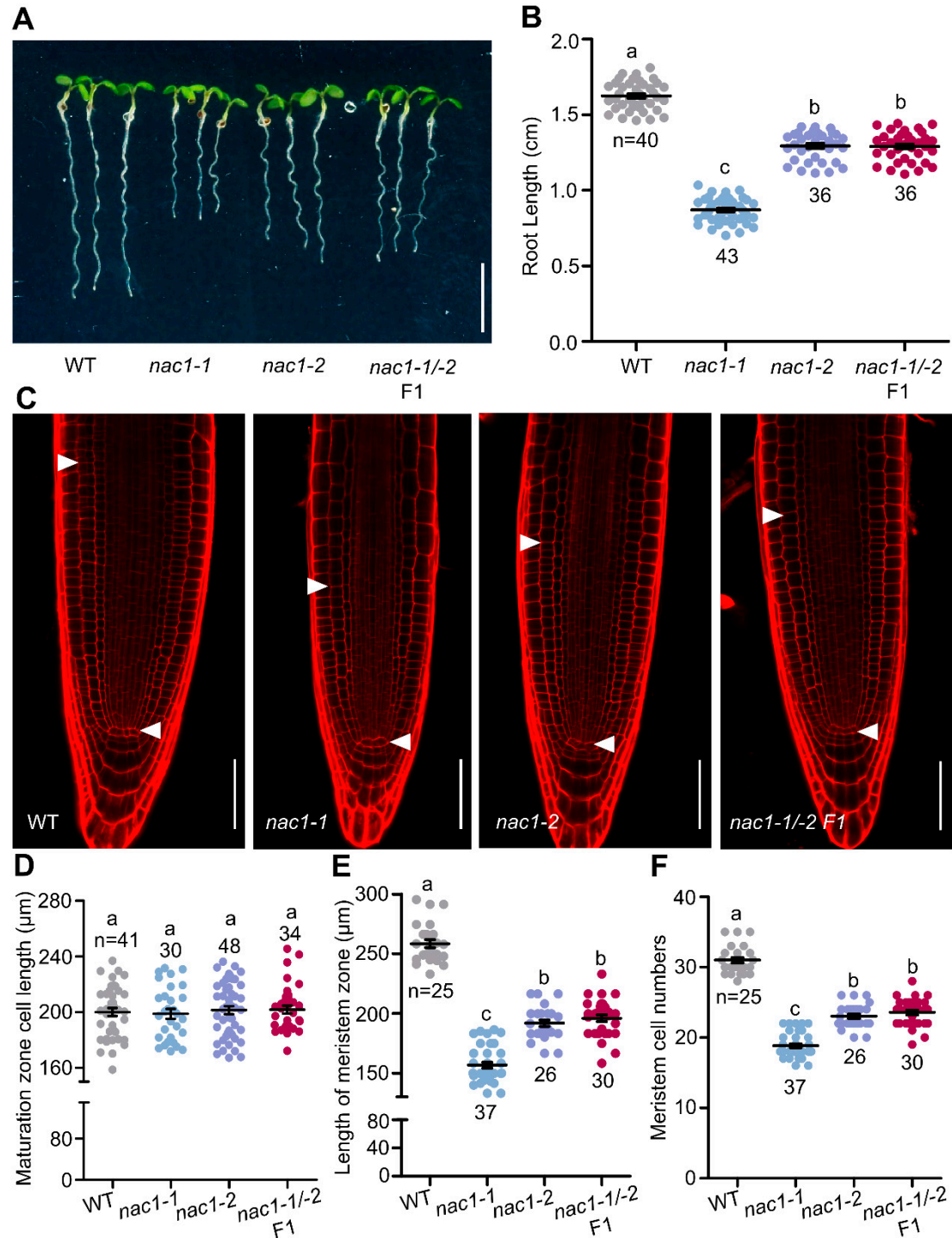
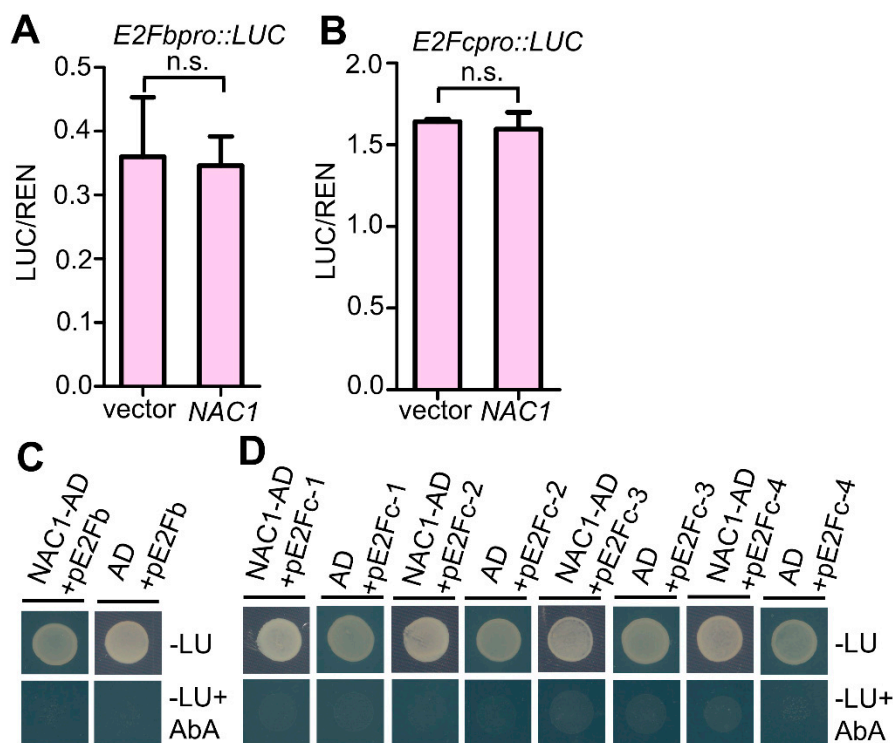


## Supplemental Figures



**Supplemental Figure S1. Analysis of *nac1-1/nac1-2* T-DNA mutants.** (A) The root growth phenotypes of WT, *nac1-1*, *nac1-2* and the first generation of *nac1-1/-2* grown on a 1/2 MS medium. The seedlings were photographed at 5 days postgermination

(dpg). Scale bar represents 0.5 cm. **(B)** Measurements of primary root length of WT, *nac1-1*, *nac1-2* and the first generation of *nac1-1/-2* as shown in (A). **(C)** Confocal images of root tips of WT, *nac1-1*, *nac1-2* the first generation of *nac1-1/-2* as shown in (A). The seedlings were used at 5 dpg for imaging. White arrows indicate the boundary between root meristem and transition zones. White arrows below indicate the QC. Scale bars represent 50  $\mu$ m. **(D)** Root cortical cell length in the maturation zone of 5 dpg seedlings as shown in (C). **(E)** Length of meristem zone of 5 dpg seedlings as shown in (C). **(F)** Cell numbers in the proliferation domain of 5 dpg seedlings as shown in (C). Data Information: In **(B,D,E,F)**, data represent mean  $\pm$  SD. *n* denotes the total number of scored samples. Individual values (black dots) are shown. Different lowercase letters indicate significant differences by one-way ANOVA followed by Tukey's multiple comparison test ( $P < 0.05$ ).



**Supplemental Figure S2. NAC1 was not bind the *E2Fb* or *E2Fc* promoter.** **(A,B)** NAC1 transactivates the *E2Fb* and *E2Fc* promoter in *A. thaliana* leaf protoplasts. The effector (35s::*NAC1*) and reporter (*E2Fbpro::LUC* or *E2Fcpro::LUC*) constructs. The empty vector pBI221 was used as a negative control. Data represent mean  $\pm$  SD of

three independent replicates in the experiment (Student's test, n.s., not significant). (C,D) Yeast one-hybrid binding assay involving NAC1 and *E2Fb* or *E2Fc* promoters. The *E2Fb*pro spans from -625 to -47 bp were PCR fragment upstream of ATG start site of *E2Fb*; *E2Fc*pro-1 spans from -4317 to -3574 bp; *E2Fc*pro-2 spans from -2946 to -2690 bp; p*E2Fc*-3 spans from -2095 to -1195 bp; p*E2Fc*-4 spans from -940 to -291 bp were PCR fragment upstream of ATG start site of *E2Fc*. The yeast transformants were dropped onto SD-L-U (-Leu,-Ura) media. AbA concentration with 250 ng/mL.