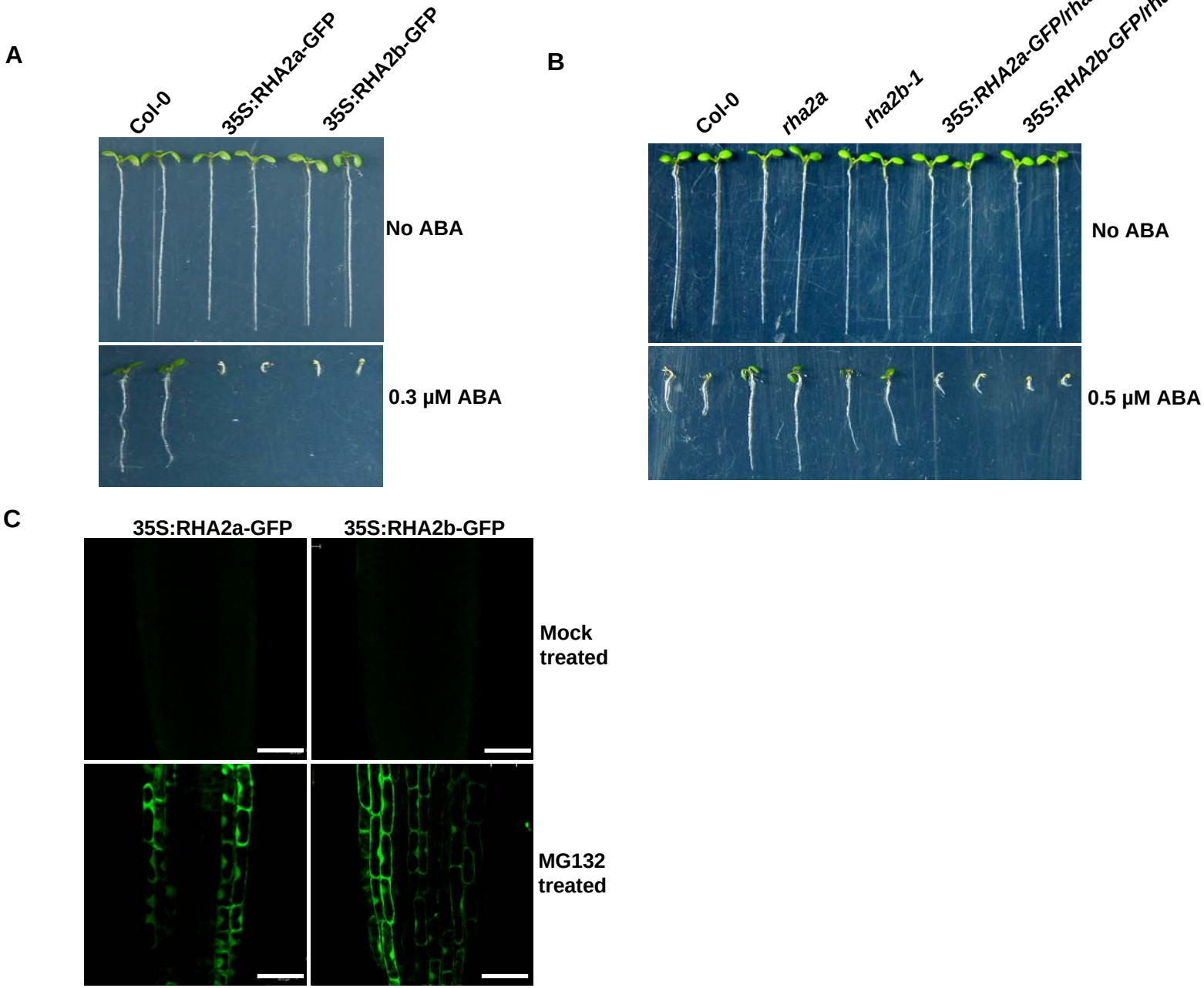
Li et al., Supplemental Figure S1

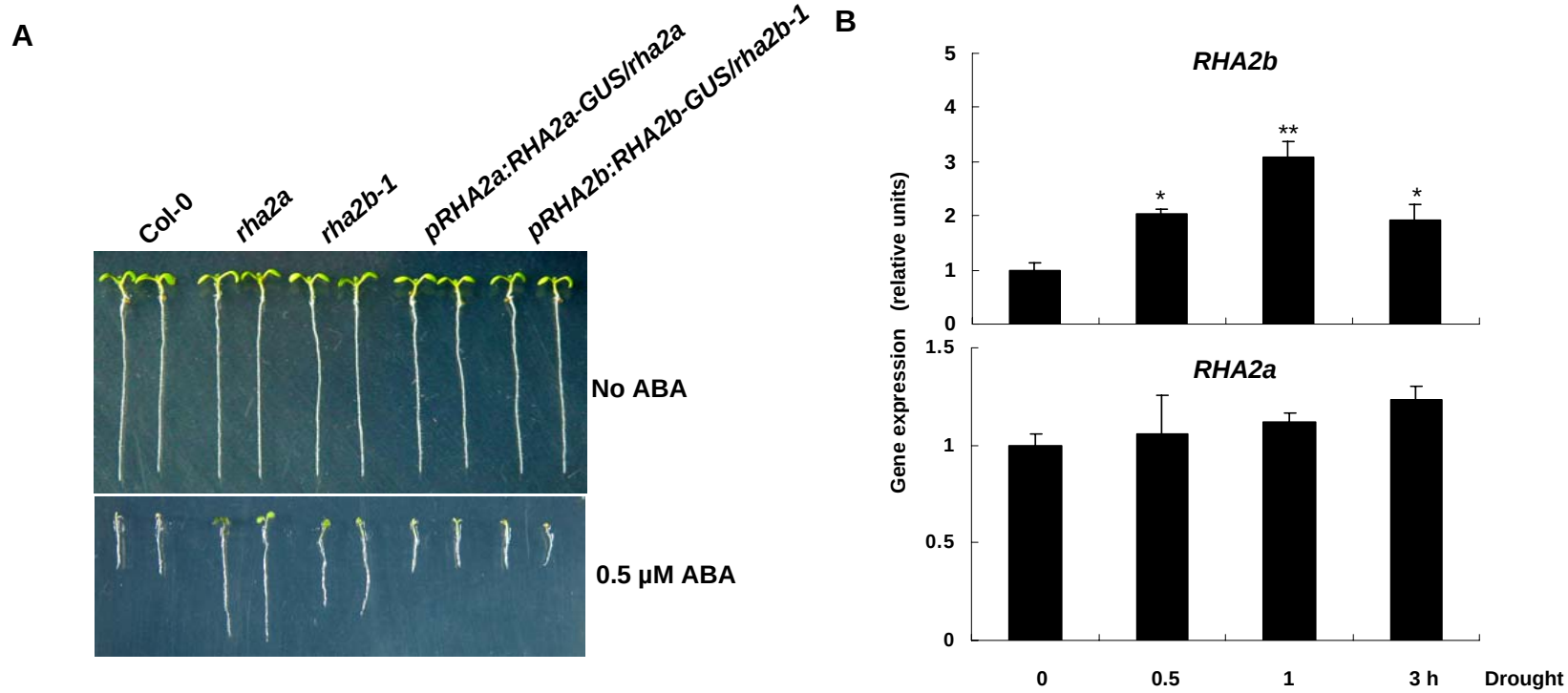


Supplemental Figure S1. Subcellular localization of the RHA2b and RHA2a.

A, ABA response of *35S:RHA2a-GFP* and *35S:RHA2b-GFP* transgenic *Arabidopsis* seedlings. Photographs of seedlings grew on medium containing 0 and 0.3 μM ABA at 5 d after the end of stratification.

B, ABA response of *35S:RHA2a-GFP*/*rha2a* and *35S:RHA2b-GFP*/*rha2b-1* seedlings. Photographs of seedlings grew on medium containing 0 and 0.5 μM ABA at 5 d after the end of stratification.

C, Photomicrographs of transgenic *Arabidopsis* roots harboring the 35S:RHA2b-GFP or 35S:RHA2a-GFP constructs. One-week-old plants treated (or mock treated) with 50 μM MG132 for 6 h under dim light overnight were observed with fluorescence microscopy. Bars=50 μm.



Supplemental Figure S2. Comparison of *RHA2b* and *RHA2a* expression.

A, ABA response of *pRHA2a:RHA2a-GUS/rha2a* and *pRHA2b:RHA2b-GUS/rha2b-1* *Arabidopsis* seedlings. Photographs of seedlings grew on medium containing 0 and 0.5 μM ABA at 5 d after the end of stratification.

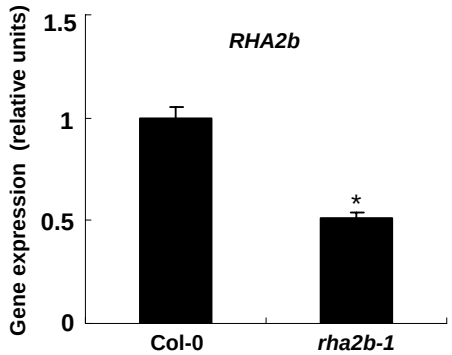
B, Drought-induced *RHA2b* and *RHA2a* expression revealed by qRT-PCR. Two-week-old wild type seedlings were subjected to drought treatment for 0, 0.5, 1 and 3 h respectively. *ACTIN2* primers were used as an internal control. Data shown are mean ± SD of three independent experiments.

Asterisks in B indicate significance of the difference from the corresponding control values determined by Student's *t*-test (* $0.01 \leqslant P < 0.05$, ** $P < 0.01$).

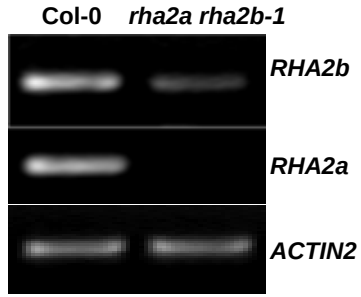
Li et al., Supplemental Figure S3

A

B

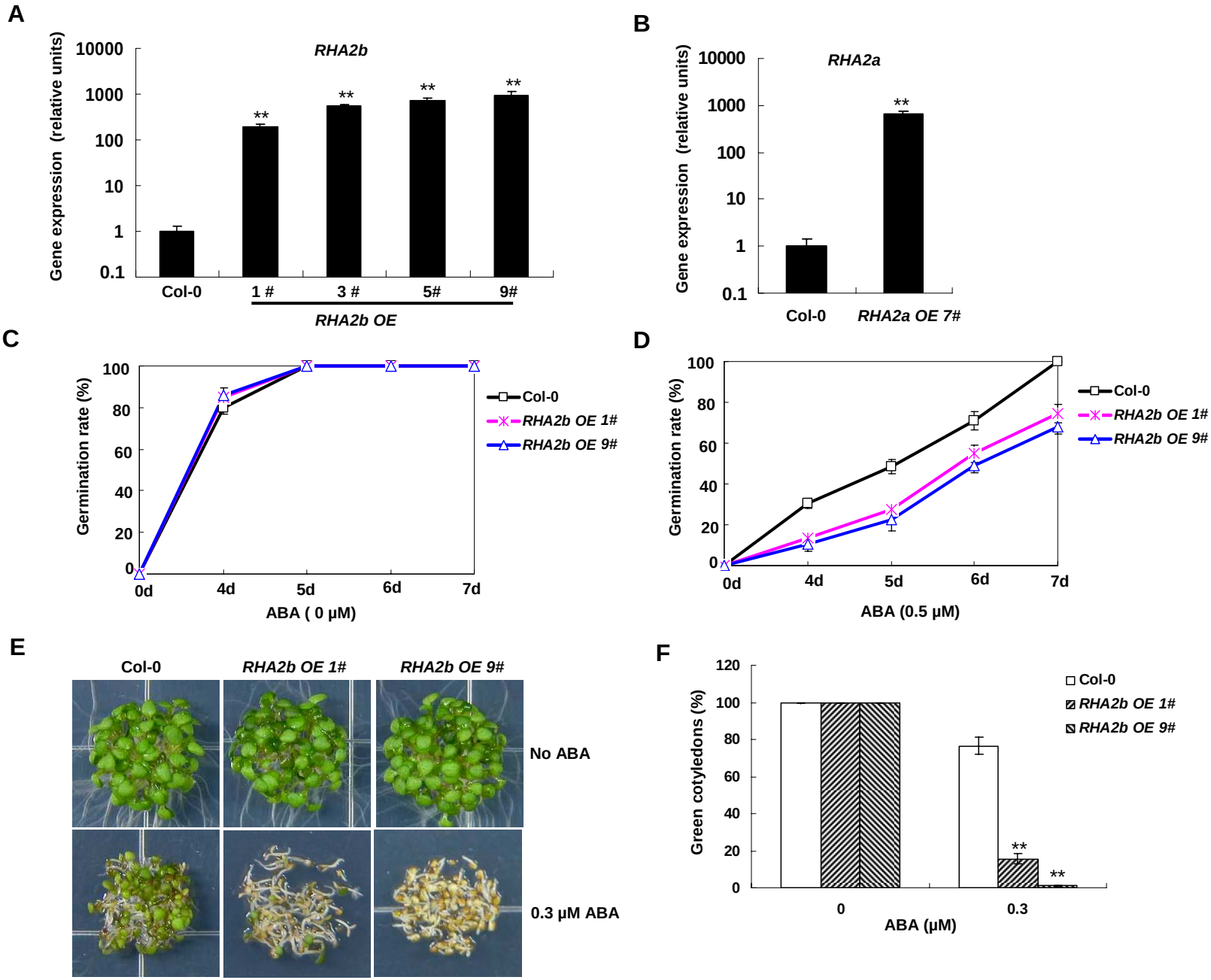


C



Supplemental Figure S3. Molecular analysis of *RHA2b*/*RHA2a* mutants.
A, Diagram of the *RHA2b* gene. The T-DNA inserted 168-bp upstream of the translation start site in Salk_014943 (*rha2b-1*).
B, Expression of *RHA2b* in *rha2b-1* revealed by qRT-PCR. *ACTIN2* primers were used as an internal control.
C, RT-PCR analysis showing reduced expression of *RHA2b* and no expression of *RHA2a* in the *rha2a rha2b-1* double mutant. *ACTIN2* primers were used as an internal control.
Asterisk in B indicate significance of the difference from the corresponding control values determined by Student's *t*-test (* $0.01 \leqslant P < 0.05$).

Li et al., Supplemental Figure S4



Supplemental Figure S4. ABA responses of *RHA2b OE* 1# and *RHA2b OE* 9# plants in seed germination and postgerminative growth.

A, qRT-PCR analysis showing elevated expression of *RHA2b* in *RHA2b* overexpression transgenic lines. *ACTIN2* primers were used as an internal control.

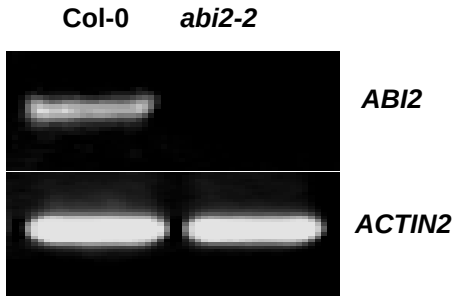
B, qRT-PCR analysis showing elevated expression of *RHA2a* in *RHA2a* overexpression transgenic line 7. *ACTIN2* primers were used as an internal control.

C and D, Seed germination time course of *RHA2b OE* 1# and *RHA2b OE* 9# grown on medium without ABA (C) or containing 0.5 μM ABA (D). Data shown are mean±SD of three replicates. At least 100 seeds per genotype were measured in each replicate.

E, Photographs of young seedlings at 5 d after the end of stratification. Seeds were germinated and allowed to grow on horizontal agar media containing 0 and 0.3 μM ABA. The pictures were taken at 5 d after the end of stratification.

F, Cotyledon greening percentage of the seedlings described in (E). Values represent mean±SD of three replicates. At least 30 seedlings per genotype were measured in each replicate.

Asterisks in A, B and F indicate significance of the difference from the corresponding wild-type values determined by Student's *t*-test (** $P<0.01$). At least three independent experiments were conducted and similar results were obtained.



Supplemental Figure S5. Expression of *ABI2* in the *abi2-2* (Salk_015166) mutant.
RT-PCR analysis showing no expression of *ABI2* in *abi2-2* mutant. *ACTIN2* primers were used as an internal control.