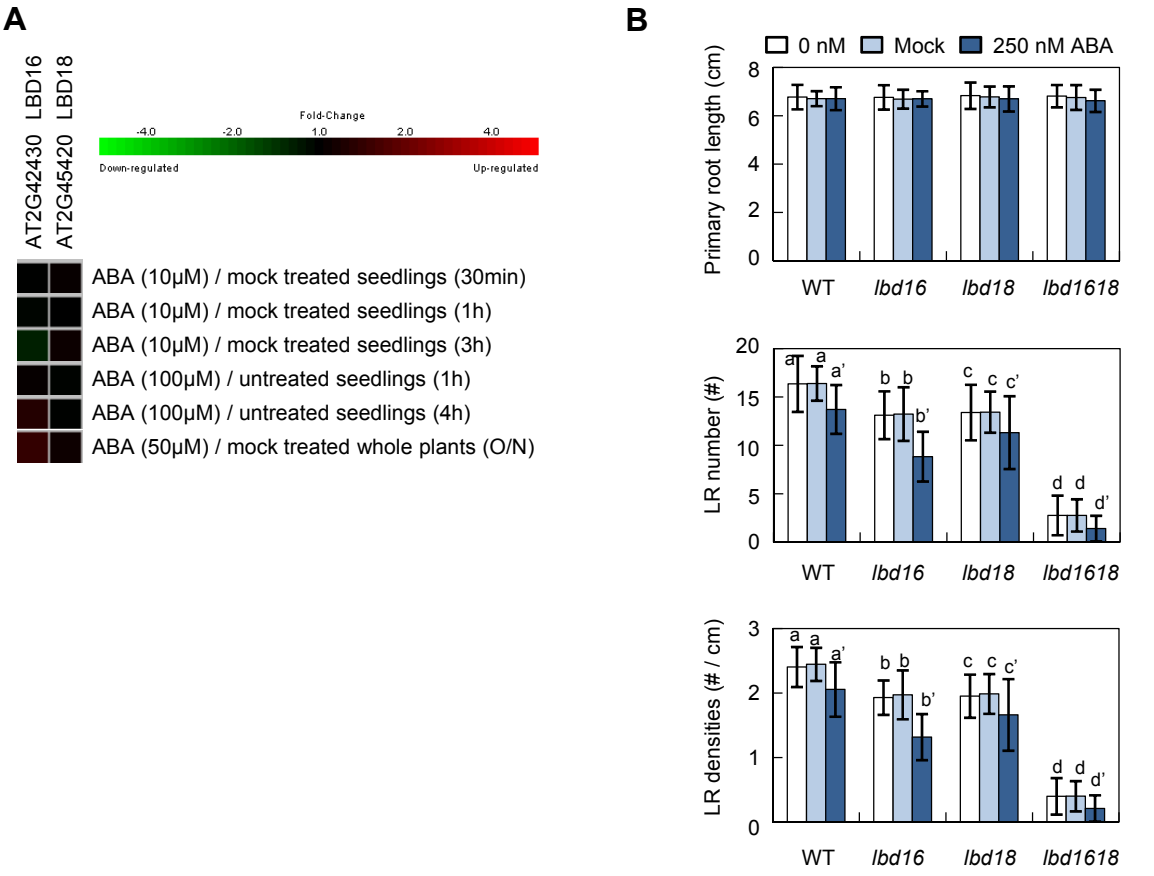
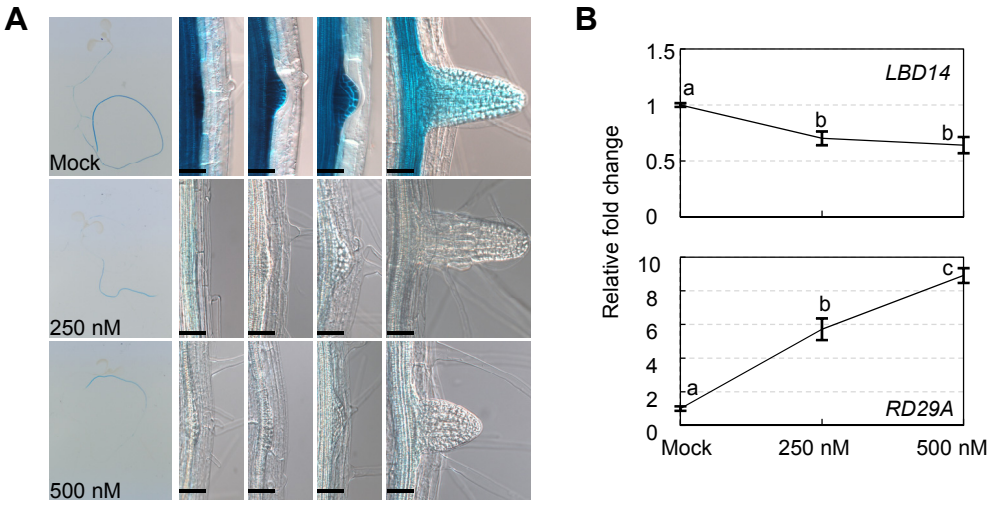
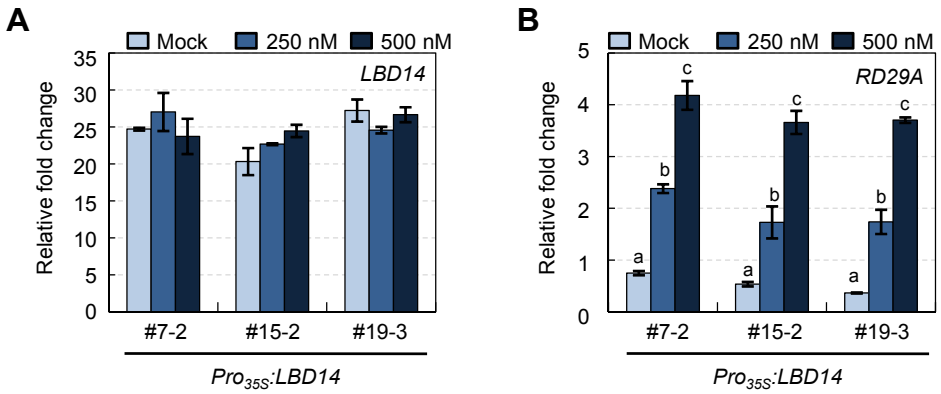



**Supplemental Fig. S4** Analysis of LR phenotype of wild-type, *lbd16*, *lbd18*, and *lbd16 lbd18* with varying concentrations of ABA. (A) *In silico* analysis of *LBD16* and *LBD18* expression in response to ABA. The heat map represents the relative values from the ratios of treatment versus control values using the perturbations tool of Genevestigator (www.genevestigator.ethz.ch). The red color, green color, and black color stand for up-, down-, and unchanged expression, respectively. (B) Primary root length, LR numbers, and LR densities of wild-type, *lbd16*, *lbd18*, and *lbd16 lbd18* mutant plants in the presence of ABA. Plants were grown and treated with ABA as described in Fig. 7A. *lbd16,18* indicates *lbd16 lbd18* double mutant. Mean ± SD values were determined from 25 seedlings. Bars with apostrophes indicate significant differences at $P < 0.05$ in the given genotype by one-way ANOVA and the Tukey's honestly significant difference test.




**Supplementary Fig. S5** Expression of *LBD14* in response to ABA. (A) GUS staining of *Pro*$_{LBD14}$*:GFP:GUS* transgenic Arabidopsis in the presence and absence of ABA. Plants were grown vertically for 3 days on a 0.5 X MS agar plate, then transferred to a 0.5 X MS agar plate containing 0, 250, or 500 nM of ABA, and incubated vertically for additional 4 days, followed by GUS staining. The first left panel shows GUS expression of root tissues. The rest four panels show GUS expression of lateral root primordium at different stages of development and the emerged LR. Scale bars = 50 ㎛. (B) The qRT-PCR analysis of *LBD14* expression in the root tissue in response to ABA. Plants were grown vertically for 7 days on 0.5 X MS agar plate, and then incubated with 0, 250, or 500 nM of ABA for additional 1 day. Total RNAs were subjected to qRT-PCR. *RD29A* was used as a marker gene for ABA response. Relative fold changes were plotted as the ratio of the given treatment relative to the transcript level of *LBD14* or *RD29A* in the wild type treated with mock after normalization to *ACTIN7*. Mean ± values were determined from three biological replicates (each biological replicate was estimated as the average of two technical qRT-PCR replicates.). Bars with different letters indicate significant differences at $P < 0.05$ by one-way ANOVA and the Tukey's honestly significant difference test.




**Supplementary Fig. S6** Quantitative RT-PCR analysis of *LBD14* (A) or *RD29A* (B) expression in the root tissue of *Pro$_{35S}$:LBD14* transgenic plants in response to ABA. Plants were grown vertically for 3 days on a 0.5 X MS agar plate, then transferred to a 0.5 X MS agar plate containing each concentration of ABA, and incubated vertically for additional 4 days. *RD29A* was used as a marker gene for ABA response. Relative fold changes were plotted as the ratio of the given treatment relative to the transcript level of *LBD14* or *RD29A* in the wild type treated with mock after normalization to *ACTIN7*. Mean ± values were determined from three biological replicates (each biological replicate was estimated as the average of two technical qRT-PCR replicates.). Bars with different letters indicate significant differences at $P < 0.05$ by one-way ANOVA and the Tukey's honestly significant difference test.