

Fig. S1. Phenotype of *RD26* overexpression and repression lines. (A) Phenotype of *35Spro:RD26* and *35Spro:RD26:SRDX* lines. Plants in the upper row are the T1 generation of *35Spro:RD26:SRDX* and those in the lower row are *35Spro:RD26*. All plants are 3 weeks old, and the corresponding Col wild type is shown on the left. (B) Phenotype of 4-week-old *35Spro:RD26* transgenic lines. Scale bar = 1 cm. (C) qRT-PCR analysis of *RD26* transcript levels. Error bars = SD (n=20).

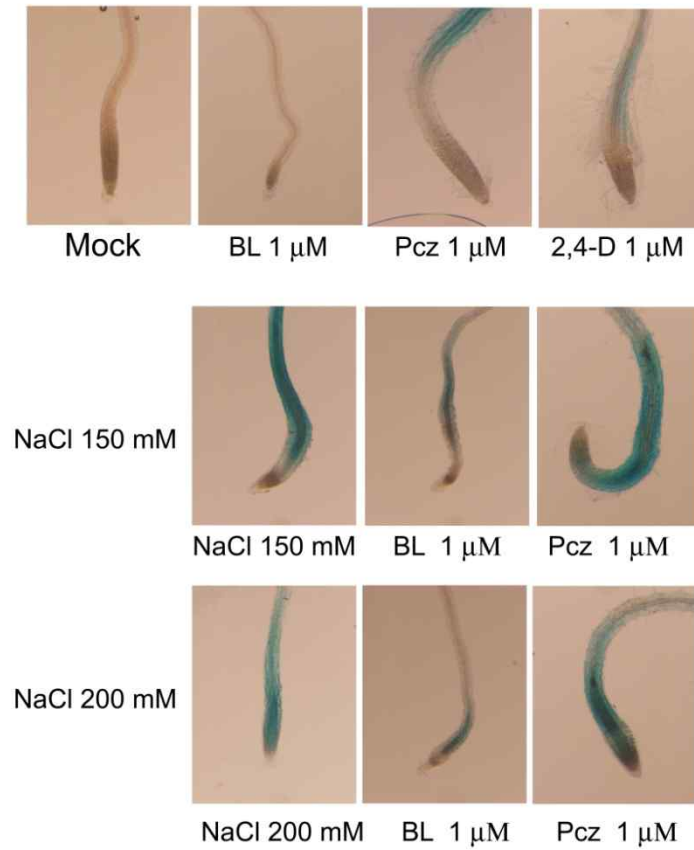


Fig. S2. Morphology and GUS staining pattern of Columbia root tips. Root tips were pre-treated with *epi*-BL or Pcz and then incubated in 200 mM NaCl plus *epi*-BL or Pcz for 2 more days.

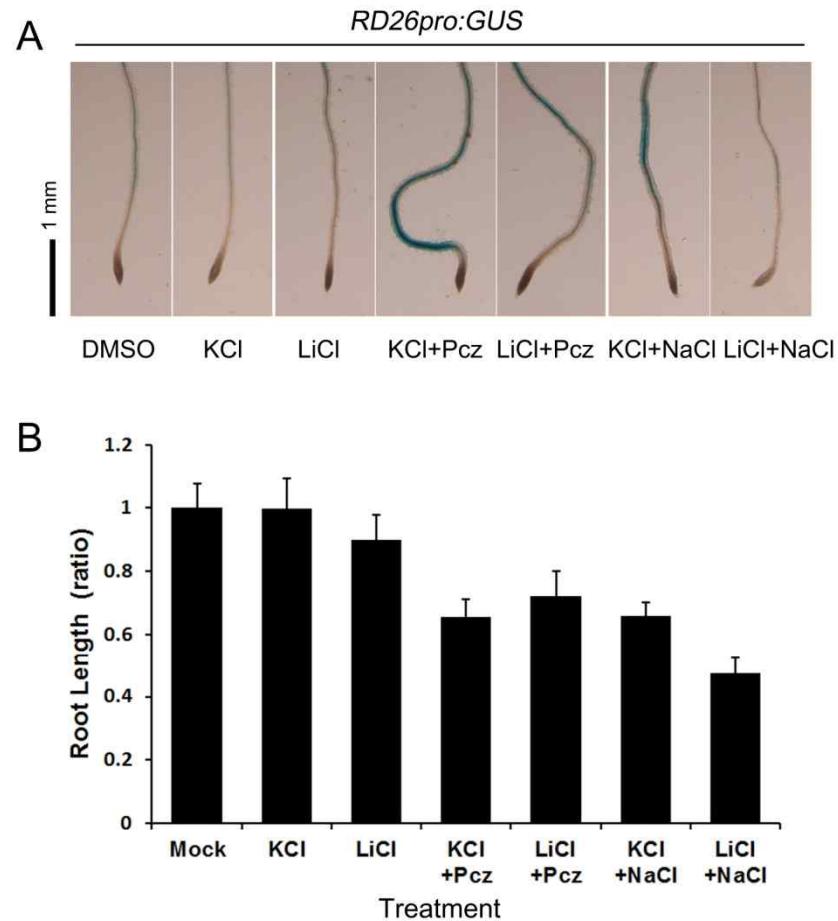


Fig. S3. Root length and GUS histochemical staining pattern of *RD26pro:GUS* in plants. (A) GUS histochemical staining pattern in the roots of *RD26pro:GUS* plants grown in the presence or absence of Pcz, LiCl, and KCl. (B) Root growth inhibition of seedlings treated with LiCl, KCl and Pcz, LiCl and Pcz, KCl and NaCl, and LiCl and NaCl. Error bar = SD (n=18).

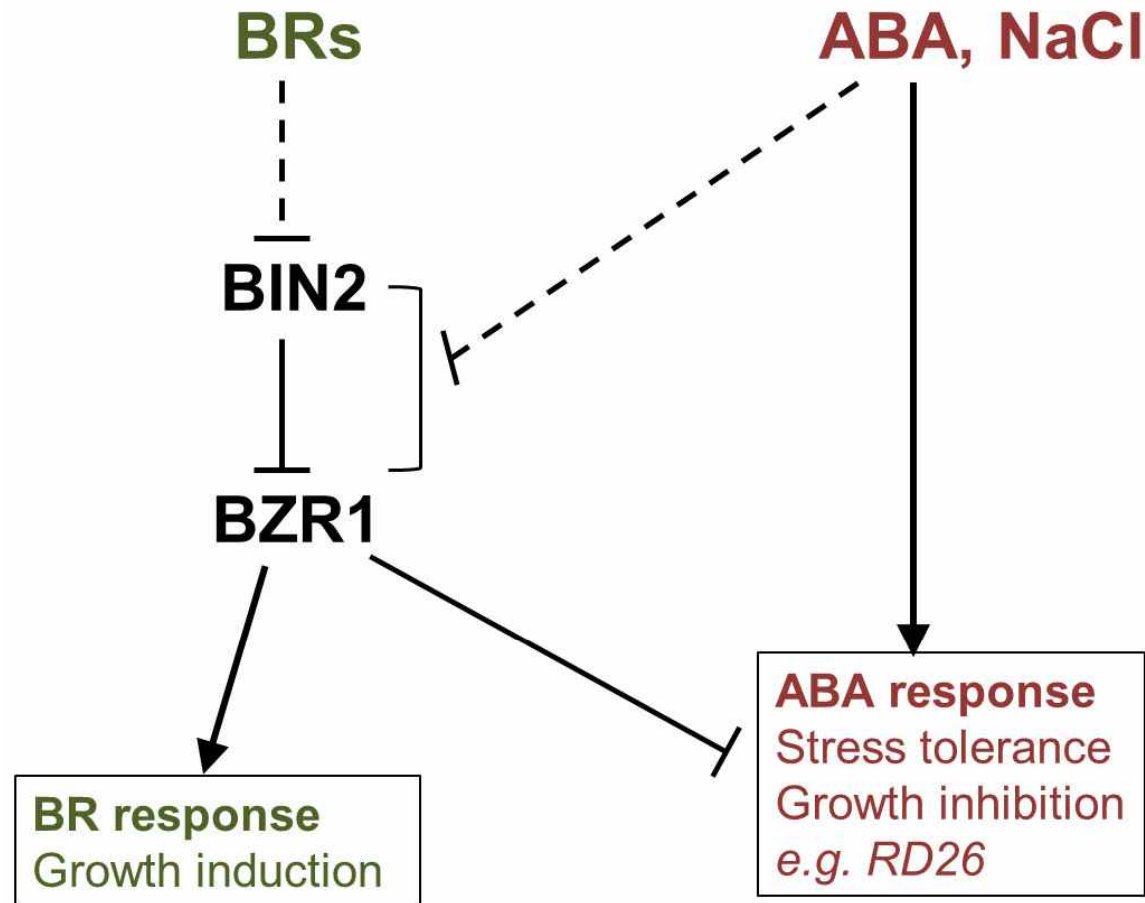


Fig. S4. Proposed model of BR and ABA cross regulation. Illustration of the proposed interaction between BRs and ABA in controlling growth and stress tolerance. BRs induce the BR response through the BZR1 transcription factor, and repress stress tolerance genes. In contrast, ABA upregulates stress tolerance genes, repressing the BIN2-dependent growth pathway of BR and thereby fine-tuning plant growth during stress conditions.