

Supporting Information

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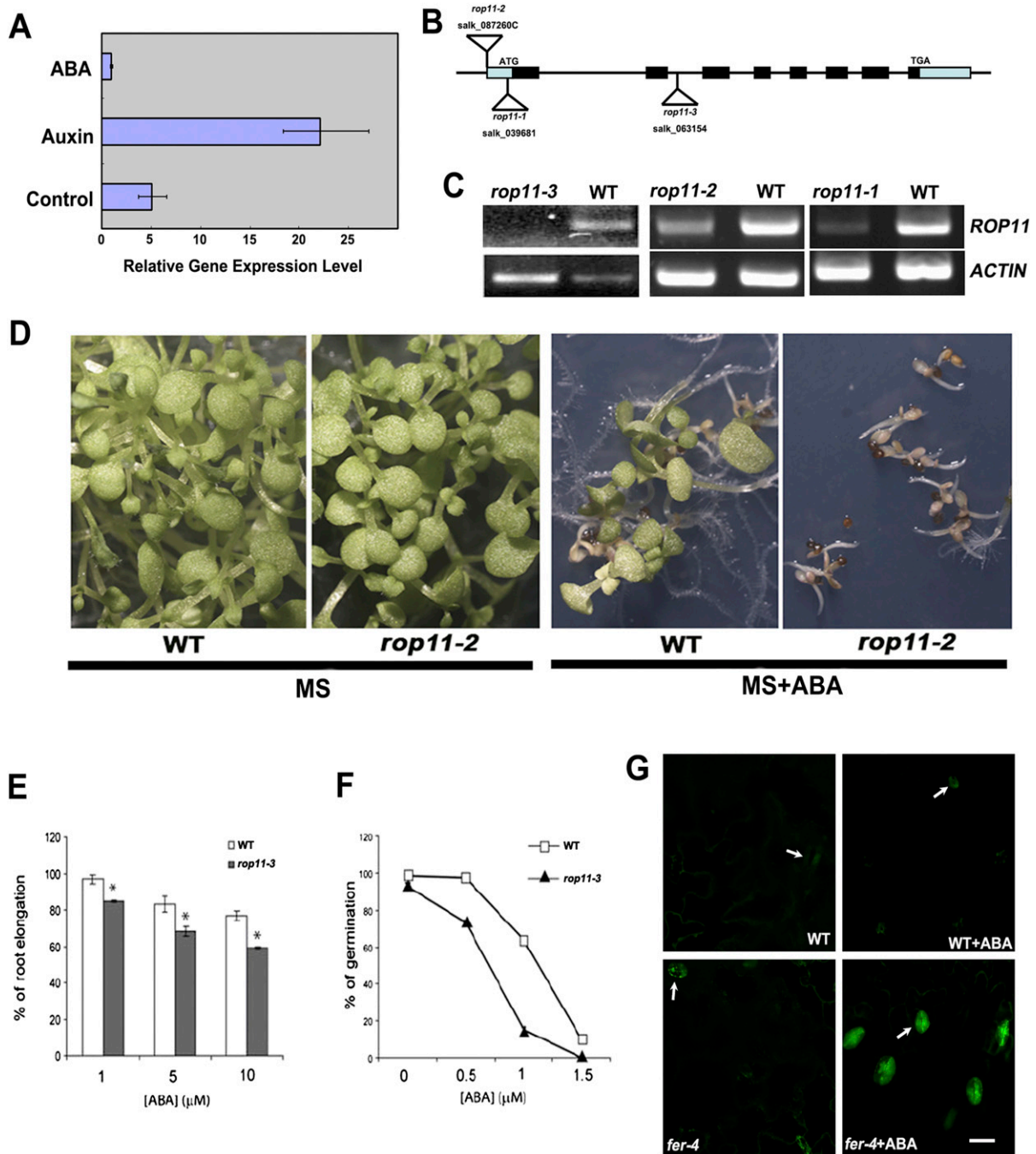


Fig. S1. Hormone-regulated *FER* expression and phenotypic analyses of *rop11/arc10*. (A) Quantitative RT-PCR analysis of *FER* transcripts under auxin and ABA treatments (*Materials and Methods*). Three independent experiments yielded similar results. (B) Scheme of *ROP11/ARAC10* gene organization and position of T-DNA insertions. The ATG start codon and TGA stop codon are indicated; boxes are exons, and lines are introns. The exact site for T-DNA insertions (indicated by triangles) was mapped by PCR and DNA sequencing of the PCR products. (C) RT-PCR analysis showing levels of *ROP11/ARAC10* transcripts in *rop11/arc10-1*, *rop11/arc10-2*, and *rop11/arc10-3* mutant lines. *ACTIN2* were used as loading control. (D) ABA sensitivity of WT and mutant seedlings. Physiologically comparable seeds of WT and *rop11/arc10-2* mutant were sterilized and plated on MS medium supplemented with 0 or 2 μ M ABA at 23 °C for 12 d. (E) ABA inhibition of root elongation. *rop11/arc10-3* seedlings are more sensitive to inhibition of root elongation by ABA compared with WT. Data represent average \pm SE of three independent experiments with 10 seedlings each. (F) *rop11/arc10-3* seeds are more responsive to ABA inhibition during germination. Data represent average \pm SE of three independent experiments with \sim 100 seeds each. (G) ROS production in guard cells of WT and *fer-4* mutant with or without ABA, indicated by fluorescent dye 2', 7'-dichlorodihydro-fluorescein diacetate.

