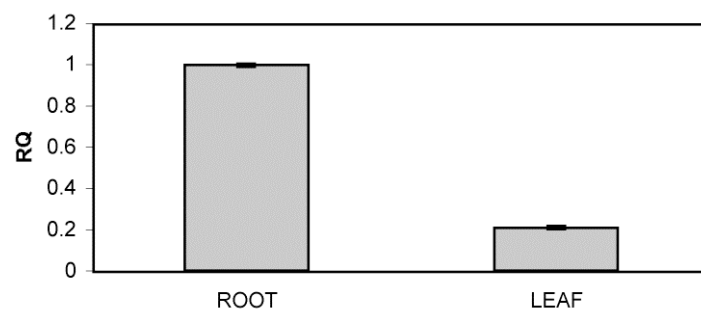
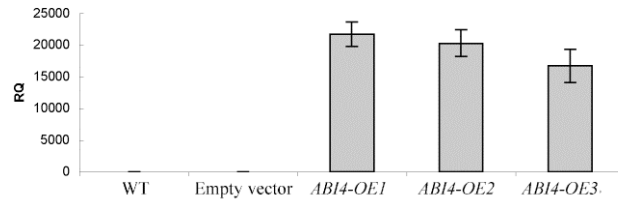


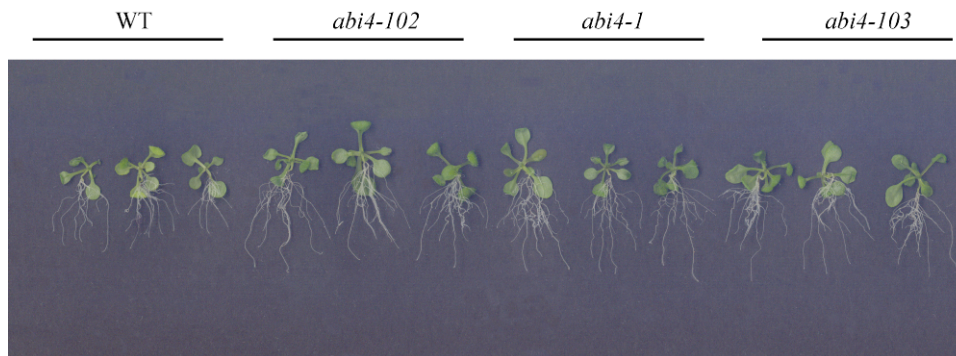
**Supplemental Figure 1.** GUS staining of *ABI4:GUS* plants. (A) Three-day-old seedlings germinating on 0.5x MS medium. (B) Three-day-old seedlings germinating on 0.5x MS medium supplemented with 7% glucose. (C) Rosette leaves of 2-week-old plant. (D) Open flower. (E) Silique. (F) Petiole base.



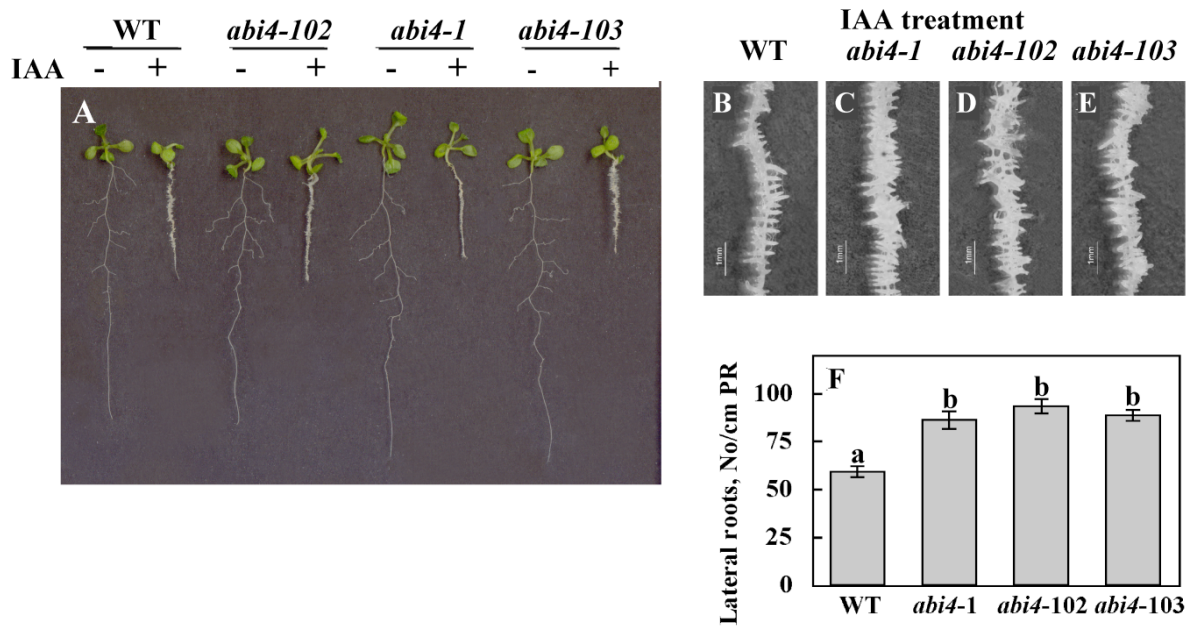
**Supplemental Figure 2.** *ABI4* overexpression in root and leaf tissues. RNA was extracted from two-week-old seedlings, and RNA levels were quantified using qRT-PCR, with the expression in the roots defined as 1.



**Supplemental Figure 3.** Quantification of dexamethasone-induced *ABI4* overexpression in transgenic *Arabidopsis* plants harboring the *pOp6:ABI4* construct. Five-day-old seedlings were treated with 10  $\mu$ M dexamethasone. RNA was extracted 9 d later, and RNA levels were quantified using qRT-PCR, with the expression of wild-type plants defined as 1.



**Supplemental Figure 4.** Auxin treatment of *abi4* mutants. Wild-type and *abi4* mutants were germinated on solid 0.5x MS medium containing 2  $\mu$ M IAA. Plants were photographed 3 weeks later.



**Supplemental Figure 5.** Lateral root formation in IAA-treated *abi4* mutants. Seventeen-day-old seedlings were transferred to 0.5x MS medium or to 0.5x MS medium supplemented with 20  $\mu$ M IAA. Photograph was taken 4 d later. **(A)** Whole seedlings. **(B)** to **(E)** Close-up of roots of IAA-treated plants shown in **(A)**: **(B)** wild-type, **(C)** *abi4-1* mutant, **(D)** *abi4-102* mutant, **(E)** *abi4-103* mutant. **(F)** Quantitative analysis of the entire root system of IAA-treated seedlings such as those shown in **(B)** to **(E)**. Bars with different letters represent statistically different values by Tukey's HSD post-hoc test ( $P \leq 0.05$ ).

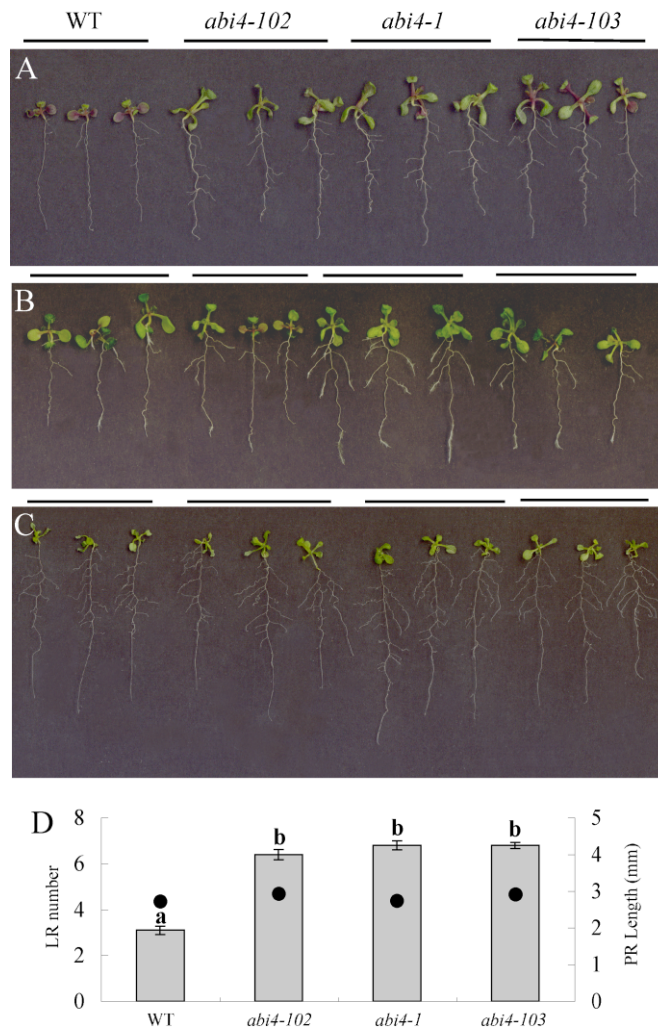


**Supplemental Figure 6.** *DR5:GUS* expression pattern is altered on the background of *abi4* mutation.

**(A)** GUS staining of *DR5:GUS*/wild type root system of 12-day-old seedling.

**(B)** GUS staining of homozygous *DR5:GUS/abi4-1* mutants 12-day-old seedlings.

Arrowheads indicate GUS staining foci.



**Supplemental Figure 7.** Lateral root formation in cytokinin-treated wild-type and *abi4*-mutant *Arabidopsis*.

(A) to (C) One-week-old seedlings were transferred to 0.5x MS medium (C) or to 0.5x MS medium supplemented with 20  $\mu$ M zeatin (A) or 20  $\mu$ M 6-benzylaminopurine (6-BA) (B). Photograph was taken 10 d later.

(D) Quantitative analysis of data shown in (A). Bars, LR number, Dots, length of primary roots. Bars with different letters represent statistically different values by Tukey's HSD post-hoc test ( $P \leq 0.05$ ).

**Supplemental Table 1.** Genes whose steady state mRNA levels are not altered in roots of *abi4* mutants and *ABI4*-OE plants. mRNA levels were determined by qRT-PCR. Expression levels between these analyzed plant lines differed from wild type by < 20%.

Gene name	Gene locus
<i>AUX1</i>	AT2G38120
<i>EIN2</i>	AT5G03280
<i>ERA1</i>	AT5G40280
<i>IAA14</i>	AT4G14550
<i>IAA19</i>	AT3G15540
<i>IAA28</i>	AT5G25890
<i>LRP1</i>	AT5G12330
<i>PIN1</i>	AT1G73590
<i>TIR1</i>	AT3G62980

**Supplemental Table 2. Primer list**

Primer	Sequence	Application
ABI4 FOR <i>Bam</i> HI	ATGGATCCATACGGTAGATTAGTCTTTCTAGG	<i>ABI4</i> promoter cloning
ABI4 REV <i>Eco</i> RI	GCCTTAAGAGATGAAGAAGAAGAAGAAGA	<i>ABI4</i> promoter cloning
ABI4 FOR <i>Sal</i> I	TAGTCGACATGGACCCTTTAGCTTC	<i>ABI4</i> coding region cloning
ABI4 REV <i>Sal</i> I	CAGTCGACTTAATAGAATCCCCCAAG	<i>ABI4</i> coding region cloning
ABI4 FOR	TTACCGTGGCGTTTCGACAA	qRT-PCR
ABI4 REV	GAGTGCGCTTACGTGGCTCT	qRT-PCR
18S FOR	AAGCAAGCCTACGCTCTGGA	qRT-PCR
18S REV	AGGCCAACACAATAGGATCGA	qRT-PCR
AUX1 FOR	TTGGCCTTGGAATGACCACT	qRT-PCR
AUX1 REV	ATGTTTCACACCTTCCGCCT	qRT-PCR
EIN2 FOR	TATGACAAGTGGACGTGCATGTT	qRT-PCR
EIN2 REV	GCAACTCCCACAACCATGGT	qRT-PCR
ERA1 FOR	ACACAGTGTGGCATTTCAGGC	qRT-PCR
ERA1 REV	TGCGTTCGATGAACTCGAG	qRT-PCR
IAA14 FOR	CCTTCTAAGCCTCCTGCTAAAGC	qRT-PCR
IAA14 REV	CCGCTCTTCTGATTAGCCATAAC	qRT-PCR
IAA19 FOR	CATCGGTGTGGCCTTGAAA	qRT-PCR
IAA19 REV	GCGAGCATCCAGTCTCCATC	qRT-PCR
IAA28 FOR	TCATTCCCTTCCAATAACAGGGTT	qRT-PCR
IAA28 REV	TGTGCCGTTAGGTTTCTCCG	qRT-PCR
LRP1 FOR	CAAGACGGAGGAGGGTCAAG	qRT-PCR
LRP1 REV	CGTCCTCCACTGCCGTTACT	qRT-PCR
PIN1 FOR	AACGACAACCAGTACGTGGAGA	qRT-PCR
PIN1 REV	GCTTATGTTGTTCCCACCGTC	qRT-PCR
TIR1 FOR	TGCAGGAATCTGAAAGAGCTTG	qRT-PCR
TIR1 REV	GGAAATGGCTAAGCCAGTGG	qRT-PCR