Fig. S1

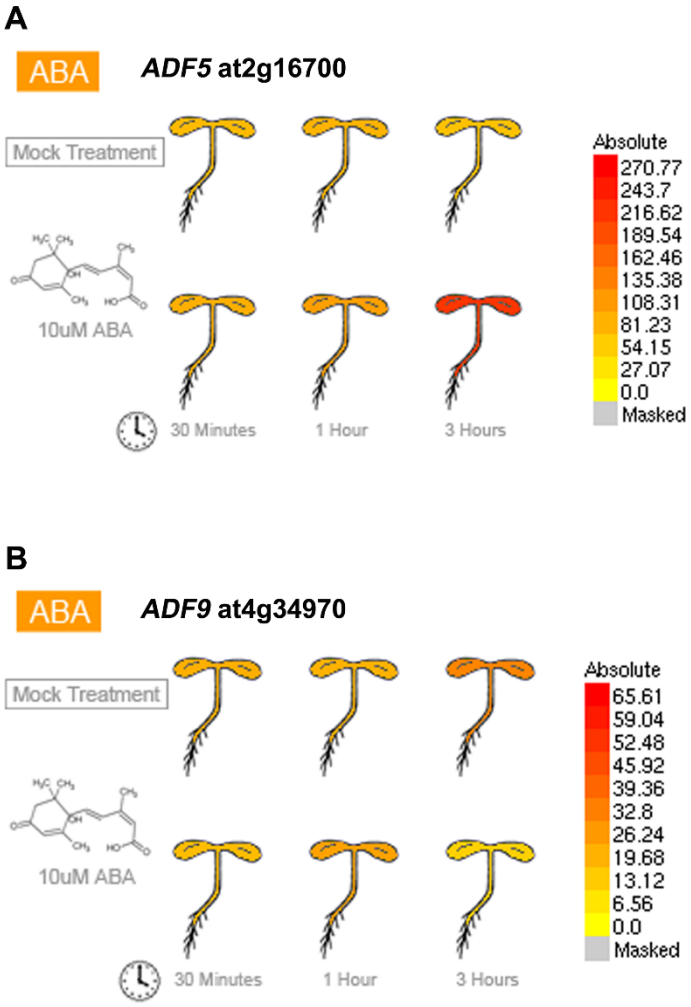

Fig. S1. *ADF5* expression is induced by ABA from microarray analysis.

(A) The expression level of *ADF5* is upregulated by ABA from the e-FP browser (http://bbc.botany.utoronto.ca/efp/cgi-bin/efp). Red indicates high expression, and blue scale denotes low expression. (B) The expression levels of ADF9 after ABA treatment from the e-FP browser (http://bbc.botany.utoronto.ca/efp/cgi-bin/efp). Red indicates high expression, and blue scale denotes low expression.

Fig. S2

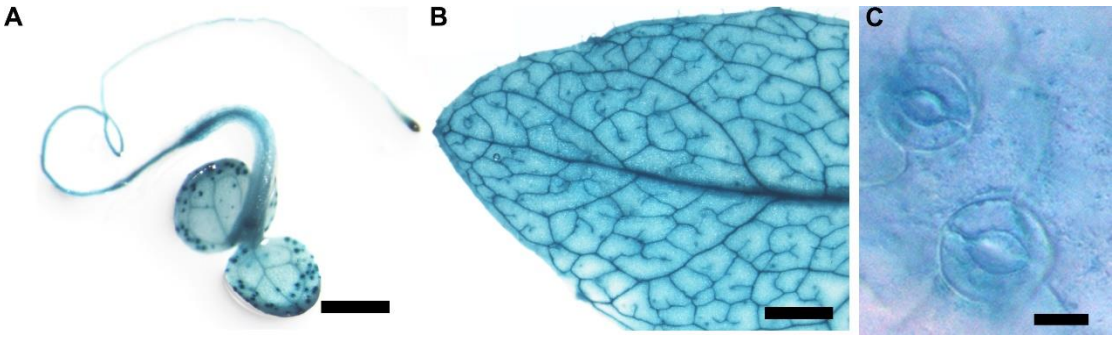

Fig. S2. Analysis of ADF5 expression patterns.

The GUS activity in the PBI121-ADF5Pro-GUS transgenic plants in cotyledon (A), rosette leaf (B) and guard cells (C).

Fig. S3

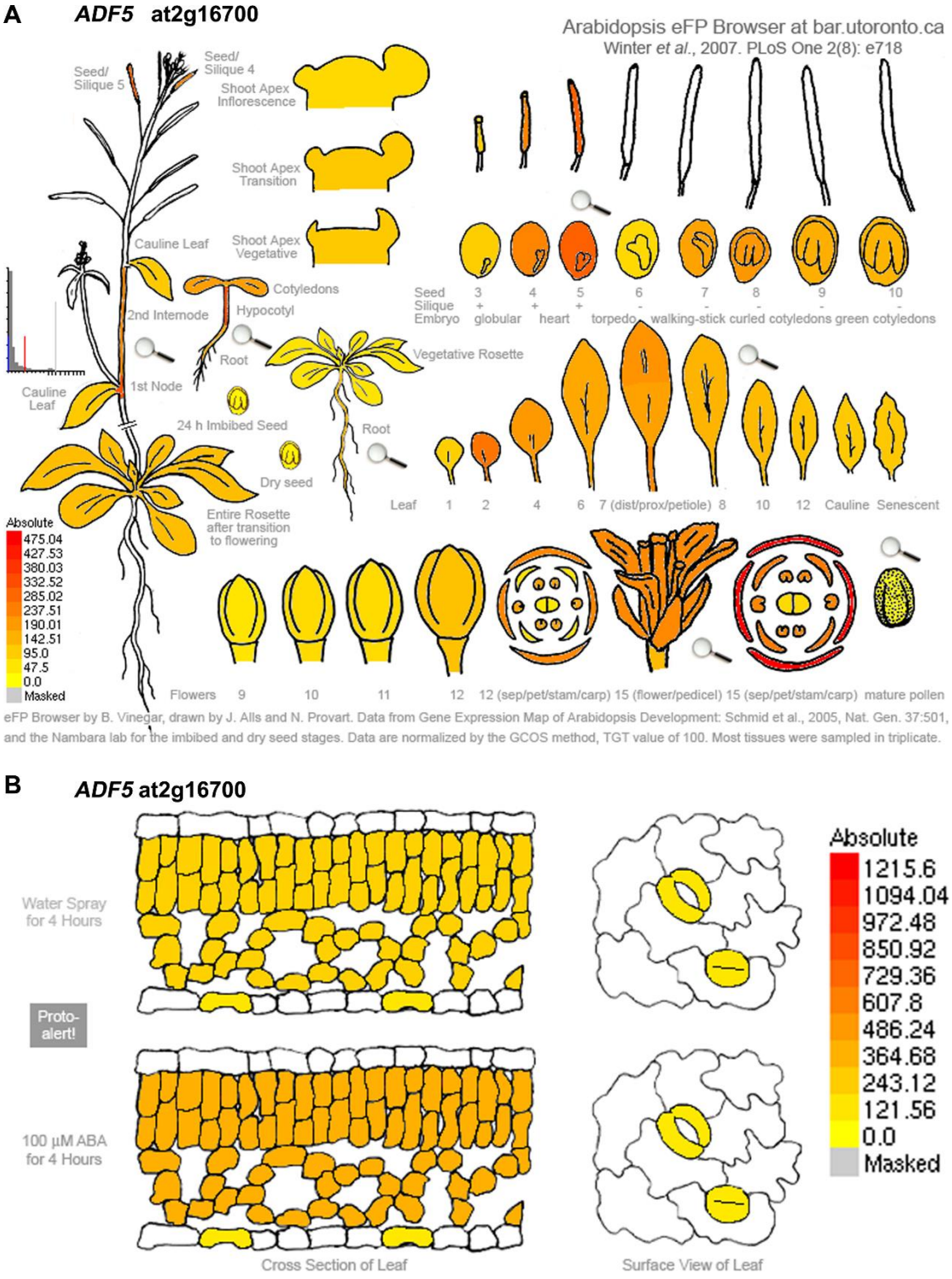

Fig. S3. *ADF5* expression in leaves and guard cells.

(A) and (B) The expression level of *ADF5* in leaves and guard cells from the e-FP browser (http://bbc.botany.utoronto.ca/efp/cgi-bin/efp). Red indicates high expression, and blue denotes low expression.

Fig. S4

Fig. S4. The prediction of ABRE core motif and GCEs in the *ADF5* promoter.

The prediction of ABRE core motif and GCEs in the *ADF5* promoter.

Fig. 5

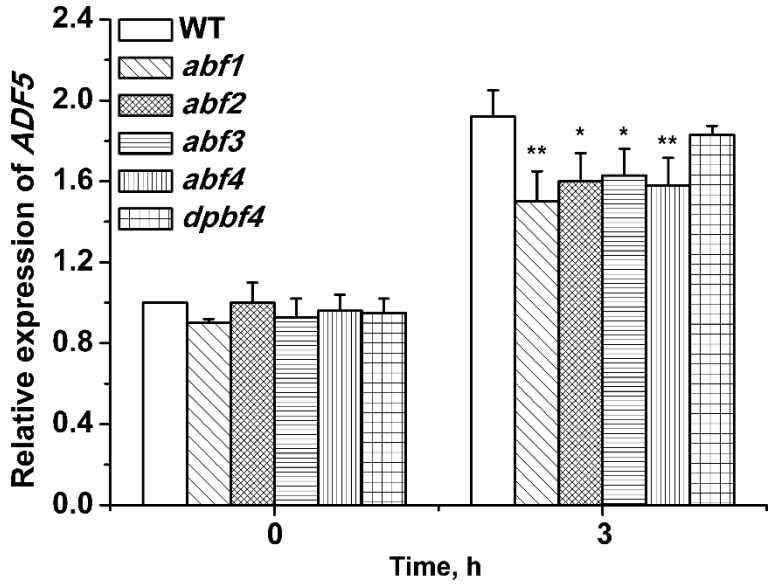

Fig. S5. Expression of *ADF5* in WT and *abf/areb* mutant plants.

qRT-PCR analysis revealed *ADF5* expression by ABA. Fourteen-day-old seedlings were treated with 40 μM ABA for different times, and the leaves of seedling were detached for RNA extraction. *UBQ11* was used as an internal gene.

Fig. S6

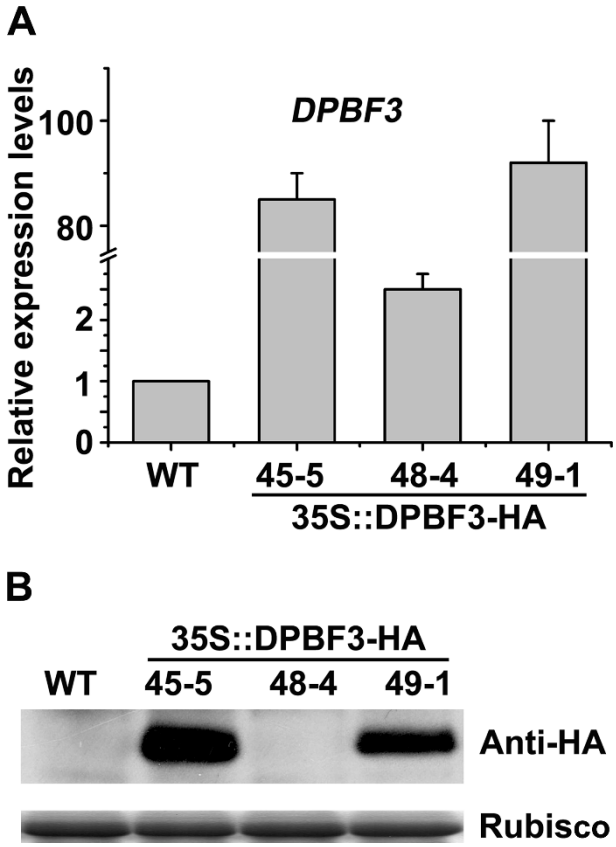

Fig. S6. Identification of the DPBF3 overexpression transgenic lines.

(A) qRT-PCR analysis of *DPBF3* expression in 35S:DPBF3-HA overexpression plants.

(B) Immunoblot analysis of DPBF3 by HA monoclonal antibody in WT and 35S:DPBF3-HA overexpression plants. Rubisco stained by Coomassie brilliant blue was used as an internal loading control.

Fig. S7

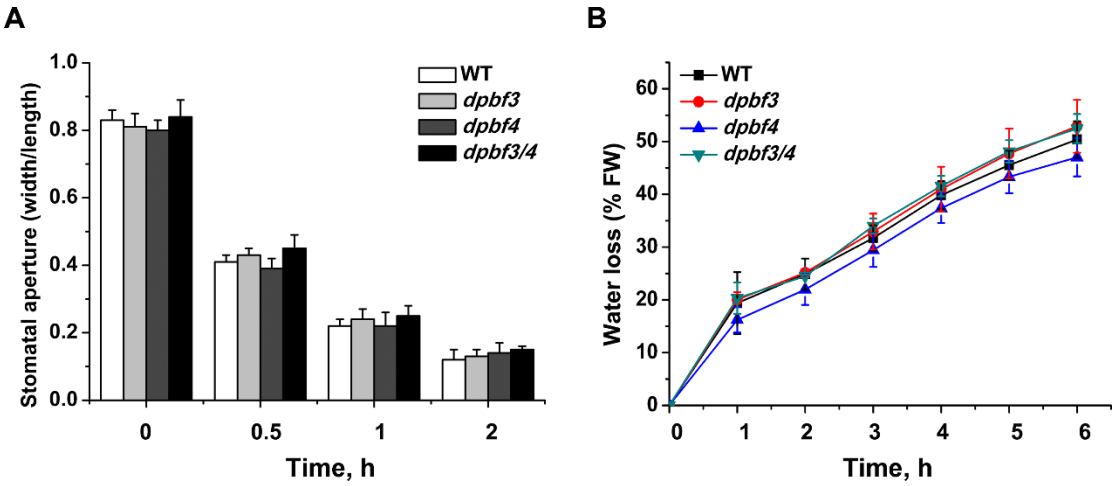

Fig. S7. Phenotypic comparison of stomatal closure and water loss among WT, *dpbf3*, *dpbf4* and *dpbf3/4* plants.

(A) The phenotype comparison of the stomatal closing rate of WT, *dpbf3*, *dpbf4* and *dpbf3/4* plants induced by ABA. (B) Analysis of water loss from the detached leaves of WT, *dpbf3*, *dpbf4* and *dpbf3/4* plants. The data represent the mean ± SE based on three independent biological replicates.

Fig. S8

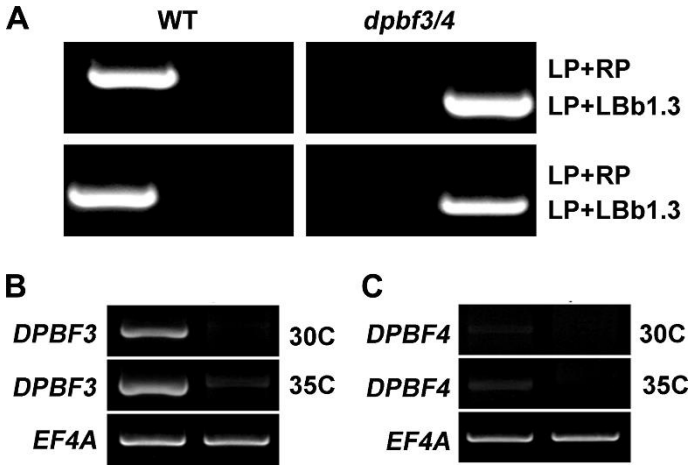

Fig. S8. Identification of the T-DNA insertion in the *dpbf3/4* homozygous mutants. (A) *dpbf3/4* homozygous T-DNA insertion mutant identification by PCR. LP and RP are mutant-specific gene primers, and LBb1.3 indicates the T-DNA left border primer. (B) and (C) RT-PCR analysis of *DPBF3* and *DPBF4* expression in WT and *dpbf3/4* double mutant lines.

Fig. S9

ADF1

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ADF2

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ADF4

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ADF9

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Fig. S9. The prediction of ABRE core motif and GCEs in the ADFs promoter.

The prediction of ABRE core motif and GCEs in the ADFs promoter.

Fig. S10

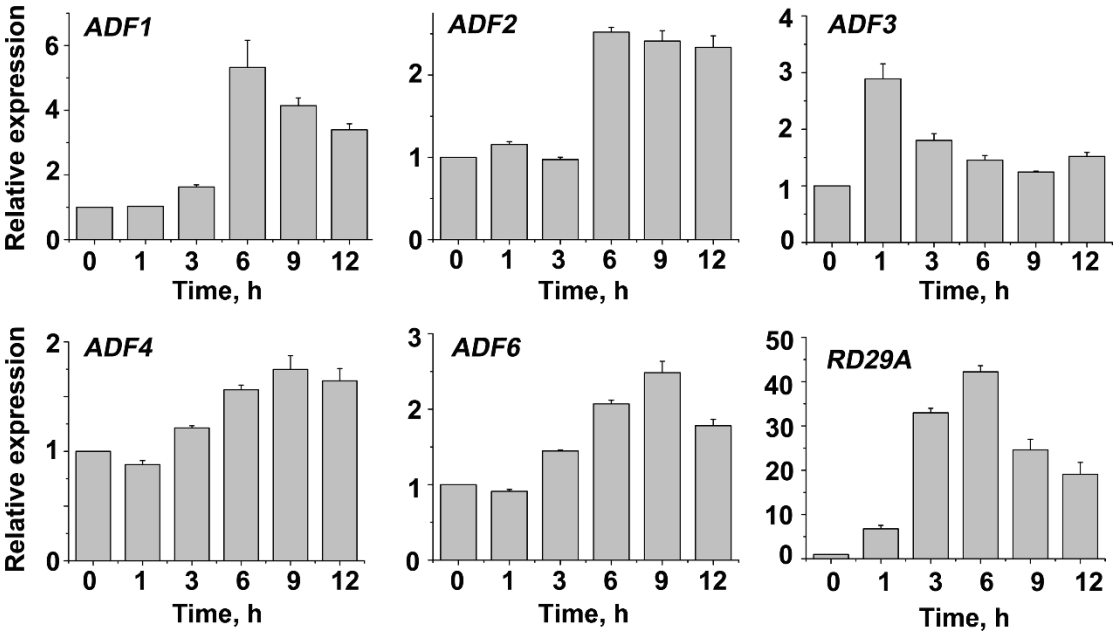

Fig. S10. The expression levels of *ADFs* induced by ABA.

qRT-PCR analysis was used to measure *ADF* (1/2/3/4/6) and *RD29A* expression by ABA. Fourteen-day-old seedlings were treated with 40 μM ABA for different times, and the leaves of seedling were detached for RNA extraction. *UBQ11* was used as an internal gene.