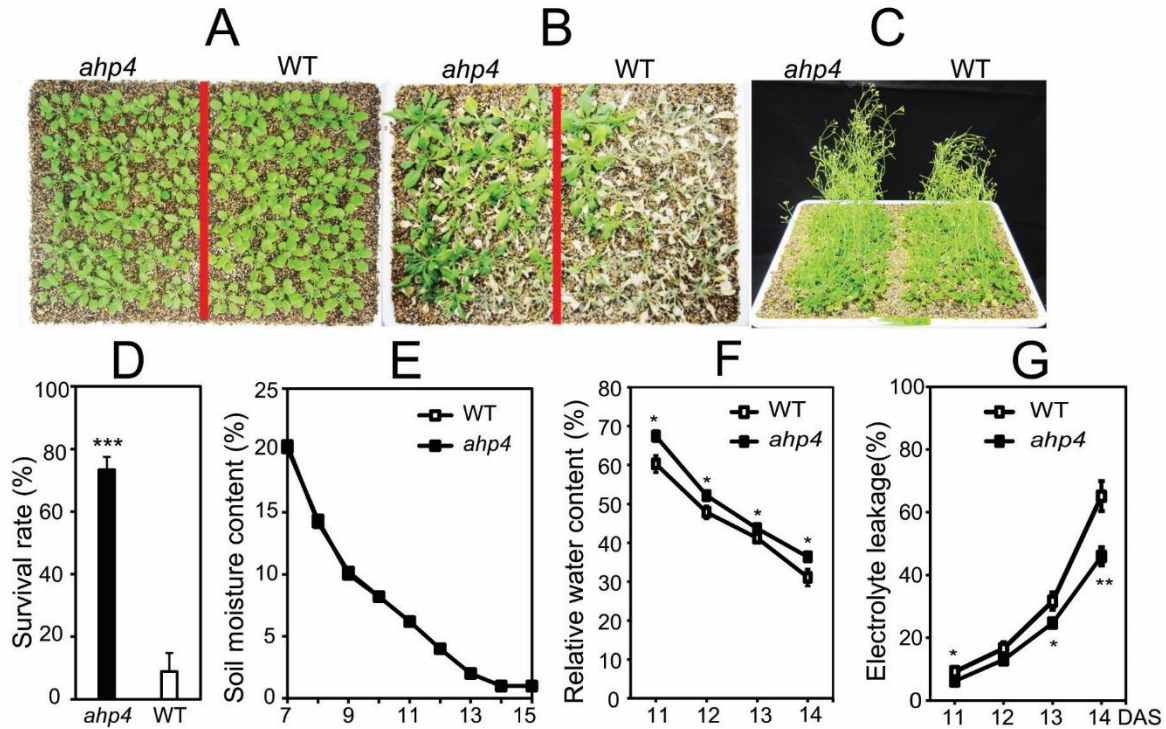
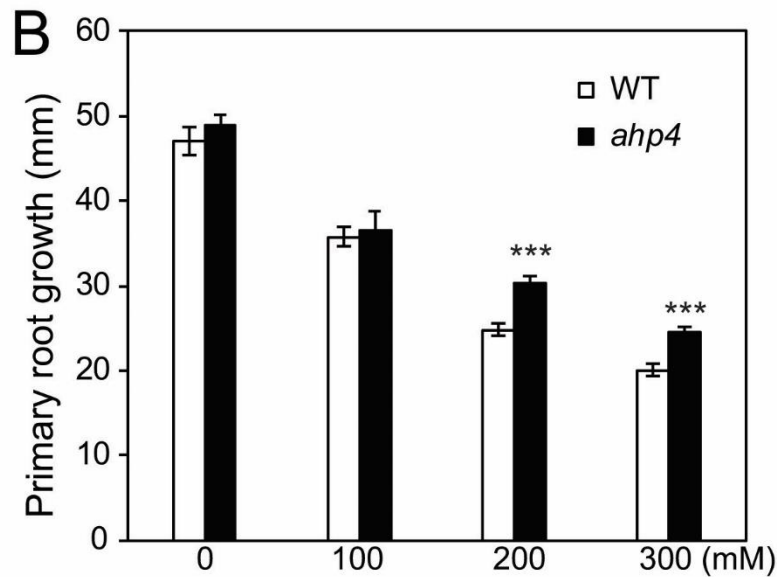
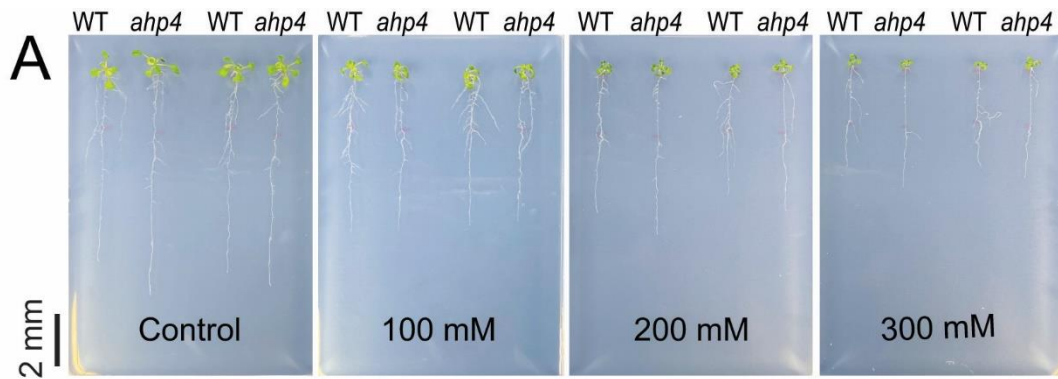


SUPPLEMENTAL DATA



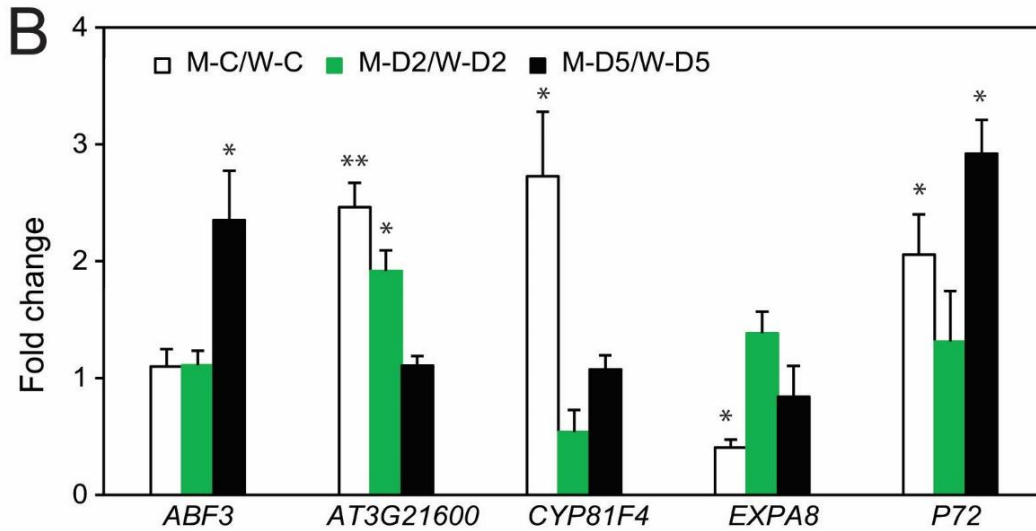
**Figure S1. Drought-tolerant phenotype of the *ahp4* mutant plants.** A, Two-week-old *ahp4* and wild-type (WT) plants were transferred from germination medium plates to soil and grown for one additional week. B, Three-week-old plants were subjected to drought for 15 days and plants were photographed three days subsequent to rewatering and after removal of inflorescences. C, Five-week-old plants were grown on the soil in well-watered control conditions. D, Plant survival rates and standard errors (SEs) ( $n = 3$ , where each replicate represents the survival plant rate of 30 plants/genotype). E, Soil moisture content was recorded during the water withholding ( $n = 5$  positions/genotype/day). F, Relative water contents of *ahp4* and WT plants grown and subjected to water withholding treatment as described in (A-B). Data represent the means and SEs ( $n = 5$ /genotype). G, Electrolyte leakage rates of *ahp4* and WT plants grown and subjected to drought treatment as described in (A-B). Data represent the means and SEs ( $n = 5$ /genotype). Asterisks indicate significant differences between the two genotypes as determined by a Student's *t*-test (\* $P < 0.05$ , \*\* $P < 0.01$ , \*\*\* $P < 0.001$ ). DAS, days after stress.



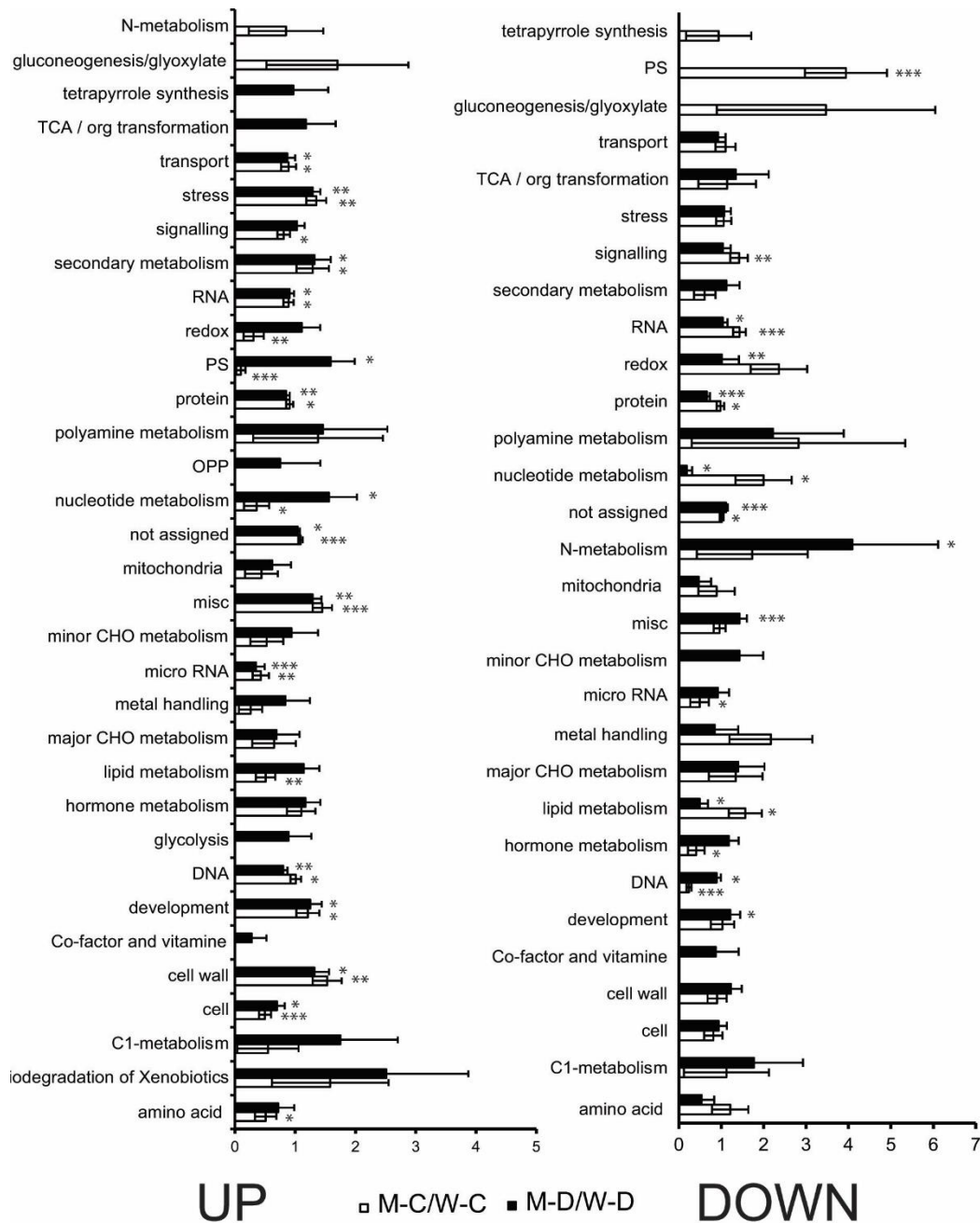
**Figure S2. A representative assay of root growth of *ahp4* mutant and wild-type (WT) plants under normal and mannitol-induced osmotic stress conditions.** A, Seven-day-old *ahp4* and WT plants grown on germination medium were transferred onto  $0.5 \times$  MS plates (1.2% w/v agar) with or without mannitol and grown for 7 additional days. B, Primary root growth of seven-day-old *ahp4* and WT plants grown under normal and mannitol conditions for 7 additional days. Data present the means and standard errors ( $n = 18$  plants/genotype). Asterisks indicate significant differences between the two genotypes as determined by a Student's *t*-test ( $***P < 0.001$ ).

**A**

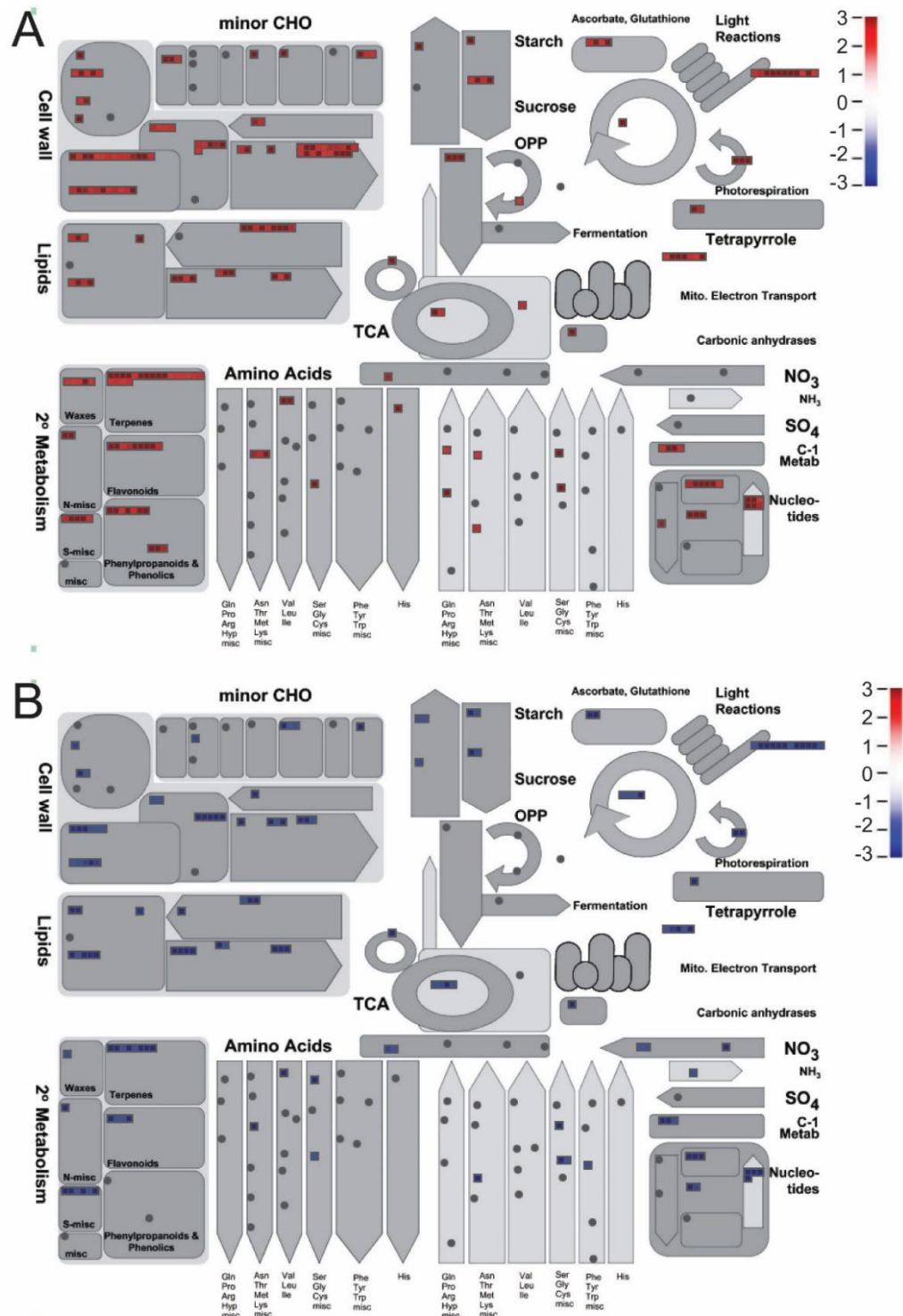
AGI	Gene description	M-C / W-C		M-D2 / W-D2		M-D5 / W-D5	
		q-value	Fold change	q-value	Fold change	q-value	Fold change
AT4G34000	<i>ABF3</i>	0.5779	0.6828	0.4793	3.4051	0.0202	5.1985
AT3G21600	Dehydration-associated protein-like protein	0.0109	2.1202	0.0878	1.3197	0.1450	0.6364
AT4G37410	<i>CYP81F4</i>	0.0285	9.8801	0.3303	0.5558	0.4122	0.6257
AT2G40610	<i>EXPA8</i>	0.0385	0.4844	0.5403	1.2889	0.7679	0.7244
AT5G66390	<i>P72</i>	0.0048	4.7093	0.6973	1.2666	0.3435	1.3136



**Figure S3. Confirmation of microarray data by real-time quantitative PCR (RT-qPCR) analysis.** Five genes were selected, and their expression patterns were examined by RT-qPCR in the leaf samples of non-dehydrated and dehydrated *ahp4* mutant and wild-type (WT) plants to validate the microarray data. A, Fold changes were extracted from microarray analysis. Red and blue colors indicate up- and down-regulated genes, respectively. B, Fold changes were obtained from RT-qPCR analysis of three independent biological replicates. Bars represent means and standard errors ( $n = 3$ ). Asterisks indicate significant differences as determined by a Student's *t*-test ( $*P < 0.05$ ,  $**P < 0.01$ ). M-C/W-C, *ahp4*-well-watered control-0 h versus WT-well-watered control-0 h; M-D2/W-D2, *ahp4*-dehydrated-2 h versus WT-dehydrated-2 h; M-D5/W-D5, *ahp4*-dehydrated-5 h versus WT-dehydrated-5 h.

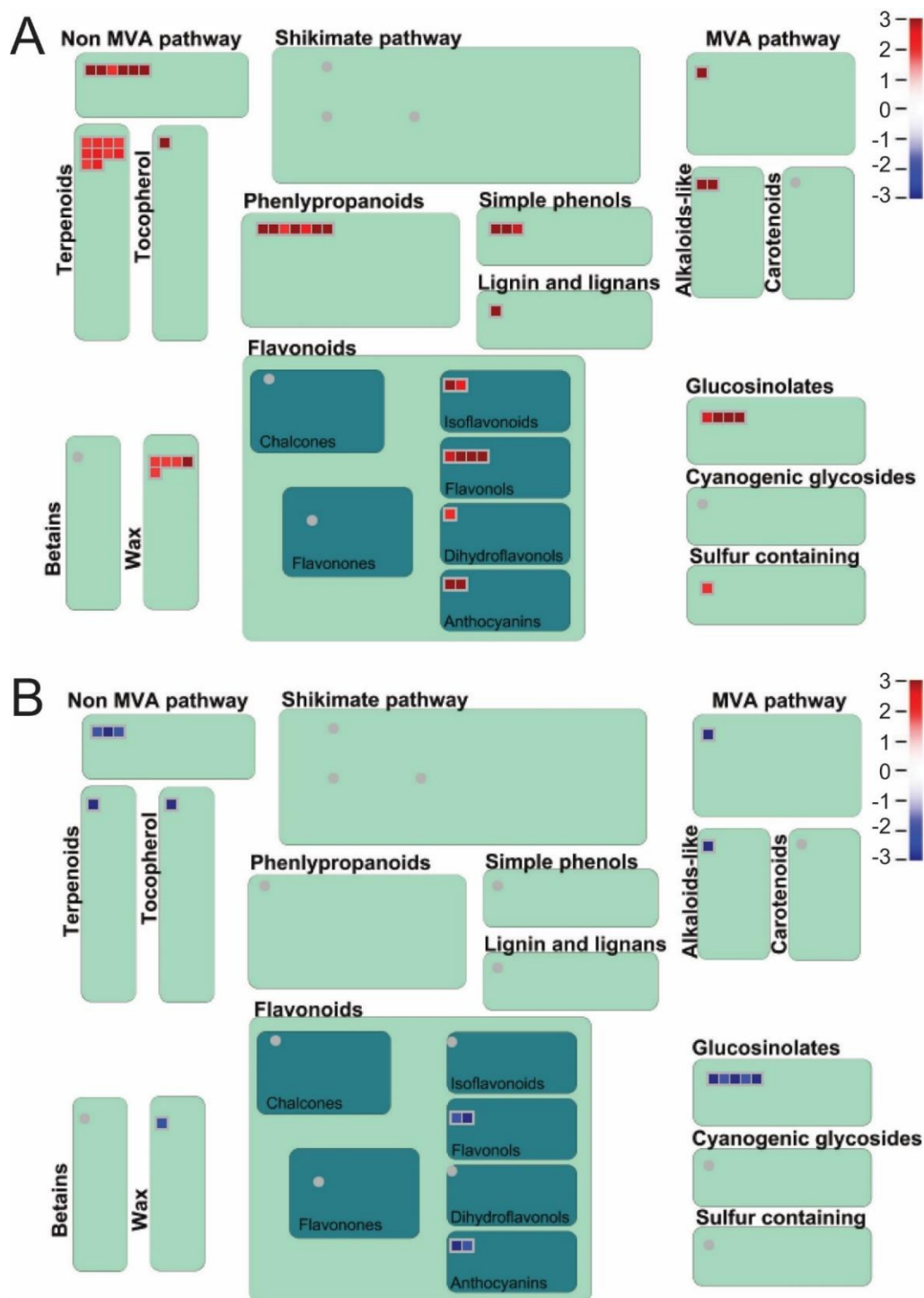


**Figure S4. MapMan-based analysis of differentially expressed genes identified in *ahp4* mutant versus wild-type (WT) plants under normal (M-C/W-C comparison) and dehydration (M-D/W-D comparison) conditions.** MapMan-based functional classification of the induced and repressed genes identified in M-C/W-C and M-D/W-D using the web-tool Classification Supersviewer (bar.utoronto.ca) with normalized class score option (\* $P < 0.05$ , \*\* $P < 0.01$ , \*\*\* $P < 0.001$ ). CHO, carbohydrate; TCA, tricarboxylic acid; M-C/W-C comparison represents *ahp4* well-watered control versus WT well-watered control; M-D/W-D comparison represents M-D2/W-D2 and/or M-D5/W-D5; W-D2, WT dehydrated 2 h; W-D5, WT dehydrated 5 h; M-C, *ahp4* well-watered control; M-D2, *ahp4* dehydrated 2 h; M-D5, *ahp4* dehydrated 5 h.

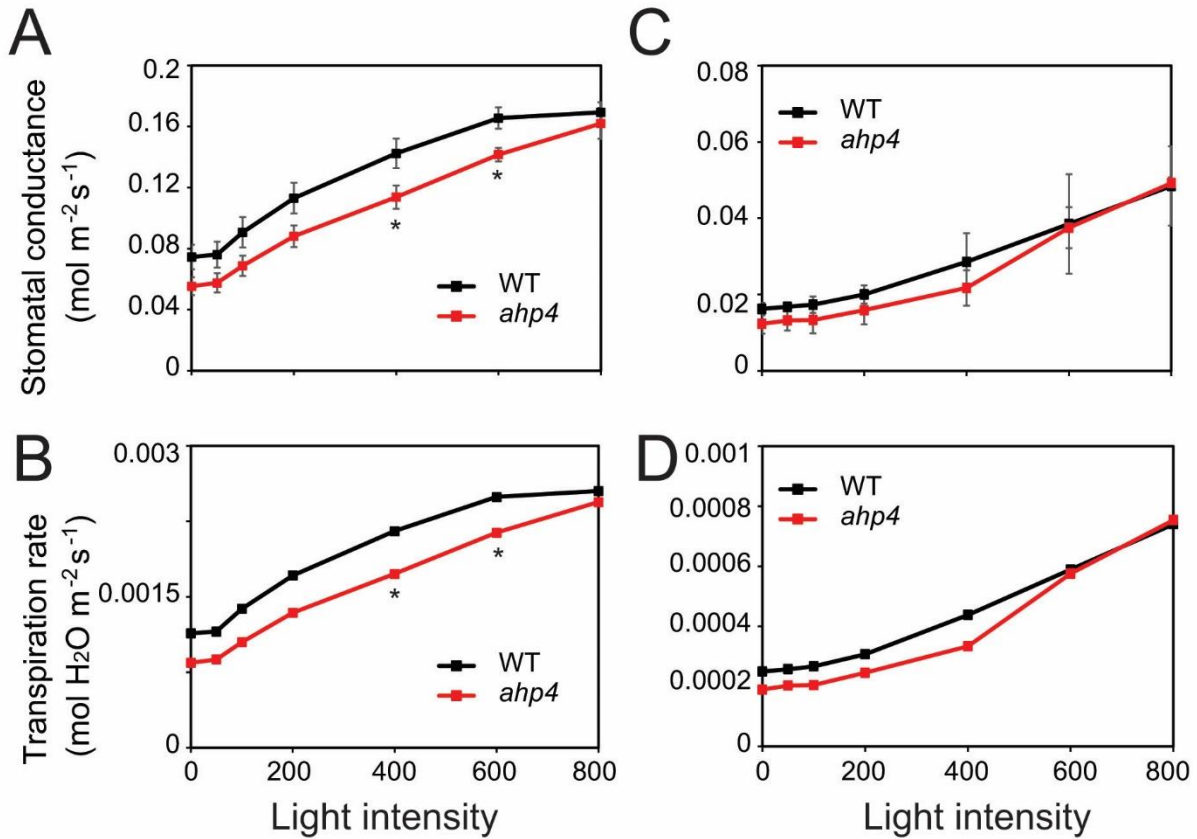


**Figure S5. Metabolism-related overview of differentially expressed genes derived from *ahp4* versus wild-type under normal and dehydration conditions using MapMan.** Metabolism-related overview of up-regulated (A) and down-regulated (B) genes. Color bar in each panel indicates fold changes in gene expression.

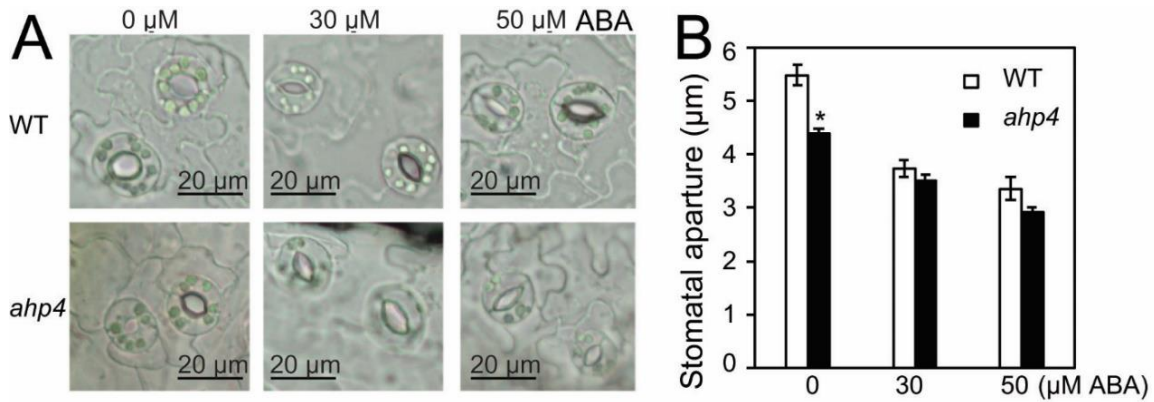




**Figure S6. Secondary metabolism-related overview of differentially expressed genes identified in *ahp4* versus wild-type under normal and dehydration conditions using MapMan. A, Up-regulated and B, down-regulated genes. Red and blue colors indicate up- and down-regulated genes, respectively. Color bar in each panel indicates fold changes in gene expression.**

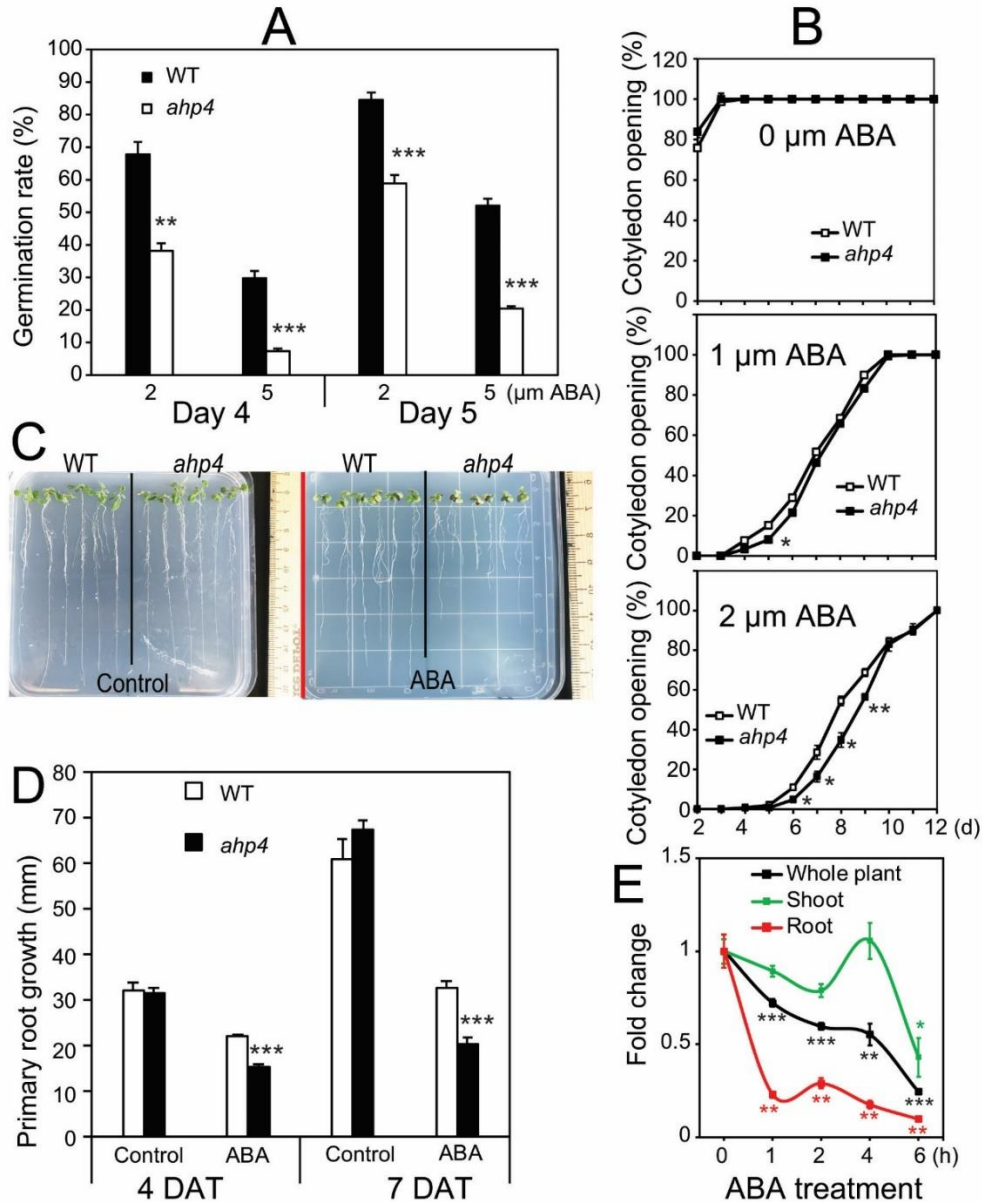


**Figure S7. Stomatal conductance and leaf transpiration rates of *ahp4* mutant and wild-type (WT) plants under well-watered and dehydration conditions.** A, Stomatal conductance, and B, leaf transpiration rates of 32-day-old *ahp4* and WT plants grown on soil under well-watered conditions. C, Stomatal conductance, and D, leaf transpiration rates of 32-day-old *ahp4* and WT plants grown on soil exposed to 30 minutes of dehydration treatment. Data represent the means and standard errors ( $n = 3$ ). Asterisks indicate significant differences between the two genotypes as determined by a Student's *t*-test ( $*P < 0.05$ ).



**Figure S8. Comparison of stomatal apertures of *ahp4* mutant and wild-type (WT) plants under abscisic acid (ABA) treatment.** A, Guard cells of 21-day-old *ahp4* and WT plants were treated with 0 (control), 30 and 50  $\mu\text{M}$  ABA for 1 h under light conditions. B, Average size of the stomatal aperture of rosette leaves from 21-day-old *ahp4* and WT plants in the presence or absence of ABA. Data represent the means and standard errors ( $n = 3$  plants/genotype; for each plant the average of eight stomatal measurements from a single leaf was calculated). Asterisks indicate significant differences between the two genotypes as determined by a Student's *t*-test ( $*P < 0.05$ ).





**Figure S9. Germination assay of *ahp4* mutant and wild-type (WT) plants on medium supplemented with different concentrations of abscisic acid (ABA), and *AHP4* expression in WT plants treated with ABA.** A, Germination rate of *ahp4* mutant and WT plants under exogenous ABA treatment. Data represent the mean and standard errors (SEs) ( $n = 8$ , where each replicate represents the radical emergence rate of  $\geq 18$  seeds/genotype). B, Cotyledon opening percentage of *ahp4* mutant and WT under exogenous ABA treatment. Data represent the mean and SEs ( $n = 3$ , where each replicate represents the cotyledon opening rate of 50 seeds/genotype). C, Seven-day-old *ahp4* and WT plants grown on germination medium were transferred onto  $0.5 \times$  MS plates (1.2% w/v agar) with or without 20  $\mu$ M ABA for 7 days. D, Primary root growth of *ahp4* and WT plants under normal and ABA conditions as described in (C). Data present the mean and SEs ( $n = 18$  plants/genotype). E, Expression of *AHP4* in 21-day-old WT plants treated with 50  $\mu$ M ABA for indicated time period. Data represent the mean and SEs ( $n = 3$ ). Asterisks indicate significant differences as determined by Student's *t*-test (\* $P < 0.05$ , \*\* $P < 0.01$ , \*\*\* $P < 0.001$ ). DAT, days after transfer.

**Table S1.** Results of the comparative microarray analysis of leaves of *ahp4* mutant and wild-type plants under well-watered and dehydration conditions.

**Table S2.** List of up- and down-regulated genes in M-C/W-C comparison ( $|\text{fold-change}| \geq 2$ ;  $q\text{-value} < 0.05$ ). A, List of up-regulated genes (fold change  $\geq 2$ ,  $q\text{-value} < 0.05$ ) in M-C/W-C comparison. B, List of down-regulated genes (fold change  $\leq -2$ ,  $q\text{-value} < 0.05$ ) in M-C/W-C comparison. M-C/W-C, *ahp4* well-watered control 0 h versus WT well-watered control 0 h.

**Table S3.** List of up- and down-regulated genes in various comparisons ( $|\text{fold-change}| \geq 2$ ;  $q\text{-value} < 0.05$ ). A, List of up-regulated genes (fold change  $\geq 2$ ,  $q\text{-value} < 0.05$ ) in M-D/W-D comparison. B, List of up-regulated genes (fold change  $\geq 2$ ,  $q\text{-value} < 0.05$ ) in M-D2/W-D2 comparison. C, List of up-regulated genes (fold change  $\geq 2$ ,  $q\text{-value} < 0.05$ ) in M-D5/W-D5 comparison. D, List of down-regulated genes (fold change  $\leq -2$ ,  $q\text{-value} < 0.05$ ) in M-D/W-D comparison. E, List of down-regulated genes (fold change  $\leq -2$ ,  $q\text{-value} < 0.05$ ) in M-D2/W-D2 comparison. F, List of down-regulated genes (fold change  $\leq -2$ ,  $q\text{-value} < 0.05$ ) in M-D5/W-D5 comparison. G, List of up-regulated genes (fold change  $\geq 2$ ,  $q\text{-value} < 0.05$ ) in W-D/W-C comparison. H, List of down-regulated genes (fold change  $\leq -2$ ,  $q\text{-value} < 0.05$ ) in W-D/W-C comparison. M-D/W-D, *ahp4* dehydrated 2 and/or 5 h versus WT dehydrated 2 and/or 5 h; M-D2/W-D2, *ahp4* dehydrated 2 h versus WT dehydrated 2 h; M-D5/W-D5, *ahp4* dehydrated 5 h versus WT dehydrated 5 h; M-D/M-C, *ahp4* dehydrated 2 h and/or 5h versus *ahp4* well-watered control 0 h; W-D/W-C, WT dehydrated 2 h and/or 5h versus WT well-watered control 0 h..

**Table S4.** Venn analysis of differentially expressed gene sets derived from various comparisons. A, List of up-regulated genes (fold change  $\geq 2$ ,  $q\text{-value} < 0.05$ ) in M-C/W-C and W-D/W-C. B, List of up-regulated genes (fold change  $\geq 2$ ,  $q\text{-value} < 0.05$ ) in M-C/W-C and W-D/W-C. C, List of down-regulated genes (fold change  $\leq -2$ ,  $q\text{-value} < 0.05$ ) in M-C/W-C and W-D/W-C. D, List of down-regulated genes (fold change  $\leq -2$ ,  $q\text{-value} < 0.05$ ) in M-D/W-D and W-D/W-C. M-C/W-C, *ahp4* well-watered control 0 h versus WT well-watered control 0 h; W-D/W-C, WT dehydrated 2 h and/or 5h versus WT well-watered control 0 h; M-D/W-D, *ahp4* dehydrated 2 and/or 5 h versus WT dehydrated 2 and/or 5 h.

**Table S5.** List of photosynthesis-related genes in *ahp4* and wild-type (WT) leaves under normal and dehydration conditions.

**Table S6.** Primers used in RT-qPCR.