Article

Transcriptomic and Metabolomic Analyses Reveal the Response to Short-Term Drought Stress in Bread Wheat (*Triticum aestivum* L.)

Xiaoyi Fu [1,2], Zhilian Liu [1,3], Xiong Du [1], Huijun Duan [1], Wenchao Zhen [1], Yuechen Zhang [1], Zhanliang Shi [2], Mingqi He [2,*] and Ruiqi Li [1,*]

Supplementary Figures



Figure S1. Image of wheat seedlings grown in pots.

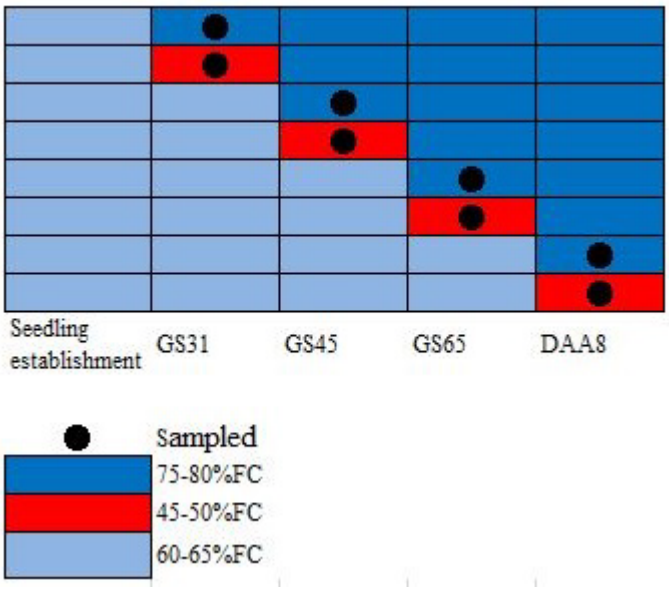


Figure S2. Schematic overview of the experimental design for the control and drought treatments. Black dots indicate the actual sampling times for the plants based on their developmental stages (light blue: watered to 60-65% of field capacity (FC); dark blue: watered to 75-80% of FC; red: watered to 45-50% of FC). All samples marked as 'watered' were irrigated 5 days prior to sample collection.

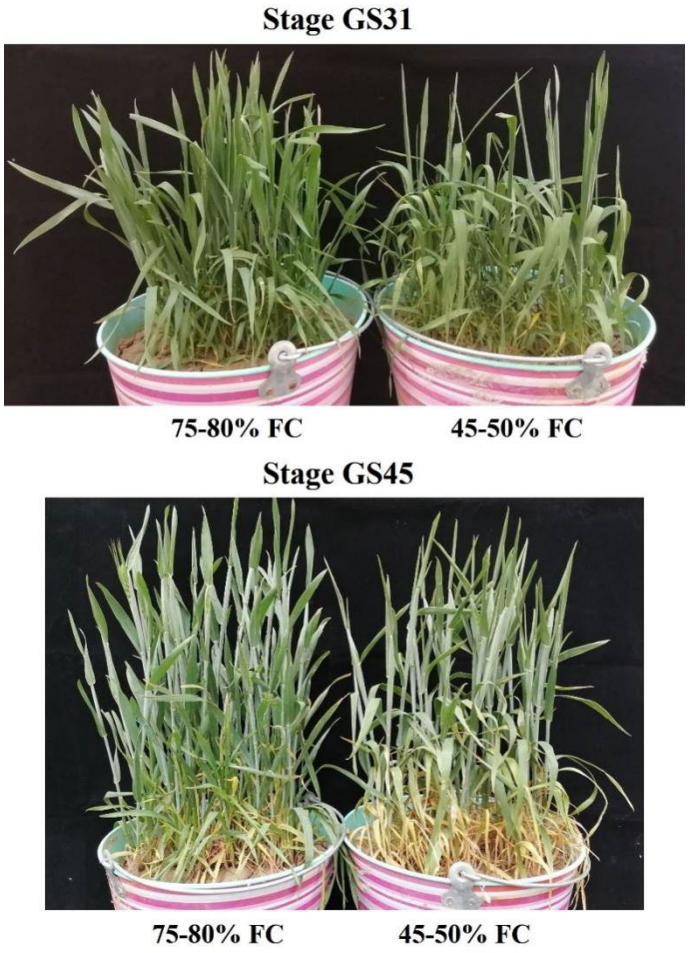


Figure S3. Images of plants before being sampled at stages GS31 and GS45.

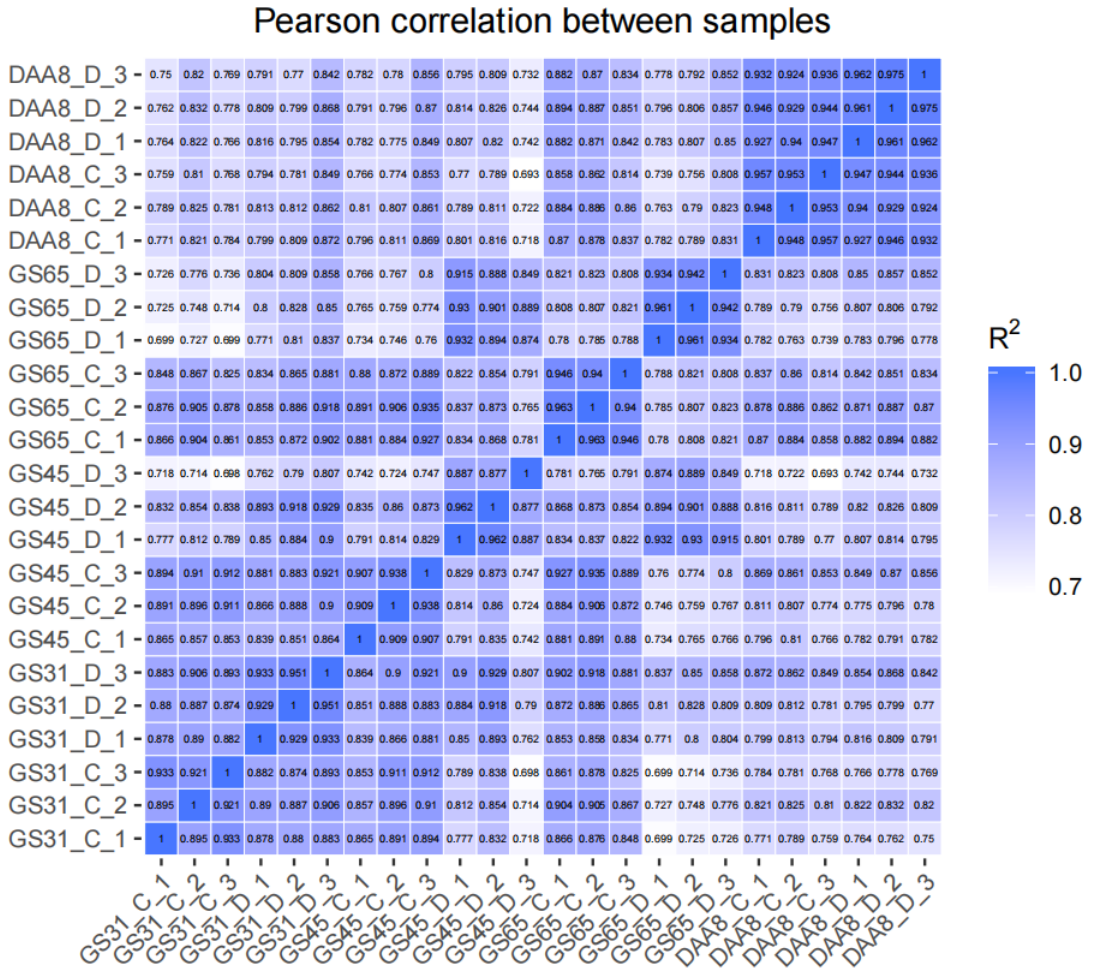


Figure S4. RNA sequencing outcomes of the wheat cultivar Jimai 418 under drought and control treatments. Heatmap representing the Pearson rank correlation coefficients between pairs of samples based on their global expression profiles under drought and control treatments at stages GS31, GS45, GS65, and DAA8.

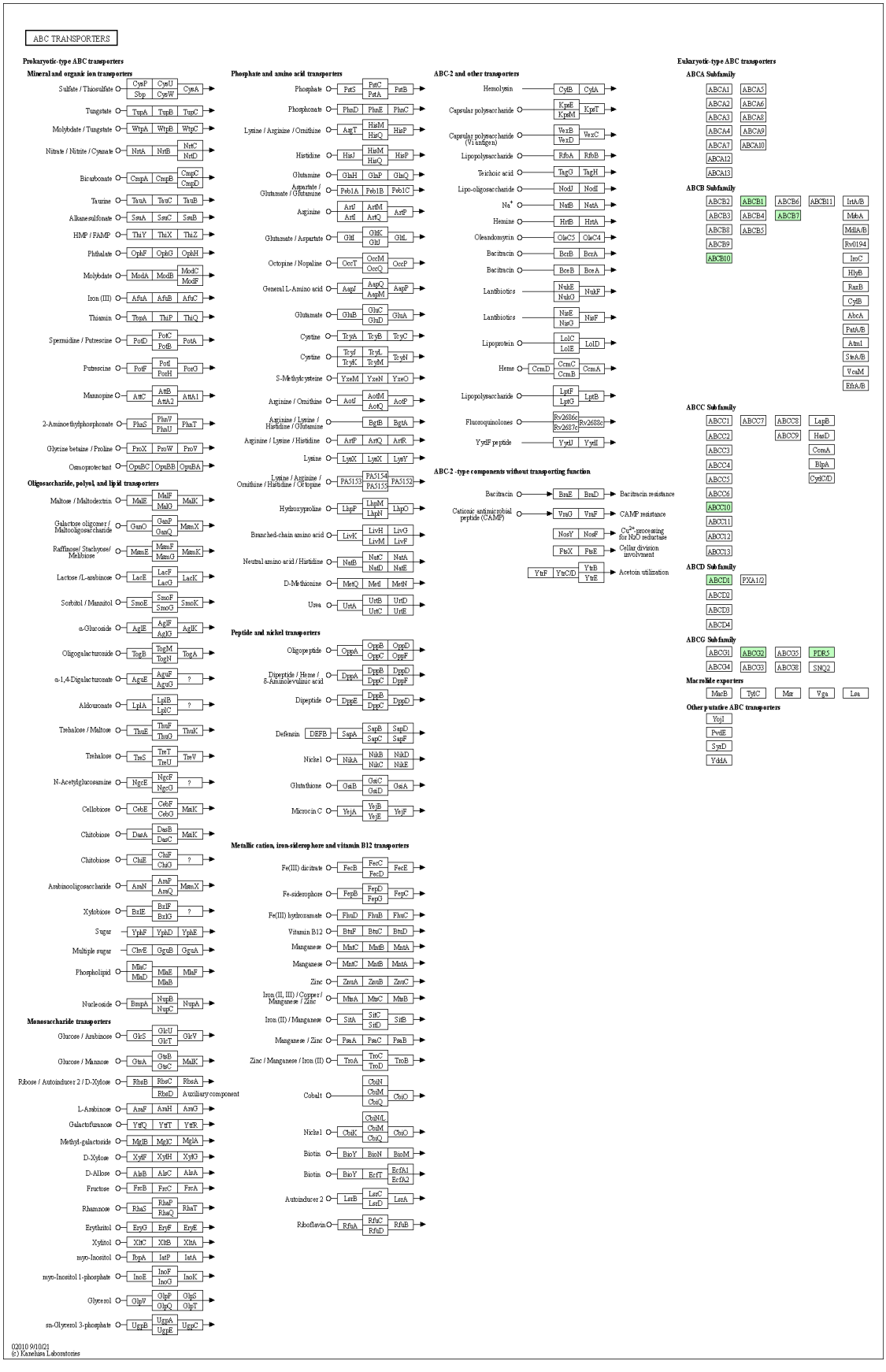


Figure S5. ABC transporter pathway map.

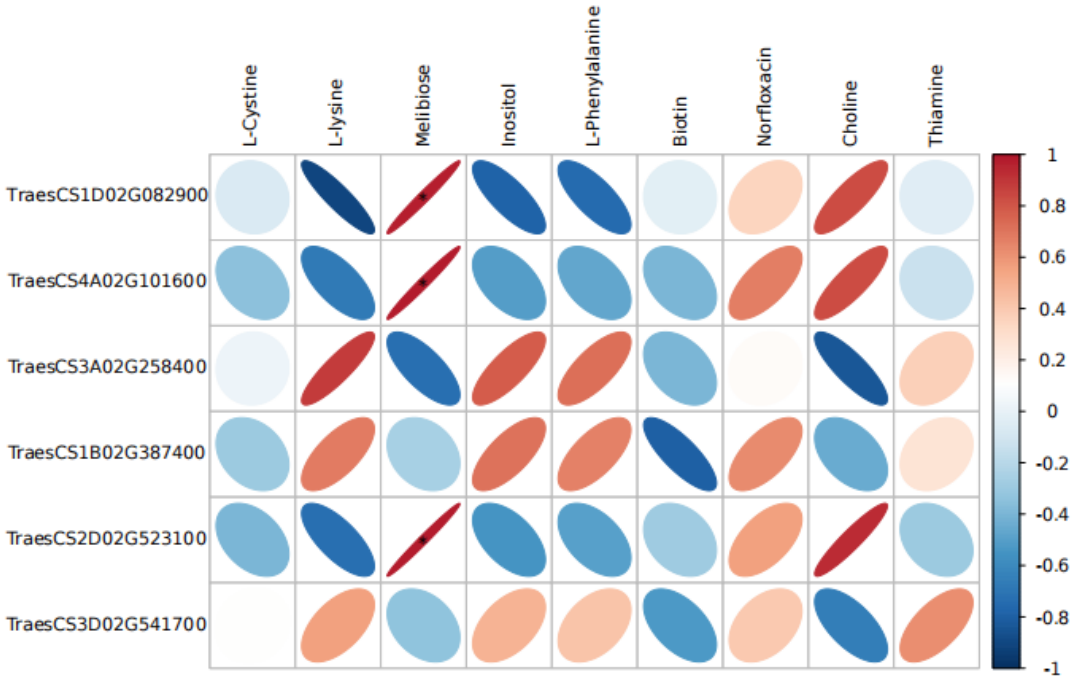


Figure S6. Correlation analysis of six genes and nine differentially accumulating metabolites (DAMs) enriched by the ABC transporter pathway.

Pearson correlation coefficients rho and P-values were calculated between the relative abundance of each DEG and each DAM. Asterisks (*) indicate statistically significant correlations ($p \leqslant 0.05$).

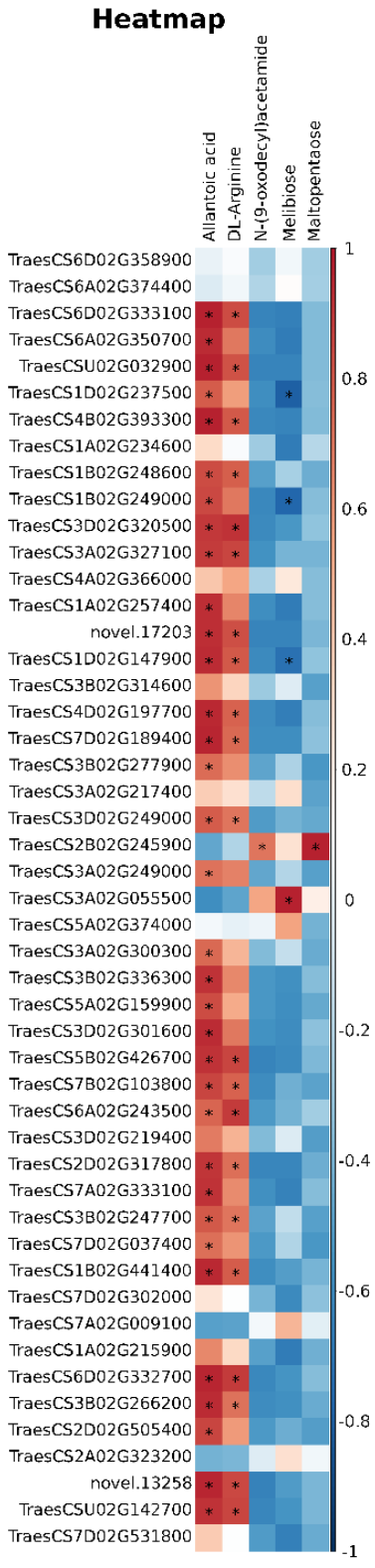


Figure S7. Correlation analysis of 49 differentially expressed genes (DEGs) and five DAMs.

Pearson correlation coefficients rho and P-values were calculated between the relative abundance of each DEG and each DAM. Asterisks (*) indicate statistically significant correlations ($p \leq 0.05$).