

Comparative physiological, metabolomic and transcriptomic analyses reveal mechanisms of improved abiotic stress resistance in bermudagrass (*Cynodon dactylon* (L). Pers.) by exogenous melatonin

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SUPPLEMENTARY DATA

Table S1. The specific primers used for real-time PCR.

Table S2. Concentrations of 54 metabolites in 28-day-old bermudagrass plants after different treatments (control or 20 μ M melatonin) under control, 300 mM NaCl, drought, and cold (4°C) stress conditions for 14 days. The concentrations of metabolites are expressed as $\mu\text{g}\cdot\text{g}^{-1}$ FW. Three biological replicates were used for each group.

Table S3. Summary of RNA-Seq data.

Table S4. List of up-regulated genes in melatonin-treated bermudagrass plants.

Table S5. List of down-regulated genes in melatonin-treated bermudagrass plants.

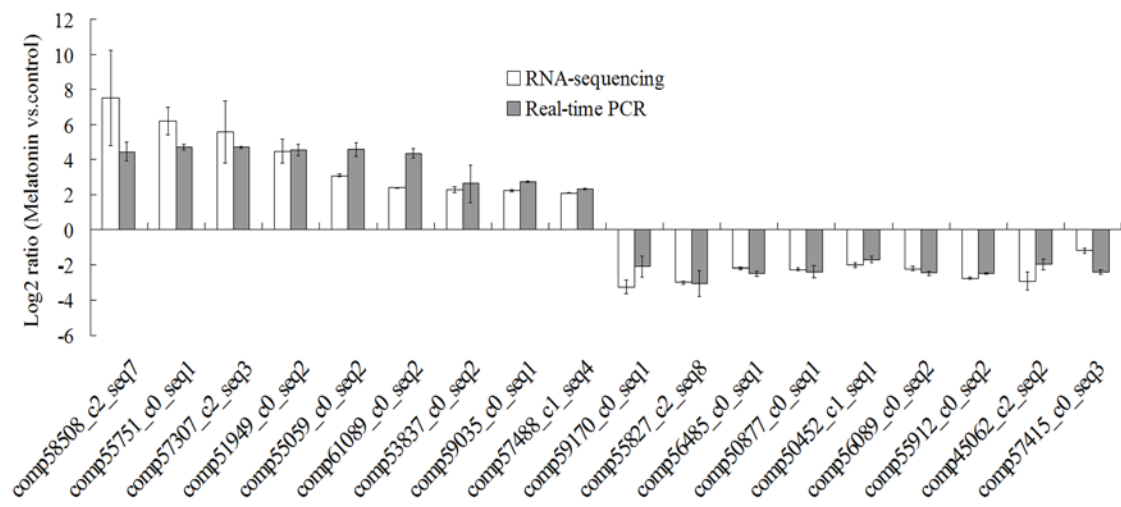


Figure S1. Validation of differentially expressed genes by quantitative real-time PCR.

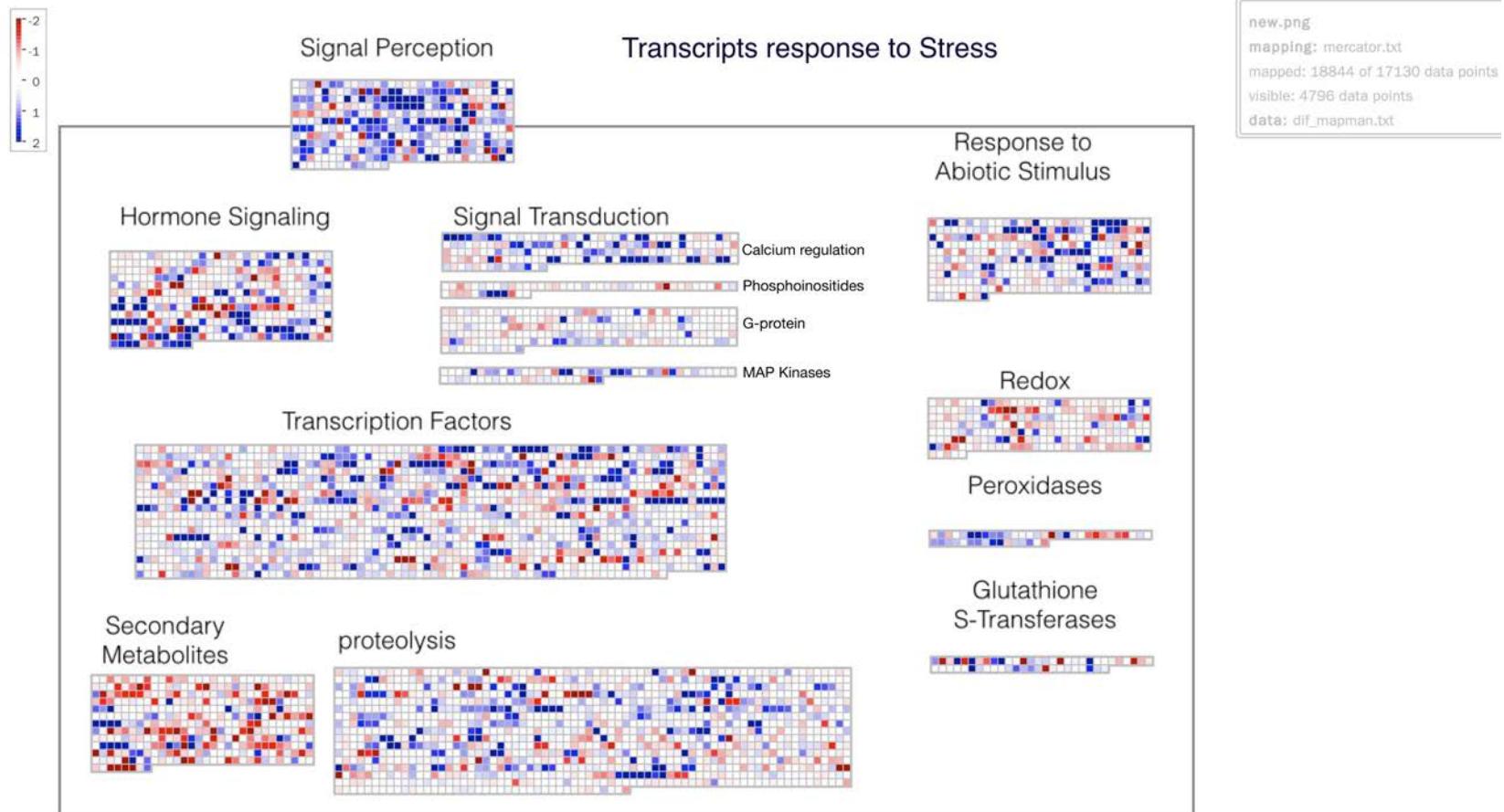


Figure S2. Effect of exogenous melatonin treatment on stress-related pathways in bermudagrass. Transcripts participate in the same pathway or homologs were represented by a set of closely-connected cubes, and the 2 based logarithm of fold change value (\log_2 FC) were denoted by colors.