

Genotype-specific physiological and transcriptomic responses to drought stress in *Setaria italica* (an emerging model for Panicoideae grasses)

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Supplementary Information

Supplementary Table S1. Chlorophyll fluorescence measurement for *S. italica* subjected to water stress treatment.

Supplementary Table S2. qRT-PCR validation of differentially expressed genes.

Supplementary Table S3. Correlation between qRT-PCR and RNA-Seq data.

Supplementary Table S4. Expression profile and gene annotation of differential expressed genes in RNA-seq.

Supplementary Table S5. GO enrichment analysis of differentially expressed genes in each of six K-means clusters.

Supplementary Table S6. KEGG enrichment analysis of differentially expressed genes in each of six K-means clusters.

Supplementary Table S7. Comparison of major agronomic traits between the 'An04' and 'Yugu1'.

Supplementary Table S8. GO enrichment analysis of genes in different category of Figure 6A.

Supplementary Table S9. Differential expressed genes involved in phytohormone metabolism and signaling.

Supplementary Table S10. List of differentially expressed transcription factors.

Supplementary Table S11. List of differentially expressed protective genes involved in drought responses in *S. italica*.

Supplementary Table S12. Quantification of endogenous phytohormones in 'Yugu1' and 'An04' in response to drought.

Supplementary information is available on the website. Please see the online Excel files for details.