

**Fig. S1 Analysis of correlation between the transcriptome among three biological replicates of both proso millet cultivars using the Pearson’s correlation coefficient.**

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**Fig. S2 Number of transposable elements expressed in SS 212 and ST 47**

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**Fig. S3 Correlation between RNA sequencing and reverse transcription-quantitative polymerase chain reaction (RT-qPCR) for the ten selected genes.** Each point represents a value of fold change of expression level at each time point comparing with that at 0 h.



**Fig. S4 Differential gene expression in ST 47 as compared with SS 212 at each treatment time point.** (A) The number of up-regulated (upper bars) and down-regulated (lower bars) genes at each treatment time point in ST 47 as compared with SS 212 is given. The number of transcription factors (TFs) up- or down-regulated at each treatment time point in ST 47 is also given; (B) Enriched gene ontology (GO) terms (process [BP], molecular function [MF], and cellular component [CC]) at each treatment time point in down- and up-regulated genes in ST 47 (up- and down regulated genes in SS 212). The color scale at the bottom represents significance (corrected *P*-value); (C) KEGG pathway at each treatment time point in down- and up-regulated genes in ST 47 (up- and down regulated genes in SS 212). The color scale at the bottom represents significance (corrected *P*-value).