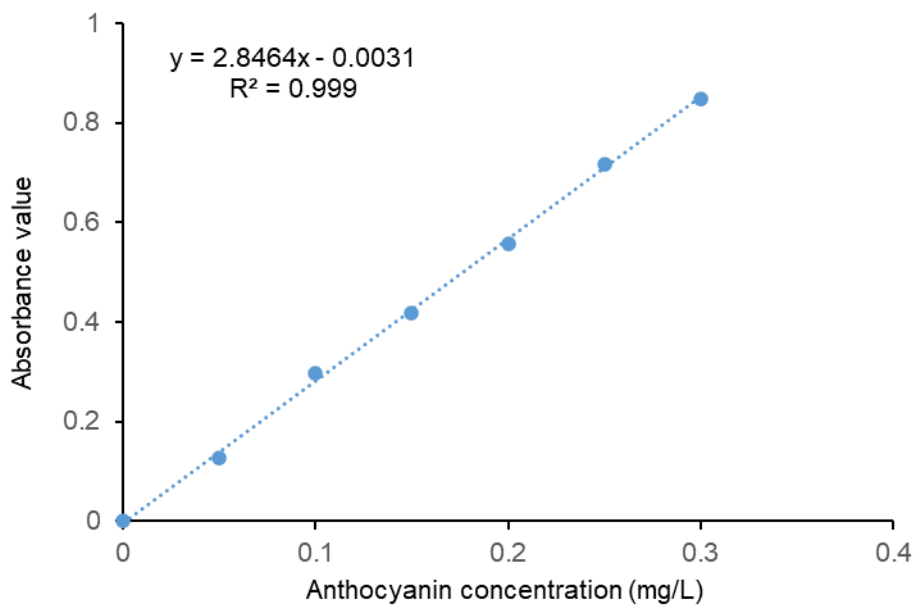
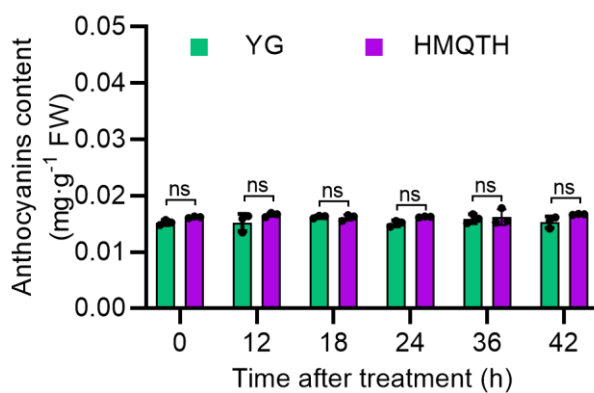


Supplementary Figure 1



Supplementary Figure 1. Standard curve for anthocyanin content determination.

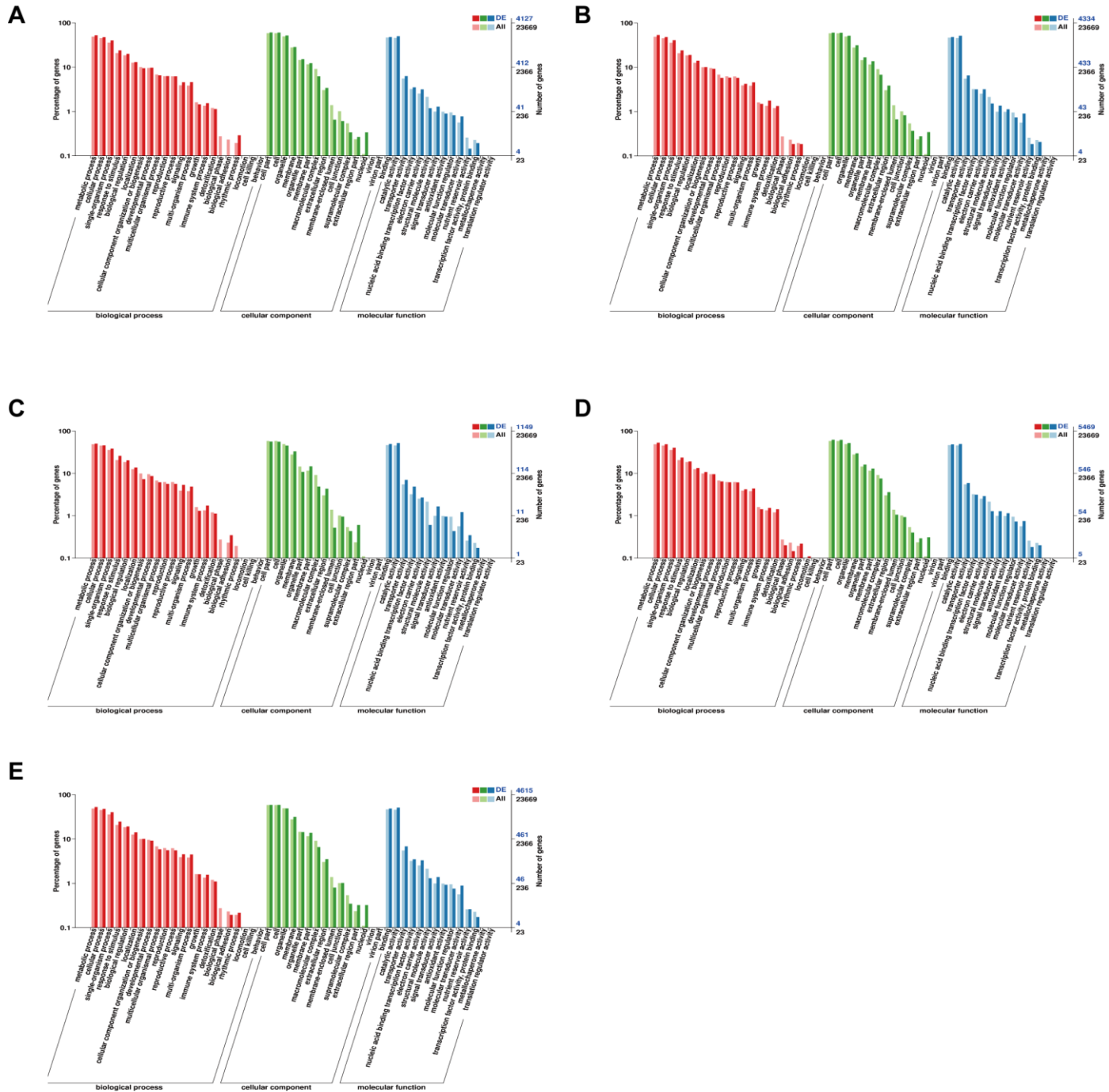
Supplementary Figure 2



Supplementary Figure 2. Anthocyanin content of untreated YG1 and HMQTH.

Bars represent mean $\pm$ SD of three biological replicates. Duncan's multiple range test was employed, ns represents no significant difference.

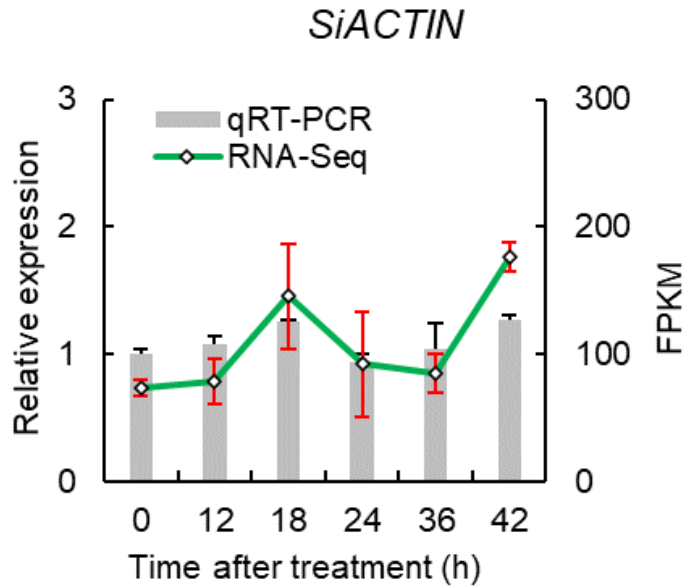
Supplementary Figure 3



Supplementary Figure 3. GO enrichment analysis of DEGs.

The percentage of DEGs enriched GO terms of the biological process, cellular component, and molecular function are shown. A: 12 h vs 0 h; B: 18 h vs 0 h; C: 24 h vs 0 h; D: 36 h vs 0 h; E: 42 h vs 0 h.

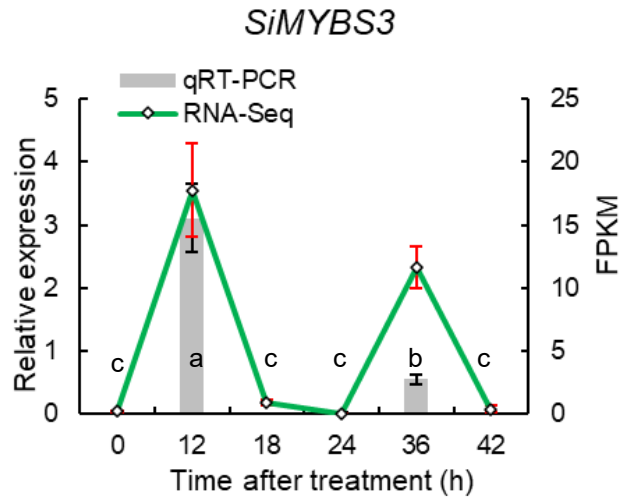
Supplementary Figure 4



Supplementary Figure 4. Quantitative RT-PCR validation of *SiACTIN*.

The relative expression levels of *SiACTIN* were detected by quantitative real time PCR and three biological replicates of each sample were used for qRT-PCR analysis. The expression level of this gene did not exhibit significant differences at different time points.

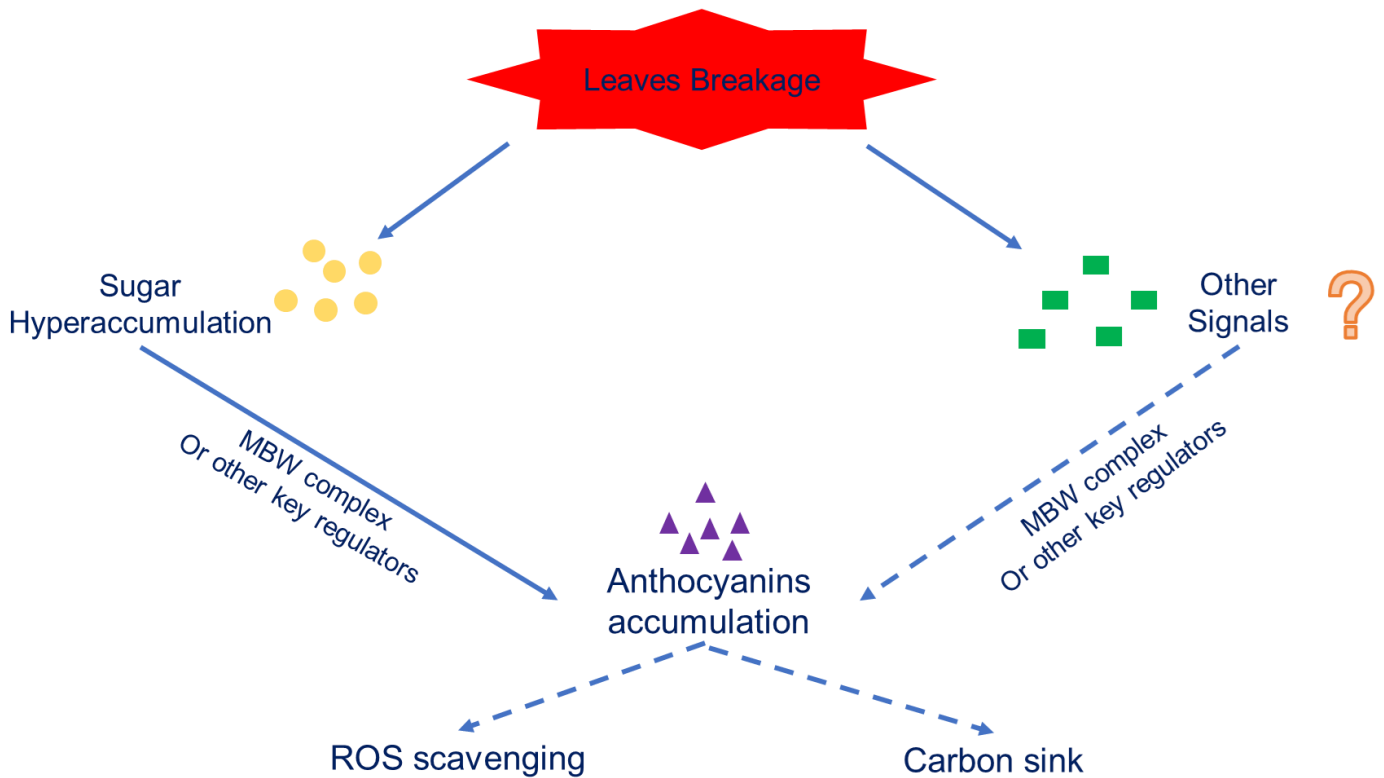
Supplementary Figure 5



Supplementary Figure 5. Quantitative RT-PCR validation of *SiMYBS3*.

The relative expression levels of *SiMYBS3* were detected by quantitative real time PCR and three biological replicates of each sample were used for qRT-PCR analysis. Bars with different lowercase letters are significantly different at $P < 0.05$ (Duncan's multiple range test). The lines show the FPKM values of the DEGs from RNA-seq data

Supplementary Figure 6



Supplementary Figure 6. Working model.

Leave breakage in foxtail millet disrupts vascular bundles and induces sugar hyperaccumulation, which may activate other signaling pathways leading to anthocyanin accumulation. The accumulated anthocyanins can function as antioxidants and act as a carbon sink.