

Figure S1. Tree map of metabolite classification

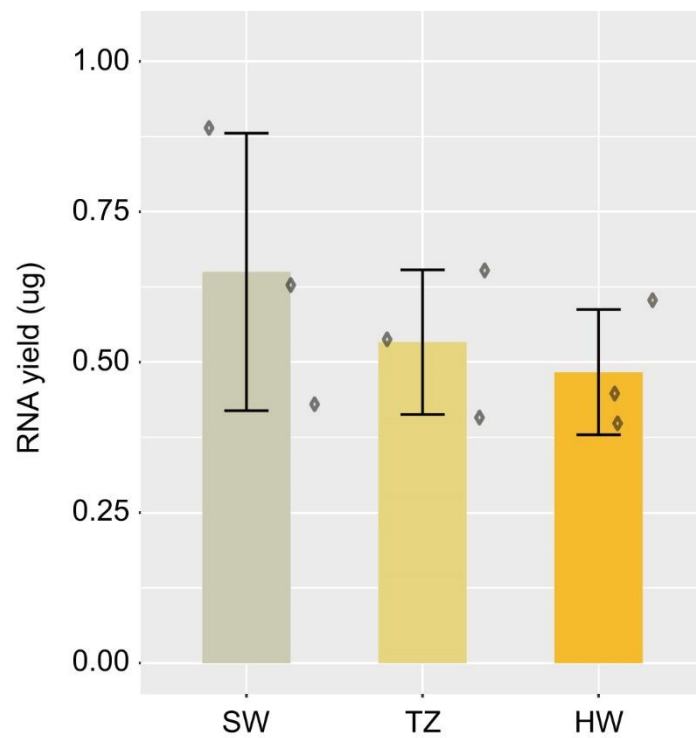


Figure S3. RNA yield of three tissues

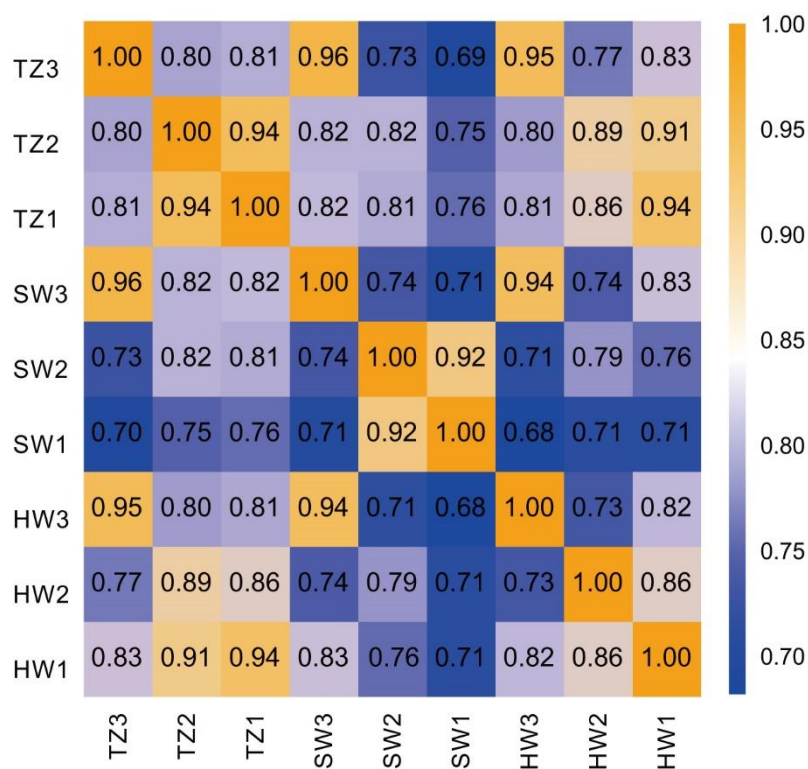


Figure S4. Correlation of transcriptomic data between replicates

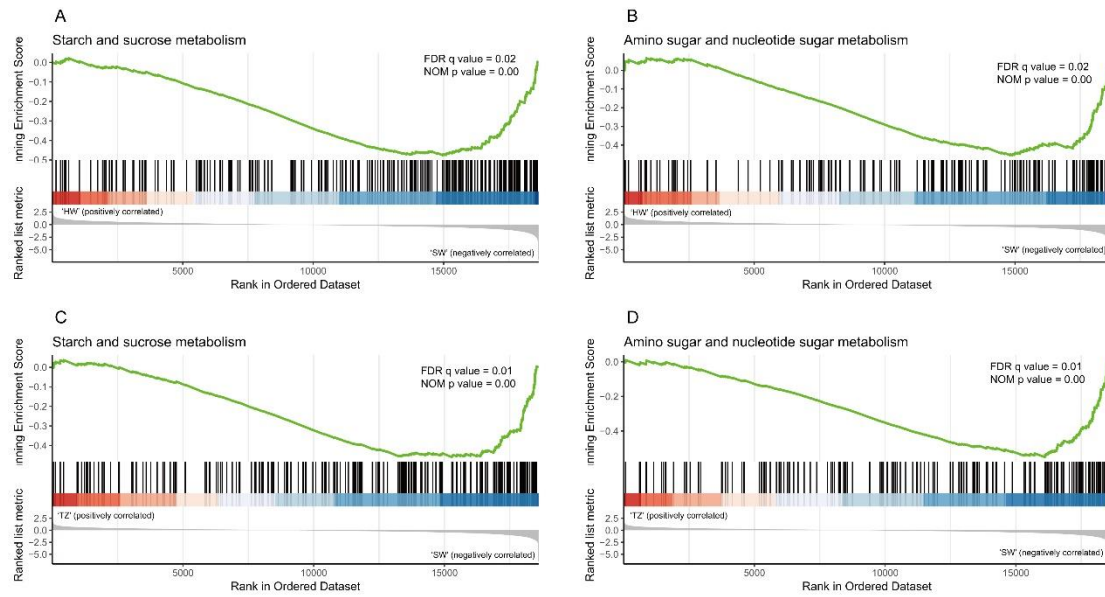


Figure S5. GSEA (gene set enrichment analysis) of starch and sucrose metabolism and amino sugar and nucleotide sugar metabolism genes. **(A)** Starch and sucrose metabolism GSEA rank was calculated by HW vs. SW. **(B)** Amino sugar and nucleotide sugar metabolism GSEA rank was calculated by HW vs. SW. **(C)** Starch and sucrose metabolism GSEA rank was calculated by TZ vs. SW. **(D)** Amino sugar and nucleotide sugar metabolism GSEA rank was calculated by TZ vs. SW

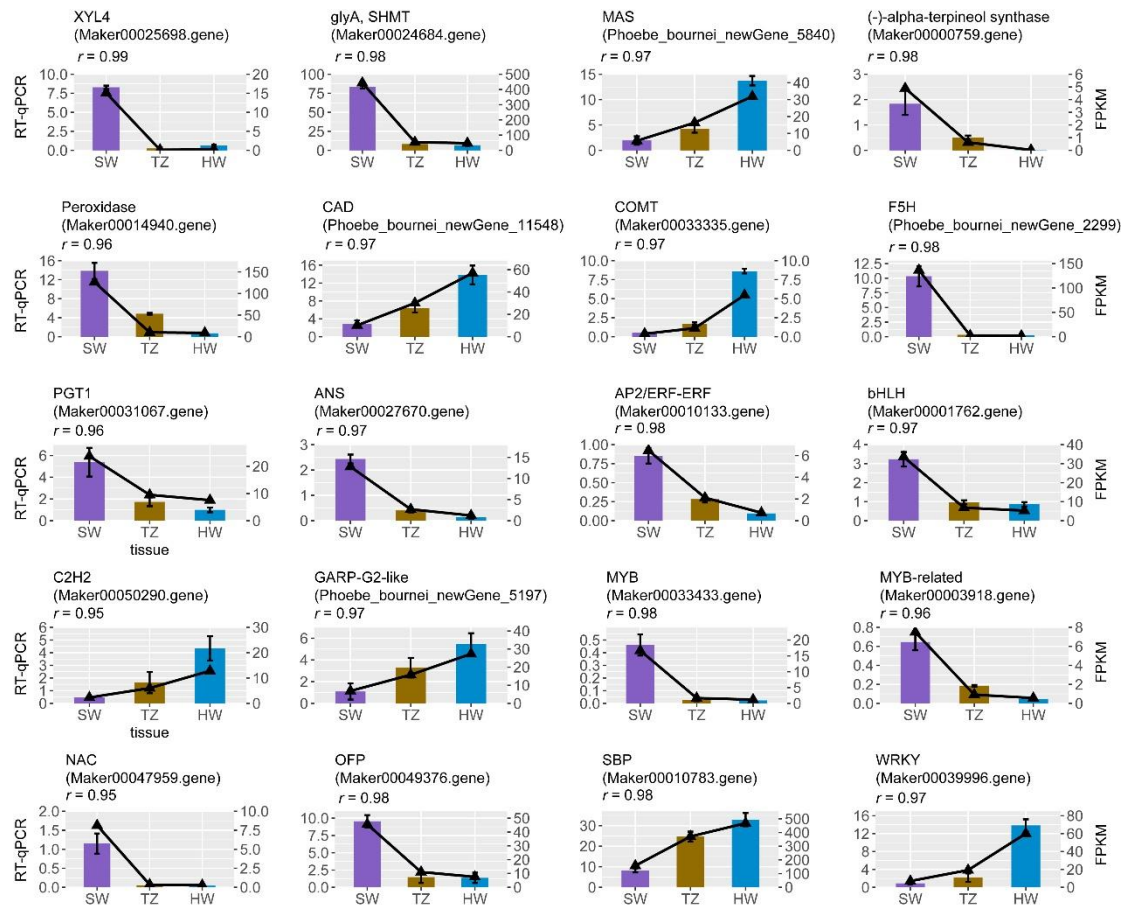


Figure S6. The RT-qPCR analysis of the expression level and fragment per kilobase per million reads (FPKM) of 20 pathway genes and transcription factors genes in HW, TZ, and SW. The column showed the relative expression level, the line showed the FPKM value.