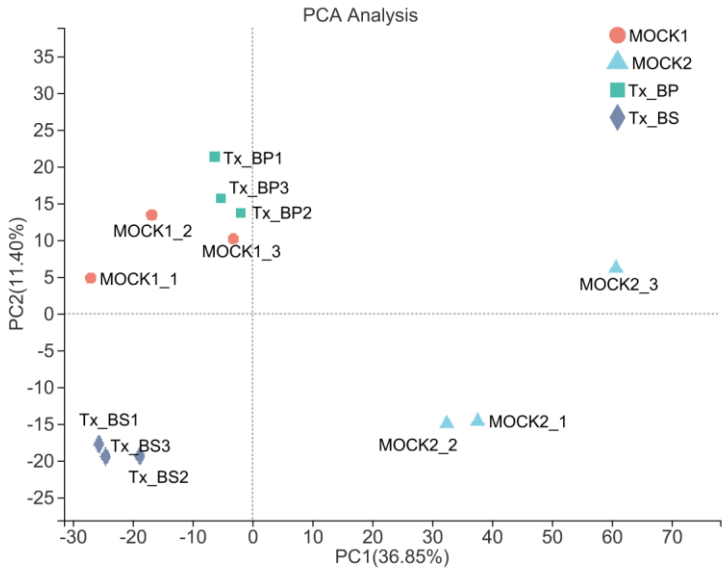


Figure S1: Principal component analysis of the RNA-Sequencing data.

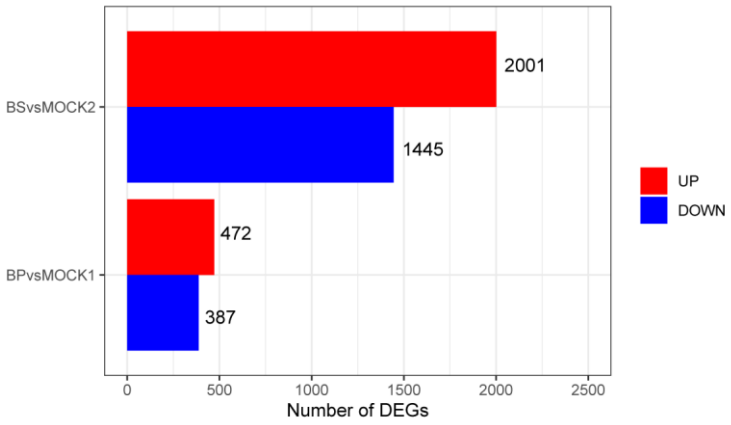


Figure S2: DEGs distribution between two groups analyzed. The number of DEGs is indicated on the right of the histograms.

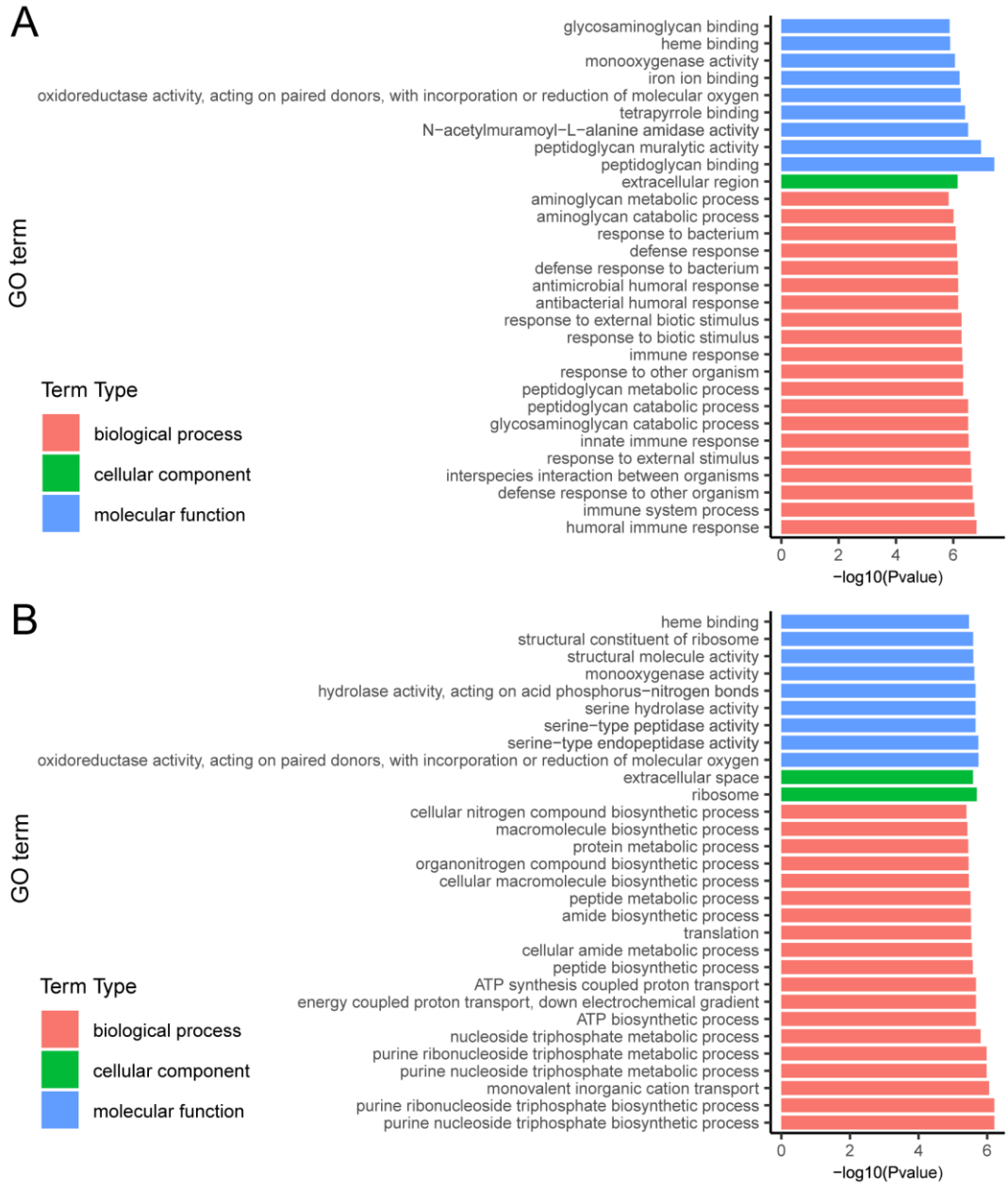


Figure S3: GO functional classification of differentially expressed genes. The blue bars represent molecular function; green bars represent cellular component; red bars represent biological process functions.

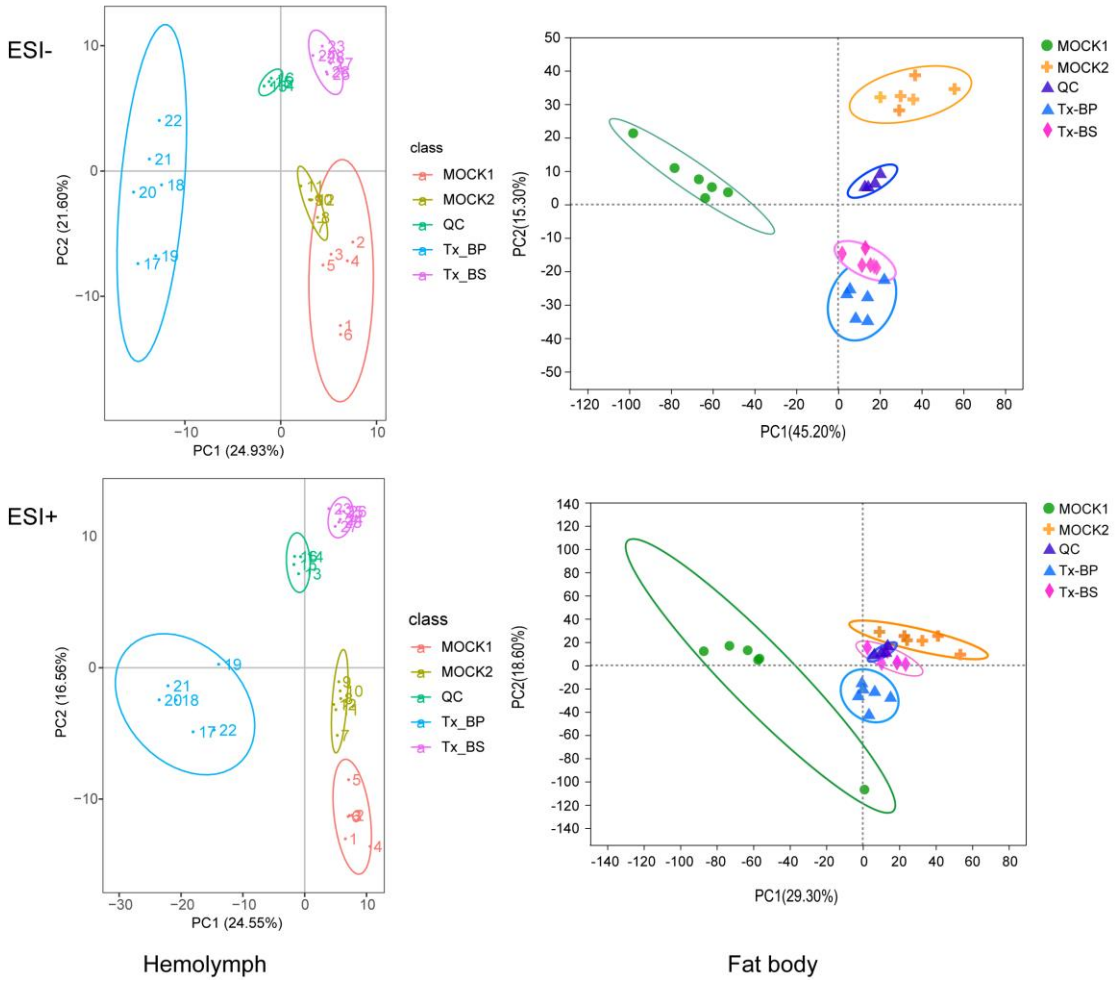
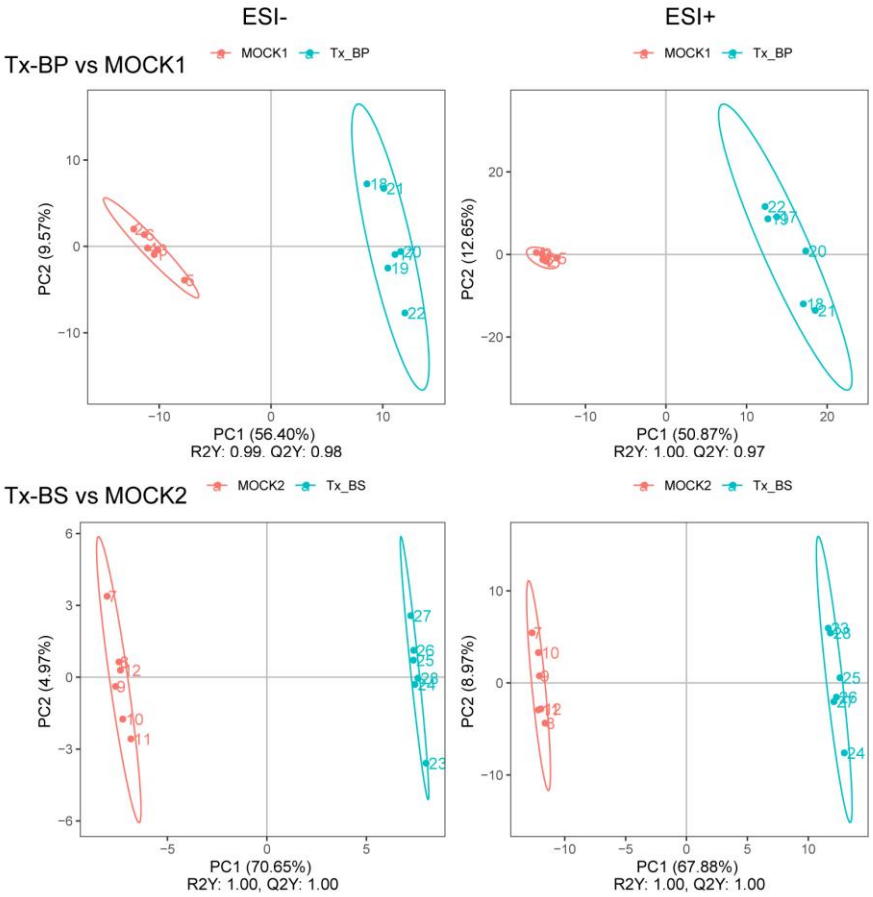


Figure S4: PCA plot of the different sample groups (MOCK1, MOCK2, Tx-BP, Tx-BS) and quality control. Each point represents a biological replicate.

Hemolymph



Fat body

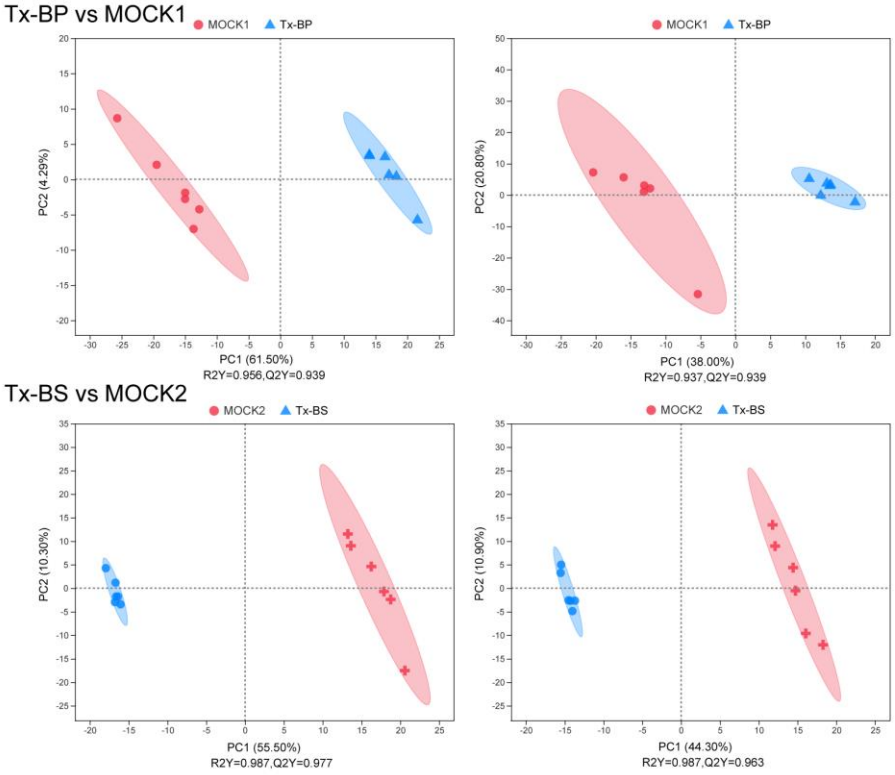


Figure S5: PLS-DA score plot and validation plots for the metabolic profiling results. The criteria for stability and credibility are as follows: R2Y greater than Q2Y values in score plots.

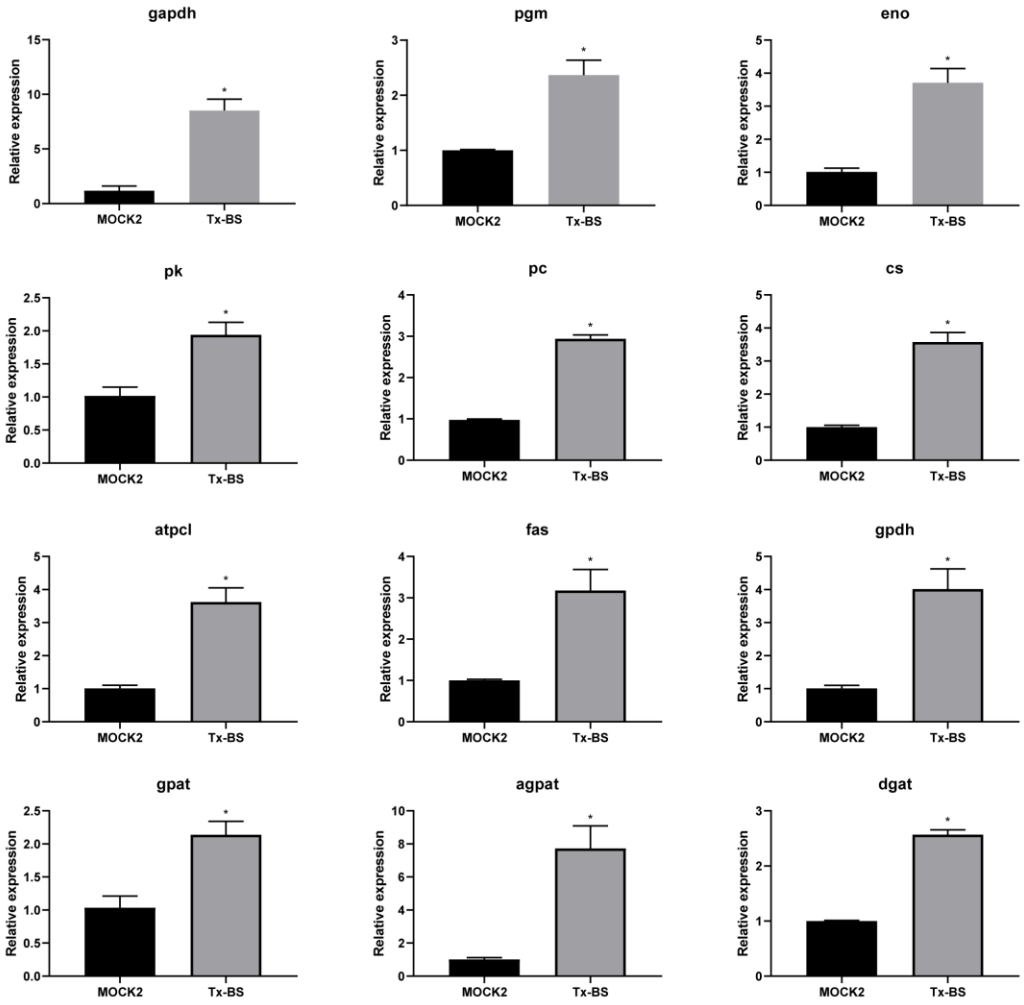


Figure S6: qRT-PCR validation of the RNA-Seq data. The ribosomal protein S3 (rpS3) used as a reference gene. The bars represent means ± SEM from three independent measurements, while letters on the bars indicate significance levels based on $p < 0.05$.

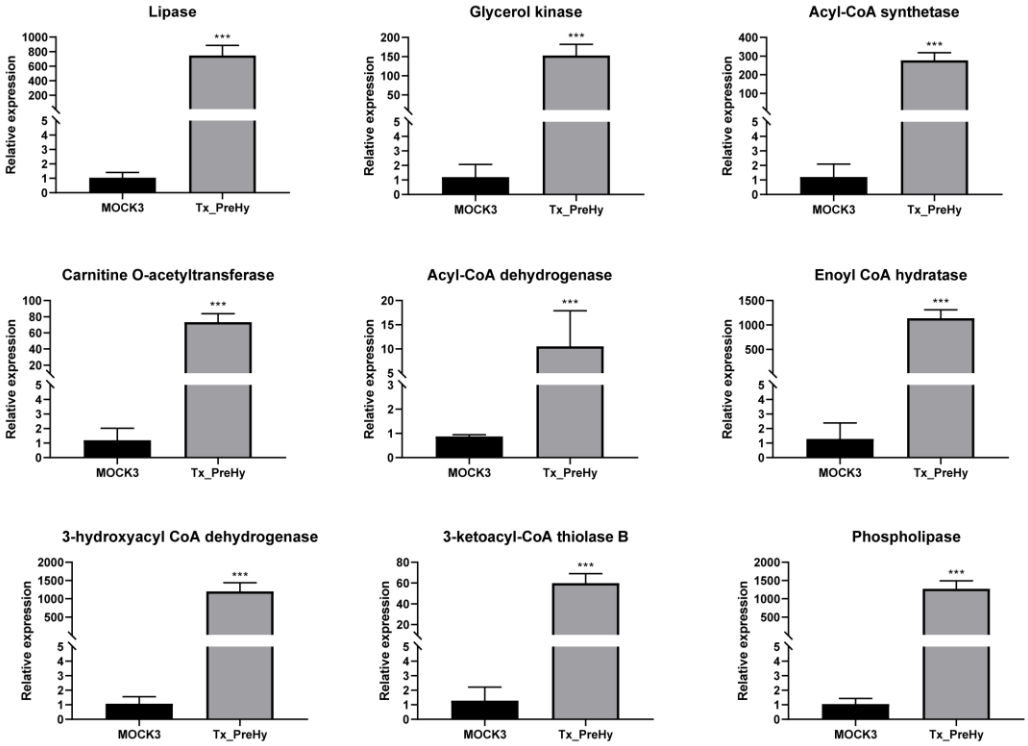


Figure S7: qRT-PCR validation of the gene associated with degradation of glycerolipids and fatty acids. The ribosomal protein S3 (rpS3) used as a reference gene. The bars represent means ± SEM from three independent measurements, while letters on the bars indicate significance levels based on $p < 0.001$. Tx-PreHy, *T. xiaojinensis* samples collected when *O. sinensis* entered PreHy stage; MOCK3, the control for Tx- PreHy.