Supplementary figures:

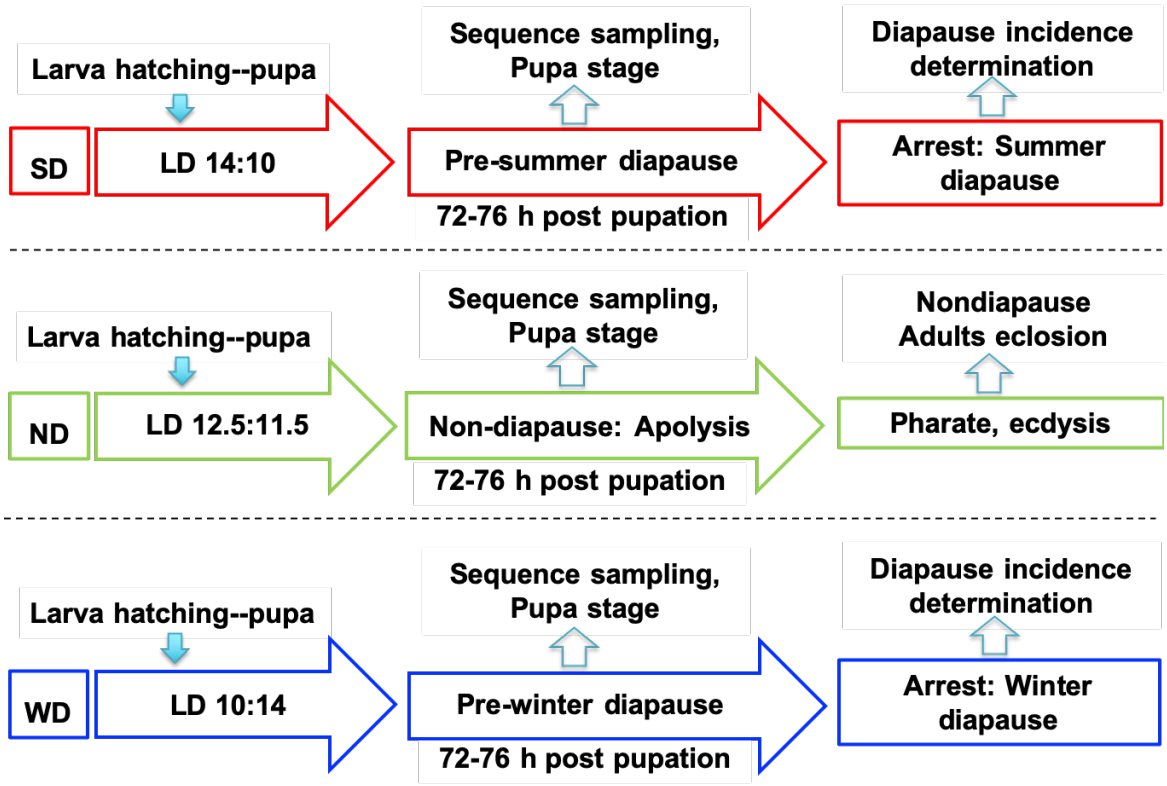

Figure S1. Protocols of the experimental design.

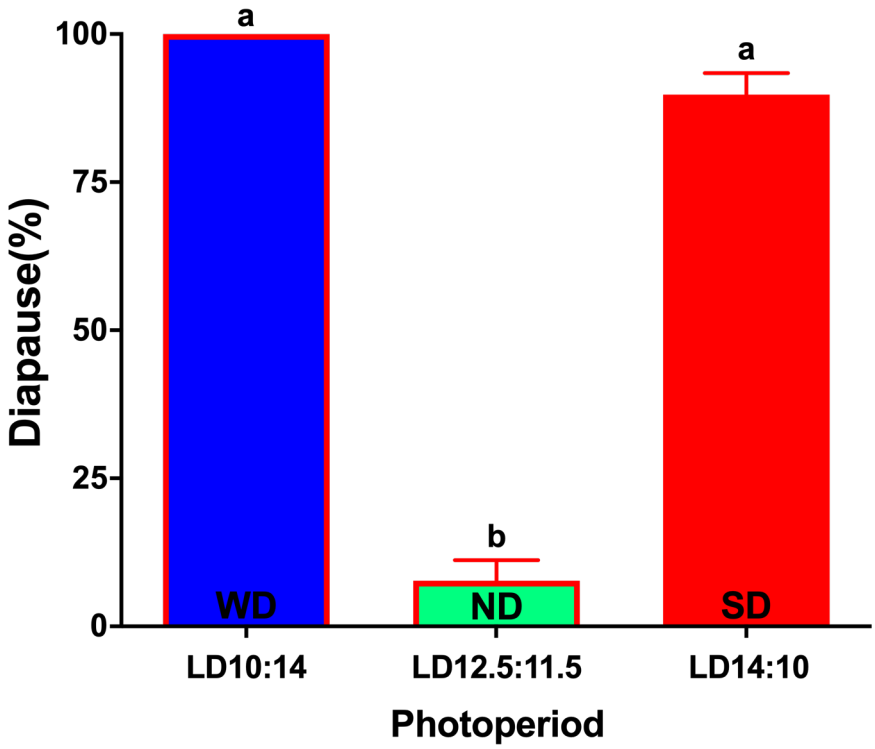

Figure S2. Incidence of diapause induced at different photoperiods of LD 10: 14, LD12.5:11.5, LD14:10, and with constant temperature of 20 °C. Values followed by different letters are significantly different based on Bonferroni test and one-way analysis of variance. Data were shown in mean and the standard error of five replicates. N = 220-327 for each treatment..

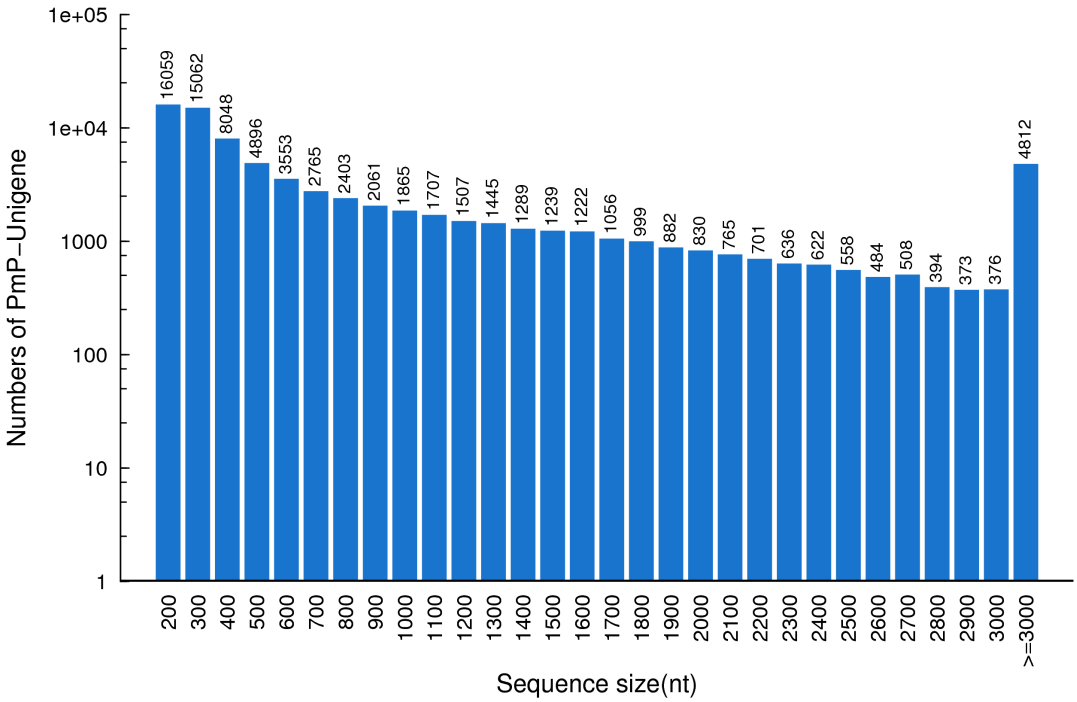

Figure S3. Unigene length distribution of transcriptome sequencing in *P. melete*.

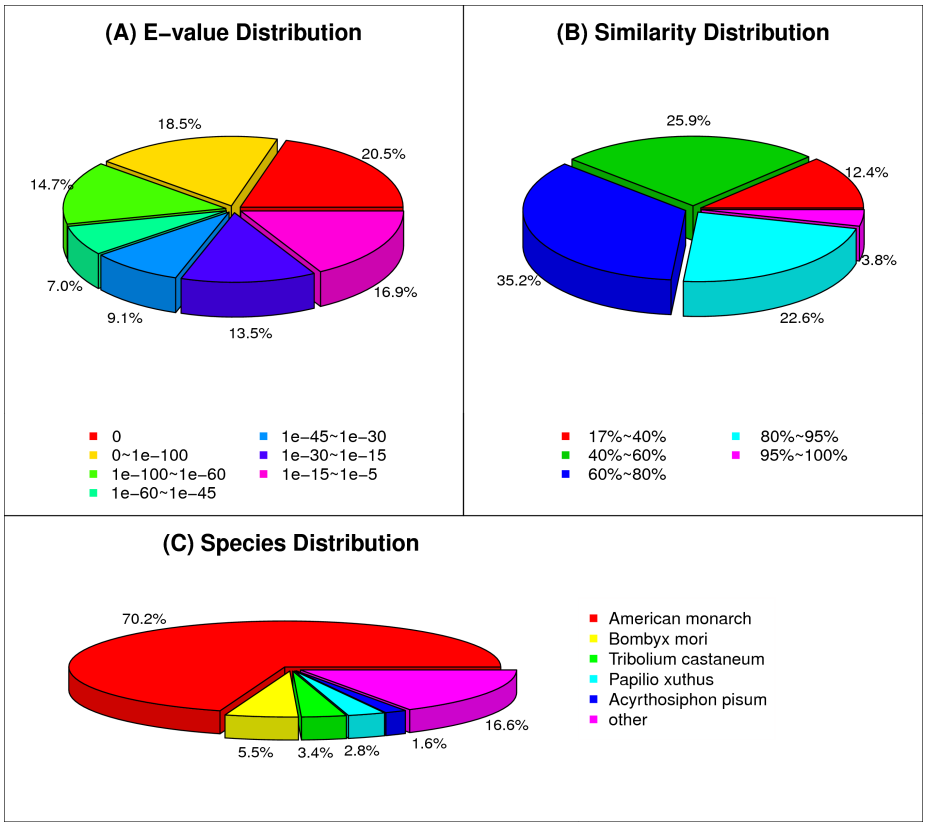

Figure S4. Classification of *P. melete* sequencing unigenes in NR database. (A). E-value distribution; (B). Similarity distribution, and (C). Species distribution.

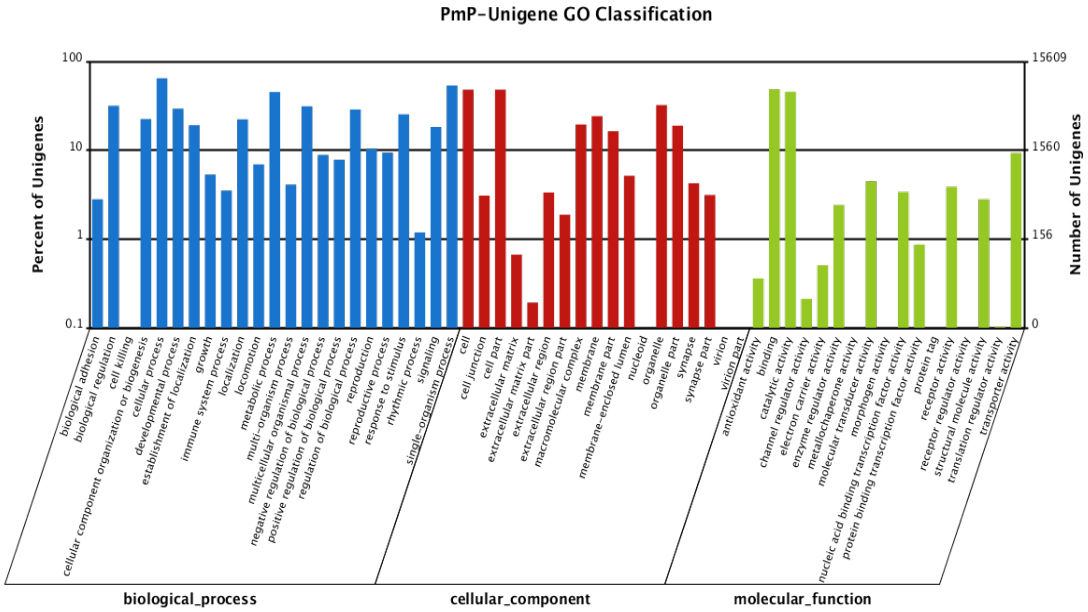

Figure S5. Gene ontology (GO) classification of *P. melete* transcriptome.

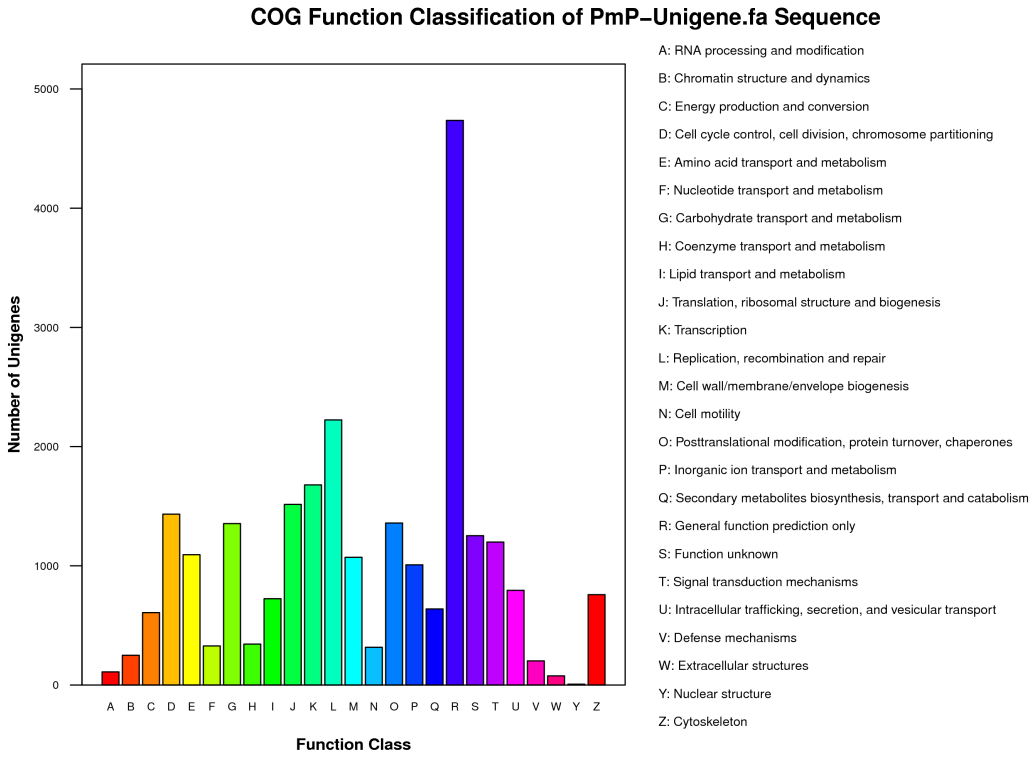

Figure S6. Clusters of Orthologous Groups (COG) function classification in the *P. melete* transcriptome unigenes. A total number of 34,534 unigenes were annotated into 25 categories.

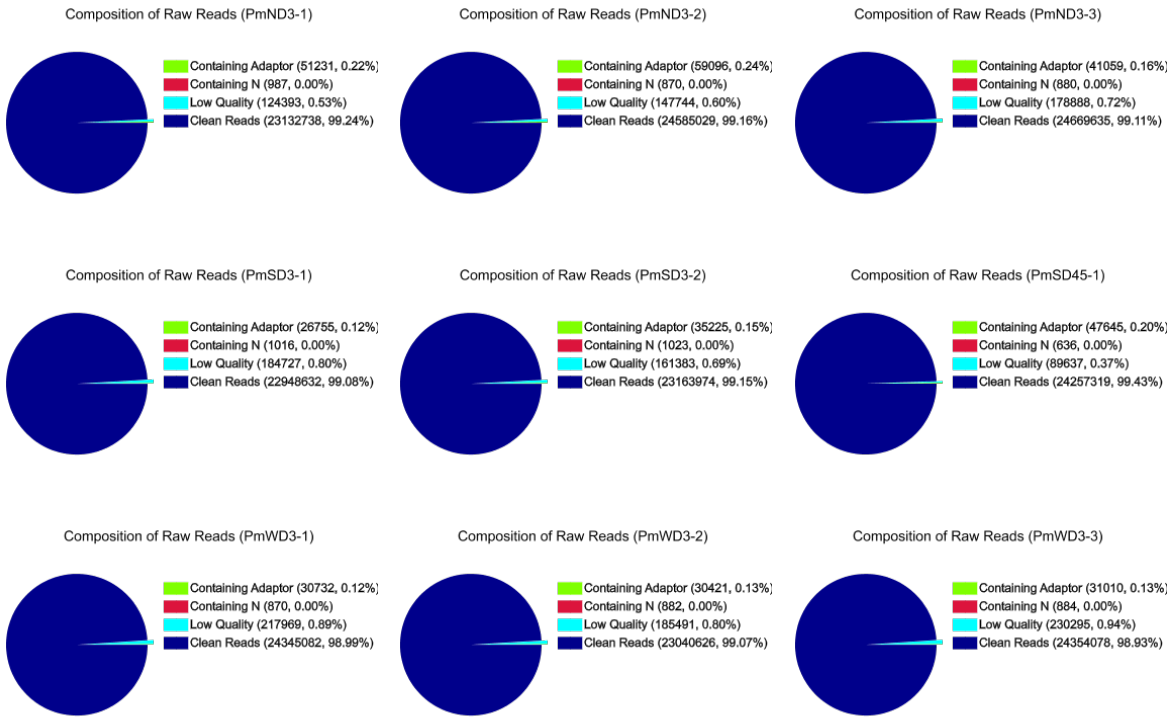

Figure S7. Different components of the raw reads and distribution of distinct clean reads in each sample in *P. melete*.

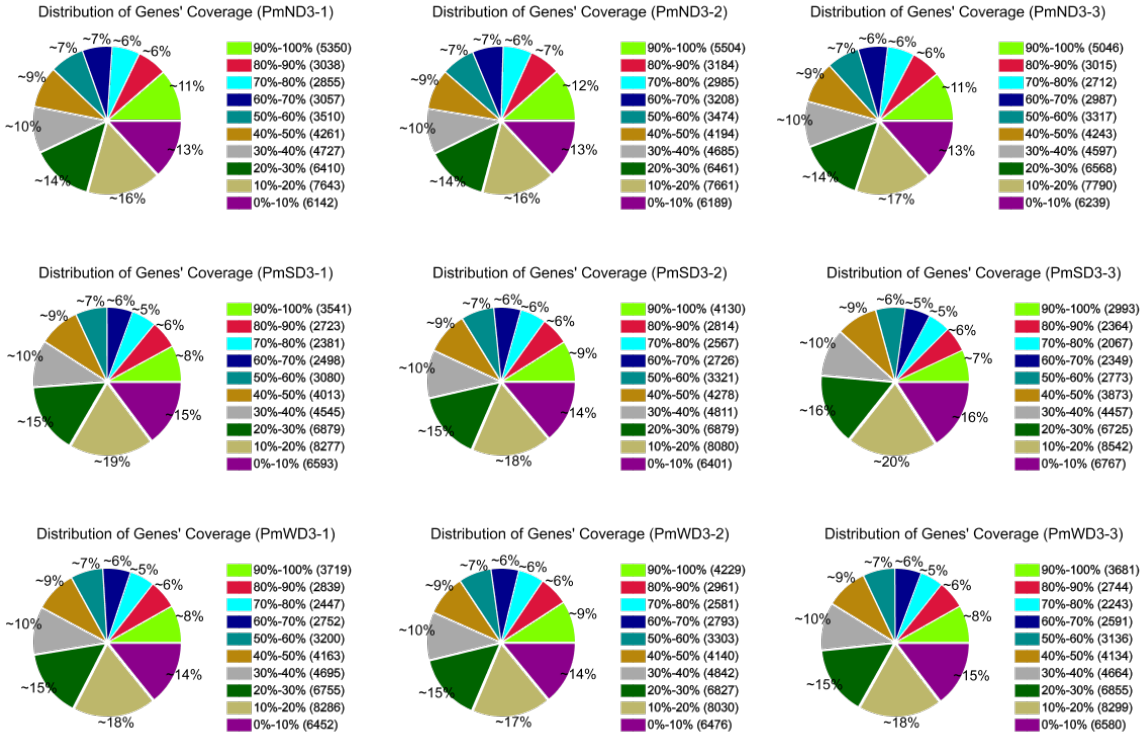

Figure S8. Distribution of genes coverage in each sample in *P. melete*.

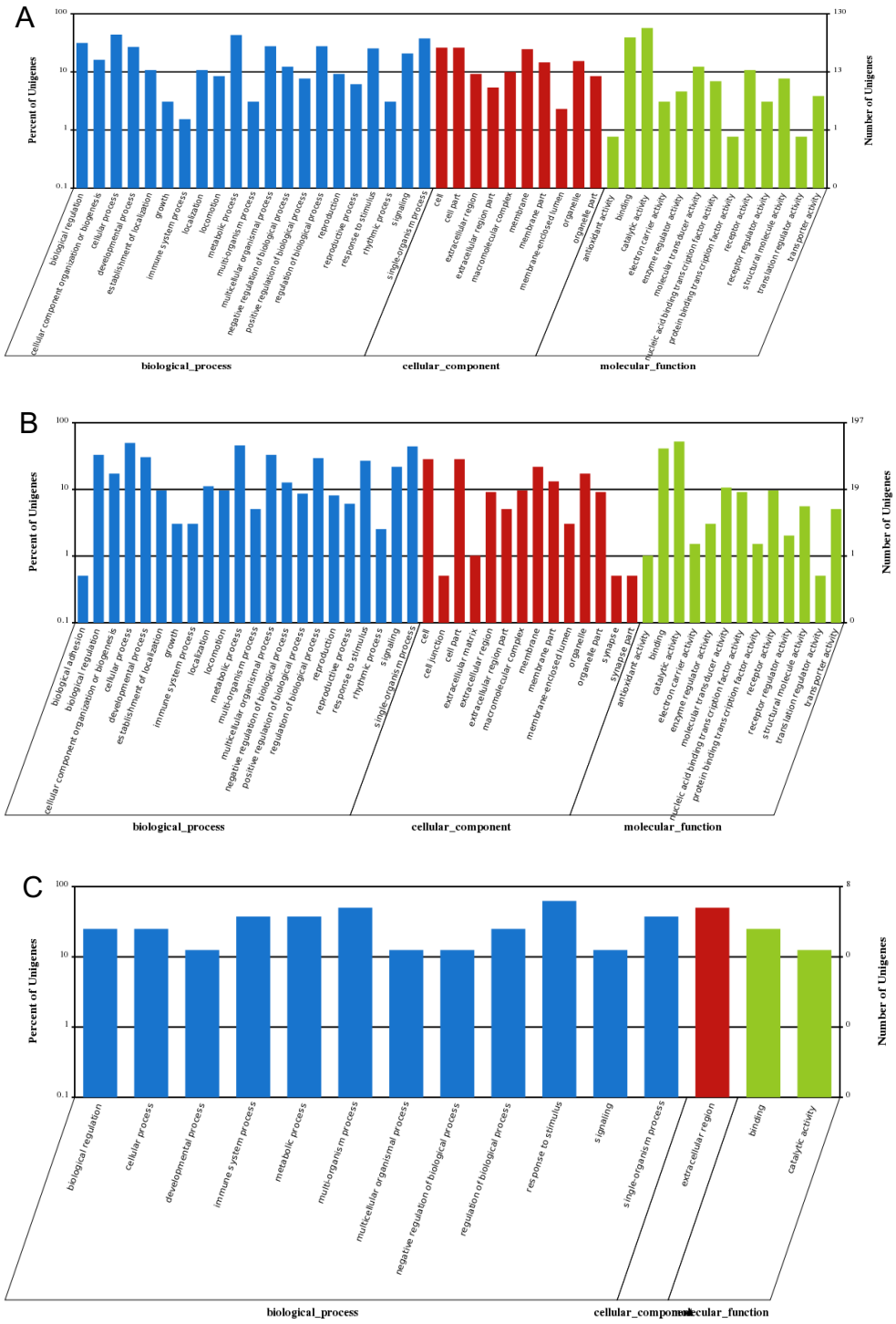

Figure S9. **Gene Ontological classification of differentially expressed genes in paired comparison among non-diapause (ND), summer diapause (SD) and winter diapause (WD)** in *P. melete*. The differentially expressed genes are grouped into three hierarchically structured GO terms of biological process, cellular component, and molecular function. The y-axis indicates the number of genes in each GO term. (**A**) Summer diapause vs non-diapause, (B) winter diapause vs non-diapause, and (C) summer diapause vs winter diapause.

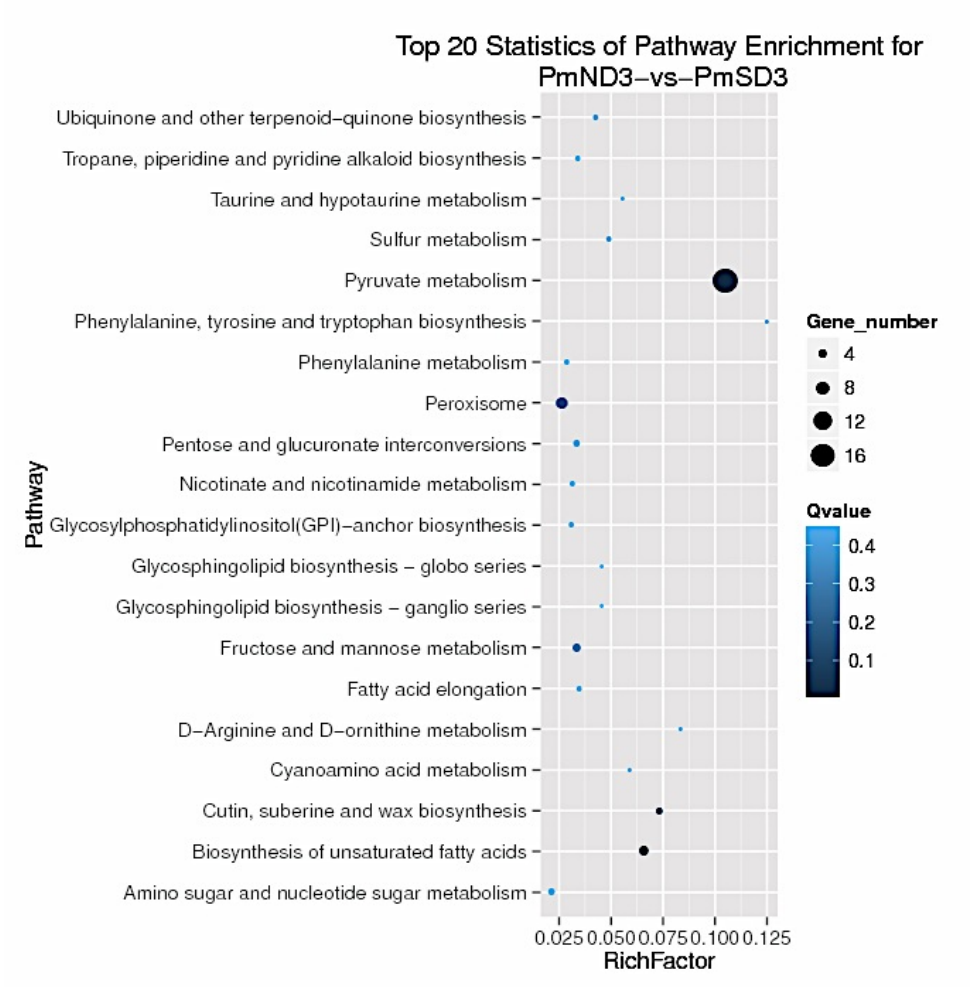

Figure S10. Significantly enriched of the top 20 statistics pathway in KEGG by differential expression genes between ND and SD treatment in *P. melete*.

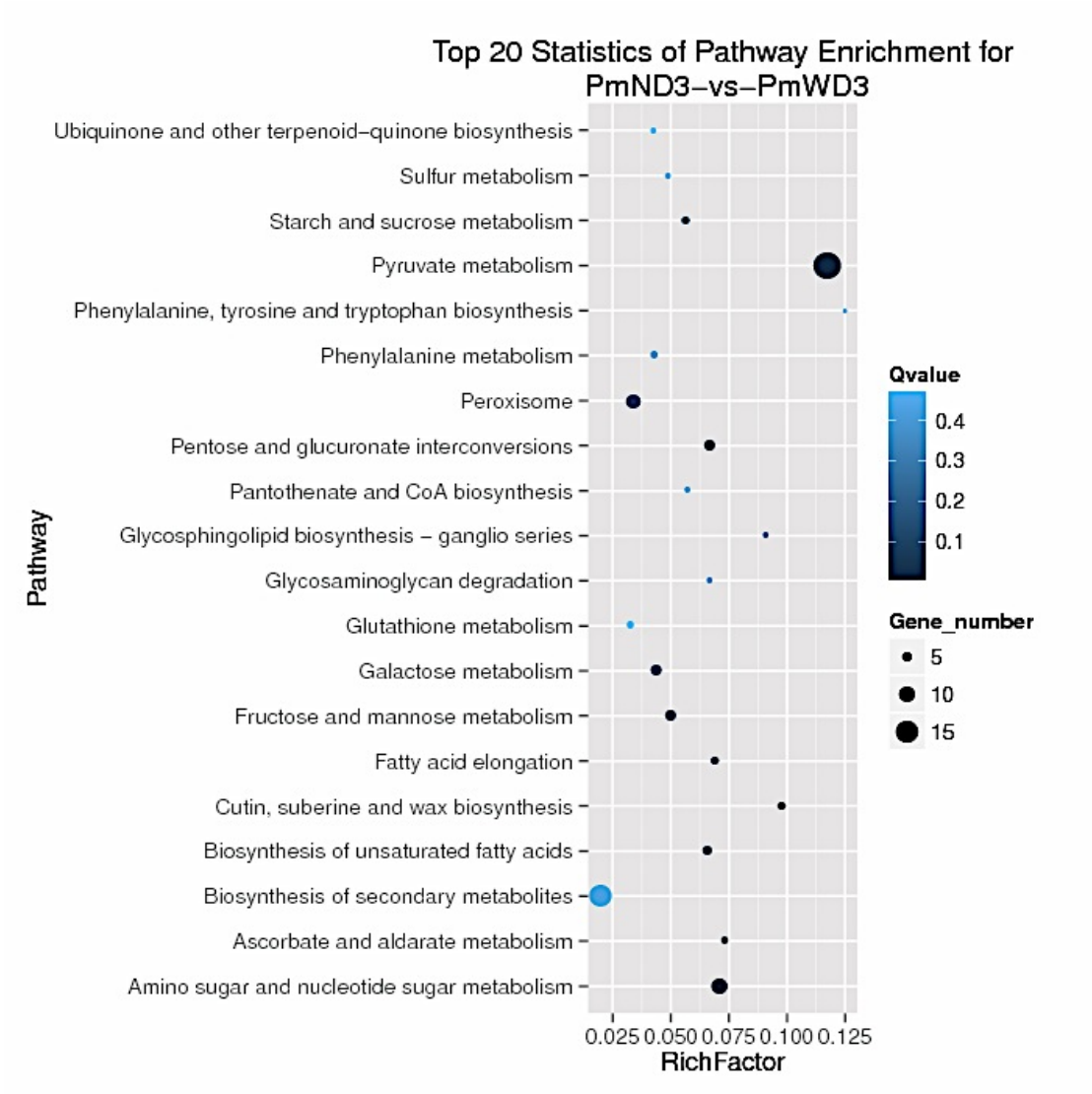

Figure S11. Significantly enriched of the top 20 statistics pathway in KEGG by differential expression genes between ND and WD treatment in *P. melete*.