

Figure S2. Proteomic assay quality analysis during the withering period of white tea. The distributions of peptide number (A) and length (B); (C) The mass error distribution of identified peptides; (D) The andromeda score distribution of identified peptides; (E) The distributions of protein molecular weight.

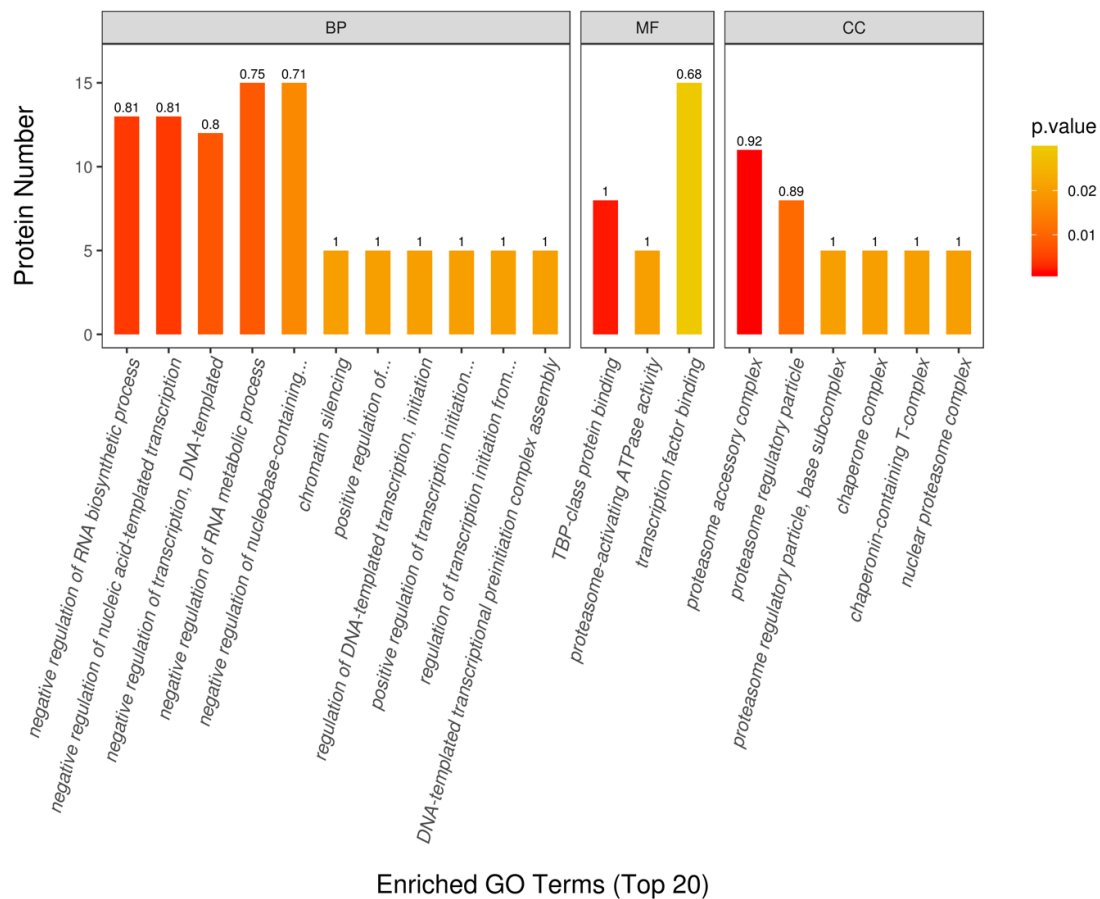
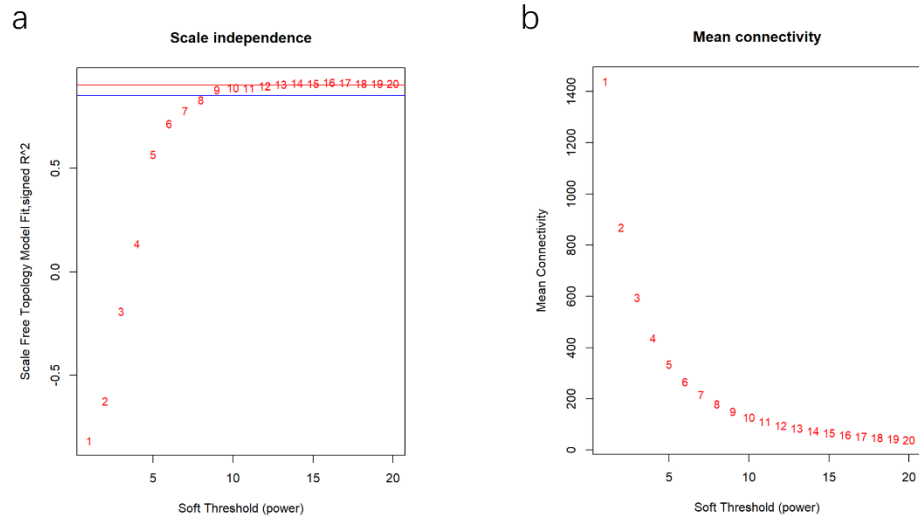


Figure S3. Top 20 significantly enriched gene ontology (GO) of the DPs in PCK vs PWP vs PWF.

A



B

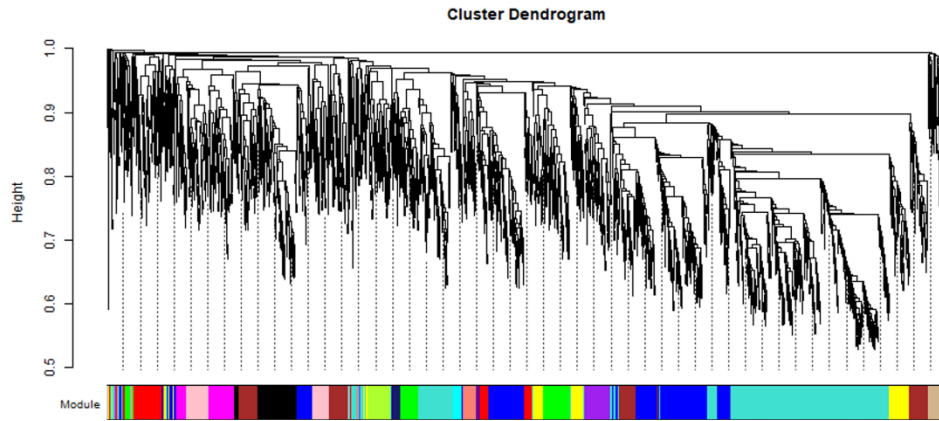


Figure S4. Clustering dendrograms of genes and module division. (A) Analysis of network topology for various soft-thresholding powers. The scale-free fit index (y-axis) as a function of the soft-thresholding power (x-axis) (a), and the mean connectivity (degree, y-axis) as a function of the soft-thresholding power (x-axis) (b). (B) Protein clustering on TOM-based dissimilarity, module division by dynamic tree cut and different colors represent different modules.

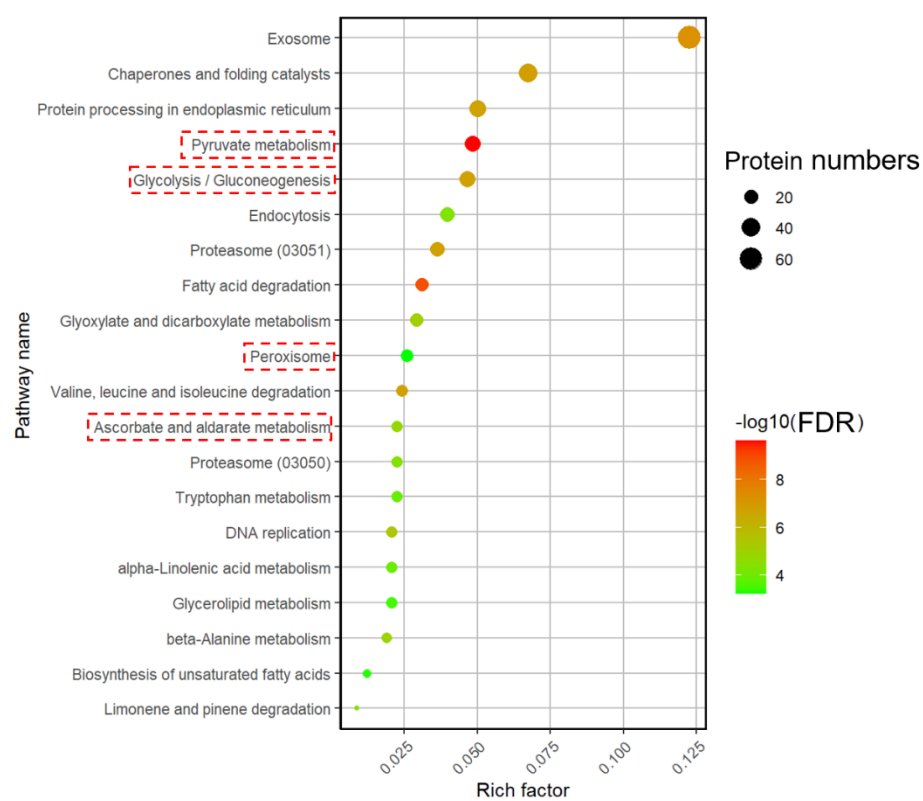


Figure S5. The significantly enriched KEGG pathways of the DPs in the MEturquiose