

Supplementary Material

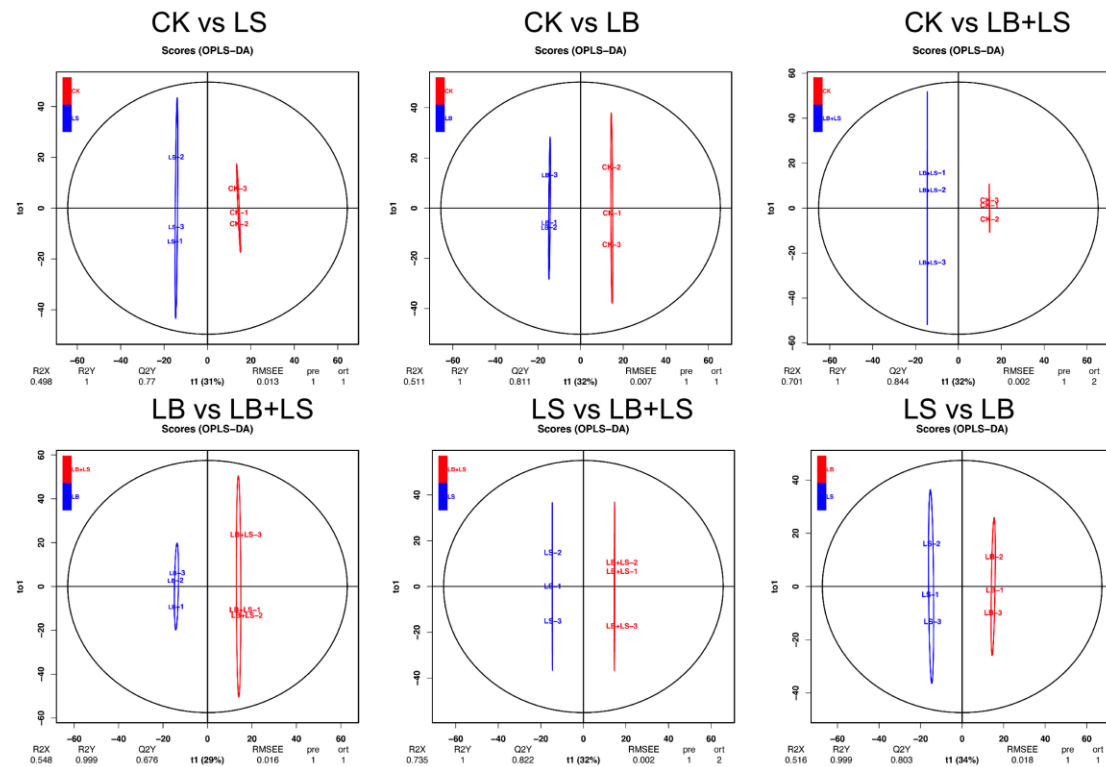


Figure S1. Orthogonal partial least squares-discriminant analysis (OPLS-DA) of metabolic profiles in each comparison.

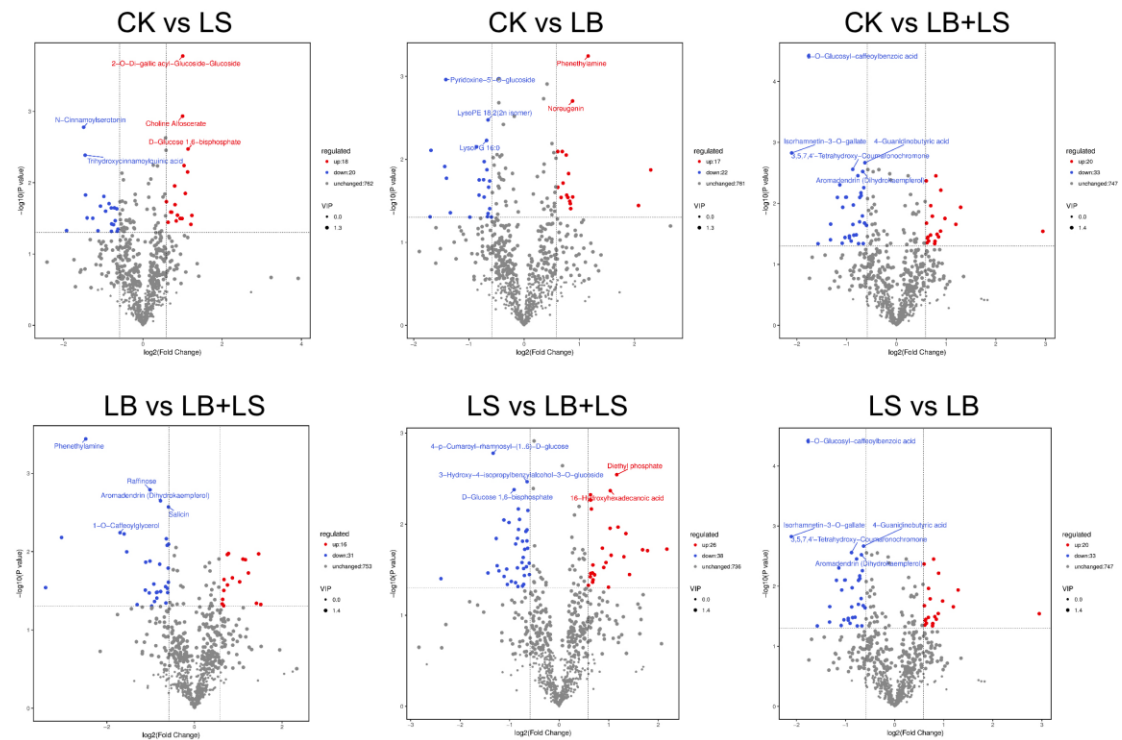


Figure S2. Volcano plots of differentially expressed metabolites (DEMs) identified in each comparison.

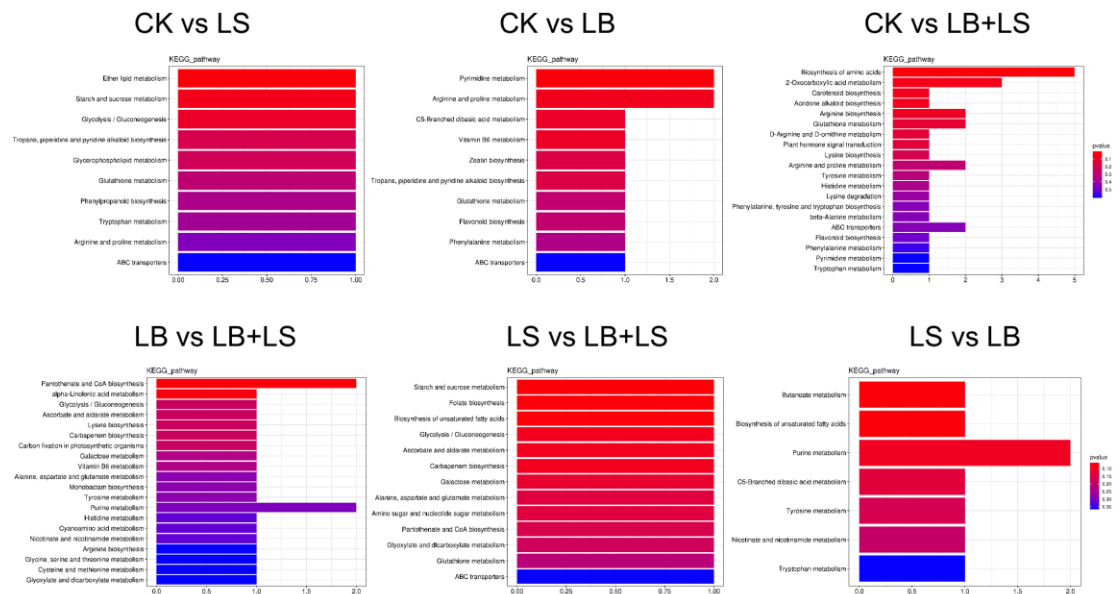


Figure S3. KEGG pathway enrichment analysis of *R. palmatum* in each comparison.

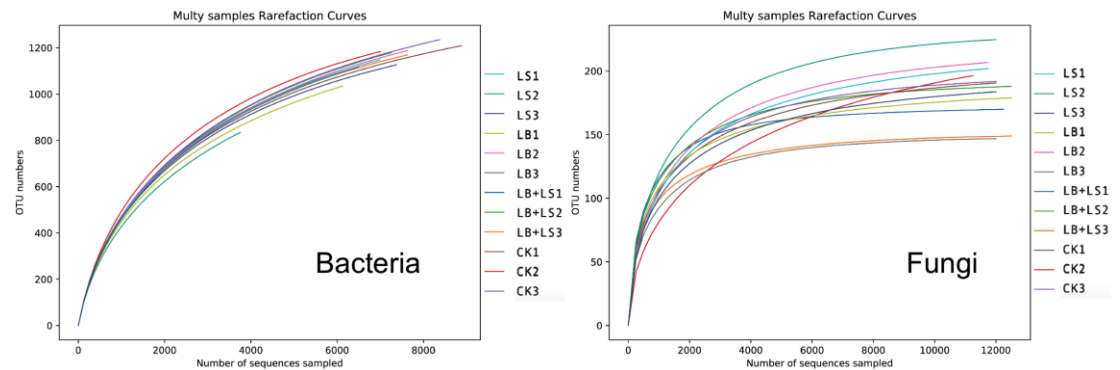


Figure S4 Rarefaction curves of the *R. palmatum* rhizosphere microbial communities.

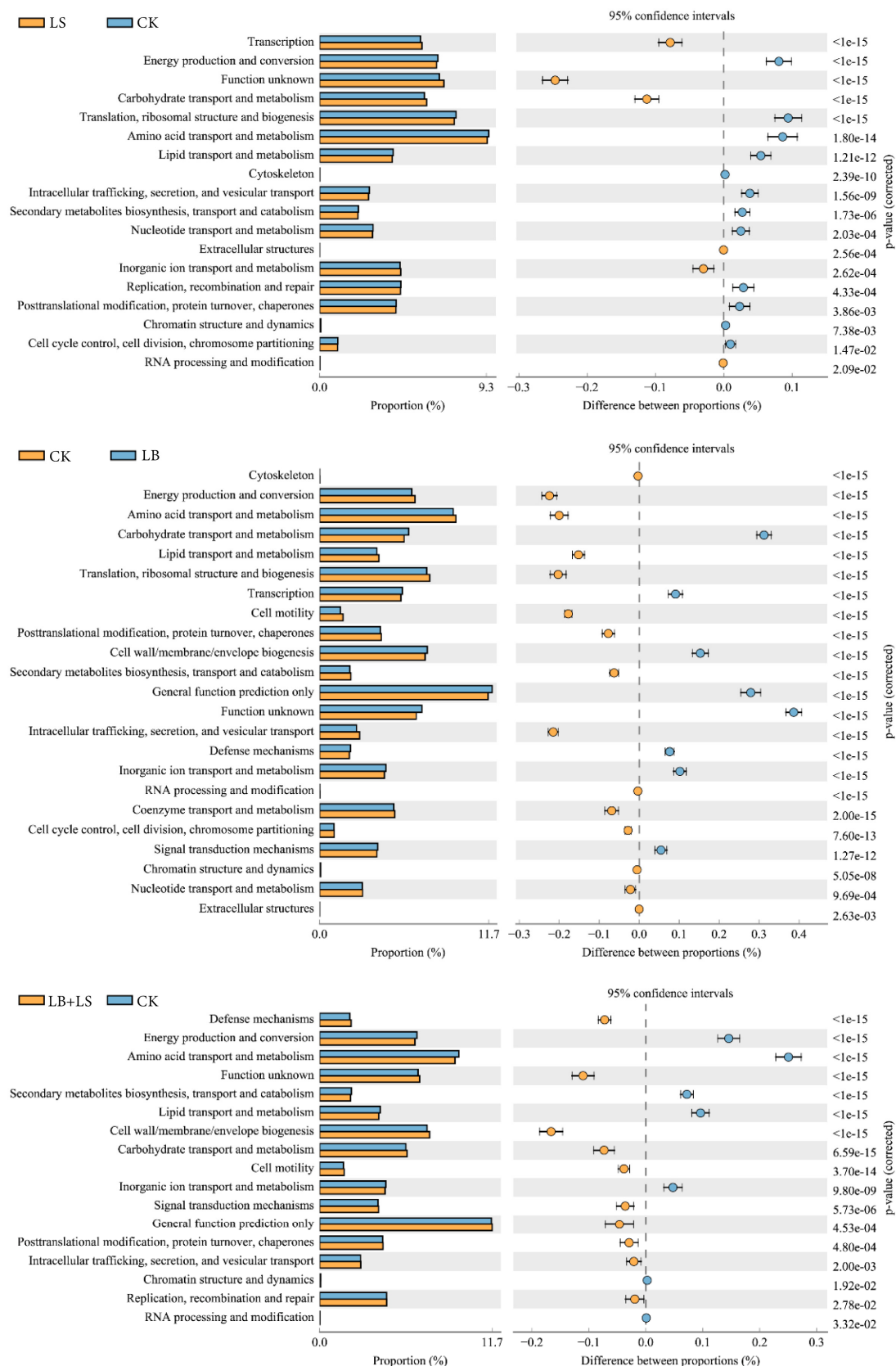


Figure S6 The COG functional classification of bacterial communities as predicted by PICRUSt.

Table S1 Metabolites' classification of the *R. palmatum* metablome.

Table S2 DEMs identified in the widely targeted metabolomics of *R. palmatum* metablome.

Table S3 KEGG pathway classification of the derived *R. palmatum* metablome.

Table S4 Results for the 16S rRNA gene-based bacterial sequencing.