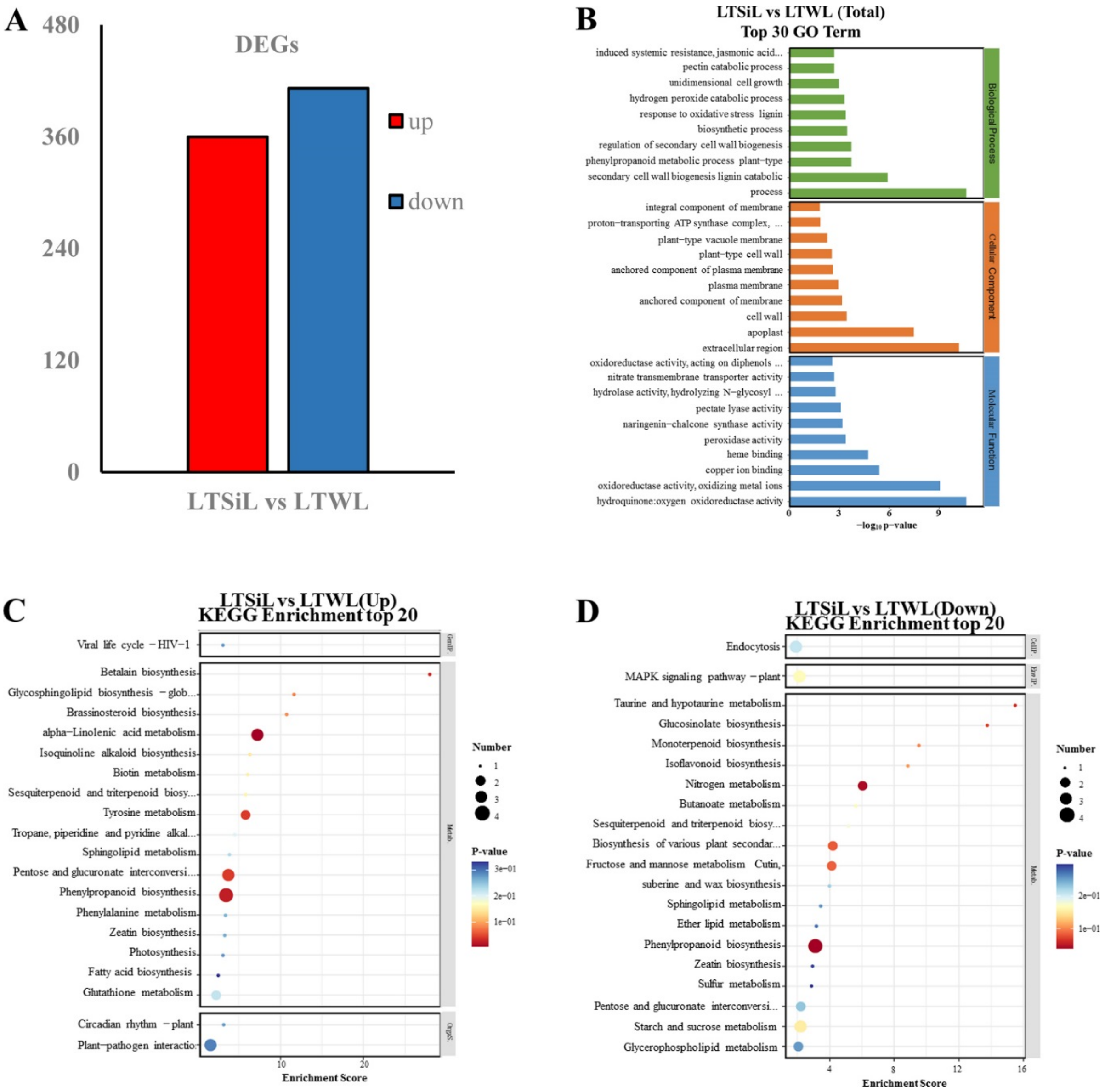

Supplemental Fig. S1 Overview of the transcriptome analysis of tea plants subjected to 4 ◦C treatment. a Number of DEGs identified in the pairwise comparison of LTSiL vs. LTWL in tea plants. b GO analysis of DEGs between LTSiL and LTWL under low temperature stress. The x-axis represents the percentage and number of DEGs, while the y-axis lists GO terms, which are categorized into three classes: cellular component, molecular function, and biological process. c KEGG pathway enrichment of the top 20 DEGs during cold stress treatment, highlighting the enriched pathways of up-regulated genes in LTSiL vs. LTWL. d KEGG pathway enrichment of the top 20 DEGs during cold stress treatment, showing the enriched pathways of down-regulated genes in LTSiL vs. LTWL. Dot size indicates the number of DEGs in a given pathway, and the rich factor is the ratio of DEG assigned to a specific pathway relative to all genes annotated in that pathway.