Figure S1 GO enrichment analysis of differentially expressed genes. The vertical axis represents GO terms, and the horizontal axis represents the Rich factor, which is the ratio of the number of enriched genes (Sample number) to the number of annotated genes (Background number) in the GO term. The larger the Rich factor, the greater the degree of enrichment. The size of the points represents the number of genes in this GO term, and the color of the points corresponds to different Padjust ranges. (A-C) GO functional enrichment classification of DEGs in WLN vs WLCK(**A**), WLNMT vs WLCK(**B**), and WLNMT vs WLN(**C**).
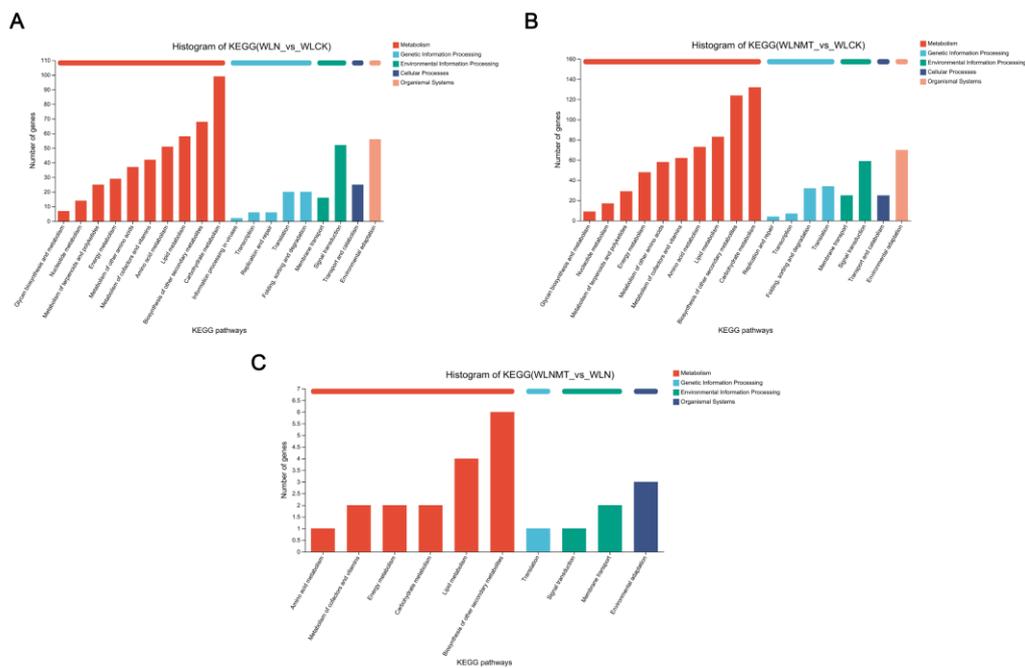
Figure S2 KEGG Functional annotation analysis of differentially expressed genes. KEGG metabolic pathways are divided into seven categories: metabolism, genetic information processing, environmental information processing, cellular processes, organismal systems, human diseases, and drug development. (A-C) KEGG

functional annotation classification of DEGs in WLN vs WLCK(**A**), WLNMT vs WLCK(**B**), and WLNMT vs WLN(**C**).