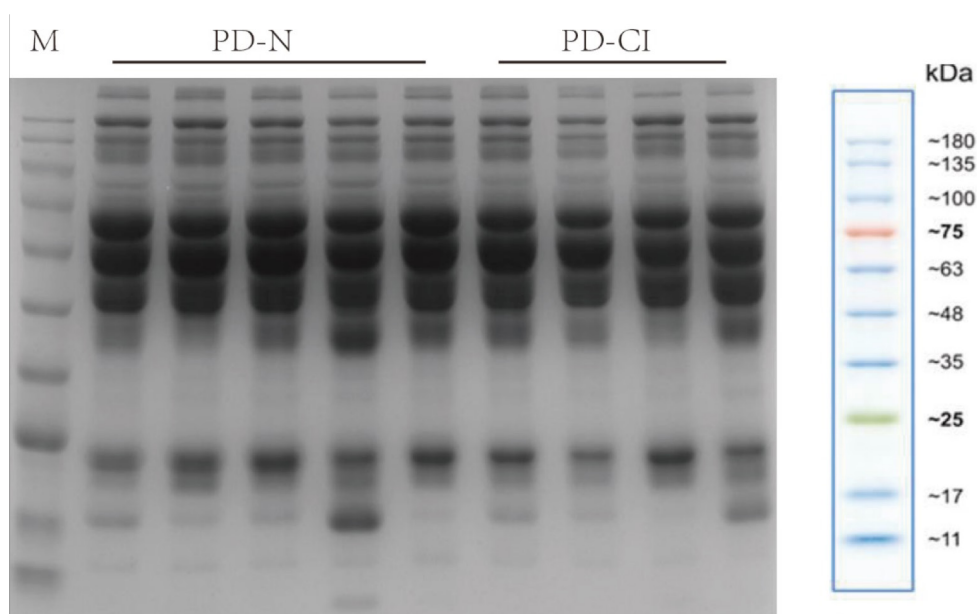**Figure S1** The concept map of O2PLS method.

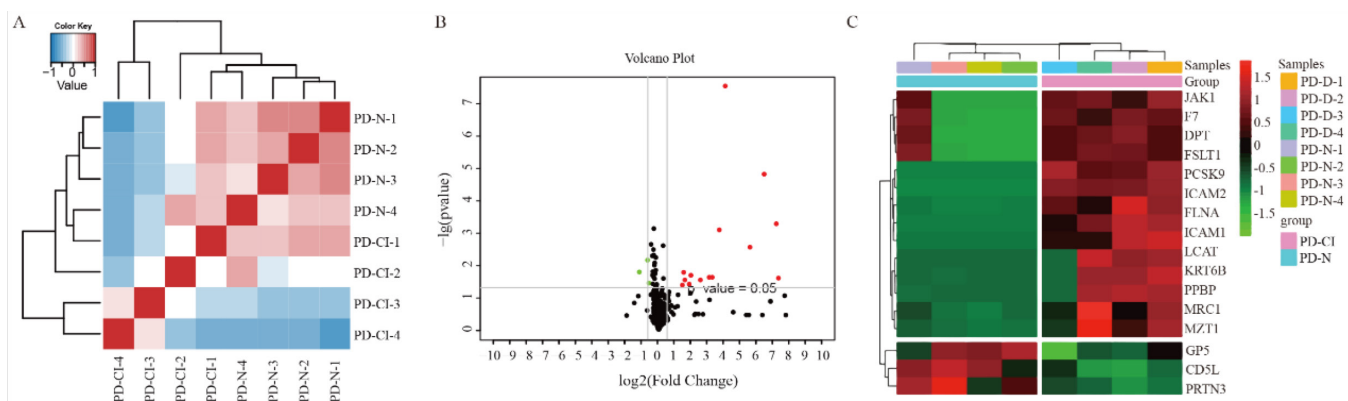**Figure S2** SDS-PAGE analysis of quality control for samples.

Figure S3 Serum differentially expressed proteins between PD-CI and PD-N. (A) Correlation analysis between samples. The color changes from white to blue, indicating negative correlation. The color varies from white to red, indicating a positive correlation. The closer the correlation coefficient is to 1 (-1), the higher the similarity of the expression patterns between samples. (B) Volcano plots of differential protein expression analysis. The red dot represents the expression of the up-regulated protein, and the green dot represents the expression of the down-regulated protein, and the black dot represents the site with no significant difference. Abscissa: the ratio of the relative expression of protein in the two groups of samples, that is Fold Change and log2 logarithmic processing. Ordinate: P value and -Log10 logarithmic processing. (C) Cluster analysis of differential protein. The color changes from green to red, indicating that the expression of protein in each sample changes from low to high.
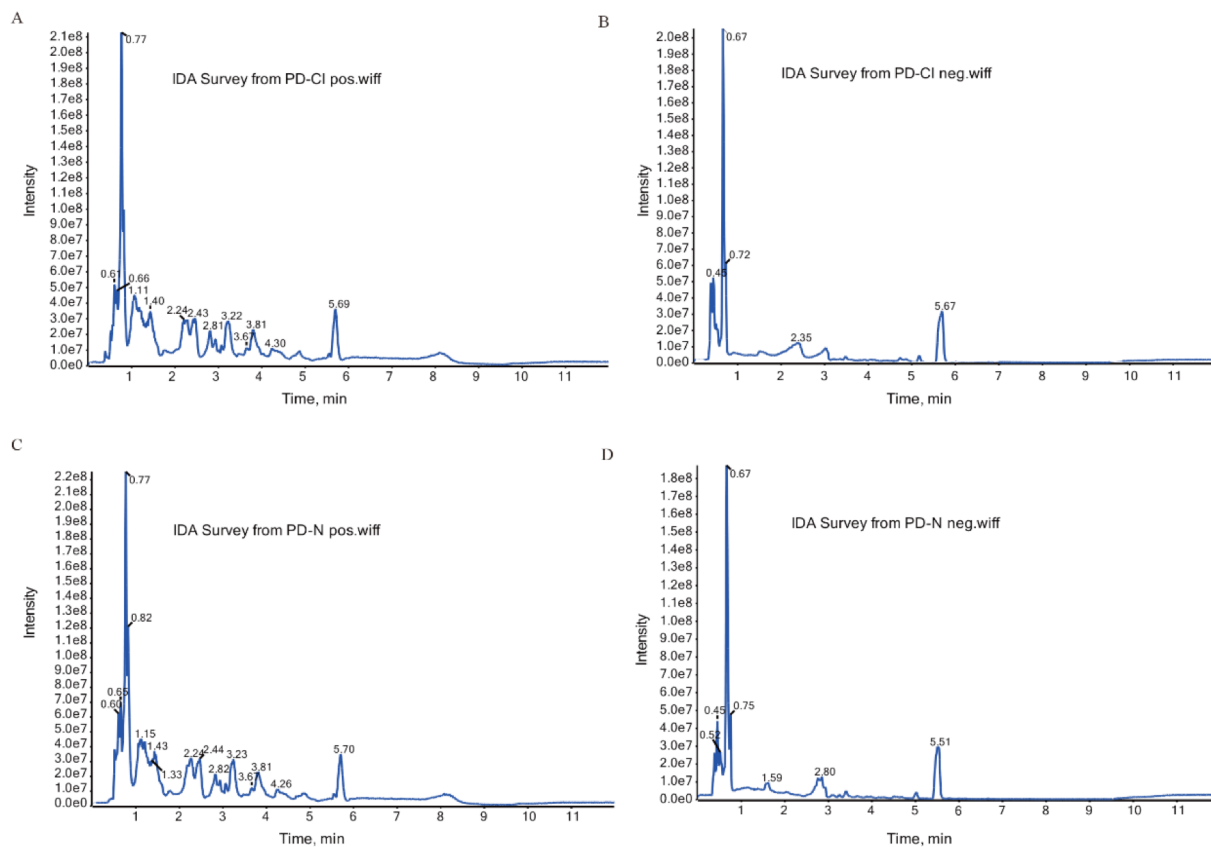

Figure S4 Typical TICs of metabolic profiles in PD-CI and PD-N based on UHPLC-Q-TOF/MS analysis. (A) positive ion mode of PD-CI; (B) negative ion mode of PD-CI; (C) positive ion mode of PD-N; (D) negative ion mode of PD-N.
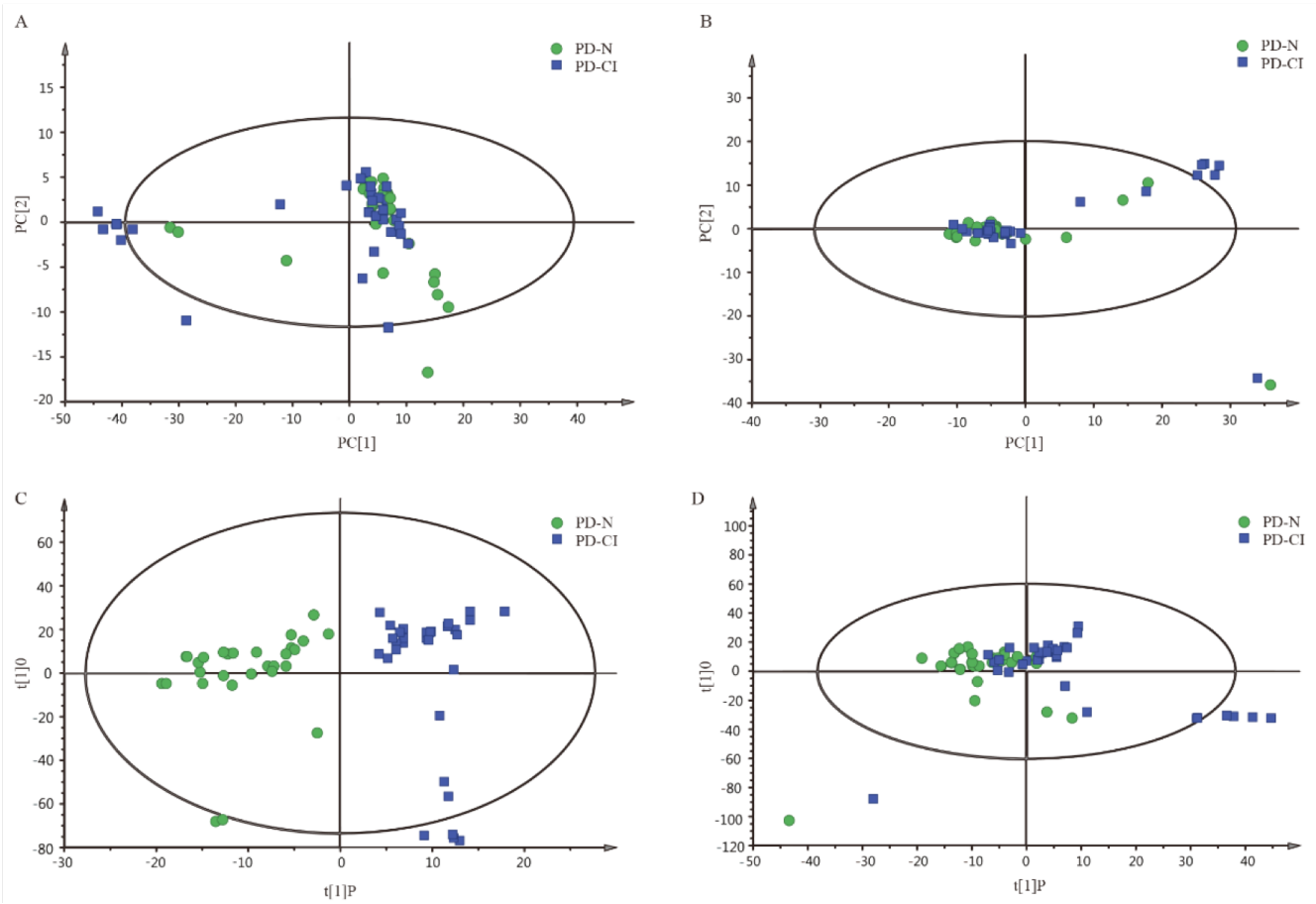
Figure S5 PCA score plots and OPLS-DA score plots of metabolic profiles in PD-CI and PD-N. (A) PCA score plot in the positive mode; (B) PCA score plot in the negative mode; (C) OPLS-DA score plot in the positive mod; (D) OPLS-DA score plot in the negative mod. Boxes and dots denote samples from PD-CI and PD-N, respectively.
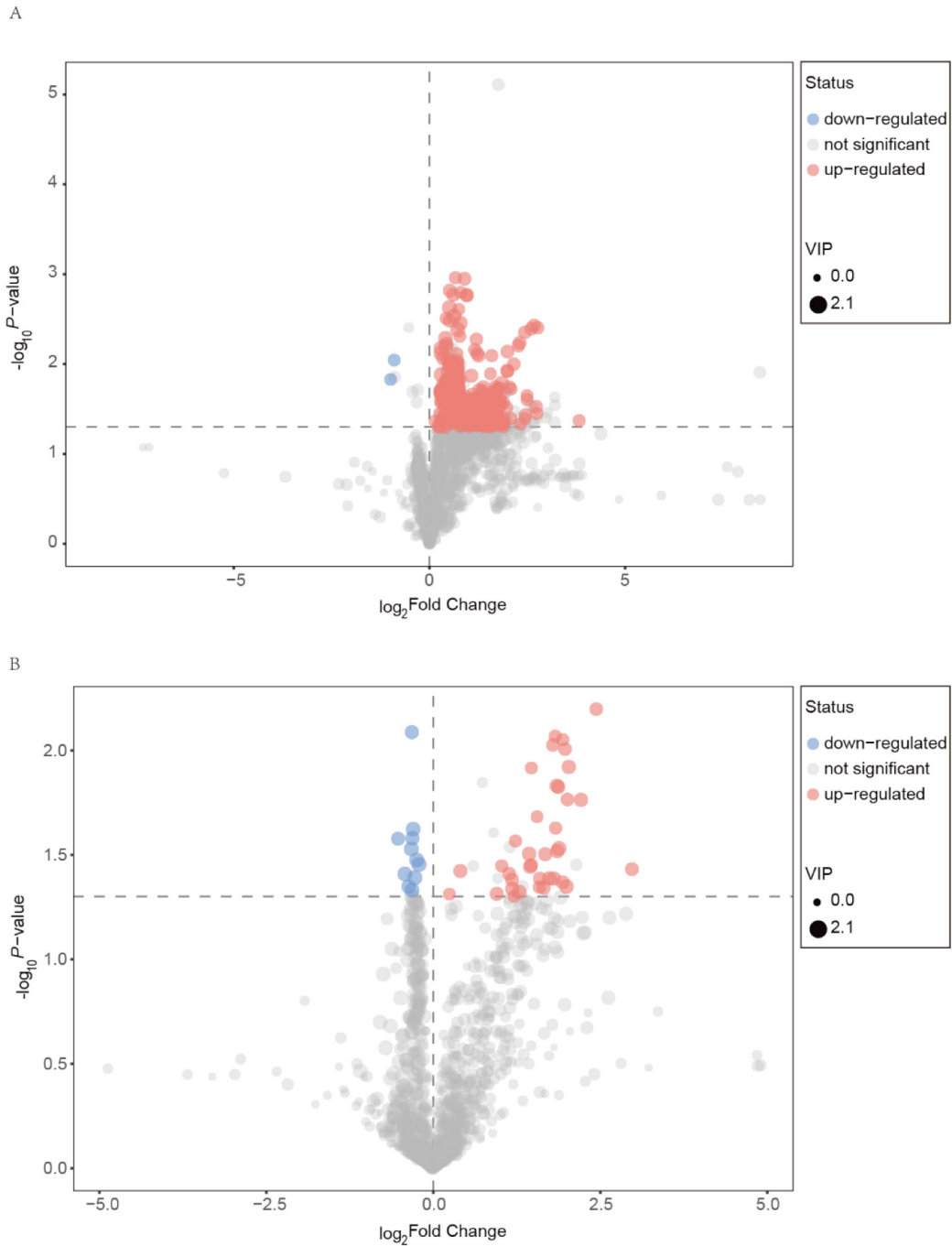
Figure S6 Volcano plot for PD-CI group versus PD-N group. (A) Volcano plot in the positive mode. (B) Volcano plot in the negative mode. Each point in the volcano plot represents a metabolite, the abscissa represents the fold change of each substance (take the base 2 logarithm), and the ordinate represents the P-value of the t test (take the negative of the base 10 logarithm). The scatter size represents the VIP value of the OPLS-DA model. The larger the VIP value, the larger the scatter. The scatter color represents the final screening result, the significantly up-regulated metabolites are shown in red, the significantly down-regulated metabolites are shown in blue, and the non-significantly different metabolites are gray.
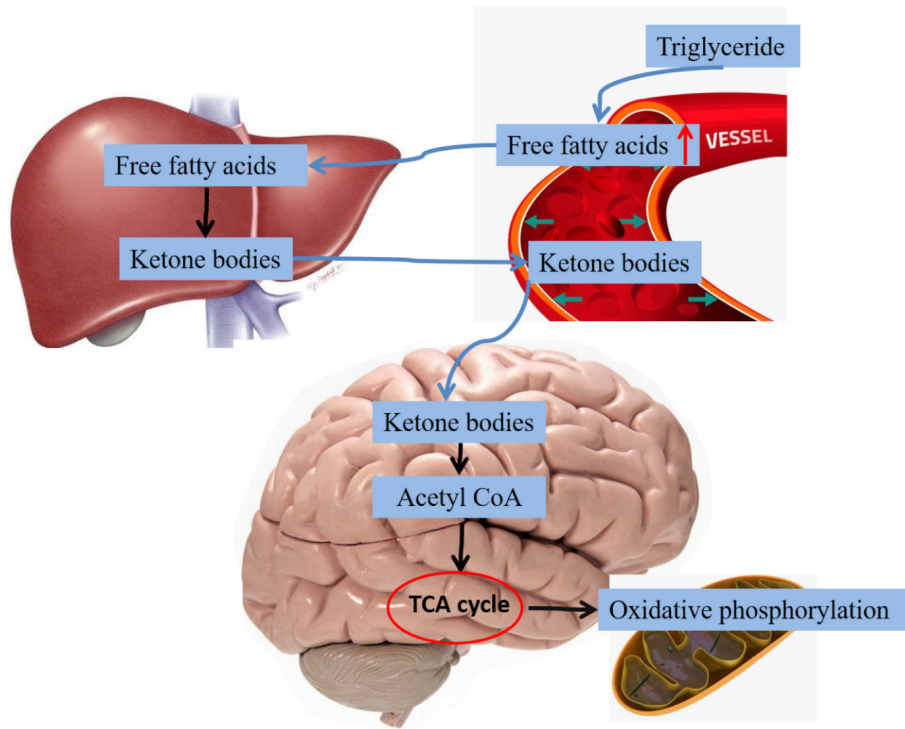
Figure S7 Concept map of fat metabolism.