

Figure S1. Overall technical route of this project.

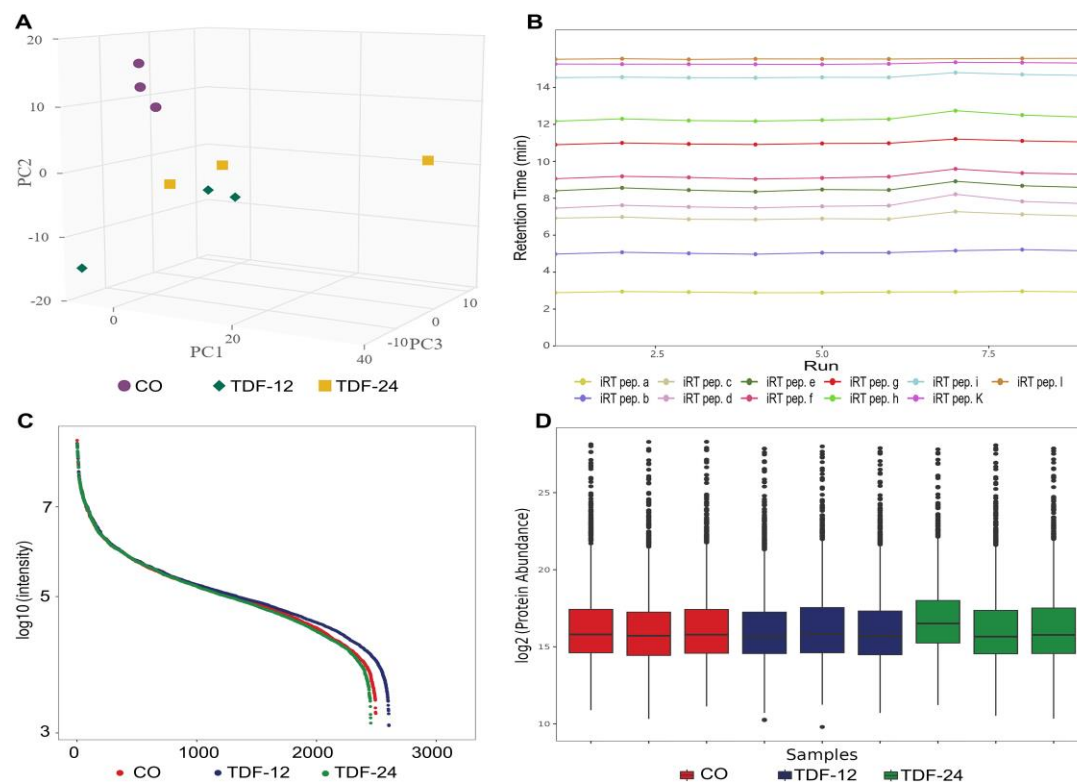


Figure S2. Quality assessment of the proteomics dataset. (A) Principal component analysis (PCA) scores. (B) IRT peptide elution time distribution. (C) Correlation scatter plot of protein abundances. (D) Sample intensity jitter profile.

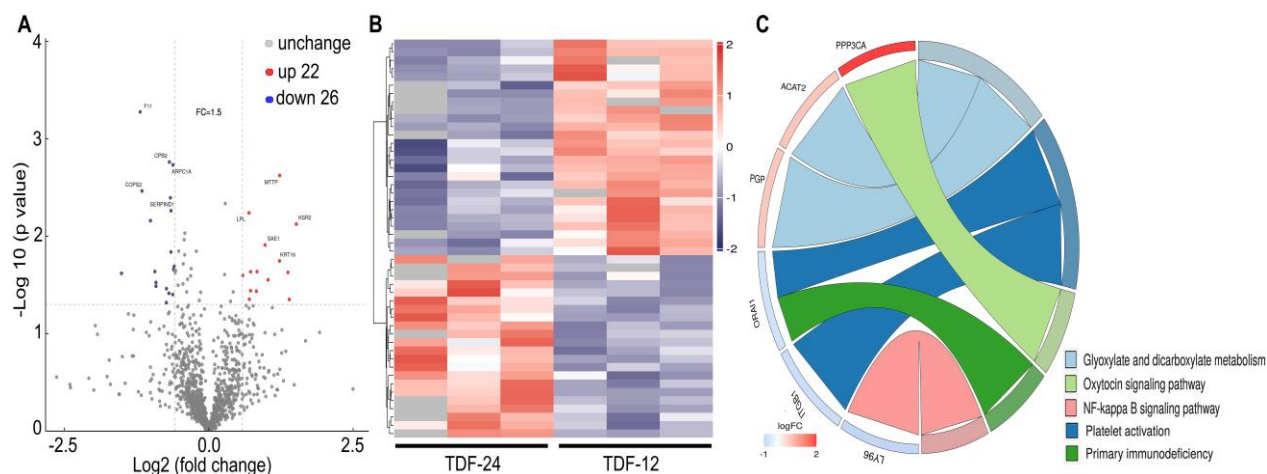


Figure S3. Bioinformatics analysis of differentially expressed proteins between the week 24 of treatment (TDF-24) and week 12 of treatment (TDF-12) groups. (A) Volcano plot of serum protein abundance differences between patients receiving TDF for 12 months and those receiving TDF for 24 months. (B) Heatmap of hierarchical clustering analysis for the differentially expressed proteins. (C) PPI network mapping of KEGG pathway enrichment analysis.

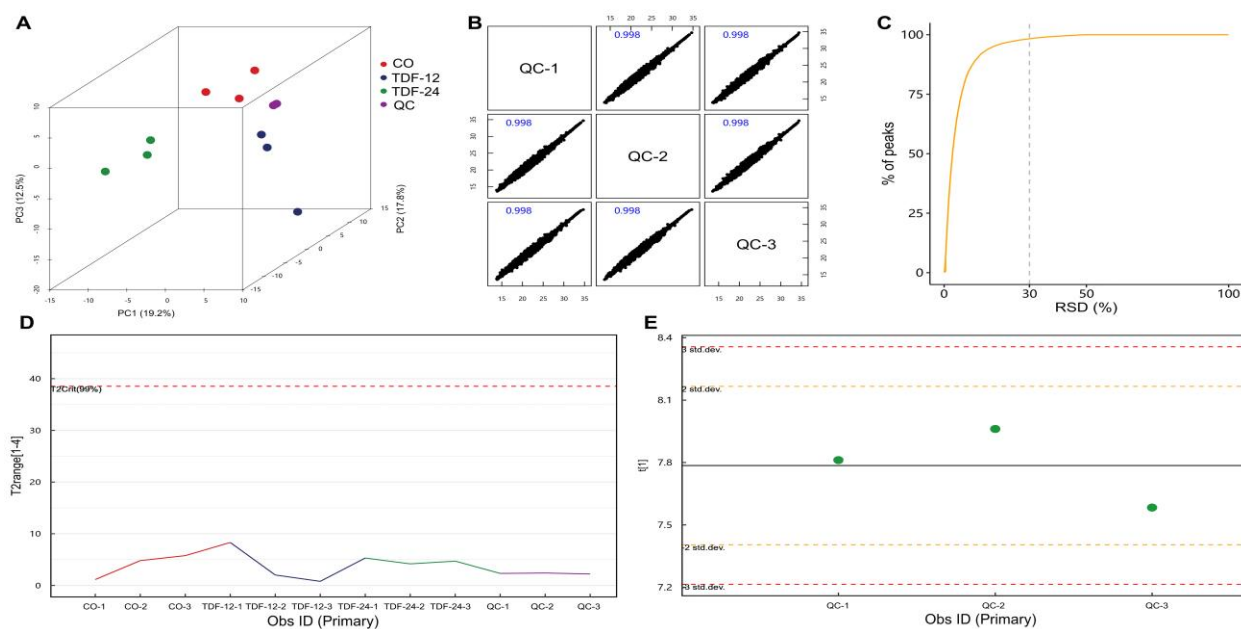


Figure S4. Quality assessment of the metabolomics dataset. (A) Principal component analysis (PCA) scores plot. (B) Correlation map of quality control (QC) samples. (C) Relative standard deviation (RSD) distribution for QC samples. (D) Multivariate statistical process control (SPC) chart. (E) Hotelling's T^2 test plot for all samples.

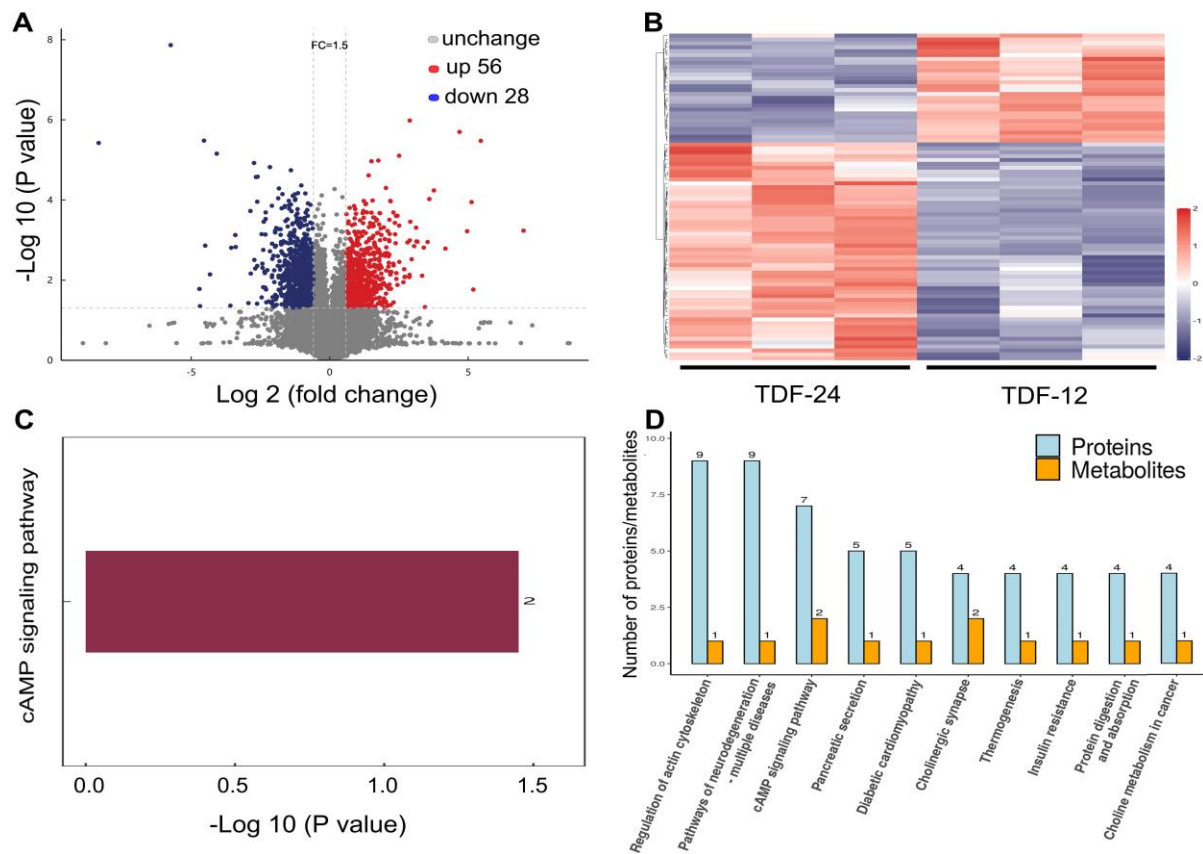


Figure S5. Bioinformatics analysis of differentially expressed metabolites between the TDF-24 and TDF-12 groups between the week 24 of treatment (TDF-24) and week 12 of treatment (TDF-12) groups. (A) Volcano plot of metabolite abundance differences in serum between the TDF-12 and TDF-24 treatment groups. (B) Heatmap from hierarchical clustering analysis of differential metabolites. (C) KEGG pathway enrichment analysis of differential metabolites. (D) Integrated KEGG pathway analysis of proteomic and metabolomic data from TDF-12 and TDF-24 patients.