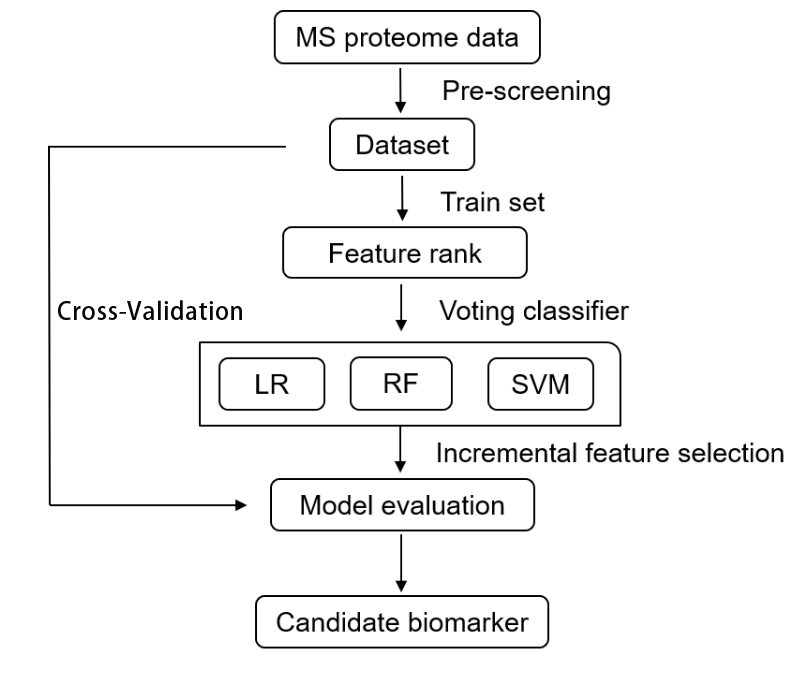
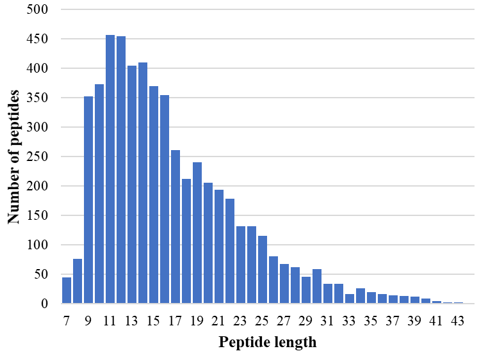
Supplementary figure S1. Flow chart of Machine Learning

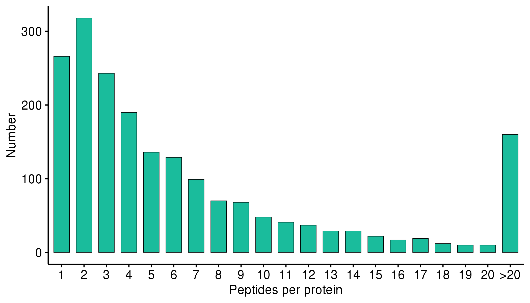


Supplementary figure S2. Quality control of the proteomics

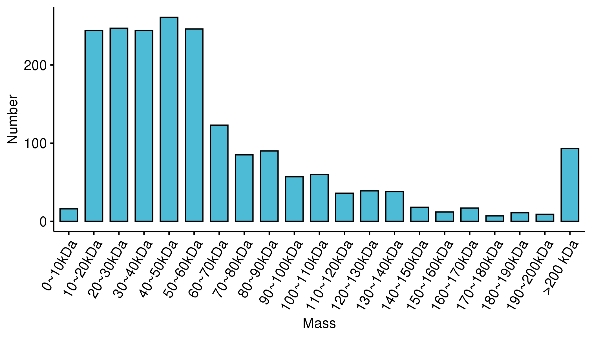
1. Length distribution of all identified peptides



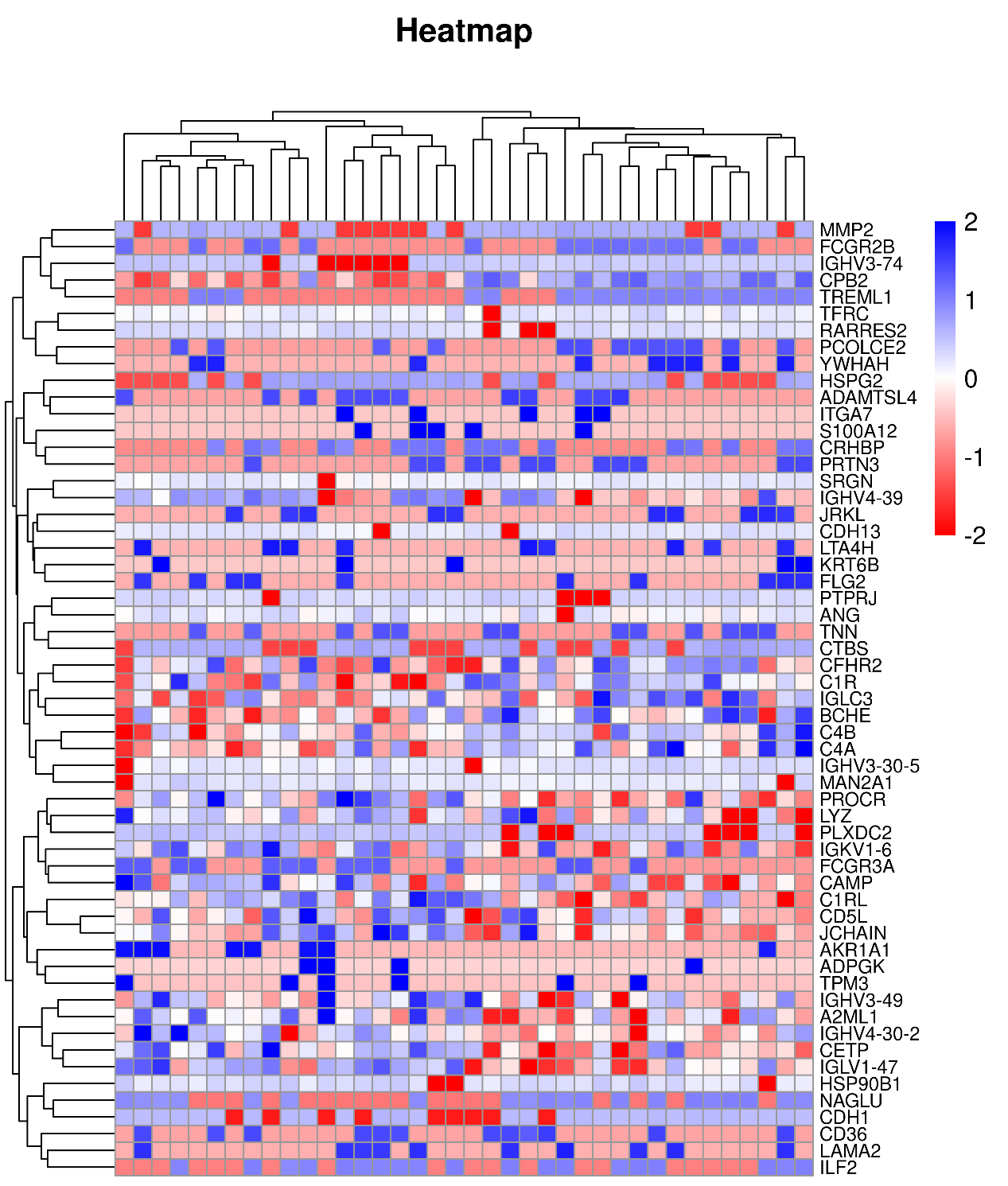
1. Distribution diagram of the number of peptides



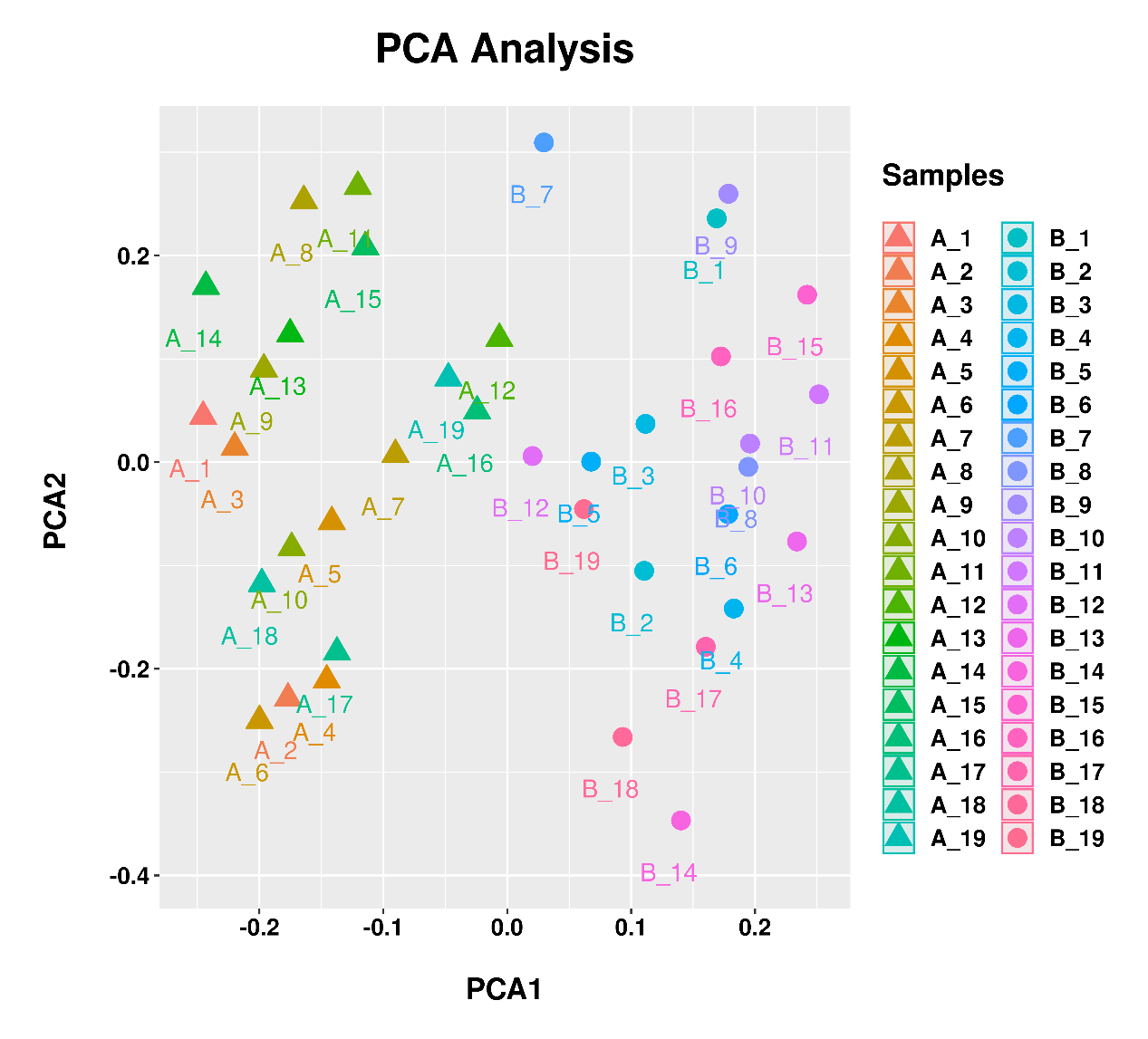
1. Distribution diagram of protein mass



Supplementary figure S3. Heatmap of unsupervised clustering analysis

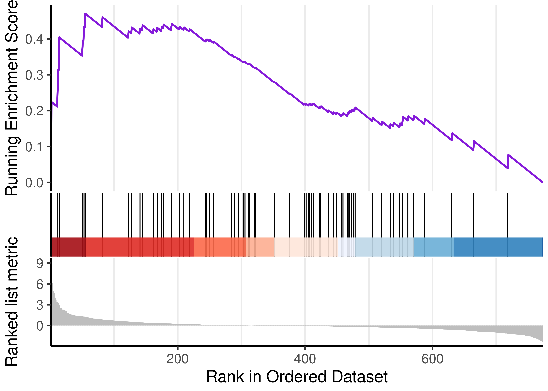


Supplementary figure S4. Principal-component analysis of differentially expressed proteins

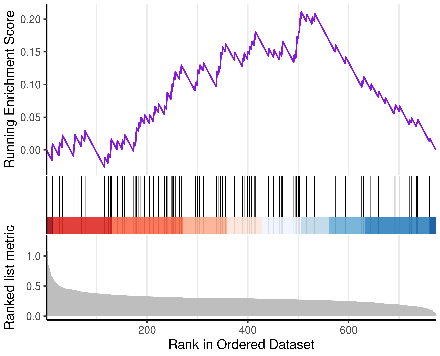


Supplementary figure S5. Gene Set Enrichment Analysis

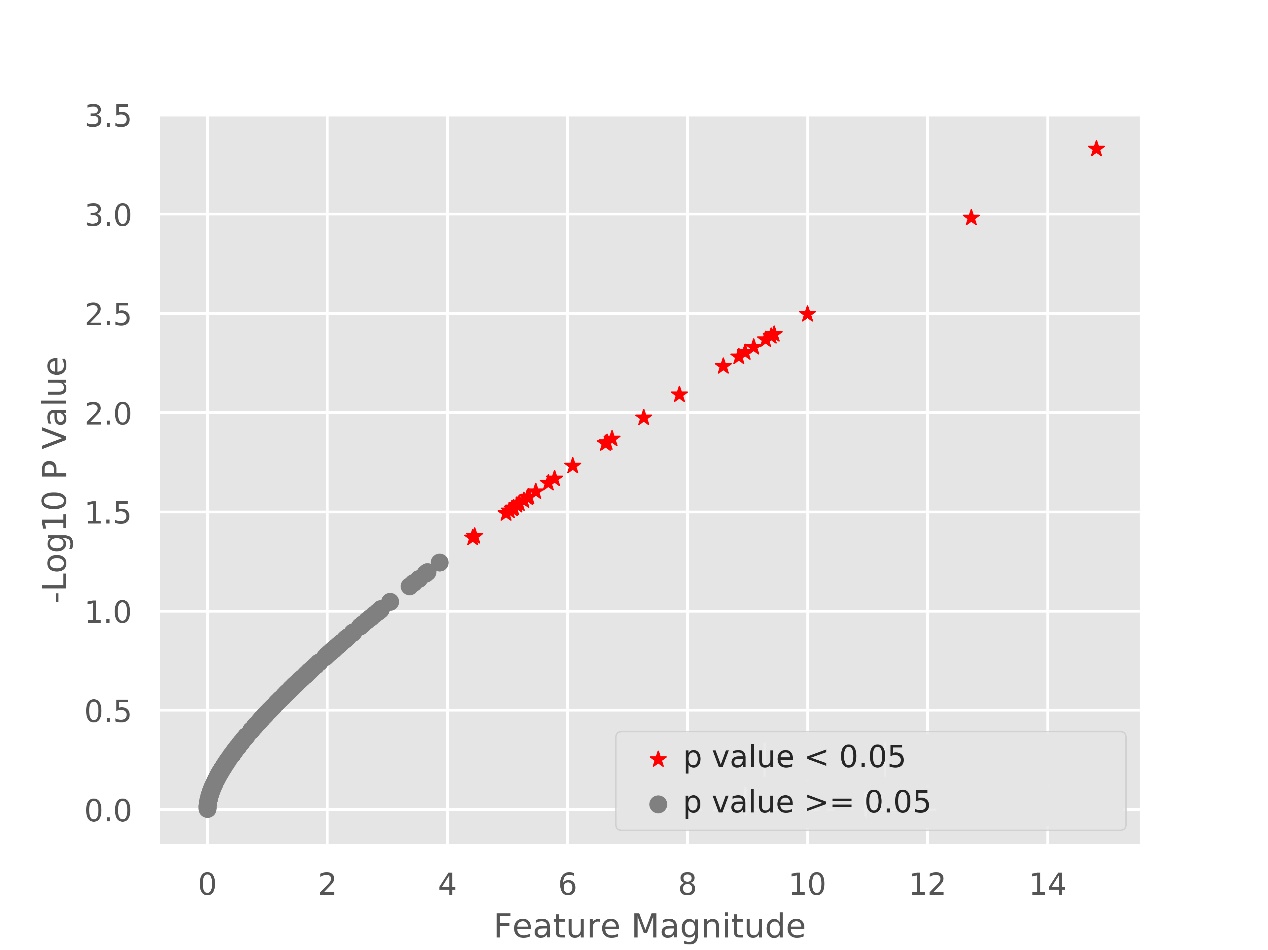
A. HALLMARK\_COAGULATION



B. GO\_LIPID METABOLIC PROCESS

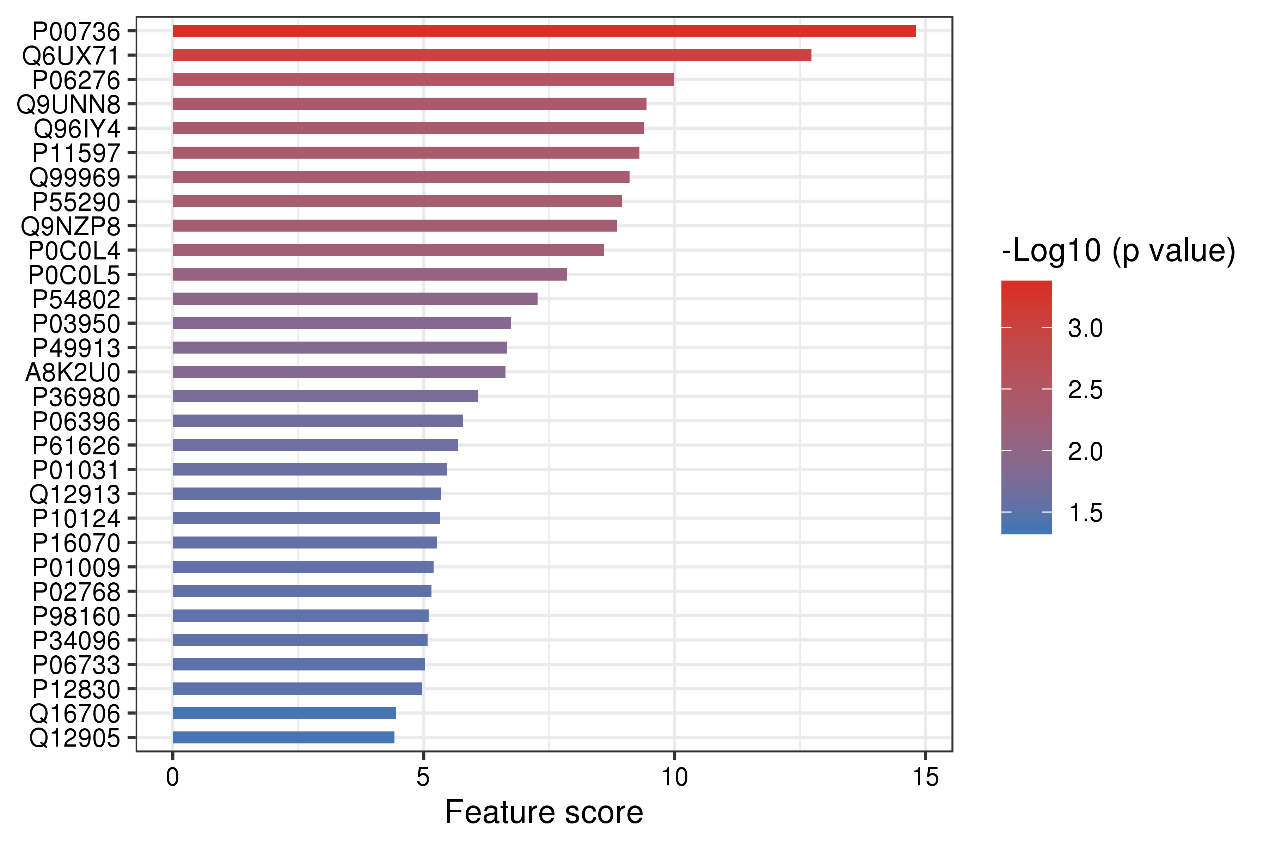


Supplementary figure S6. Feature analysis



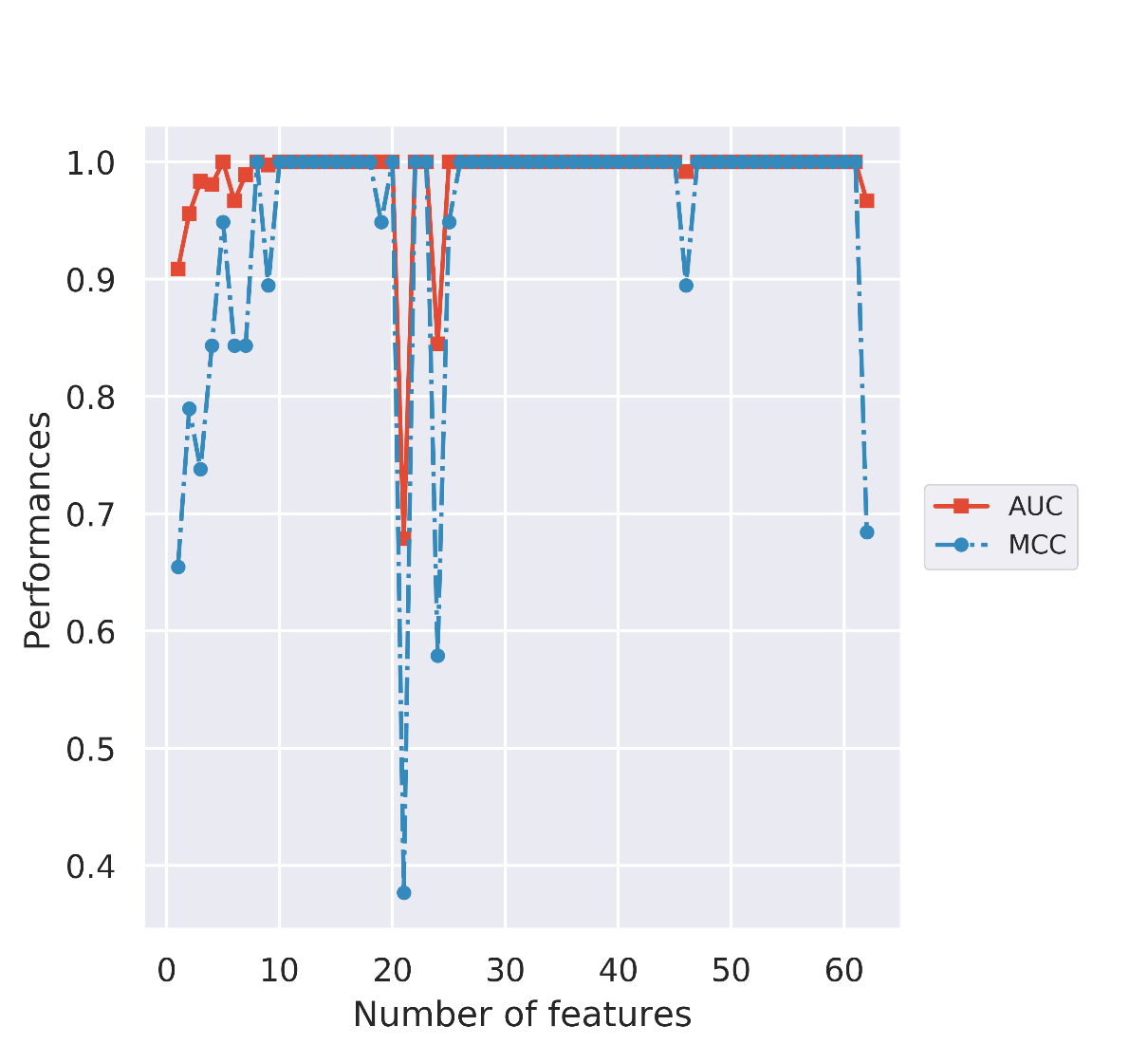
Note: In this figure, X-axis was the score of each expression feature, and Y-axis was the p-value of corresponding expression feature converted to -log10. Among them, the expression characteristics with a p value < 0.05 were indicated in red, and the expression characteristics with a p value > 0.05 were indicated in gray.

Supplementary figure S7. Ranking histogram

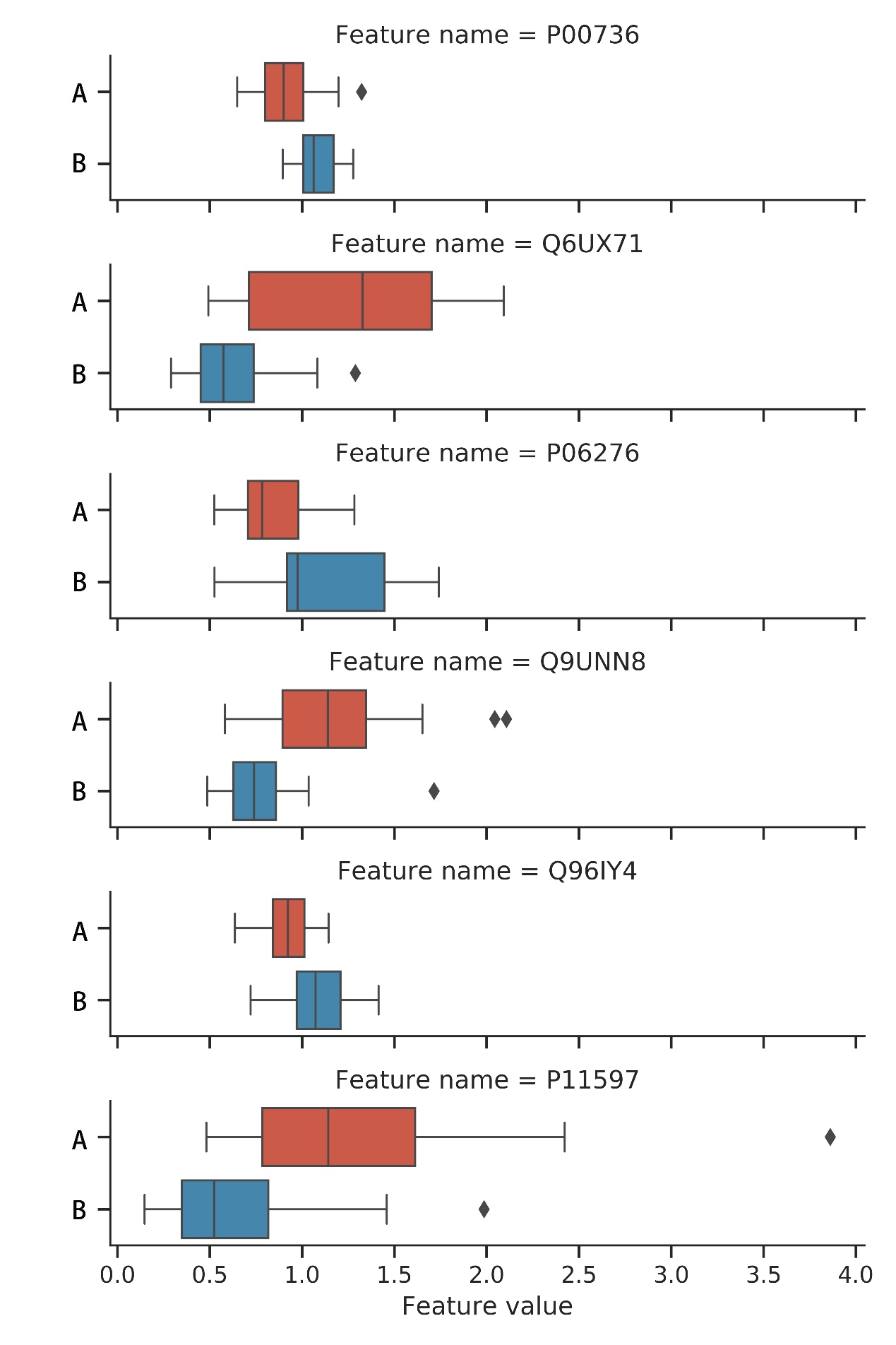


Note: In the figure, the expression feature was sorted according to the score, and the color of the histogram was filled with the feature's -log10 p value.

Supplementary figure S8. Incremental feature selection curve



Supplementary figure S9. Box plot of the levels of six candidate proteins in two groups



Supplementary figure S10. Correlation scatter plot of target proteins and biochemical parameters

A. CETP and HDL-C



B. CETP and TG



C. EPCR and fibrinogen

