**Text S2.** Proteomics instrument parameters

The Agilent LC system and AB Sciex 5600 Q-TOF-MS were used for LC-MS/MS analysis. The chromatography was performed on Agilent Poroshell 120 EC-C18 columns (50 mm×2.1 mm, 1.9 μm). The mobile phase is as follows: phase A is ultra-pure water (containing 0.1% formic acid), phase B is acetonitrile (containing 0.1% formic acid); Gradient elution conditions: 0~1 min, 5% B; 1~28 min, 5~35% B; 28~29 min, 35%~90% B; 29~31 min, 90% B; 31~32 min, 90%~5% B; 32~35 min, 5% B; Flow rate: 0.4 mL/min; Column temperature: 30℃; Sample size: 2 μL. Mass spectrum conditions: Using an electrospray ionization source (ESI), capillary voltage: 3 kV, capillary temperature: 350℃; Heater temperature: 50℃; Injection voltage: 3.00 kV; Both the solvent removal and the cone gas are nitrogen, the flow rate of the solvent removal gas is 600 L/h, and the scanning range is 300~900 m/z.

Raw proteomic .wiff files were processed using DIA-NN 1.8 for peak alignment, retention time correction, peak area extraction, and protein identification. Protein database searching was performed against the UniProt (Mus musculus) protein sequence FASTA database, downloaded on July 6, 2022. The peptide length was restricted to 7–30 amino acids, the precursor ion charge range was set to 1–4, and the precursor-level false discovery rate (FDR) was controlled at 1%. Missing values in the protein quantification matrix were imputed using half of the minimum non-zero peak intensity observed across all samples. The imputed data were then $\log_2$-transformed, followed by standardization and normalization. Differences between groups were assessed using the Mann–Whitney U test, and differentially expressed proteins were screened based on the criteria of $p < 0.05$, combined with $FC > 1.3$ or $FC < 1/1.3$ (i.e., $FC < 0.769$).