

Supplementary figure legends

Figure. S1 Statistical histogram of protein identification and quantitative results.

Total spectrum: the total number of secondary spectra; Matched spectrum (PSM, Peptide Spectrum Match): the total number of database matching spectra; Peptides: the total number of peptides; Unique peptides: the total number of unique peptides; Identified proteins: total number of identified proteins; Quantified proteins: identified proteins that can be quantified.

Figure. S2 Quality control of peptides. (A) The mass deviations of all identified peptides are mainly distributed within 10 ppm, indicating that the identification results are accurate and reliable. (B) About 65.64% of the peptides have a MASCOT score of more than 20. The median MASCOT score is 27.49. (C) The abundance ratio of most proteins is close to 1.

Figure. S3 Diagram of the fatty acid biosynthesis. Red boxes represent the up-regulated DEPs, and green boxes represent the down-regulated DEPs.

Figure. S4 Diagram of PPAR signaling pathway. Red boxes represent the up-regulated DEPs, and green boxes represent the down-regulated DEPs.

Figure. S5 Diagram of Ras signaling pathway. Red boxes represent the up-regulated DEPs, and green boxes represent the down-regulated DEPs.

Figure. S6 Diagram of HIF-1 signaling pathway. Red boxes represent the up-regulated DEPs, and green boxes represent the down-regulated DEPs. The yellow boxes represent that there are multiple proteins, and the up or down-regulated expression is inconsistent.

Figure. S7 Diagram of apoptosis pathway. Red boxes represent the up-regulated DEPs, and green boxes represent the down-regulated DEPs. The yellow boxes represent that there are multiple proteins, and the up or down-regulated expression is inconsistent.

Table S1 Parameters and instructions of MASCOT engine search

Item	Value
Enzyme	Trypsin
Max Missed Cleavages	2
Fixed modifications	Carbamidomethyl (C), iTRAQ 4/8plex (N-term), iTRAQ 4/8plex (K) TMT 6/10/16 plex (N-term), TMT 6/10/16 plex (K)
Variable modifications	Oxidation (M), iTRAQ 4/8plex (Y), TMT 6/10/16 plex (Y)
Peptide Mass Tolerance	± 20 ppm
Fragment Mass Tolerance	0.1Da
Database	See the project report
Database pattern	Decoy
Peptide FDR	≤ 0.01
Protein Quantification	The protein ratios are calculated as the median of only unique peptides of the protein
Experimental Bias	Normalizes all peptide ratios by the median protein ratio. The median protein ratio should be 1 after the normalization.