Supplementary Figure 1: The electron microscopy structure of fibrillar Aβ

Followed by Aβ incubation (1 mM) for 24 h at 37°C, 5 μl Aβ (1 mg/ml) were added to 300-mesh copper grids with carbon support film, then the samples were stained with 2% phosphotungstic acid, and the grids were analysed by transmission electron microscopy at 120kV (Tecnai G² 20, Hong Kong).
The reproducibility of SILAC quantification of the biological replicates is illustrated by the protein ratio correlations.
Supplemental Figure 3

KEGG pathway analysis of 13 differentially expressed proteins using GeneCodis 3.
Supplemental Figure 4

GO Cellular Component analysis of 13 differentially expressed proteins using GeneCodis 3.
BV2 cells were transfected with 10 nM siRNA specific for LPL (siRNA\text{LPL}) and control siRNA (siRNA\text{CON}) for 36 h.

A: The mRNA of the cells were extracted by Trizol reagent as the provided standard protocol. Quantitative PCR (qPCR) of LPL was executed using these cDNA reverse-transcripted by mRNA. LPL mRNA level examined showed significant changes after knock-down.

B: The cells were washed in cold PBS three times, harvested using 4% SDS lysis buffer. The bands of Western blotting were analysed by Image J, and the relative gray-scale was presented by the bar. (**p < 0.01; comparison against control siRNA teams, two-tailed t test.). Bars, means ±S.D. (n= 3).
Supplemental Figure 6

Among 13 significantly altered proteins detected in our SILAC quantitation results, 5 proteins were found to be single peptide identification (Trim23, CD63, HIC2, Slc6a17, and Slc23a3). The annotated spectra are provided for these 5 proteins as below:
Scan number 5743 Raw file 2_20
Method ITMS; CID Genenames Slc23a3

m/z (full)

m/z (zoom)

Relative Abundance

Intensity [10e4]