Supplementary Information For:

Quantitative proteomics study of the neuroprotective effects of B12 on hydrogen peroxide-induced apoptosis in SH-SY5Y cells

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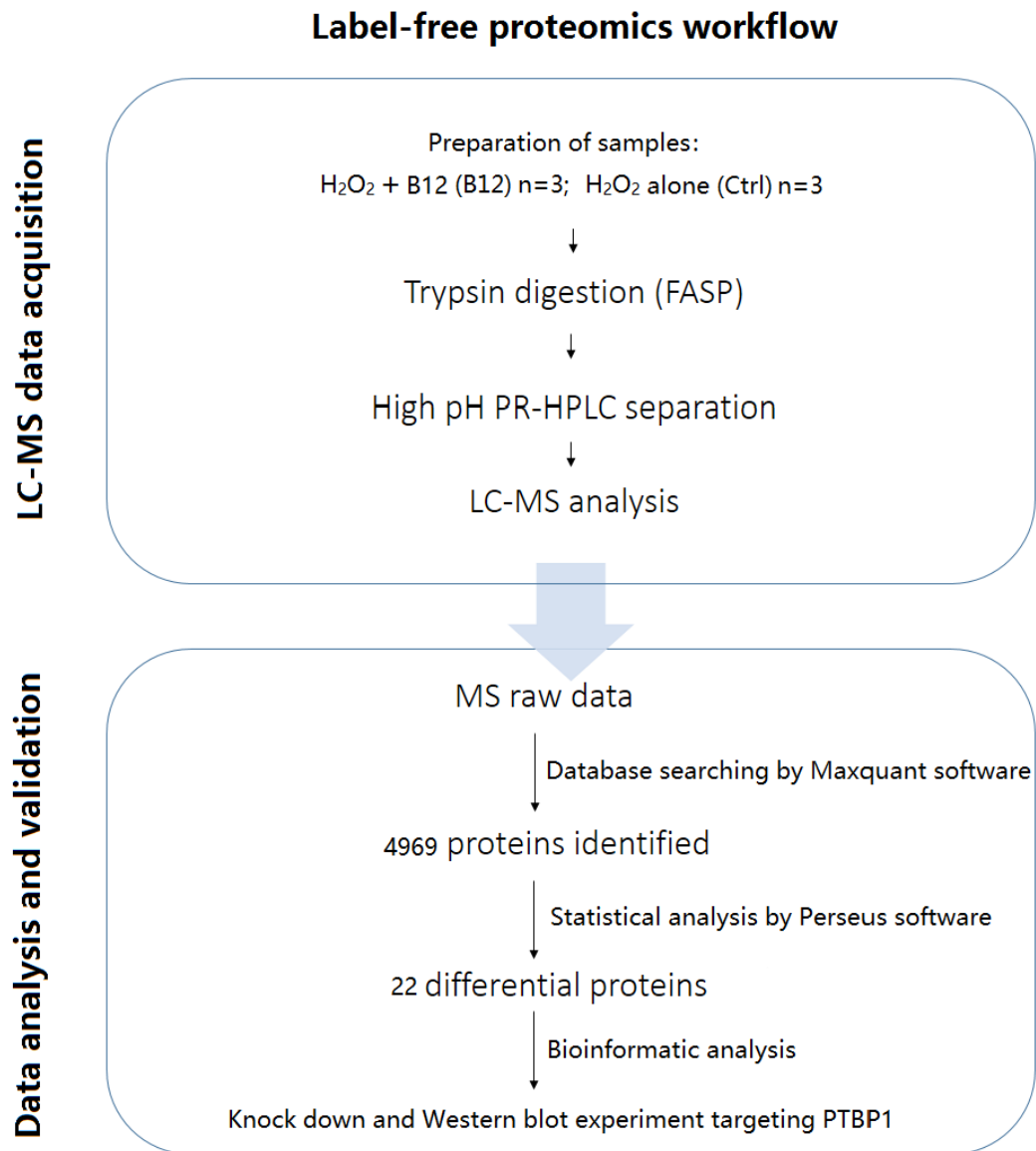
Supplementary figures and figure legends

Label-free proteomics workflow

LC-MS data acquisition

Preparation of samples:
H_2O_2 + B12 (B12) n=3; H_2O_2 alone (Ctrl) n=3

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Trypsin digestion (FASP)

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High pH PR-HPLC separation

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LC-MS analysis

Data analysis and validation

MS raw data

Database searching by Maxquant software

4969 proteins identified

Statistical analysis by Perseus software

22 differential proteins

Bioinformatic analysis

Knock down and Western blot experiment targeting PTBP1

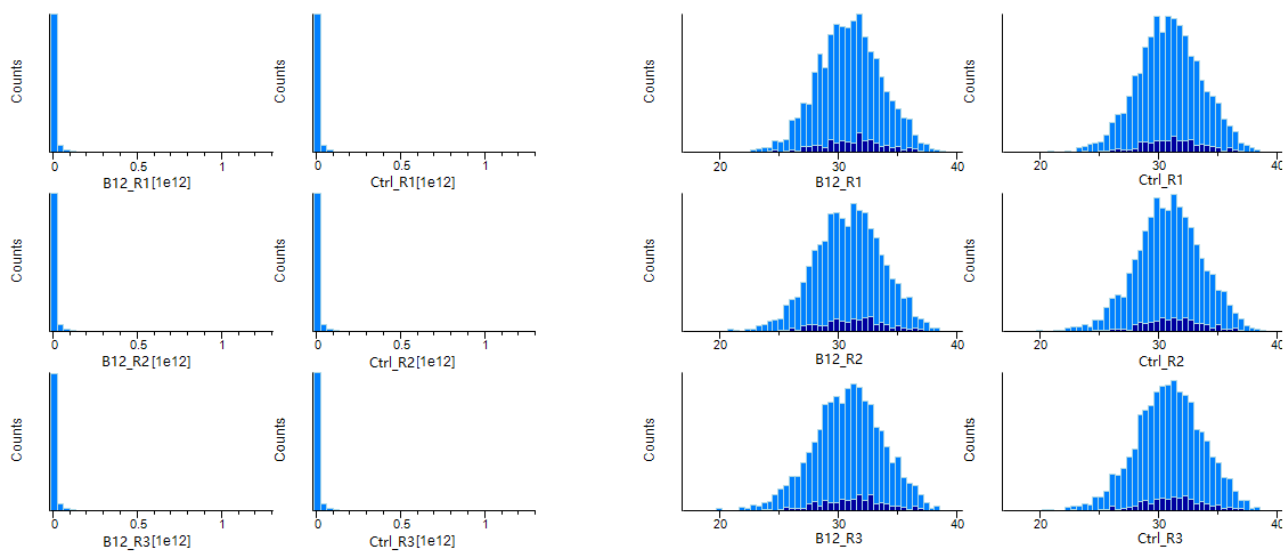Figure S1 |. The workflow flowchart of the proteomic study.

Figure S2 |.Histograms of the LFQ intensity of proteins before (left) and after (right) a logarithm transformation (base 2). Blue represents total proteins identified in SH-SY5Y cells and dark blue represents proteins that had a t-test p-value less than 0.05 between the two groups (B12 and Ctrl group).

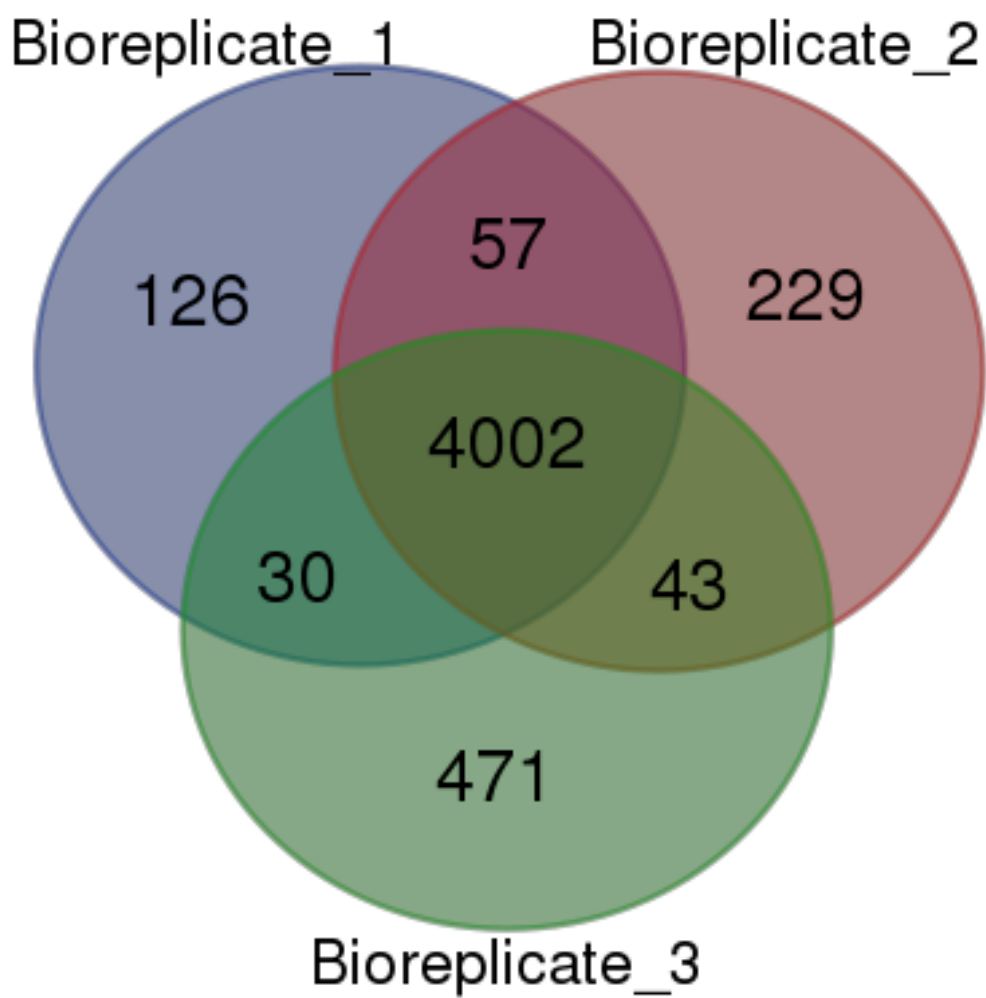| List names	number of elements	number of unique elements
Bioreplicate_1	4215	4215
Bioreplicate_2	4331	4331
Bioreplicate_3	4546	4546
Overall number of unique elements		4958

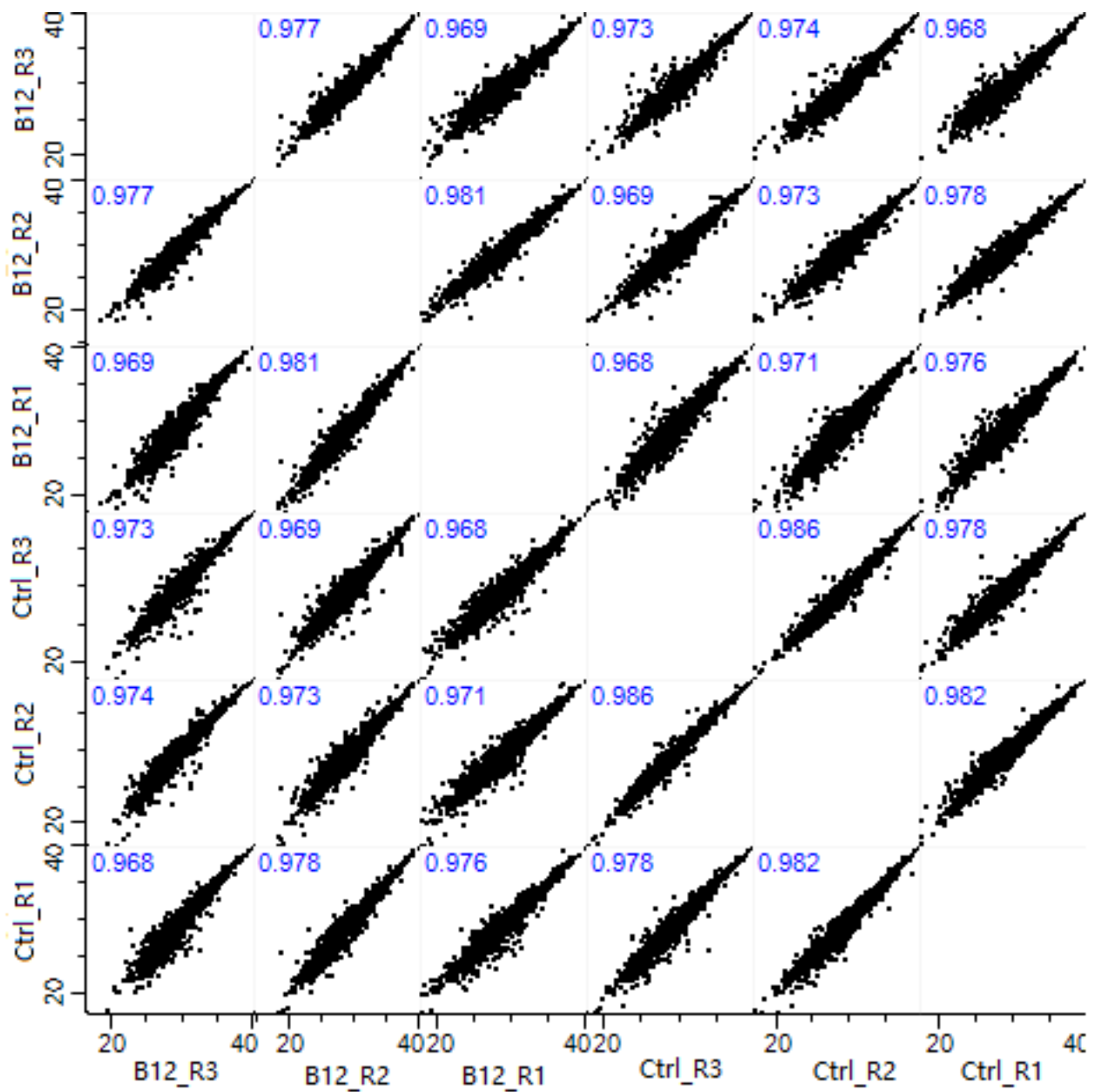Figure S3 |.Venn diagram of identified proteins in the three biological replicates.

Figure S4 |.Scatter plots of log2 LFQ intensities of identified proteins of all samples. The number in plots was the

Pearson correlation coefficient.