Figure S1

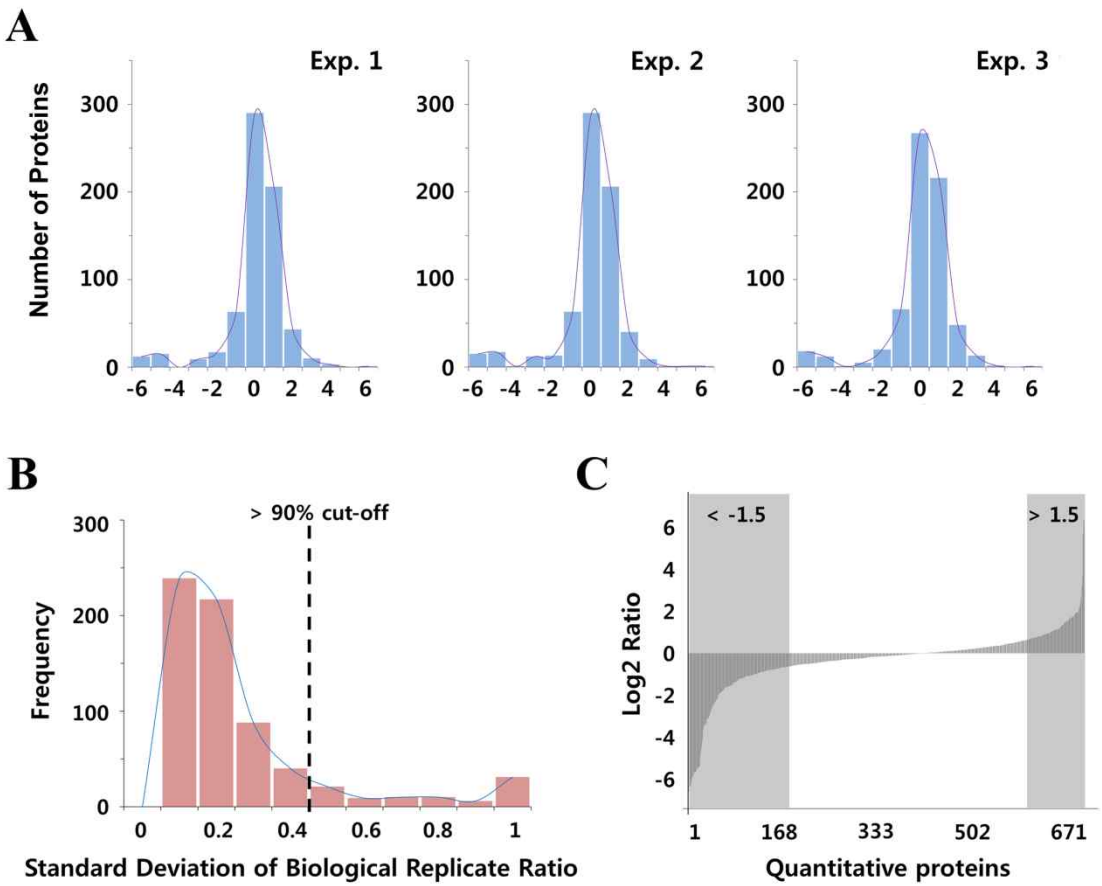

Figure S1. Distribution of log2 NSAF ratios and differentially expressed proteome

(A) The distributions of log2 NSAF ratios for primary cancer cells versus metastatic cancer cells were obtained by comparing 3 biological replicates from the label-free quantification experiments. (B) Fold-change cutoff of protein expression was considered the standard deviation of the 3 replicates. Ninety percent of all identified proteins were within less than 0.5 standard deviations. (C) Protein ratios are arranged in ascending order, resulting in a sigmoidal curve. The light shaded area represents unregulated protein groups with a less than 1.5-fold change in expression, and the dark shaded area represents protein groups that undergo more than a 1.5-fold change.

Figure S2

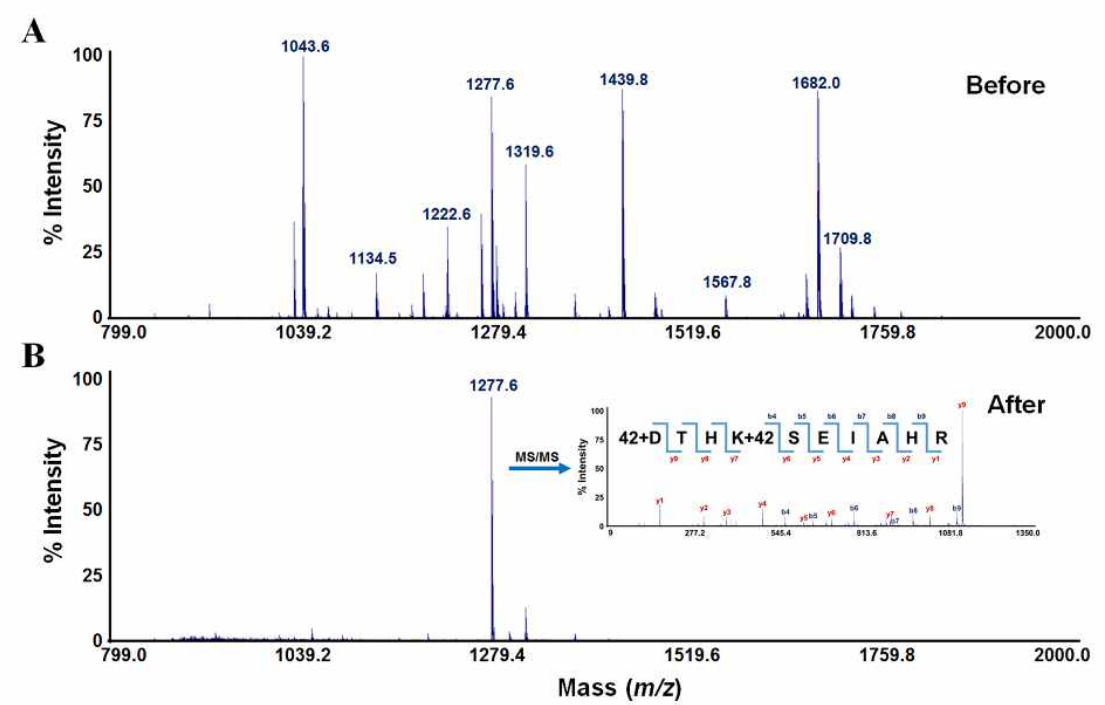

Figure S2. N-terminal peptide analysis of BSA control
(A) MS peaks are trypsin-digested peptides of acetylated BSA. (B) With our protocol, the labeled major ions correspond to the N-terminal peptides from BSA.

Figure S3

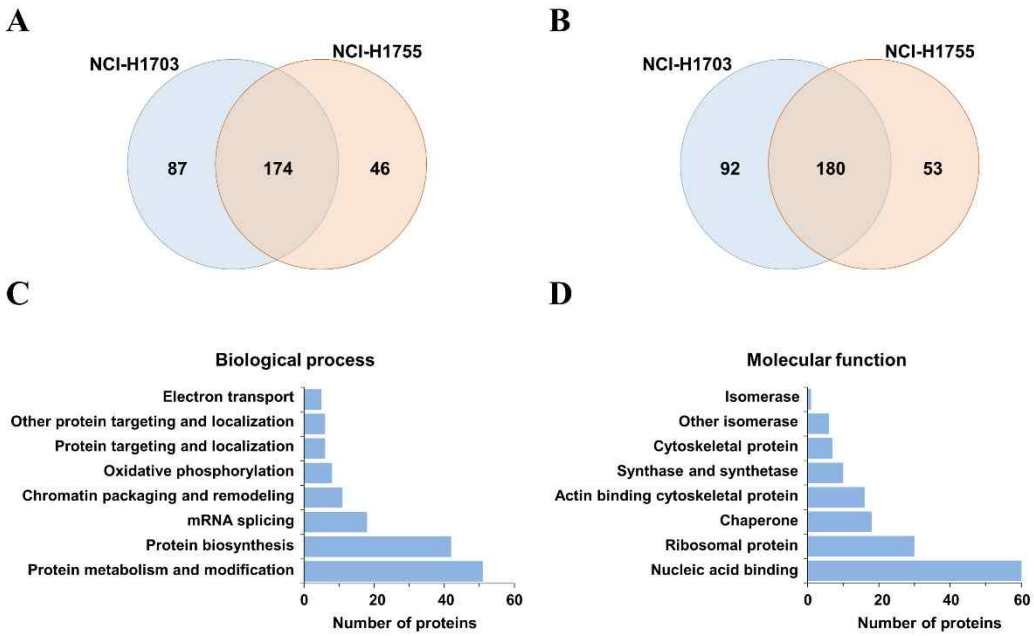

Figure S3. Summary of the identification of N-terminal peptides
(A) Numbers of all identified proteins and (B) peptides were shown in Venn diagrams. (C) Gene ontology (GO) for biological process and (D) molecular function of all identified proteins was performed using the DAVID bioinformatics tool.

Figure S4

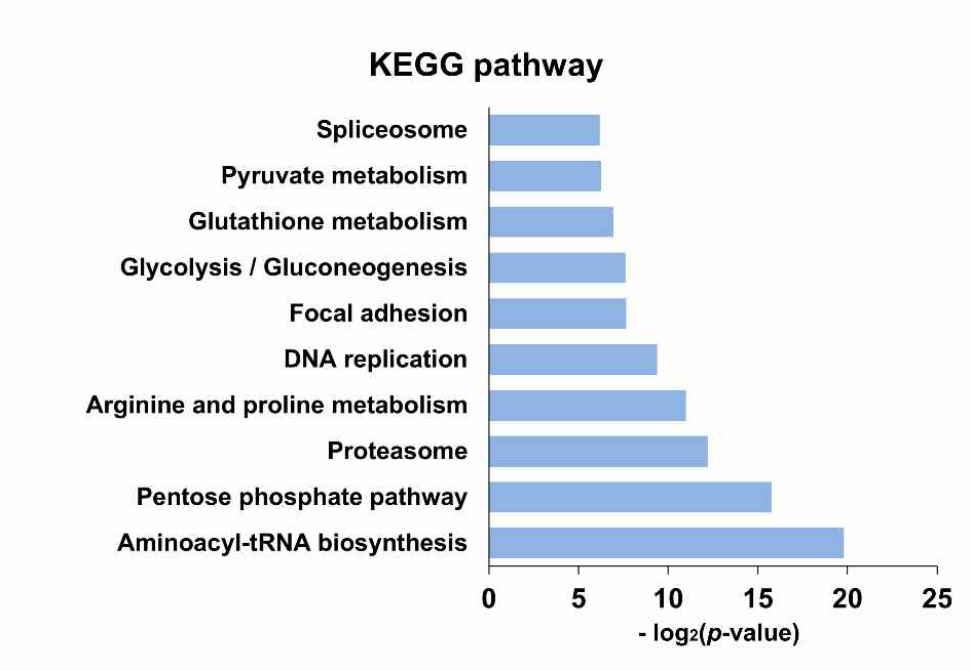

Figure S4. Pathways identified using differentially expressed proteins from both experiments

The numbers of significantly differentiated proteins associated with each pathway are shown in the bar graph.