

Supporting Information Fig. S9. (A) Scheme of the bioinformatics pipeline for analysis of the proteomics expression data. (B) Volcano plot of differentially expressed peptides analyzed using iPathwayGuide algorithm, combining significantly differentially expressed genes information with pathway-inflicted gene topological position within enriched signaling pathways. Cutoff criteria: 0.05 - Significance threshold, and 0.5 as Minimum fold change. The significantly expressed genes are colored in red.

