

Description of Additional Supplementary Files

Supplementary Data 1: raw proteomics data related to Figure 1C. Statistics calculated using limma's moderated t-test (empirical Bayes) with adjusted p-value using the Benjamini-Hochberg procedure as implemented in the Protti R package (two-sided p-values).

Supplementary Data 2: raw proteomics data related to Figure 3F. Statistics calculated using limma's moderated t-test (empirical Bayes) with adjusted p-value using the Benjamini-Hochberg procedure (two-sided p-values).

Supplementary Data 3: raw proteomics data related to Figures 4B and 5B. Statistics calculated using limma's moderated t-test (empirical Bayes) with adjusted p-value using the Benjamini-Hochberg procedure (two-sided p-values).

Supplementary Data 4: Reactome data related to Figure 5C Size: number of genes associated with the Reactome category; ES: enrichment score; NES: normalised enrichment score. Reactome pathway enrichment was performed using gene set enrichment analysis (fgsea, V1.20.0) on a pre-ranked gene list from Figure 4B. GSEA was run with min/max gene set sizes of 5/500 respectively and default weighting ($0 \geq p \leq 1$). Normalized enrichment scores (NES) and adjusted p-value were reported.

Supplementary Data 5: raw proteomics data related to Figure 6D. Statistics calculated using limma's moderated t-test (empirical Bayes) with adjusted p-value using the Benjamini-Hochberg procedure as implemented in the Protti R package (two-sided p-values).

Supplementary Data 6: The modified version of the code used to develop the model/perform the analyses and generate results in this study.