Quantitative density gradient analysis by mass spectrometry (qDGMS) and complexome profiling analysis (ComPrAn) R package for the study of macromolecular complexes

Supplementary Figures

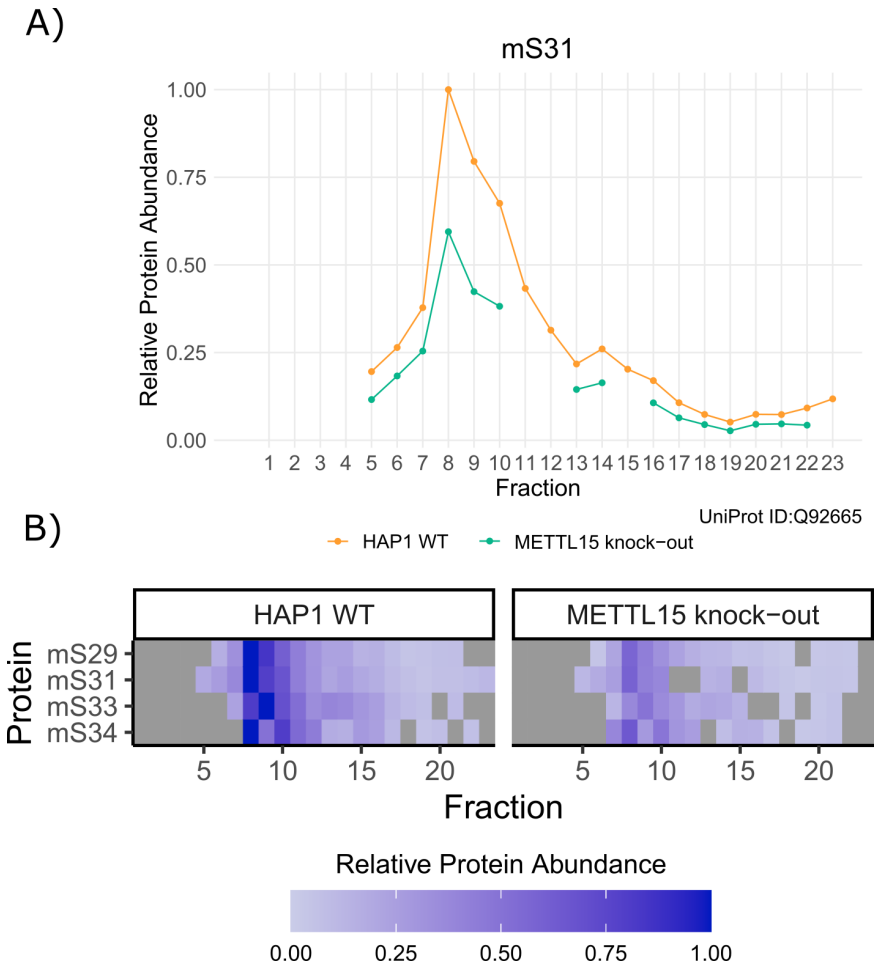

Figure S1: *Handling of missing data in visualizations. Occasionally in qDGMS and other complexome profiling experiments, a protein is not detected in a continuous range of fractions leading to incomplete data. The representation of missing data differs based on the software chosen for visualization. In ComPrAn outputs, incomplete data are clearly identifiable by break in the line (A) or by colour (B, grey rectangles).*

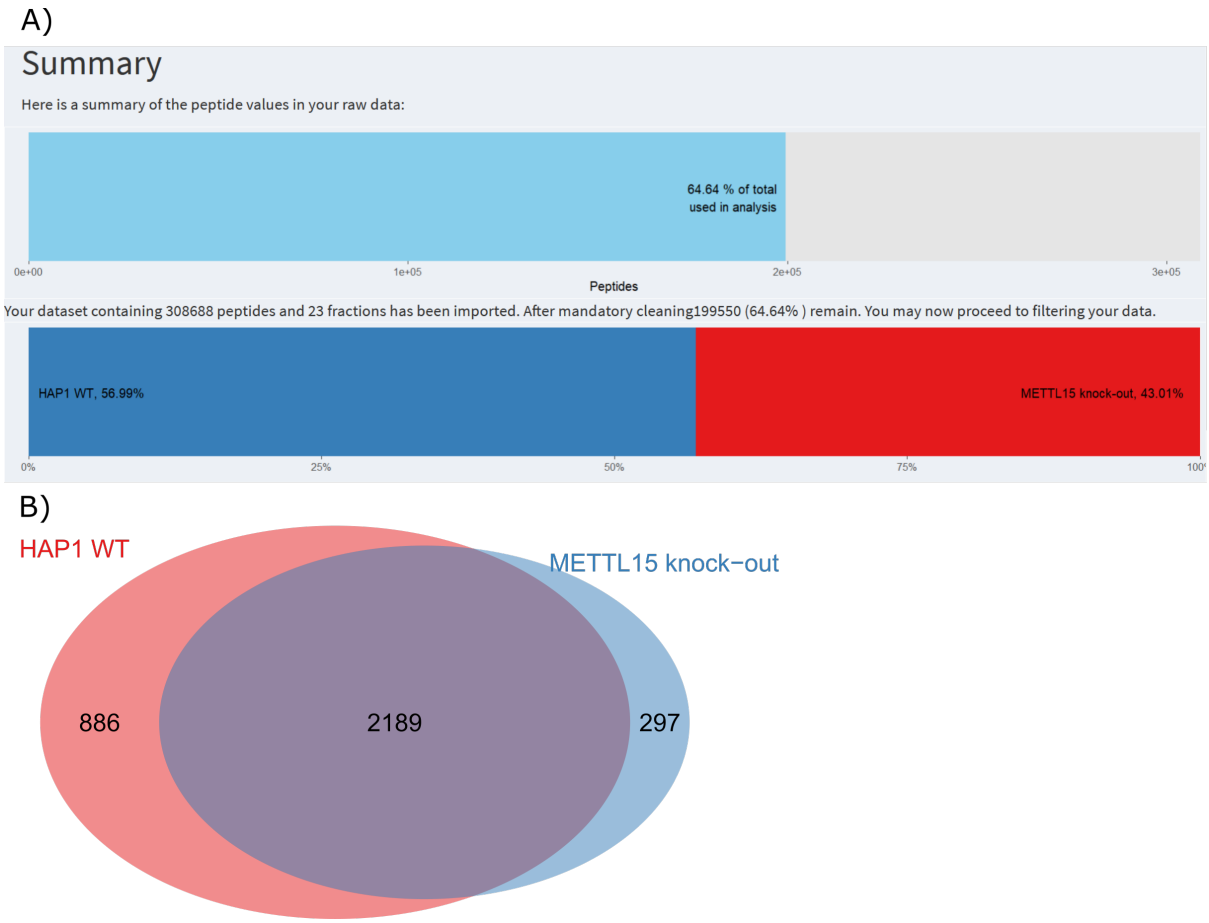

Figure S2: *Summary plots available in ComPrAn Shiny app. After initial filtering of data, fraction of peptides used for analysis and distribution of peptides between "heavy" and "light" samples is shown (A) as a rough indication of the sample pooling quality. Overall numbers of proteins detected in each sample is shown in a Venn diagram (B).*

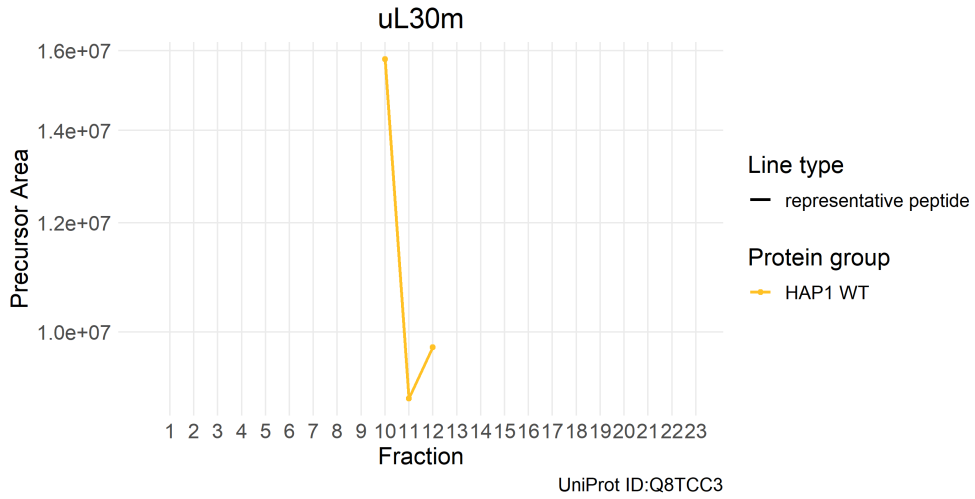

Figure S3: *Visual representation of all detected peptides for uL30m protein in the qDGMS experiment. Peptides for uL30m were detected only in the HAP1 wild-type sample. As a result, no representative peptide (Scenario B) of uL30m between wild-type and METTL15 knock-out sample was selected for quantitative comparison. Therefore, no values for this particular protein are shown in the heatmap in Figure 6A.*