





**Supplementary Figure 2:** Histograms of key quality control parameters for mass spectrometric proteome analysis (peptides  $n=42,641$ , proteins  $n=4,268$ , all before filtering). Mean and median values are given in the respective panels. (a) distribution of missed cleavages in the identified peptides, (b) distribution of peptide lengths, (c) distribution of MS/MS counts per peptide, (d) binned molecular weight distribution of proteins (bin size 10 kDa), (e) sequence coverage distribution of proteins. Histograms of (f) peptide and (bg) protein log<sub>2</sub> SILAC ratio distributions before (red) and after (blue) normalization (peptides  $n=42,641$ , proteins  $n=4,268$ , all before filtering). Mean and median values are given in the respective panels. Distribution shifts indicate a slight over-spiking of the heavy-labeled SILAC standard, which however is desirable to obtain near-complete coverage of endogenous peptide/proteins by the standard.