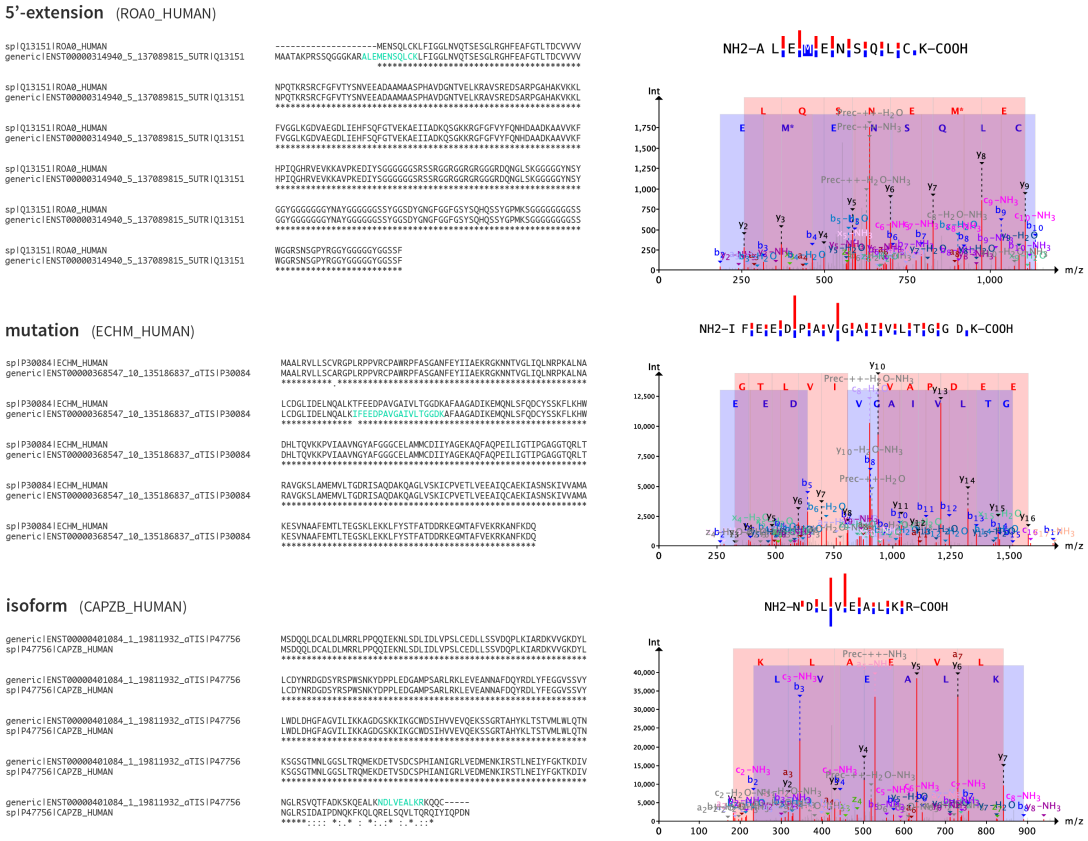

Figure S1. Examples of improved identifications in the shotgun proteomics experiment. The addition of ribo-seq data to the proteomics experiment improved the identification and score significance for 69 proteins and three representative examples are depicted here. The left column shows the Clustal Omega [37] alignment of the ribo-seq-derived amino acid sequences to the Swiss-Prot sequences with the relevant peptide identifications highlighted in cyan. The column on the right shows the corresponding fragmentation spectra and peptide sequence fragmentations.

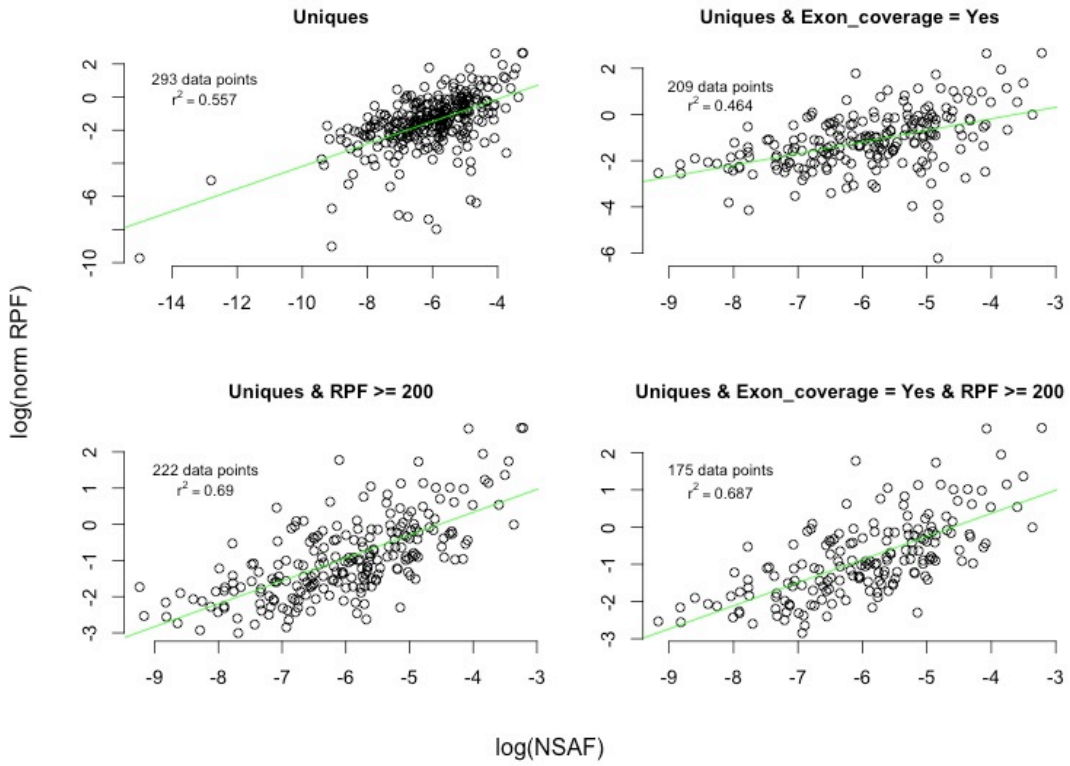

Figure S2. Correlation plots of protein abundance based on NSAF values and RPF counts for the proteins uniquely identified in Swiss-Prot. Some transcripts were not contained in our custom database because the LTM treatment and/or TIS calling failed to identify these TISs. Correlations could still be calculated as the CHX treatment did result in detectable coverage for these transcripts. The number of data points used in every plot was lower than the total number of unique Swiss-Prot identifications (312), because whenever a Swiss-Prot protein corresponded to multiple transcripts only the transcript with the highest normalized RPF value was used. Top left: all transcripts; top right: transcripts with ribo-seq coverage in all exons; bottom left: all transcripts with an RPF count ≥ 200; bottom right: transcripts with both coverage in all exons and an RPF count ≥ 200. The regression line is shown in green. For each plot, the number of data points used (i.e. the number of dbTIS transcripts) as well as the corresponding Pearson correlation coefficient (r^2) is shown.