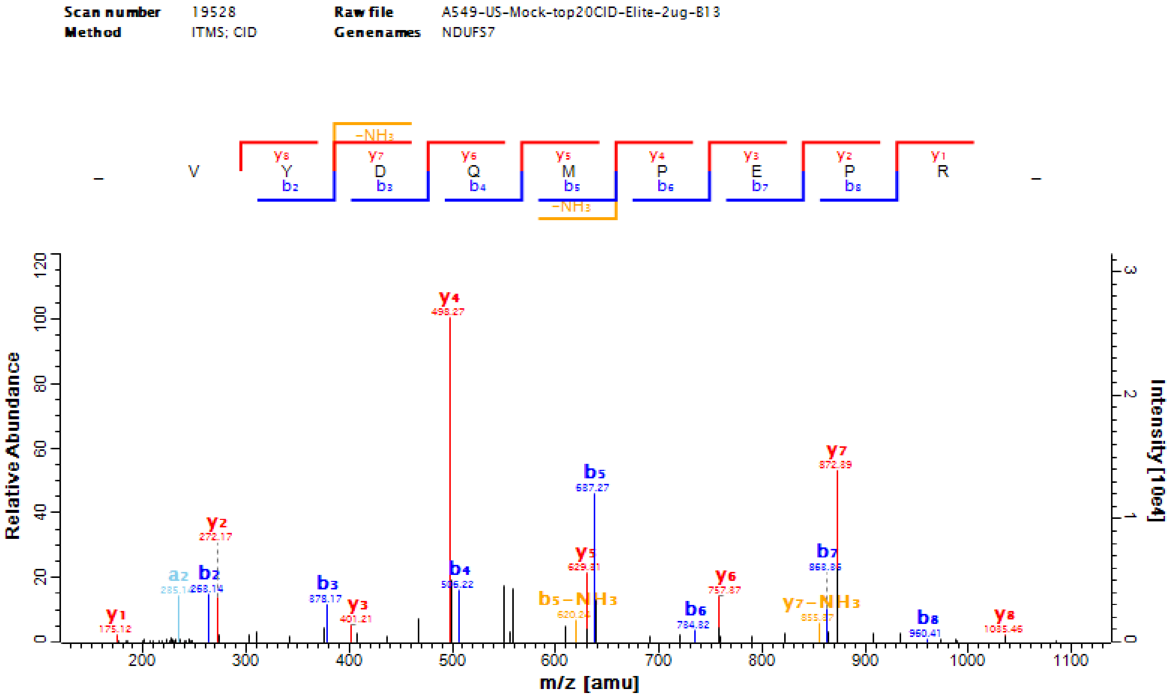
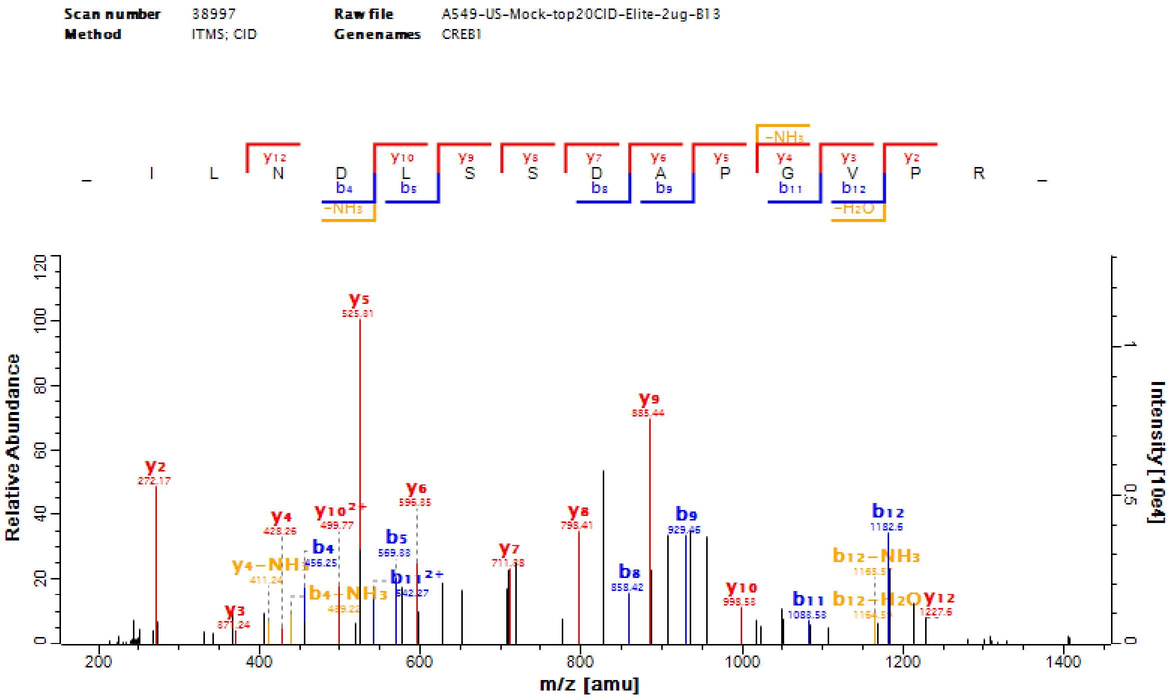
Supplemental Fig. 3. Annotated spectra for differentially abundant protein groups (FDR less than 1%) identified by a single peptide in the protein fractionation-free workflow. The full list of differentially abundant protein groups are listed in supplemental Table 2. Where multiple spectra match the peptide sequence, the annotated spectrum corresponding to the best match is reported.

Protein Group ID: 198
Protein Accession Numbers: F5GXJ1; O75251; B3KRI2; F5H5N1
Gene Names: NDUFS7
Peptide Sequence: VYDQMPEPR
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 129.89
Best Match Posterior Error Probability: 0.00014101
Best Match Spectrum:

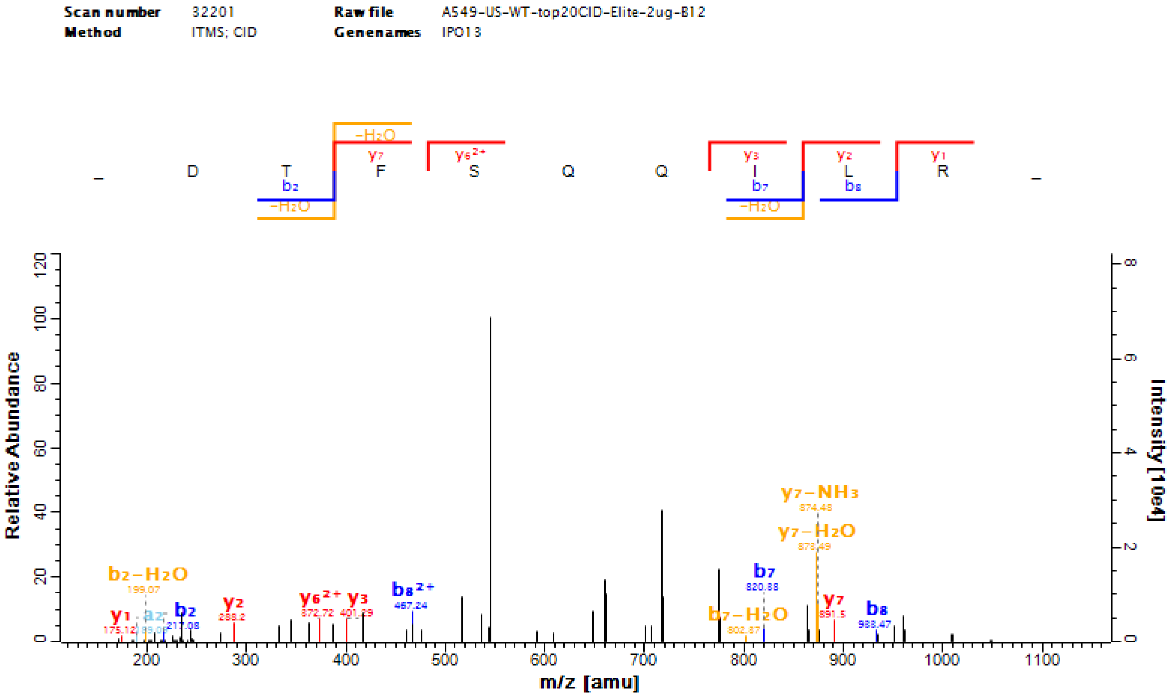


Protein Group ID: 412
Protein Accession Numbers: P16220; P16220-2; C9J896; F5H0V3; P16220-3; E7EWP8; H7C3I0; C9JBT4; B7Z7P1; C9J4L5
Gene Names: CREB1
Peptide Sequence: ILNDLSSDAPGVPR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 103.14
Best Match Posterior Error Probability: 0.0002839
Best Match Spectrum:



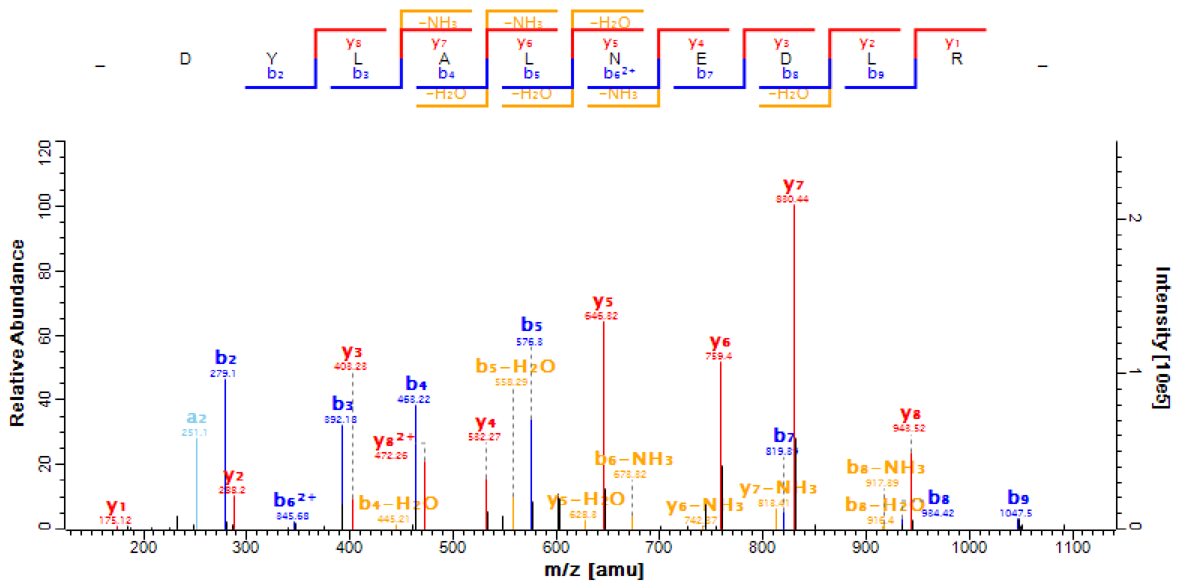
Scan number 38997 **Raw file** A549-US-Mock-top20CID-Elite-2ug-B13
Method ITMS; CID **Genenames** CREB1

Protein Group ID: 2006
Protein Accession Numbers: O94829; Q5T4X2
Gene Names: IPO13
Peptide Sequence: DTFSQQILR
Total Number of Spectra: 1
Number of Replicates (out of 8): 1
Best Match Score: 87.639
Best Match Posterior Error Probability: 0.0040876
Best Match Spectrum:

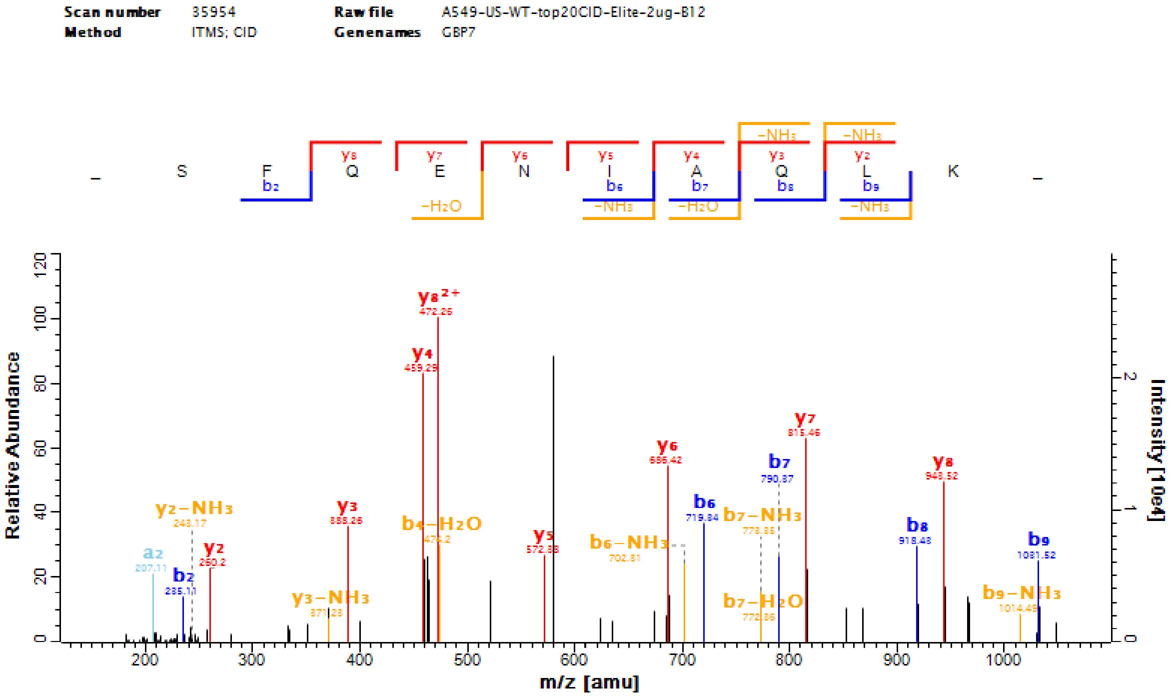


Protein Group ID: 2399
Protein Accession Numbers: Q5RJ85; P17693
Gene Names: HLA-G
Peptide Sequence: DYLALNEDLR
Total Number of Spectra: 2
Number of Replicates (out of 8): 2
Best Match Score: 172.8
Best Match Posterior Error Probability: 8.33E-06
Best Match Spectrum:

Scan number 43326 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** HLA-G



Protein Group ID: 4052
Protein Accession Numbers: Q8N8V2
Gene Names: GBP7
Peptide Sequence: SFQENIAQLK
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 130.98
Best Match Posterior Error Probability: 2.45E-05
Best Match Spectrum:



Scan number 35954 **Raw file** A549-US-WT-top20CID-Elite-2ug-B12
Method ITMS; CID **Genenames** GBP7

Protein Group ID: 4651
Protein Accession Numbers: Q9C002
Gene Names: NMES1
Peptide Sequence: LITINQQWKPIEELQNVQR
Total Number of Spectra: 4
Number of Replicates (out of 8): 4
Best Match Score: 115.8
Best Match Posterior Error Probability: 0.00010399
Best Match Spectrum: