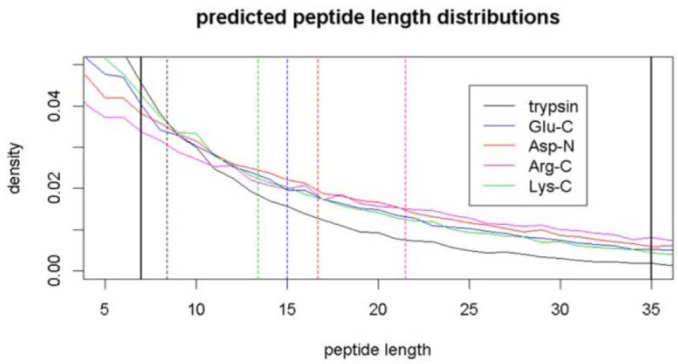
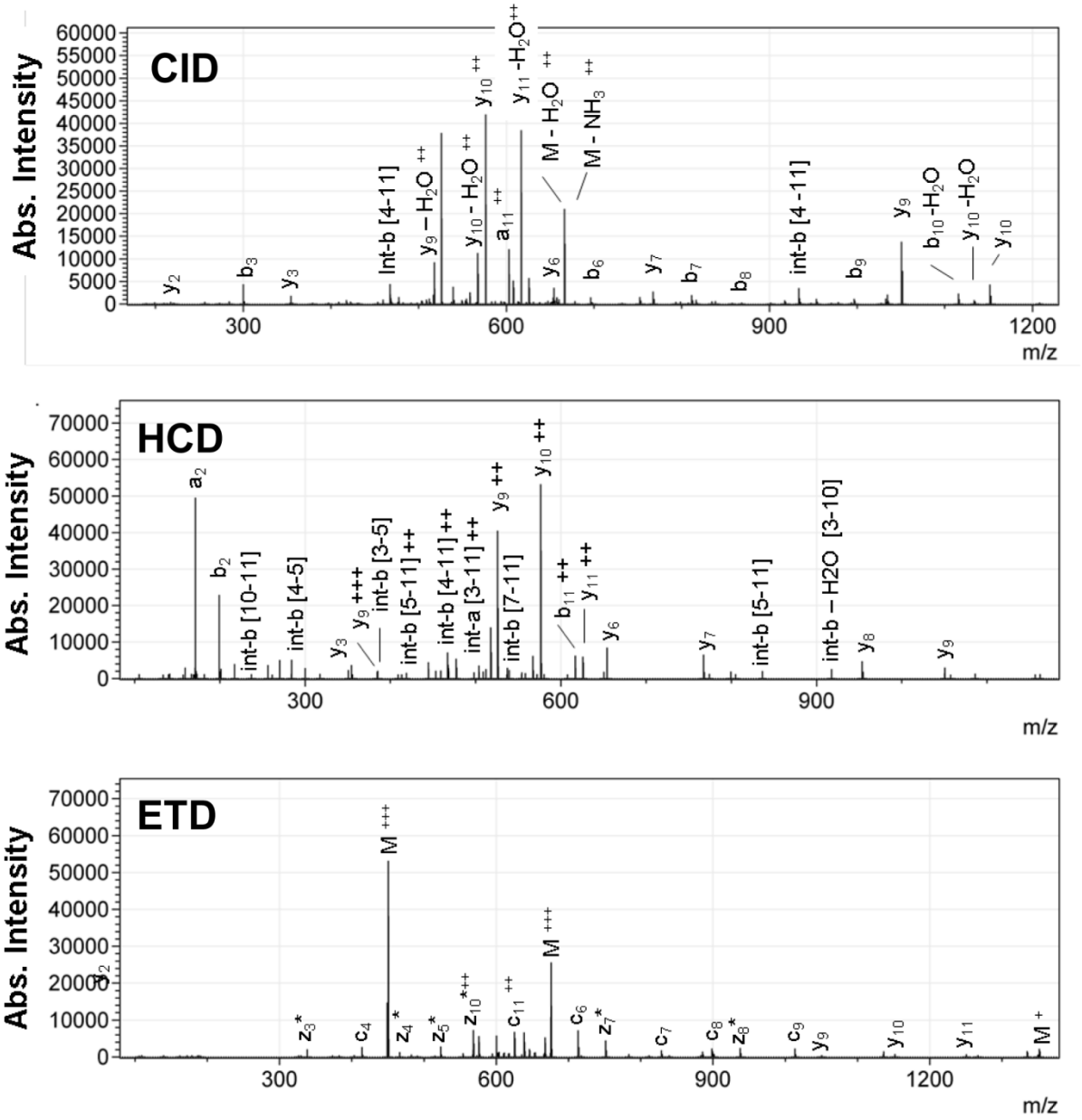
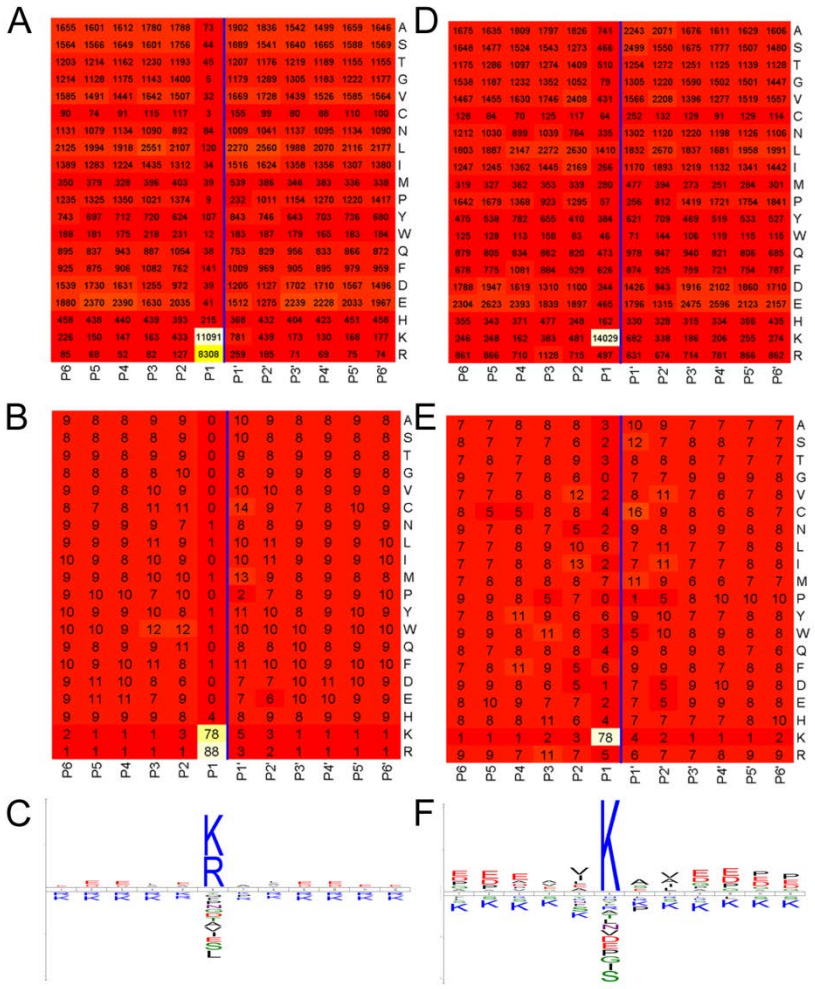


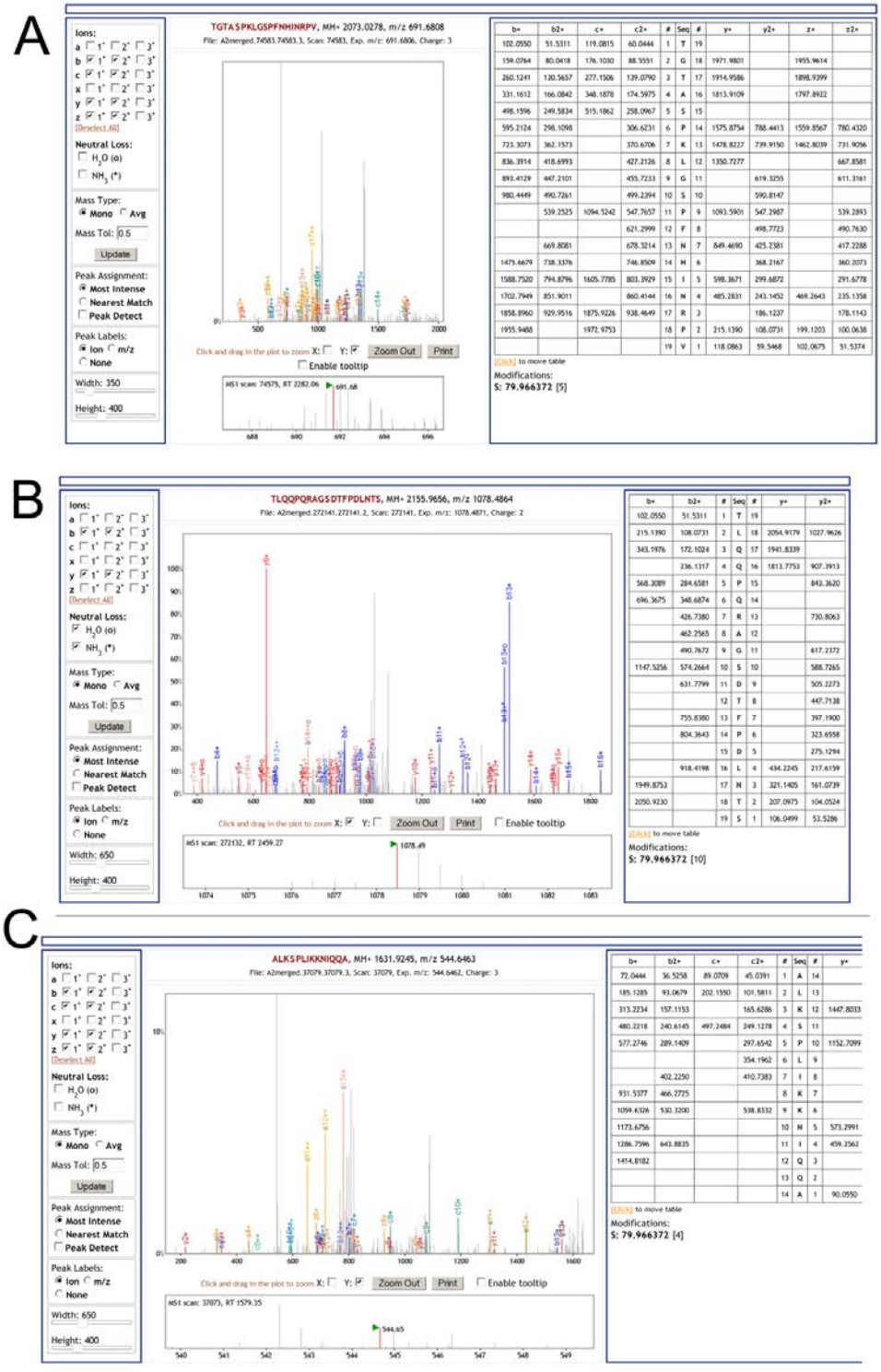
Supp. Fig. 1. Predicted length distributions of peptides generated by in silico digestion of the S. cerevisiae proteome with trypsin, Glu-C, Asp-N, Arg-C, and Lys-C.



Supp. Fig. 2. CID, HCD, and ETD spectra of a peptide from WaLP digestion: VVTPWLDGKHVV
CID and HCD (M+2H=675.3824), ETD (M+3H=450.5907)



Supp. Fig. 3. Heat maps from trypsin (A-C) and Lys C (D-F) data collected at the same time as those shown in Figure 3 for MaLP and WaLP digests. Figures A and D show the raw counts of frequency of each amino acid at each position, Figures B and E show the counts normalized for the occurrence of each amino acid at each position, Figures C And F show the IceLogos depicting the enrichment and depletion of specific amino acids (relative to the whole proteome).



Supp. Fig. 4. Annotated MS2 spectra for the three phosphorylation sites in MPD2; S175 was covered by the peptide TGTA*p*SPKLGSPFNHINRPV (+3 charge state) fragmented by ETD, a previously reported phosphorylation site. Two new phosphorylation sites were discovered; S223 covered by the peptide TLQQPQRAG*p*SDTFPDLNTS (+2 charge state) fragmented by CID and S750 covered by the peptide ALK*p*SPLIKKNIQQA (+3 charge state) fragmented by ETD.