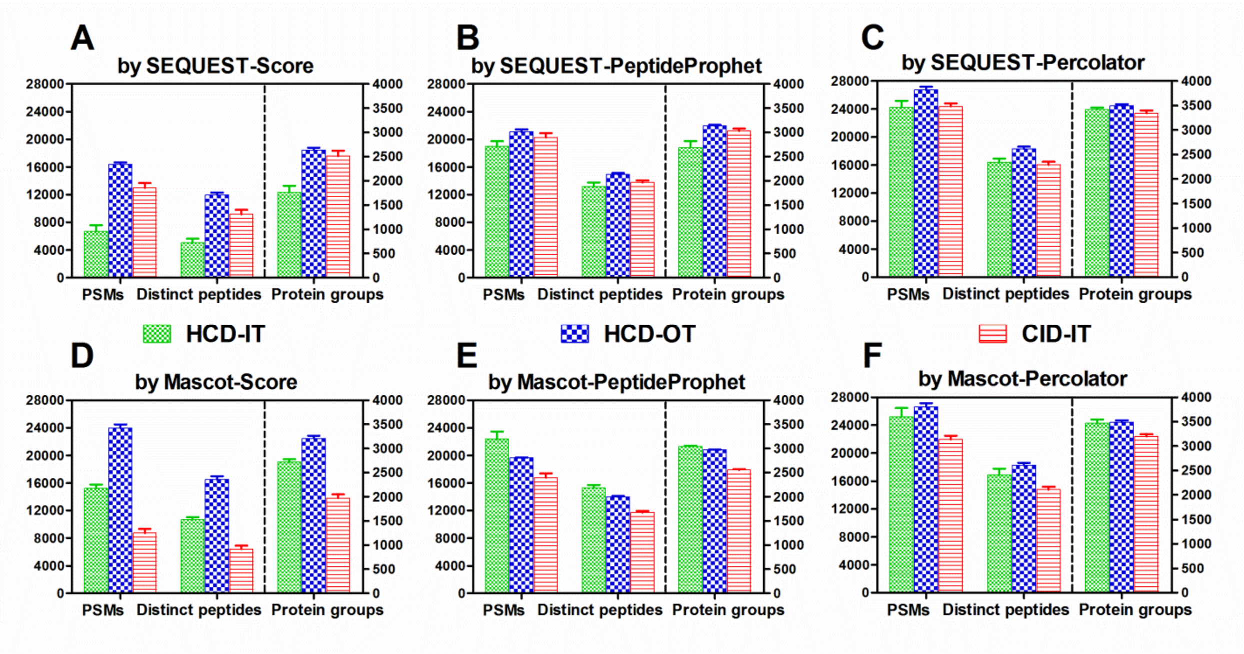
S4 Fig



S4 Fig. Peptide spectra matches (PSMs), distinct peptides and protein groups from the separate LC-MS/MS analyses for the comparison of HCD-OT, HCD-IT, and CID-IT. Six different MS data interpretation approaches were used in this study (A-F) by combining SEQUEST or Mascot with different post-processing methods such as score-based, PeptideProphet, and Percolator.