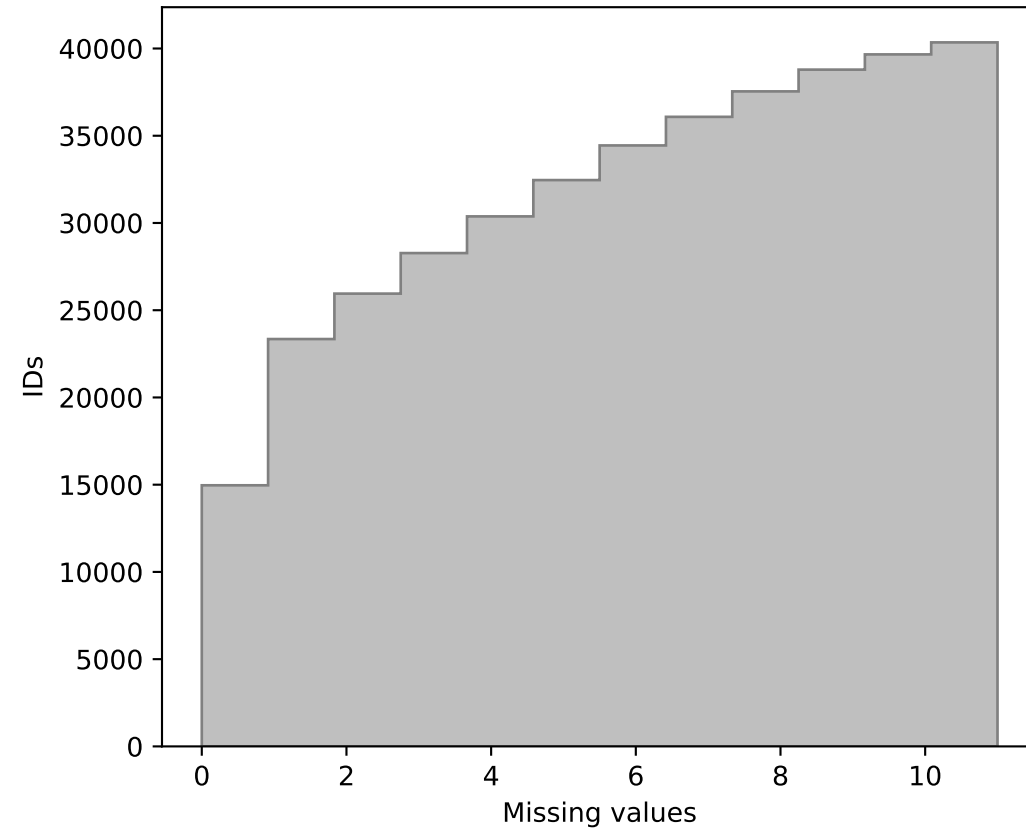
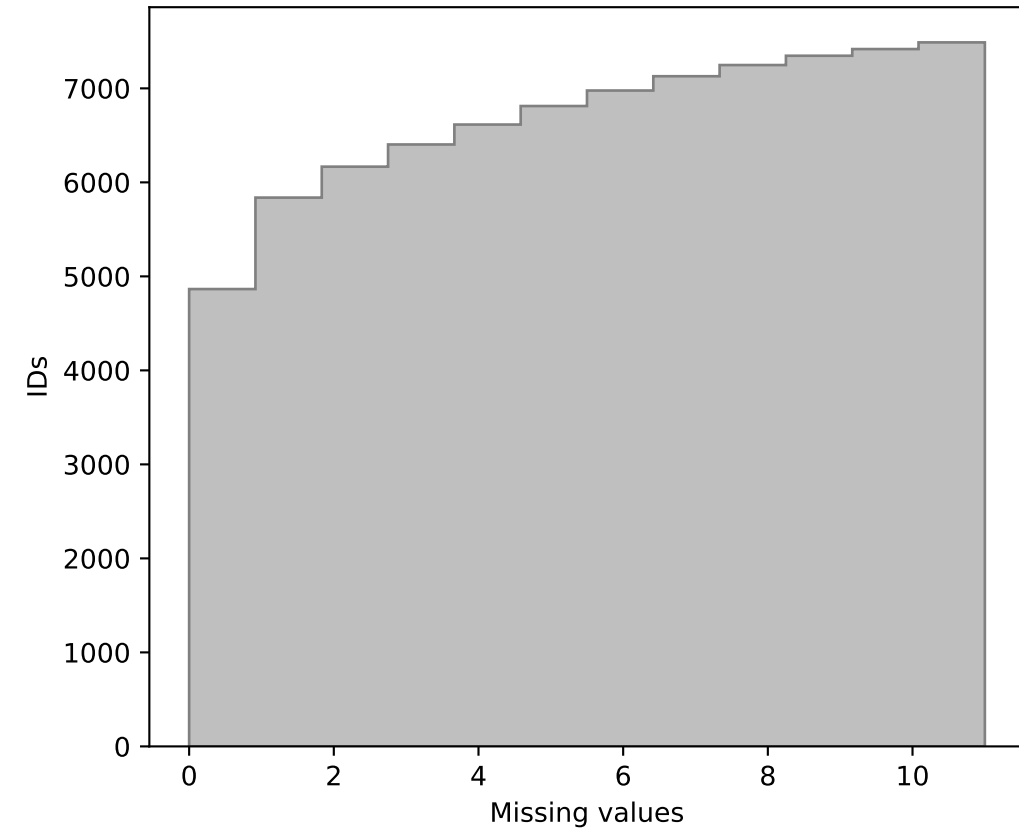


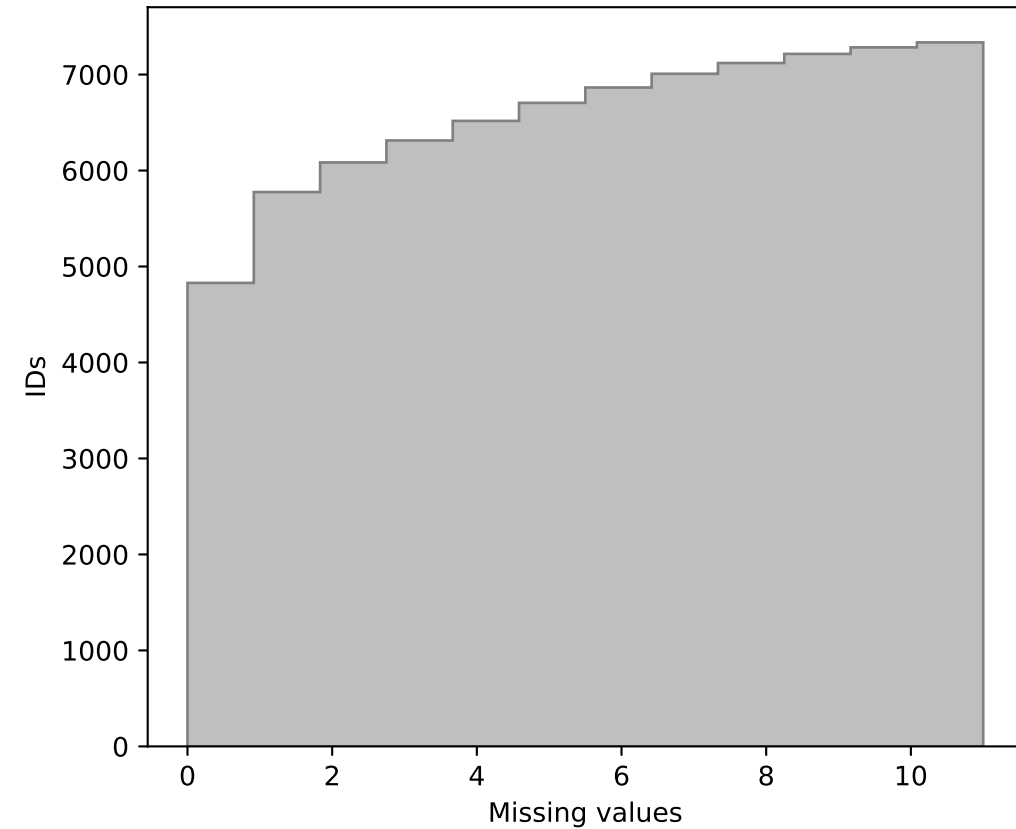
Identification consistency: precursors, CDF



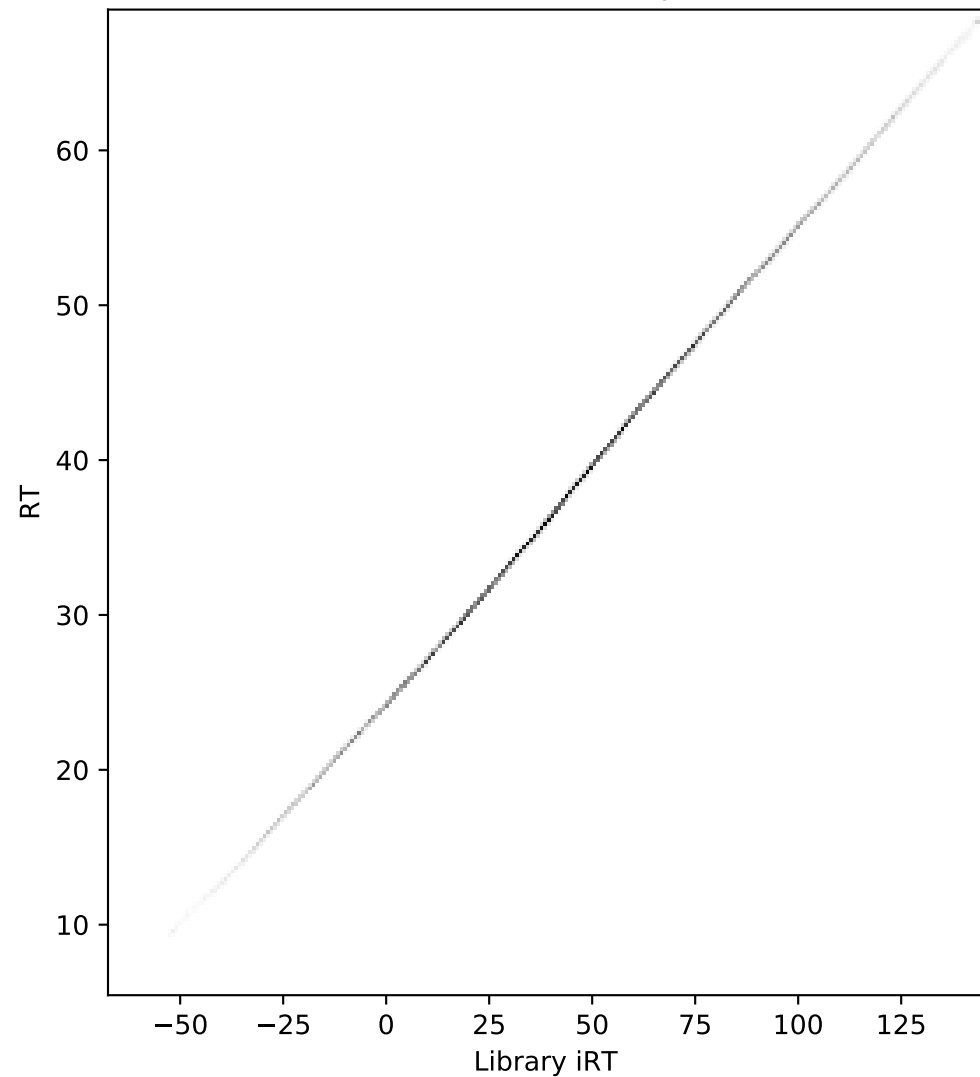
Identification consistency: protein groups, CDF



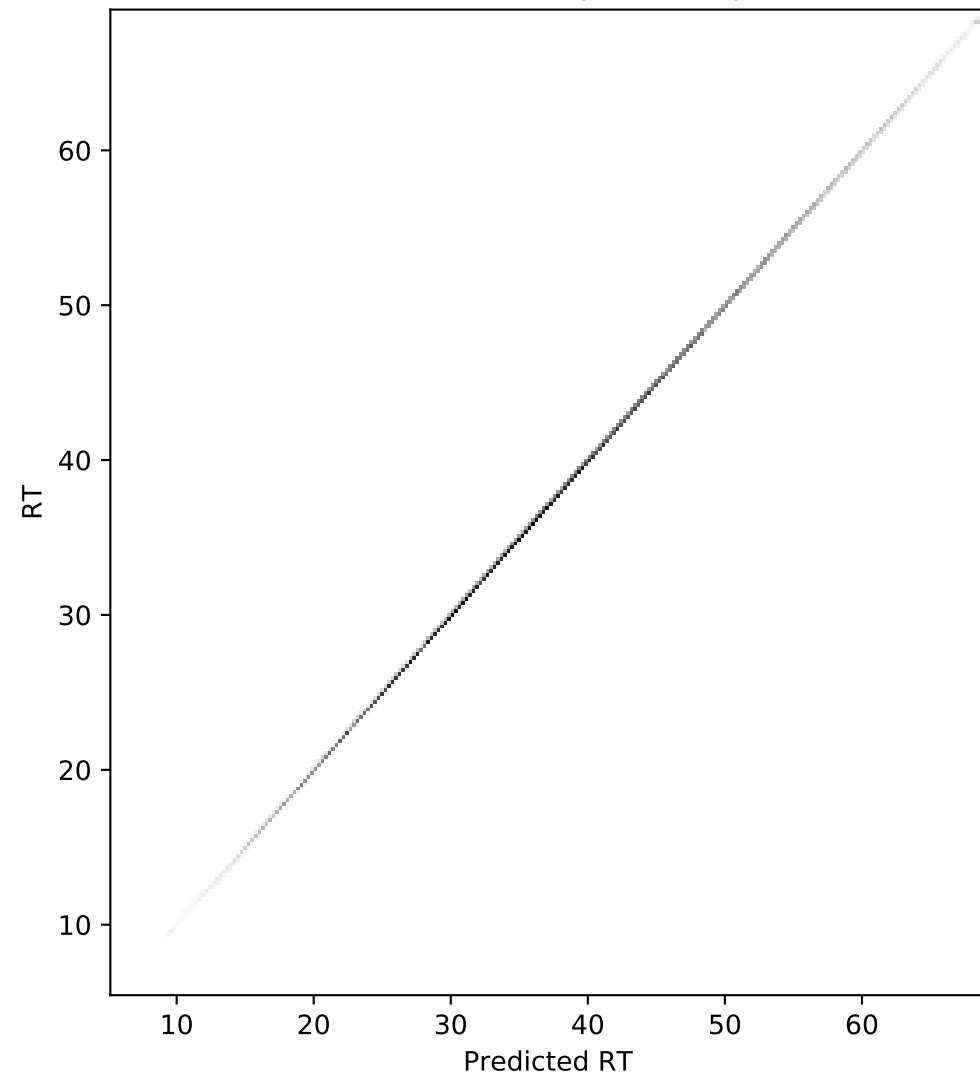
Identification consistency: genes groups, CDF



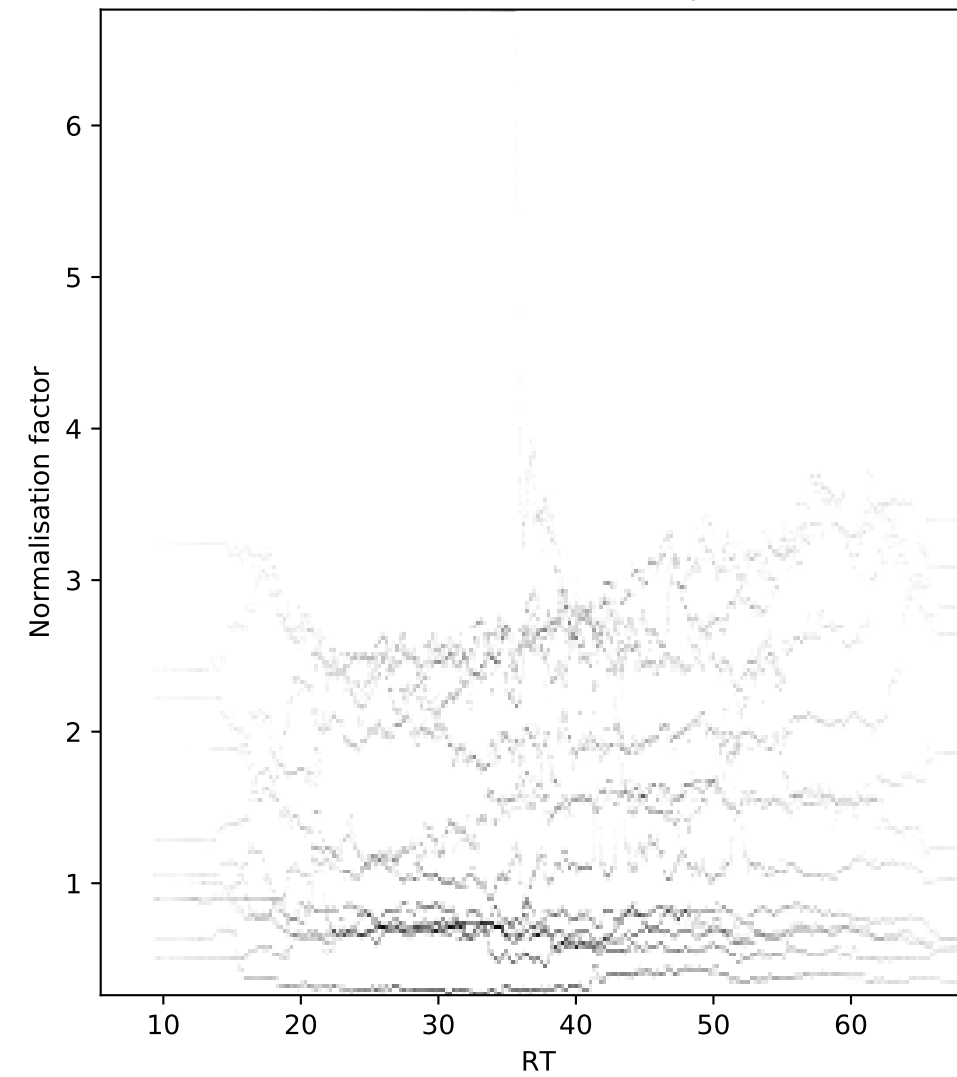
Retention times heatmap, all runs

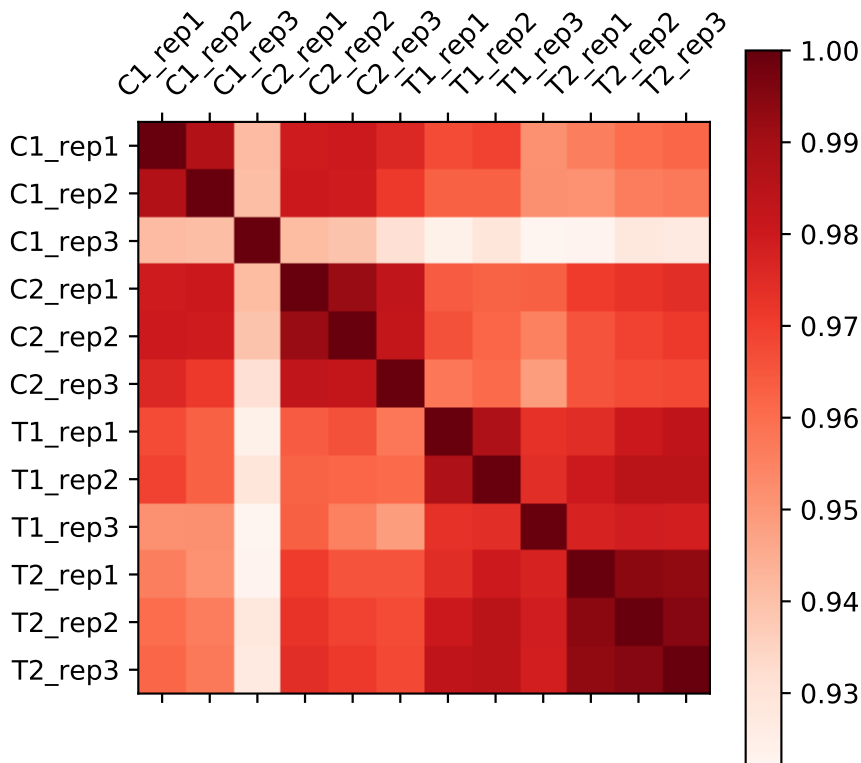


Retention time accuracy heatmap, all runs

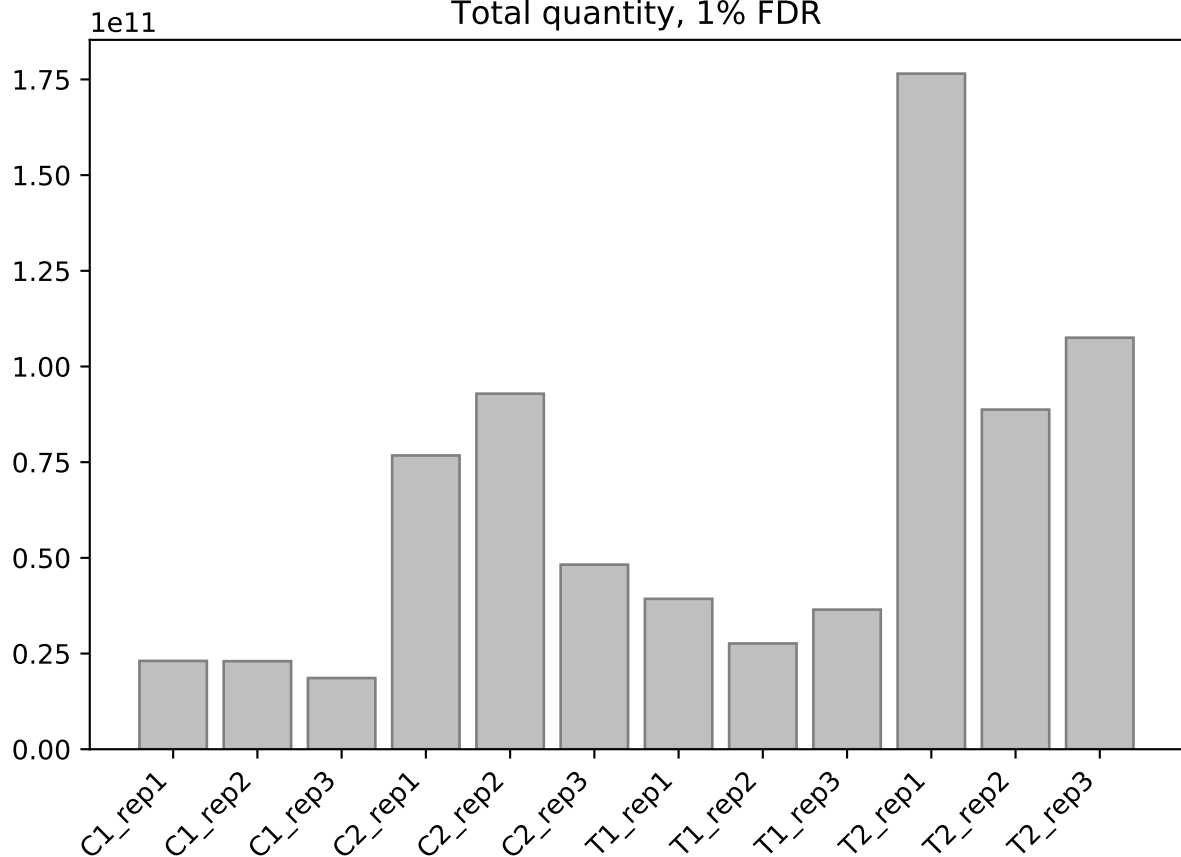


Normalisation factor heatmap, all runs



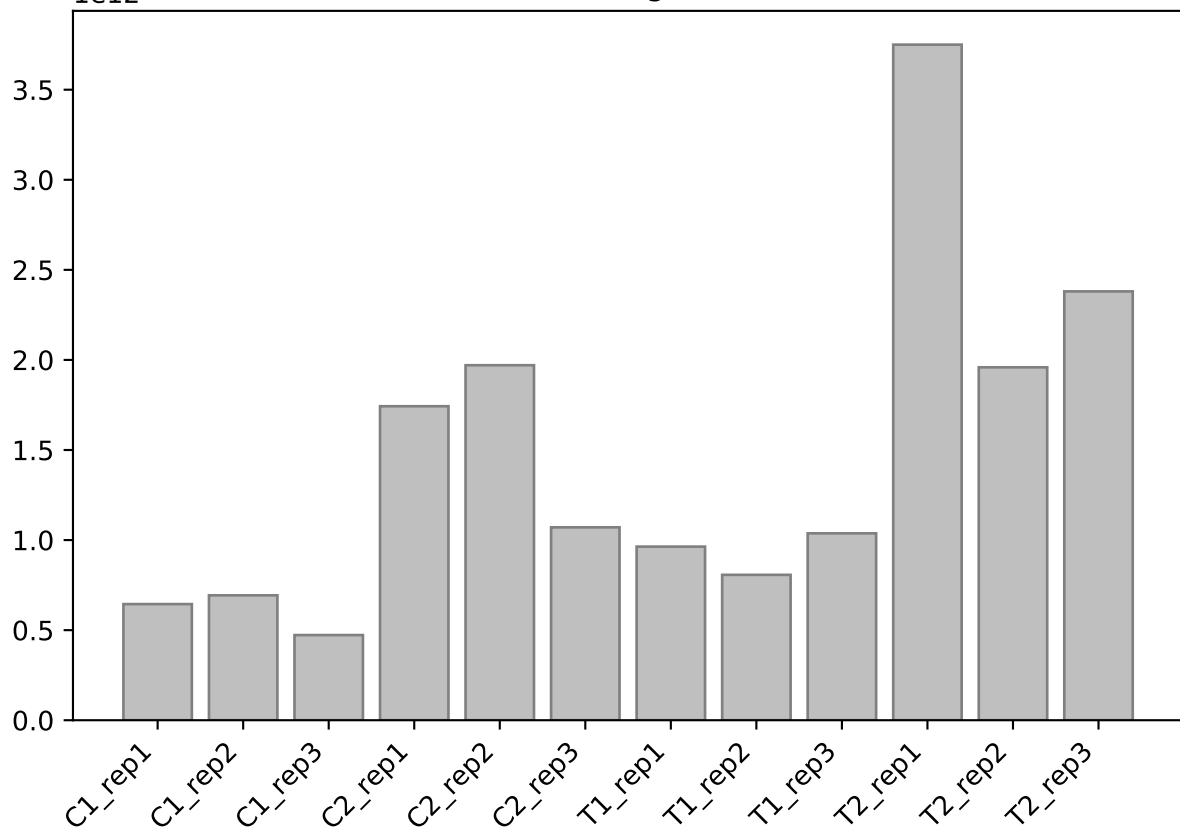


Total quantity, 1% FDR



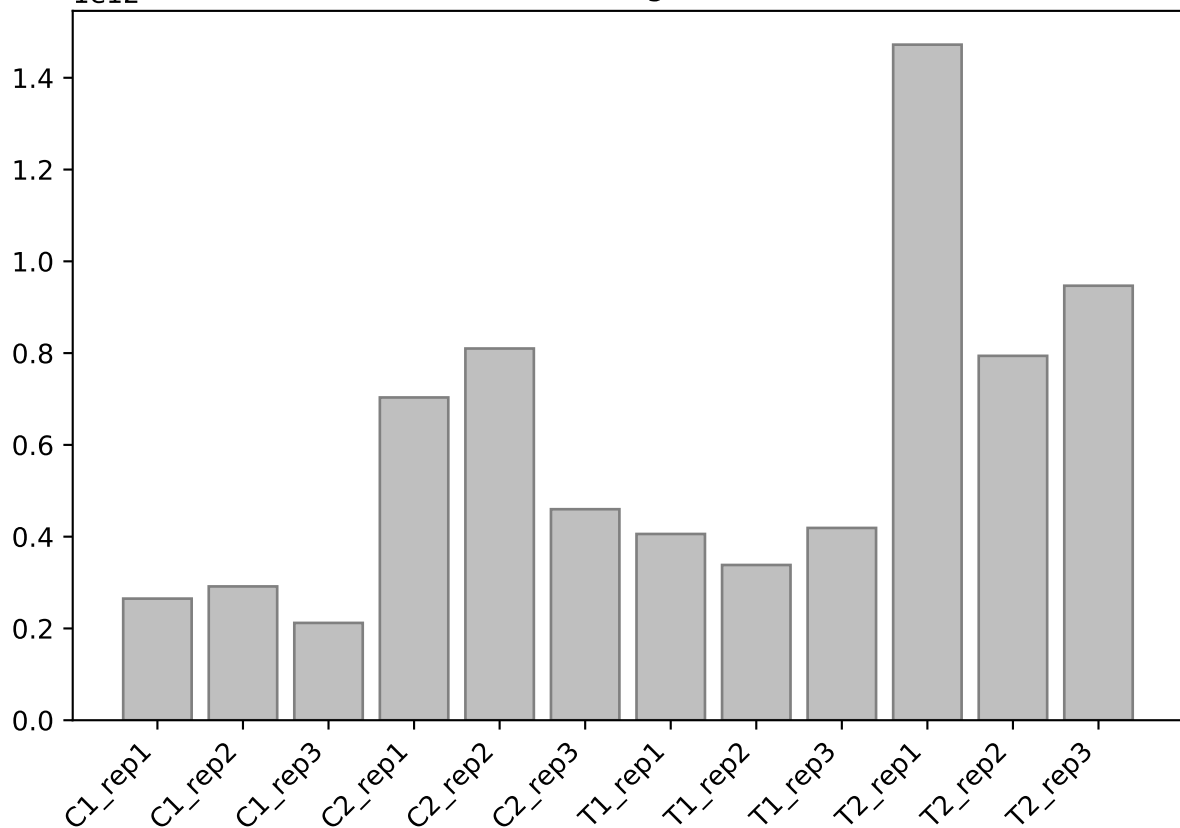
MS1 signal

1e12

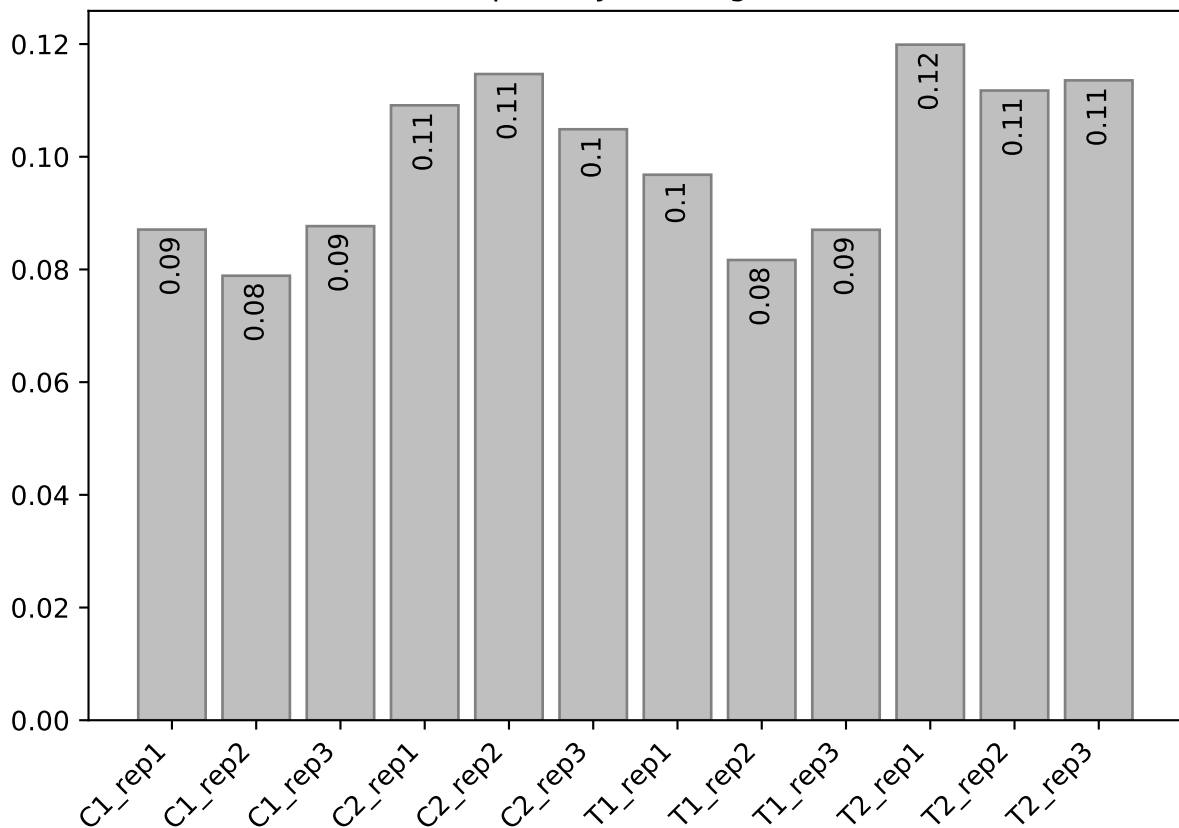


MS2 signal

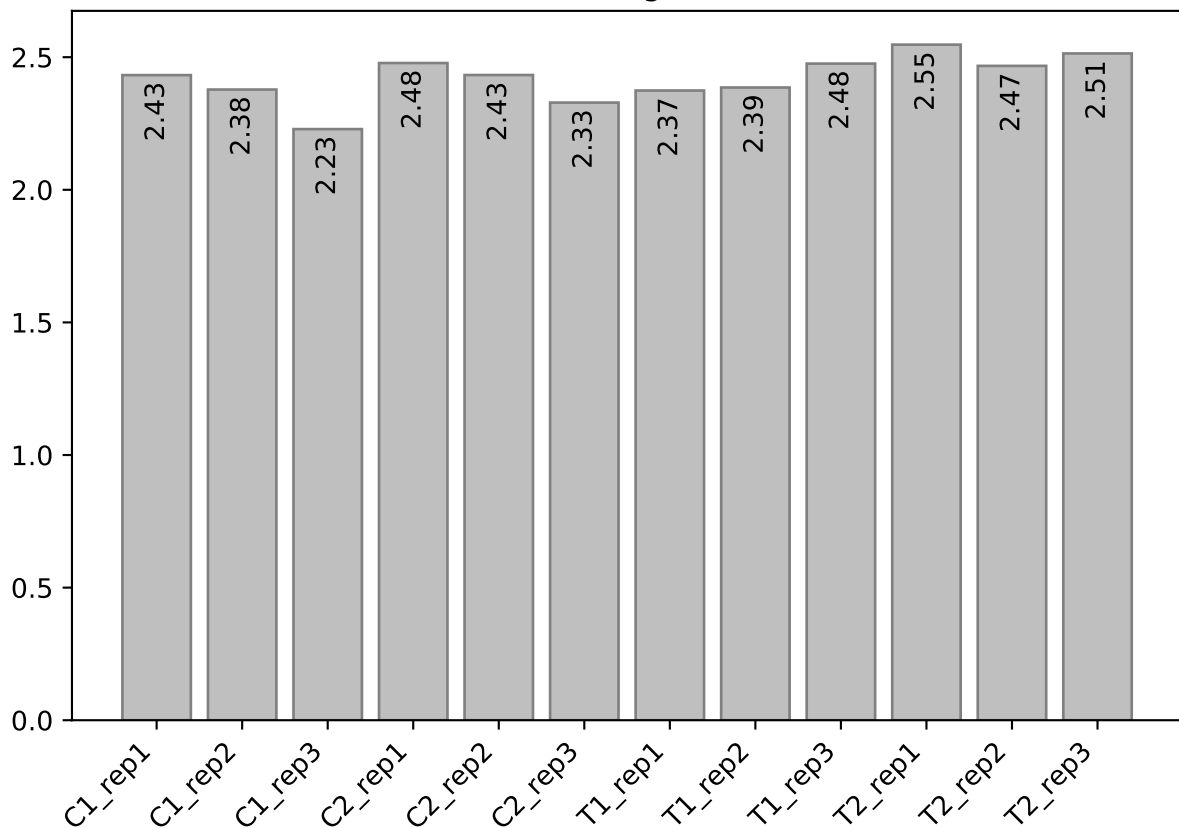
1e12



Total quantity/MS2 signal ratio

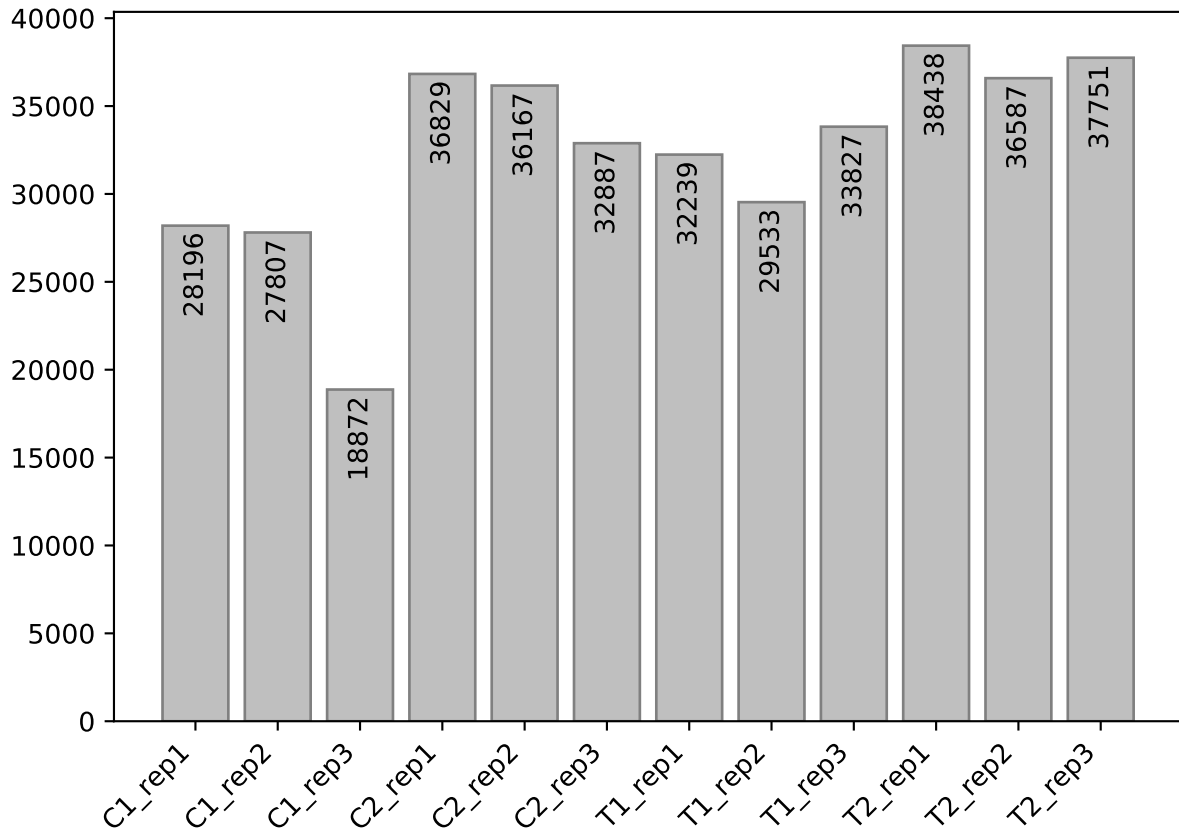


MS1/MS2 signal ratio

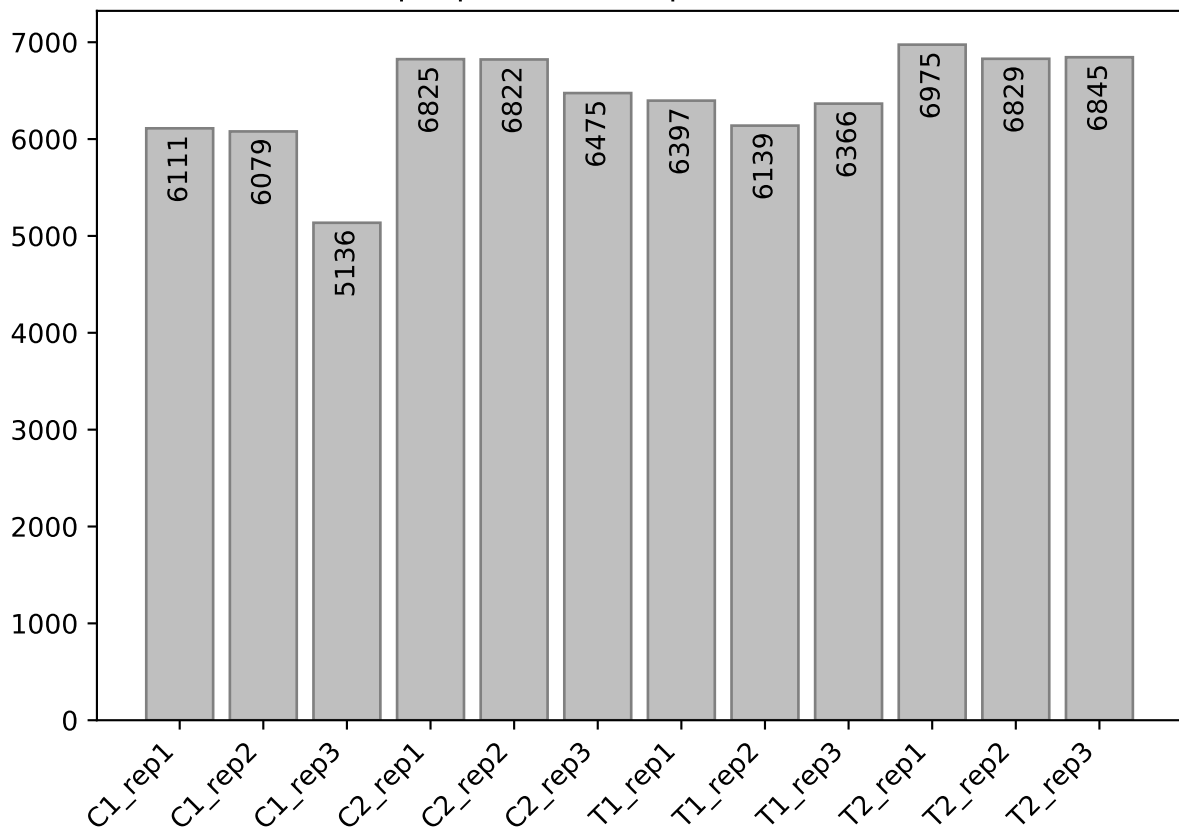




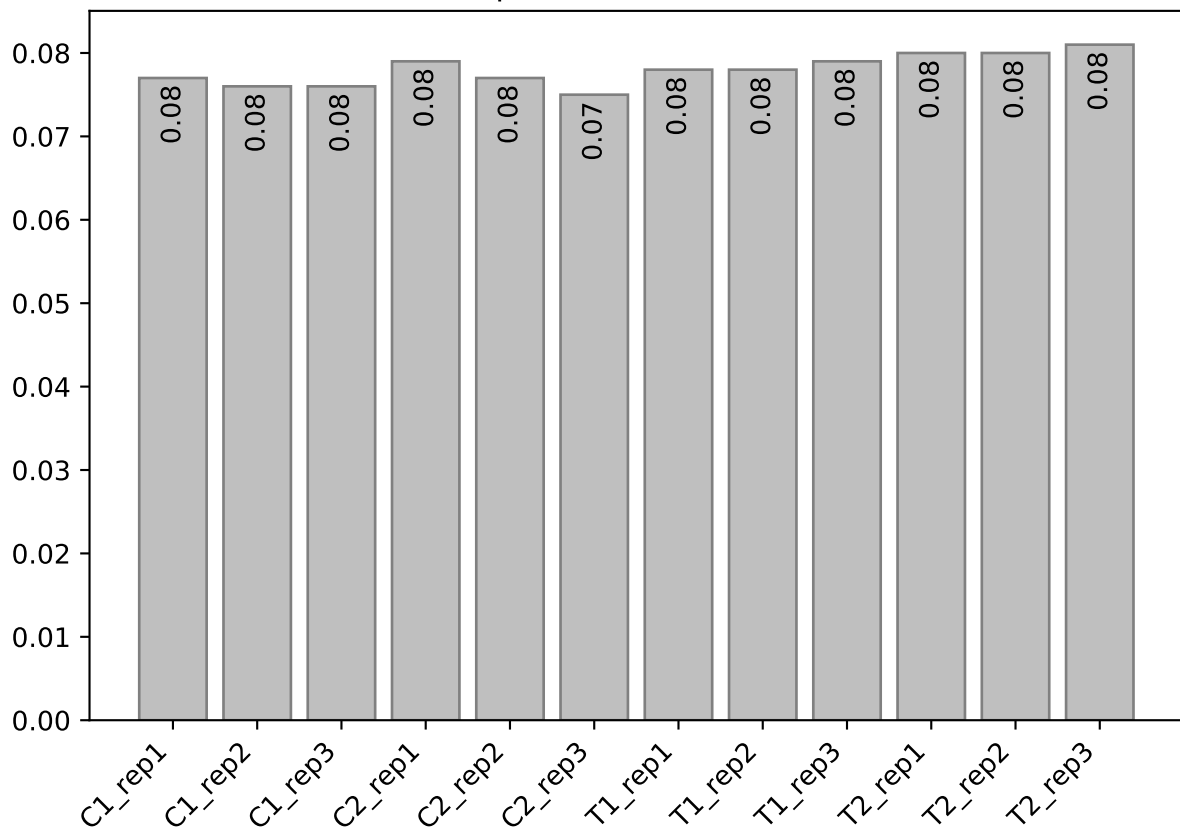
Precursors, 1% FDR



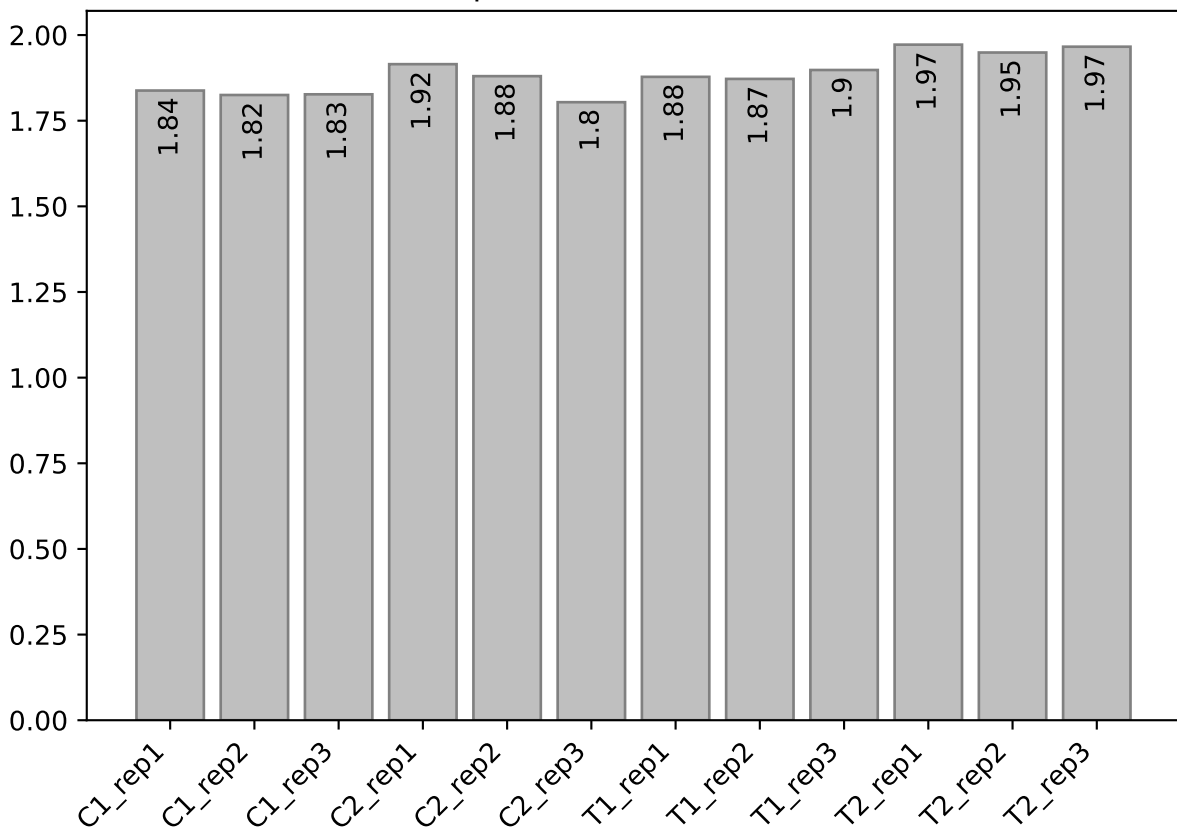
Unique proteins, 1% protein-level FDR



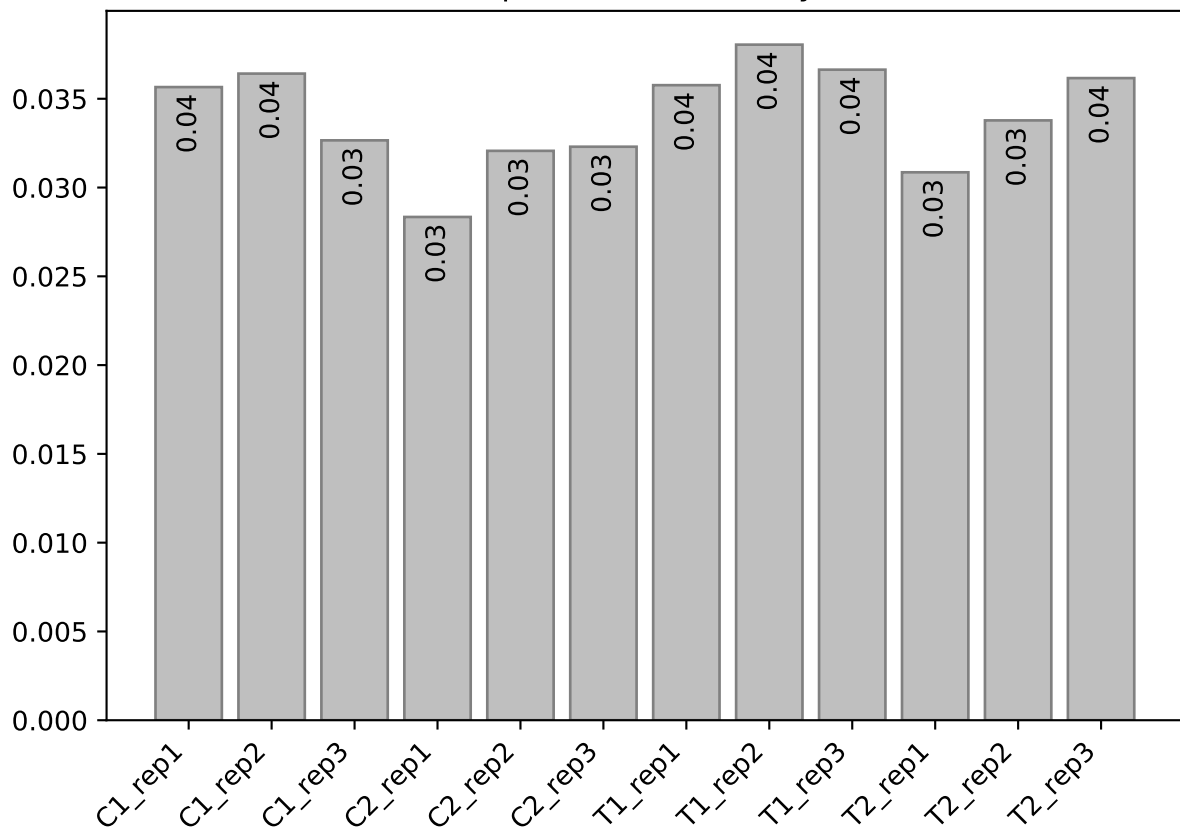
Mean peak FWHM, in minutes



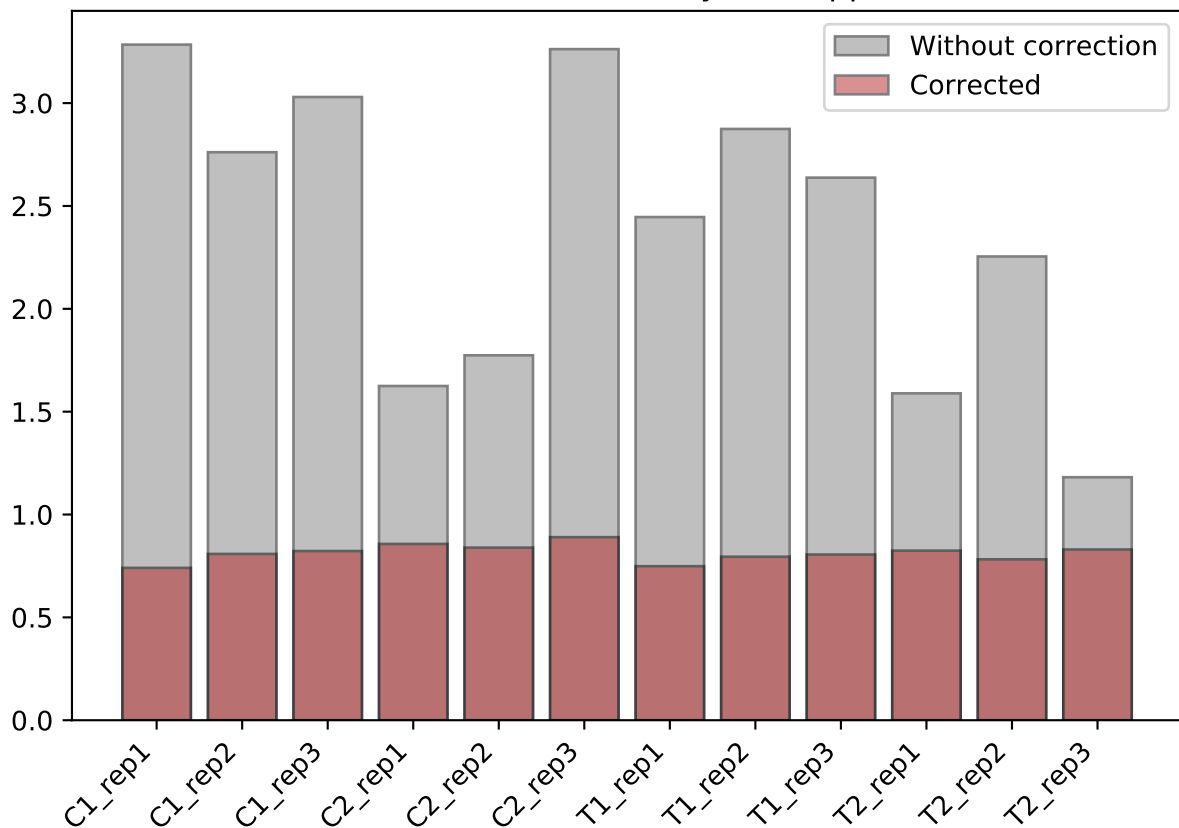
Mean peak FWHM, in MS2 scans



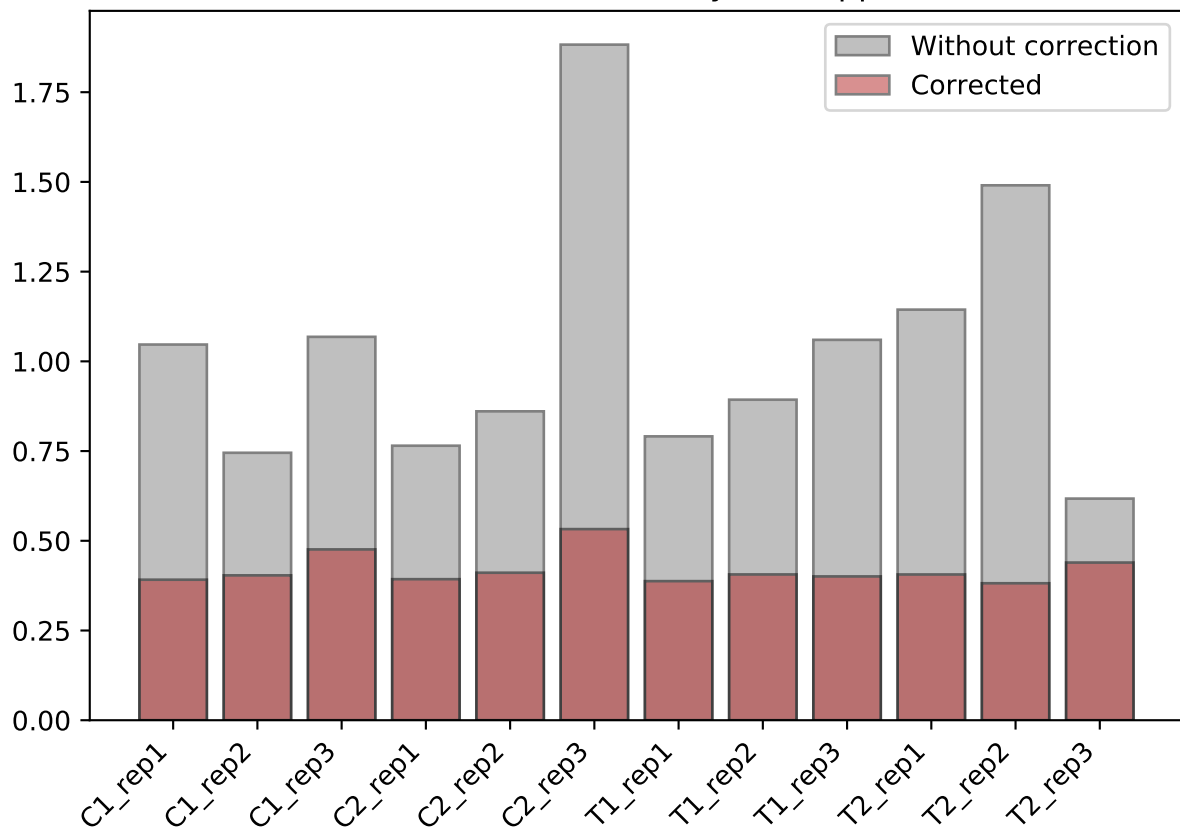
Median RT prediction accuracy, minutes



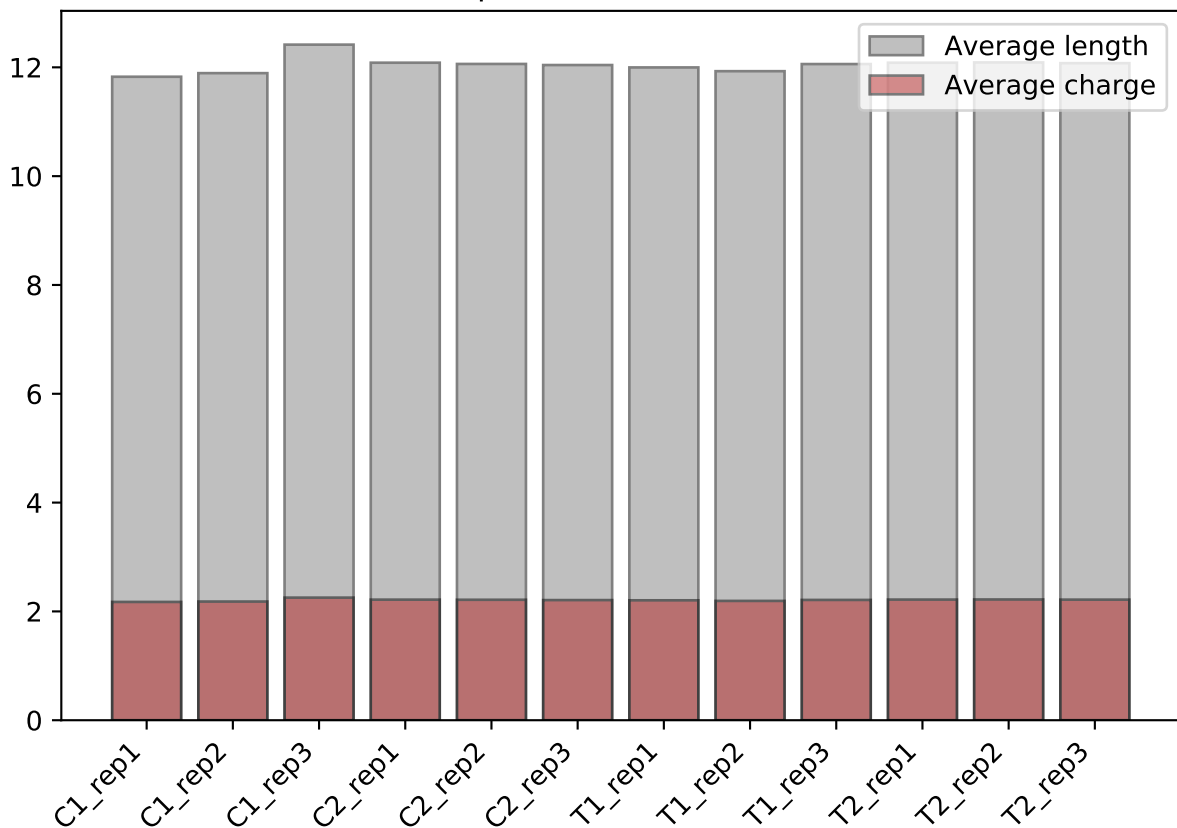
Median mass accuracy, MS2, ppm



Median mass accuracy, MS1, ppm

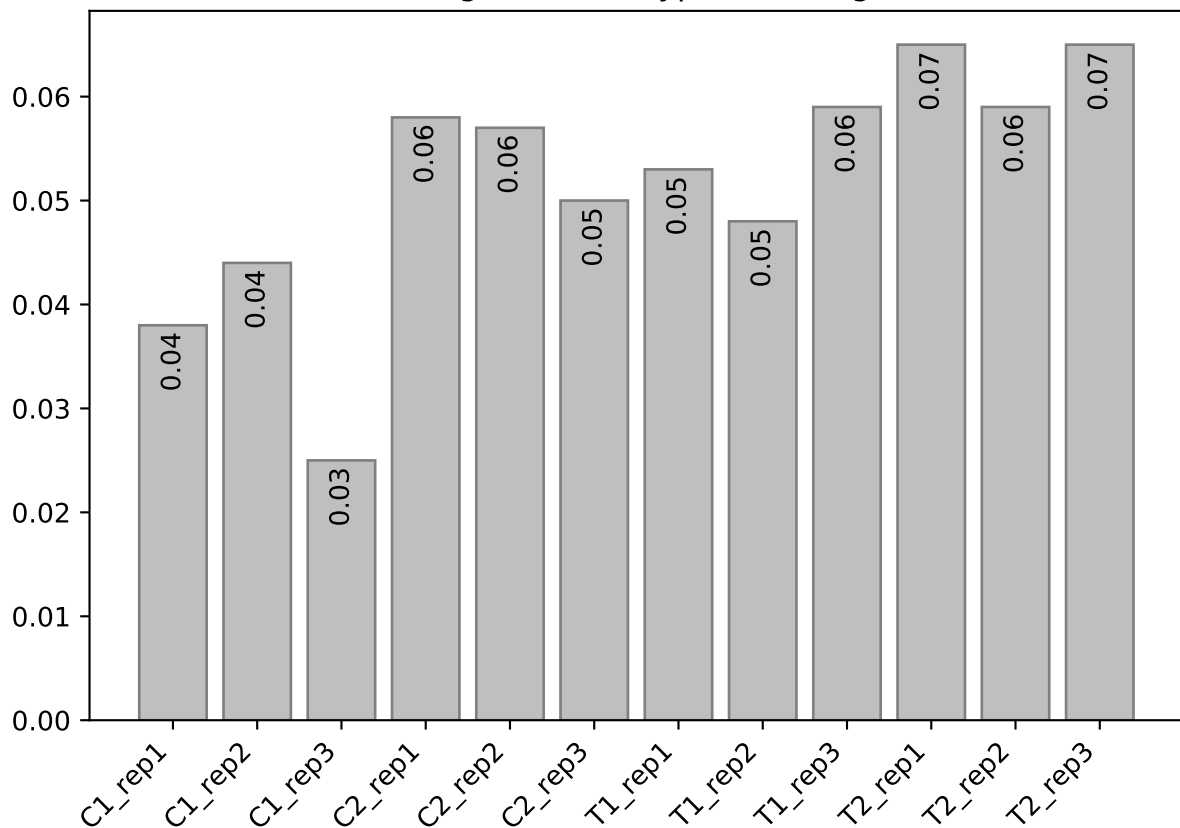


Peptide characteristics

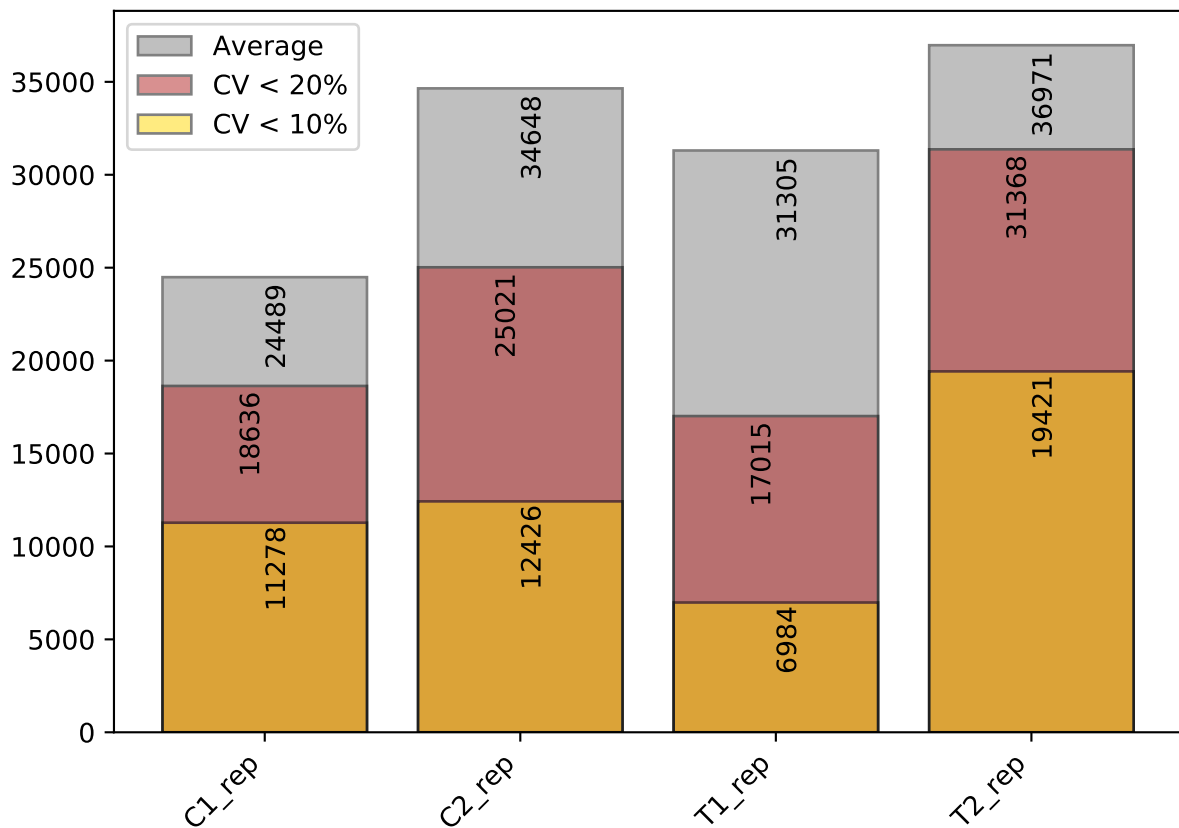




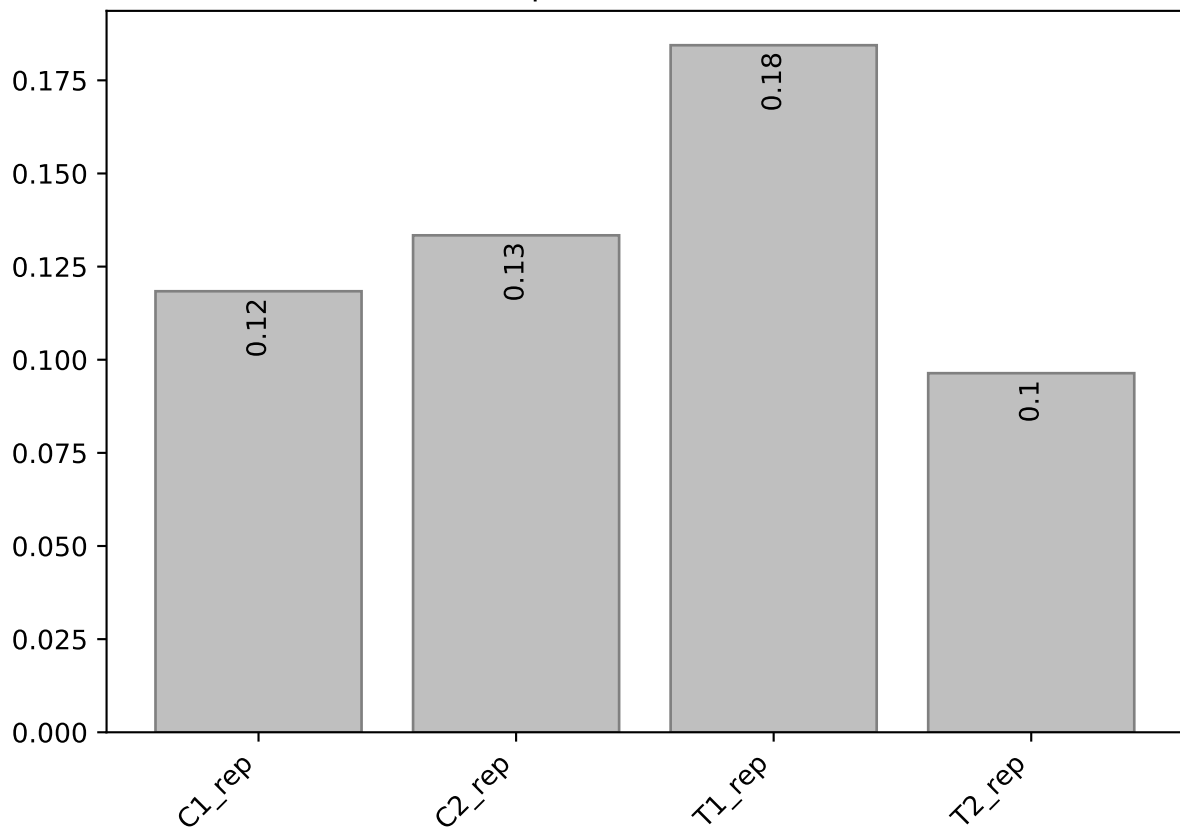
Average missed tryptic cleavages



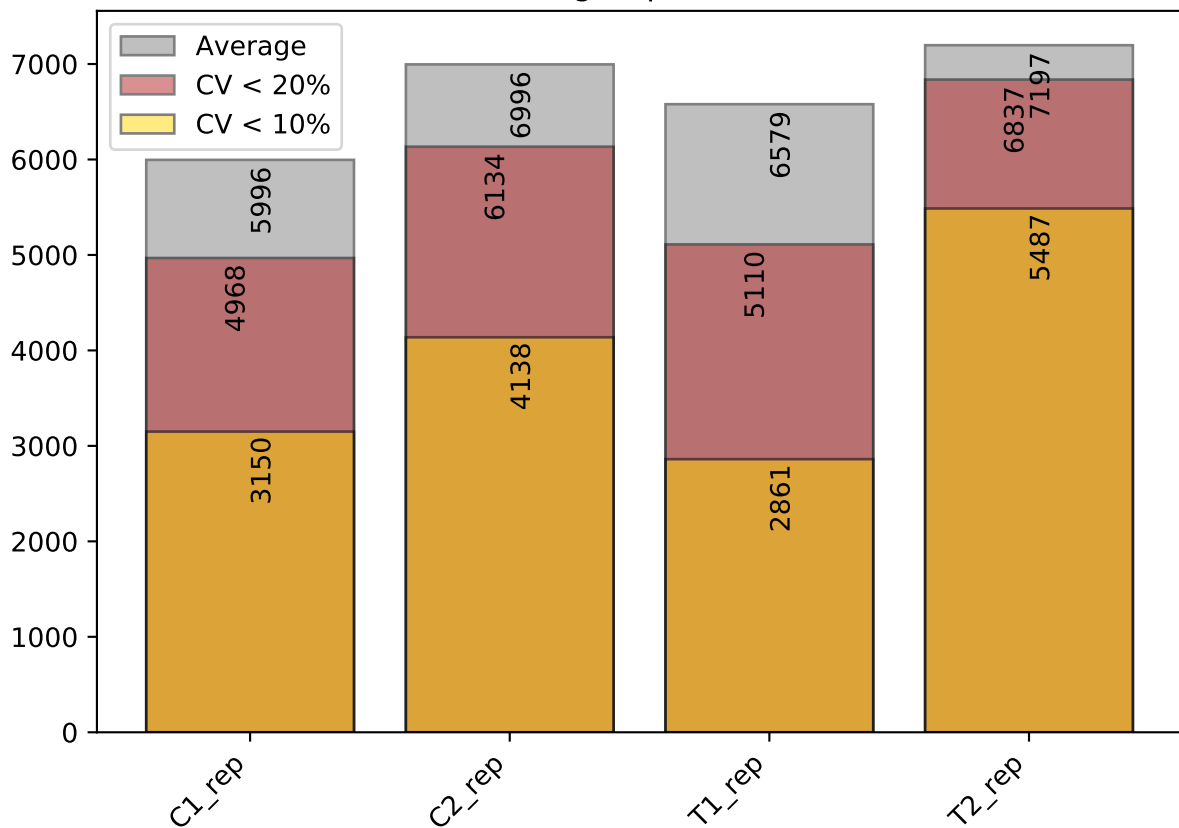
Precursors, 1% FDR



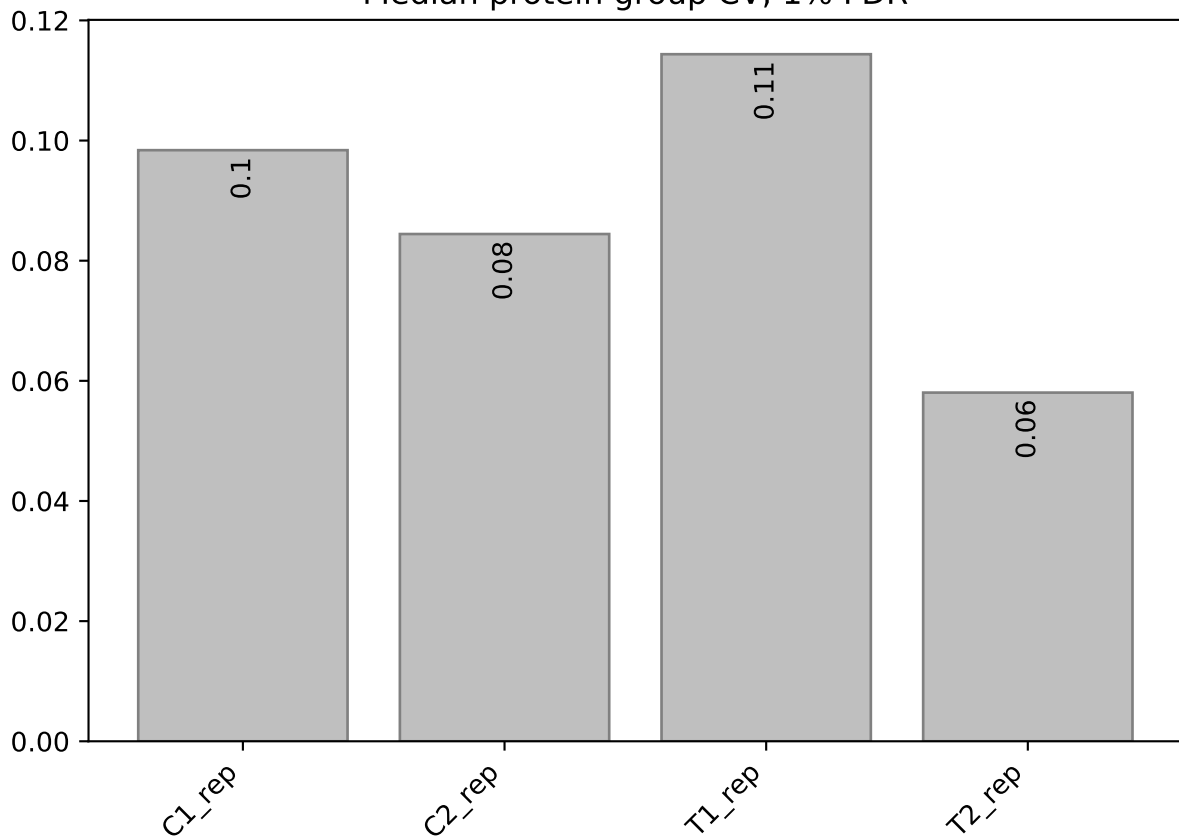
Median precursor CV, 1% FDR



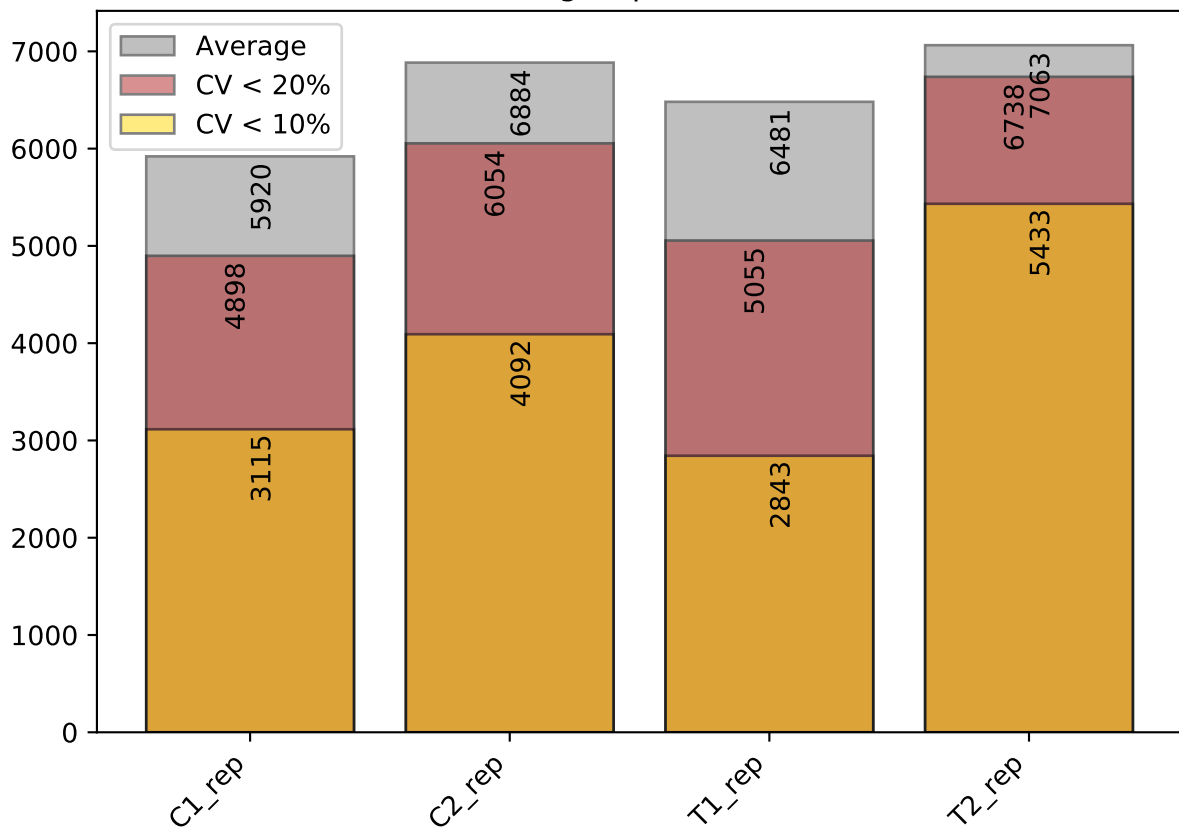
Protein groups, 1% FDR



Median protein group CV, 1% FDR



Gene groups, 1% FDR



Median gene group CV, 1% FDR

