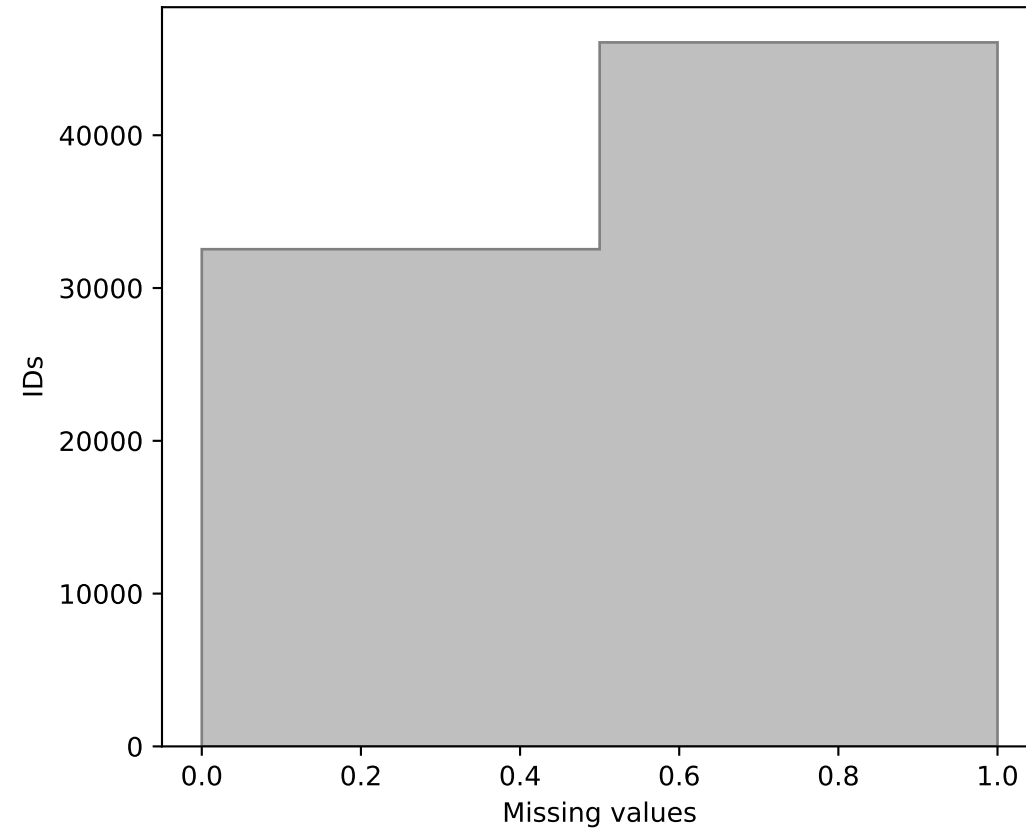
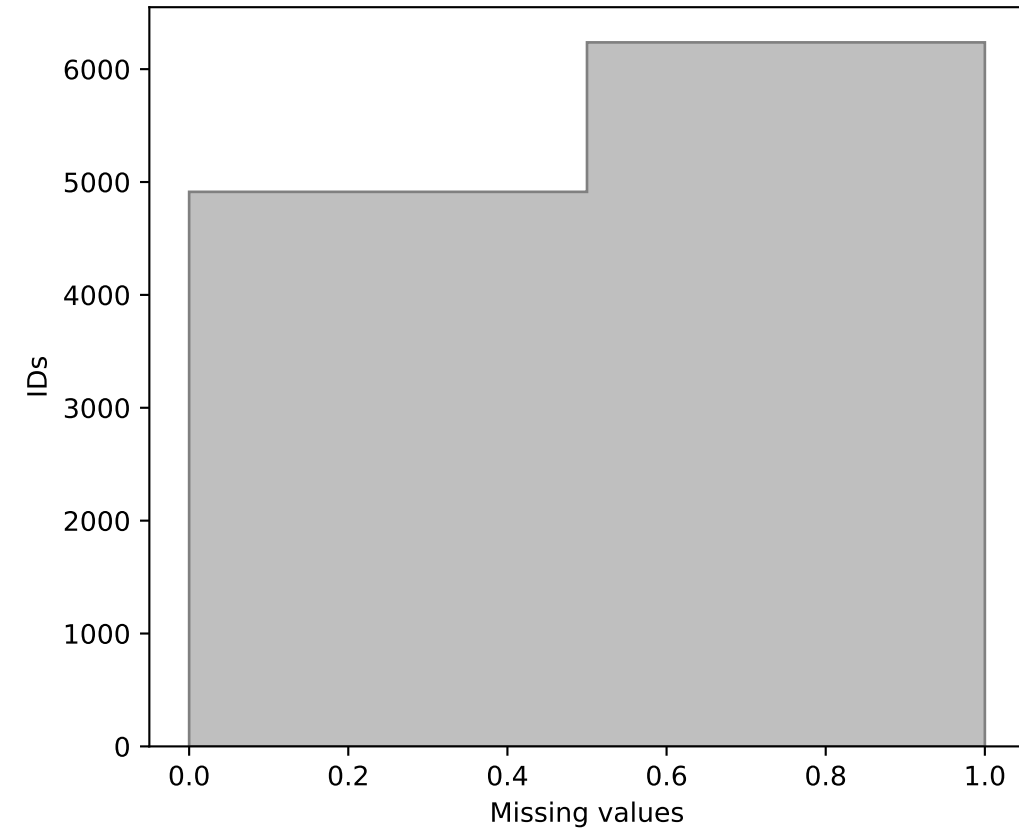


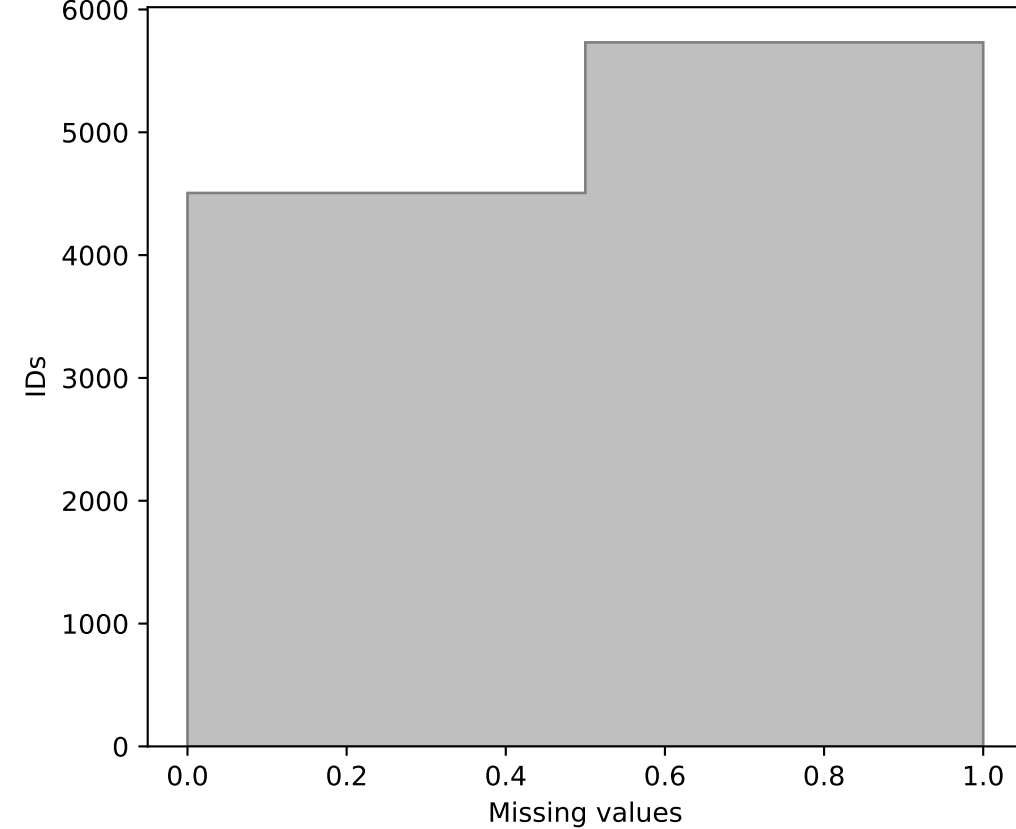
Identification consistency: precursors, CDF



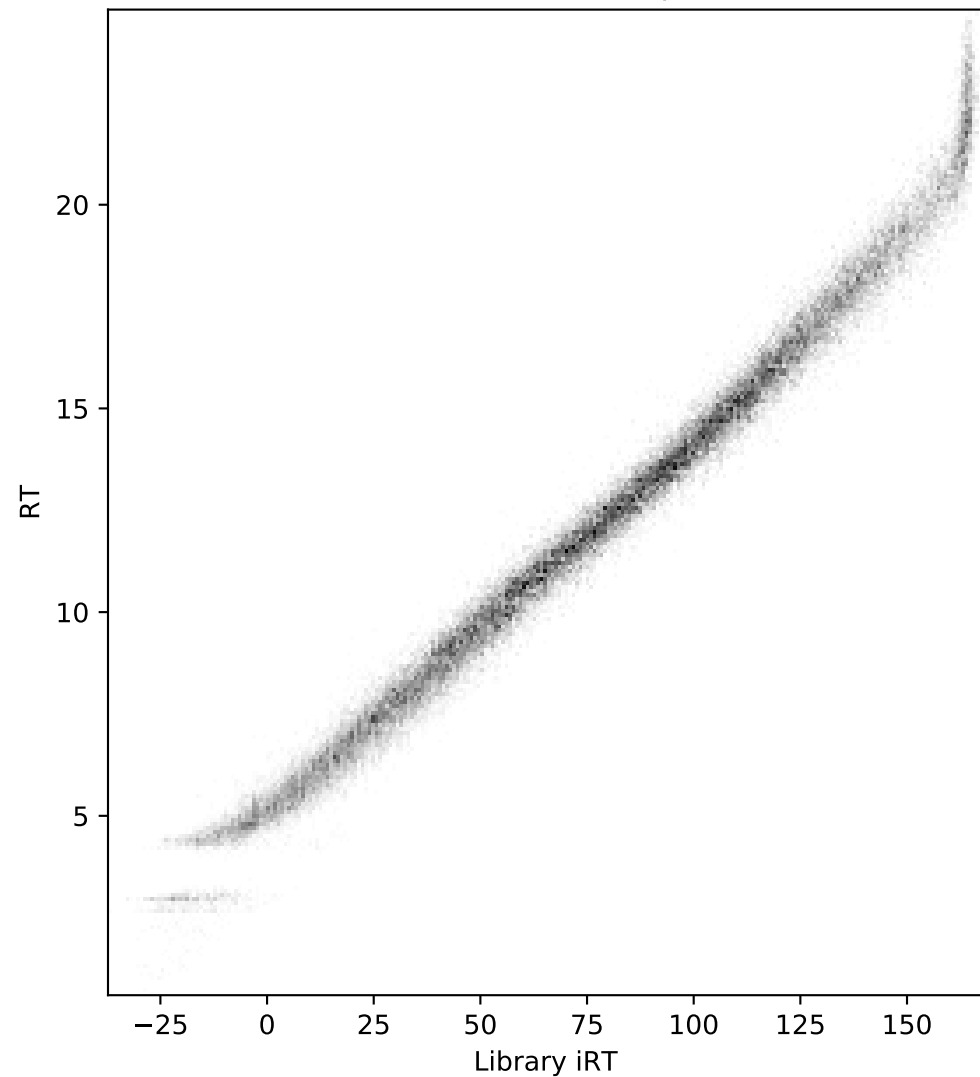
Identification consistency: protein groups, CDF



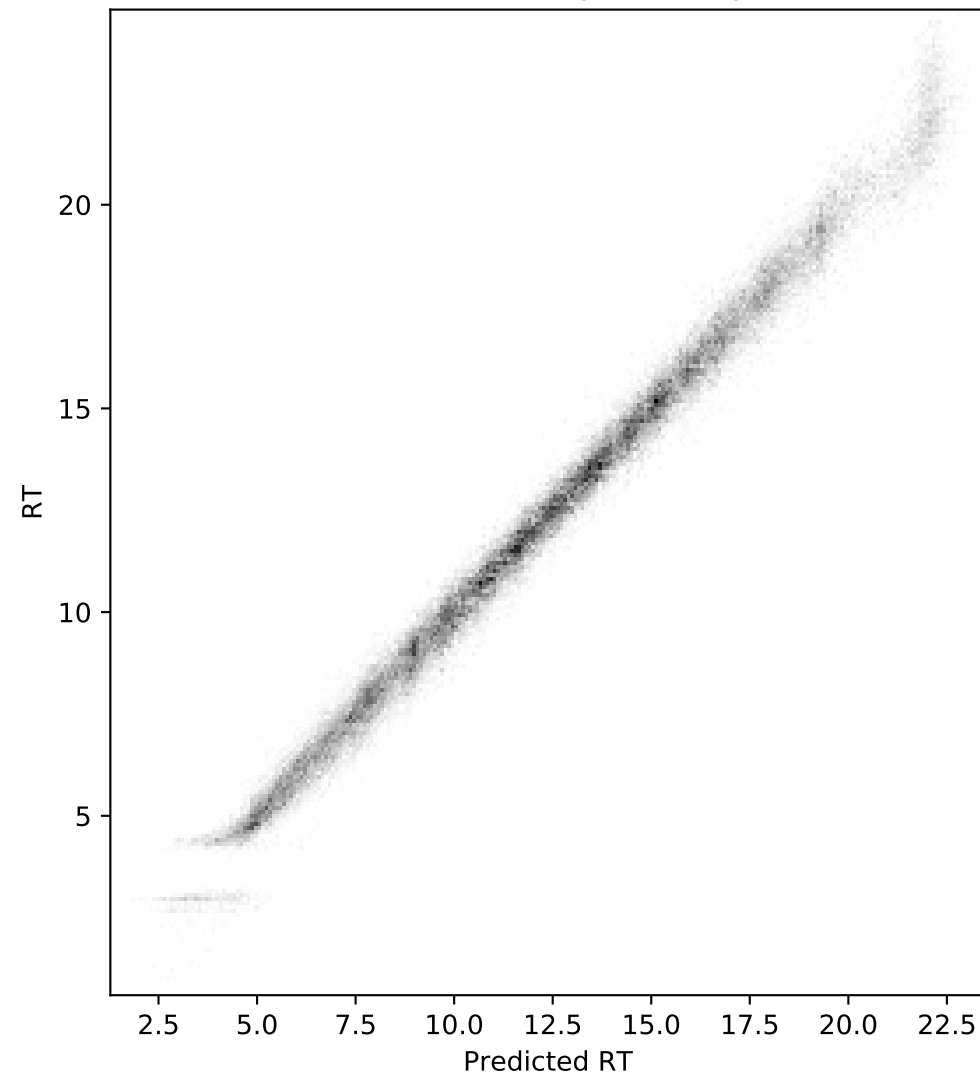
Identification consistency: unique genes, CDF



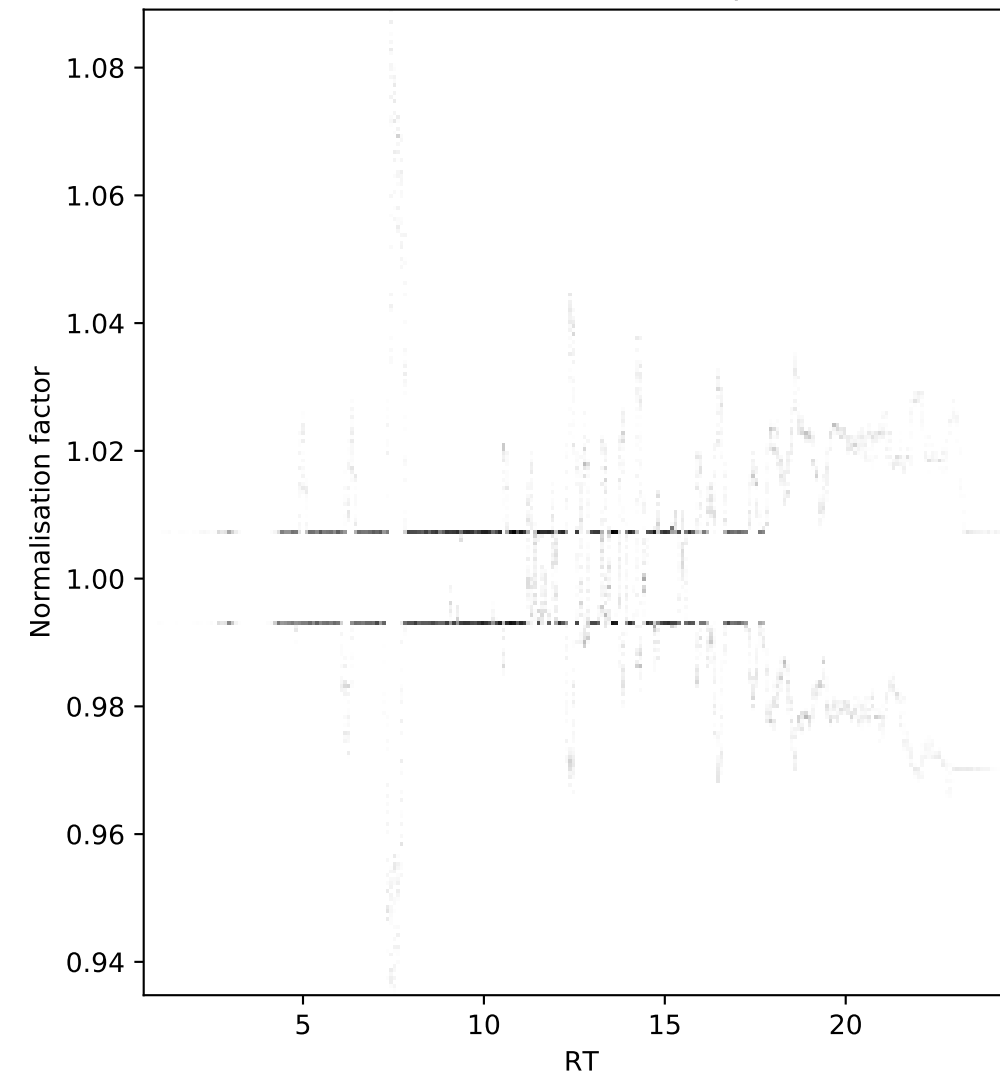
Retention times heatmap, all runs

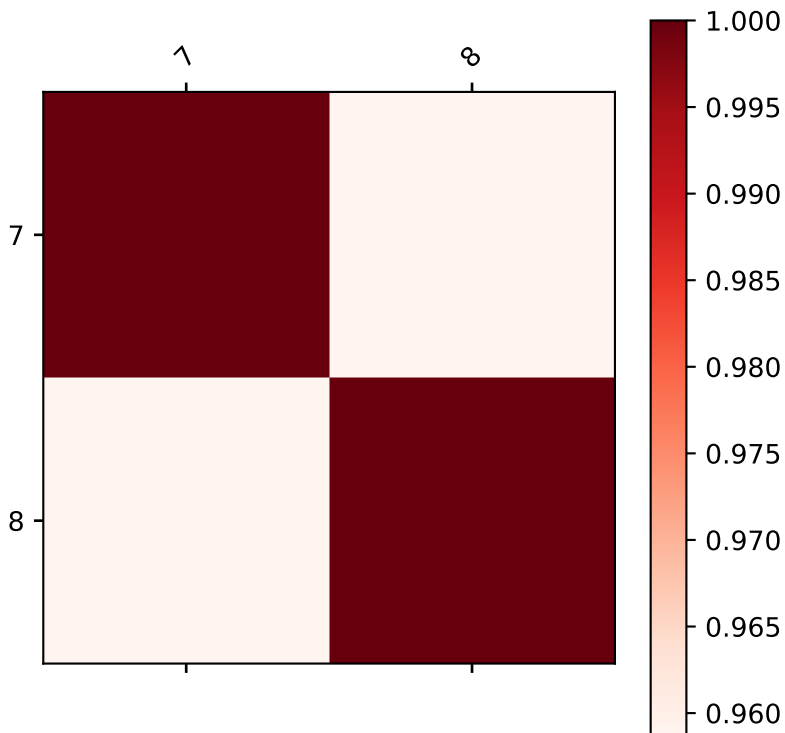


Retention time accuracy heatmap, all runs

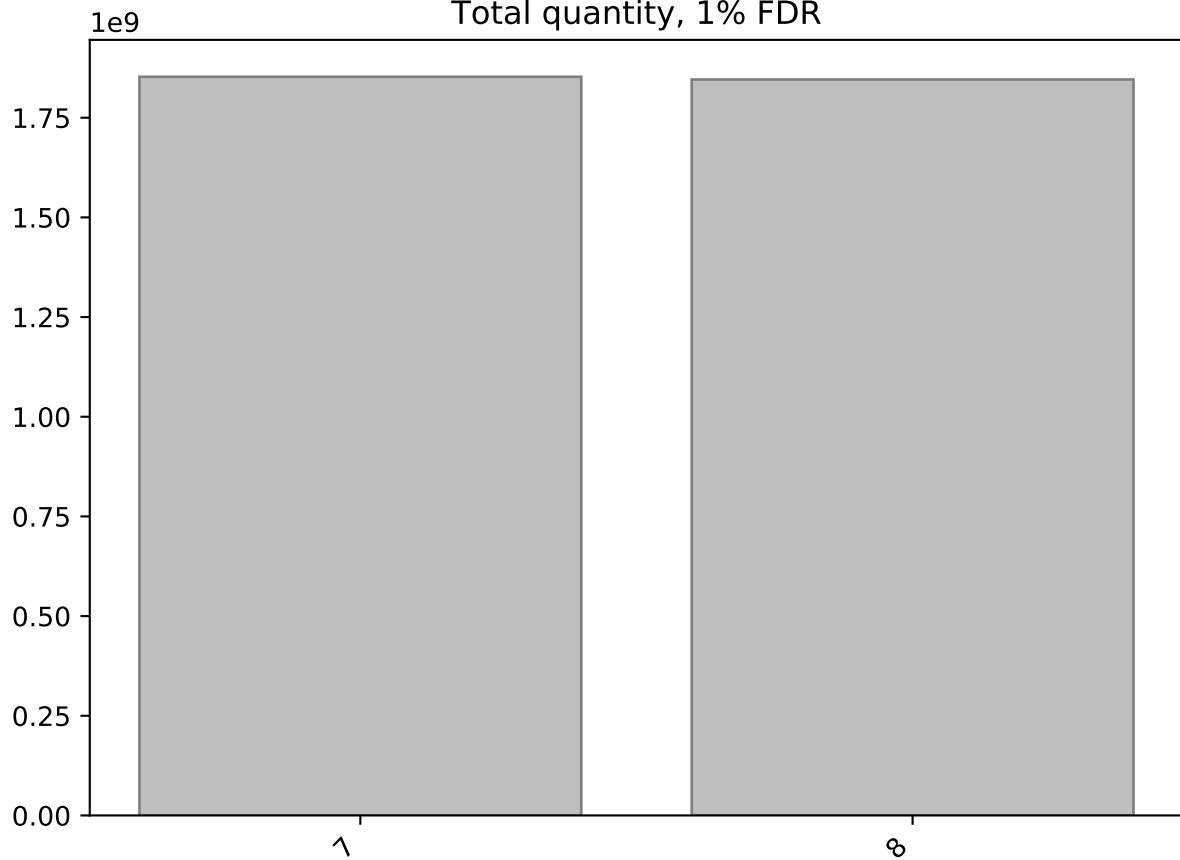


Normalisation factor heatmap, all runs

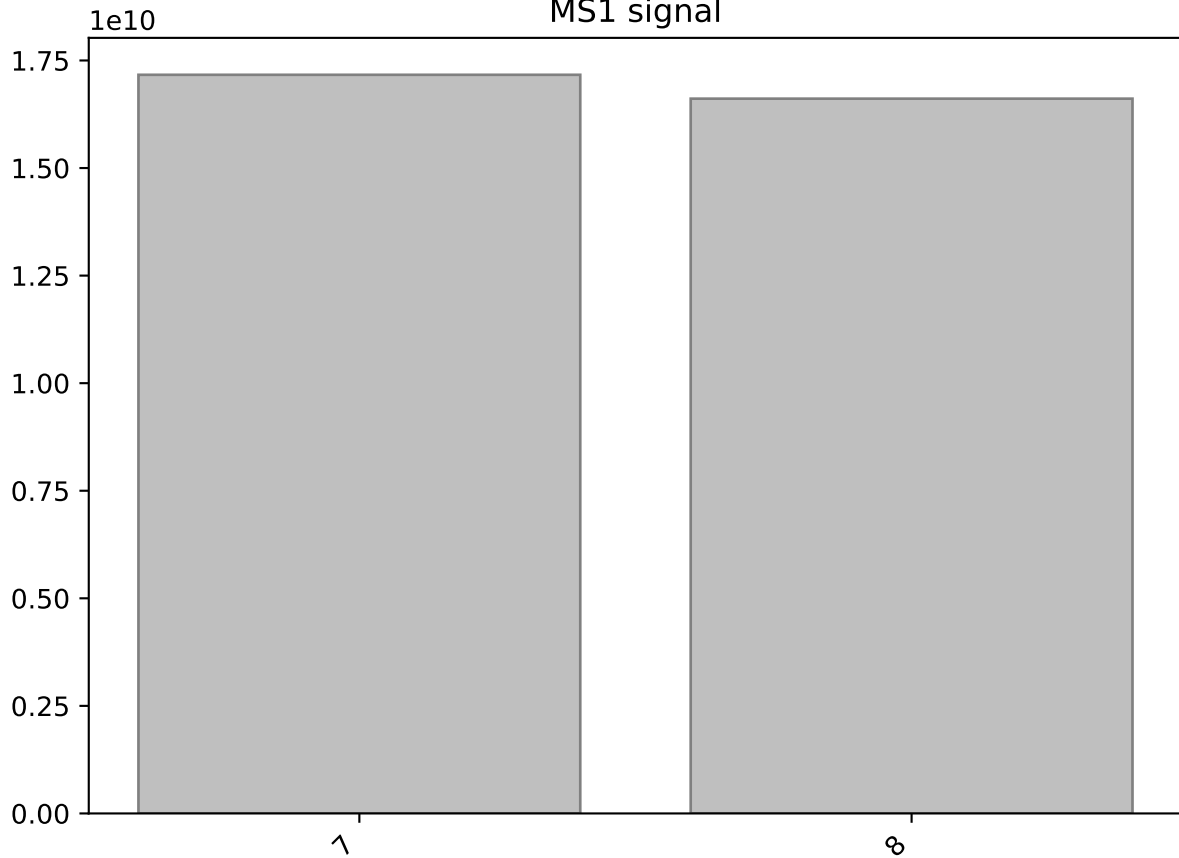




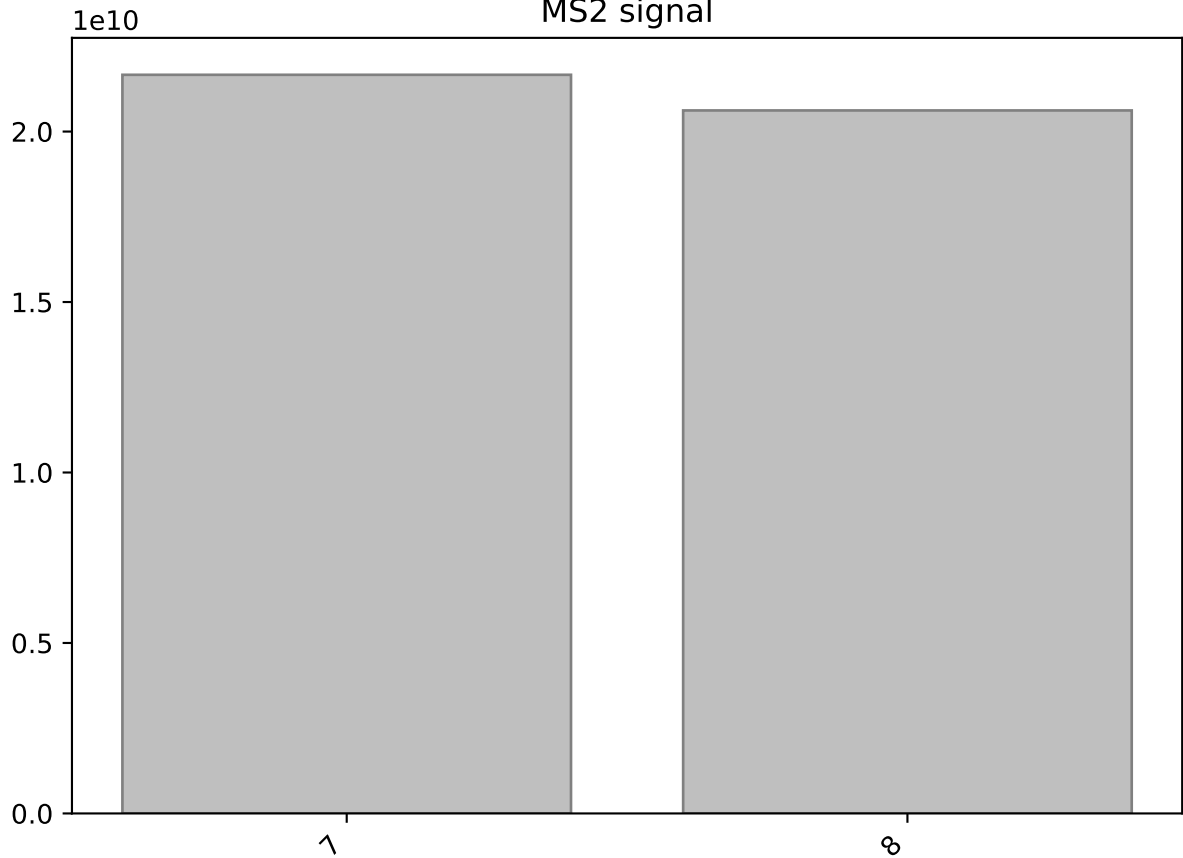
Total quantity, 1% FDR



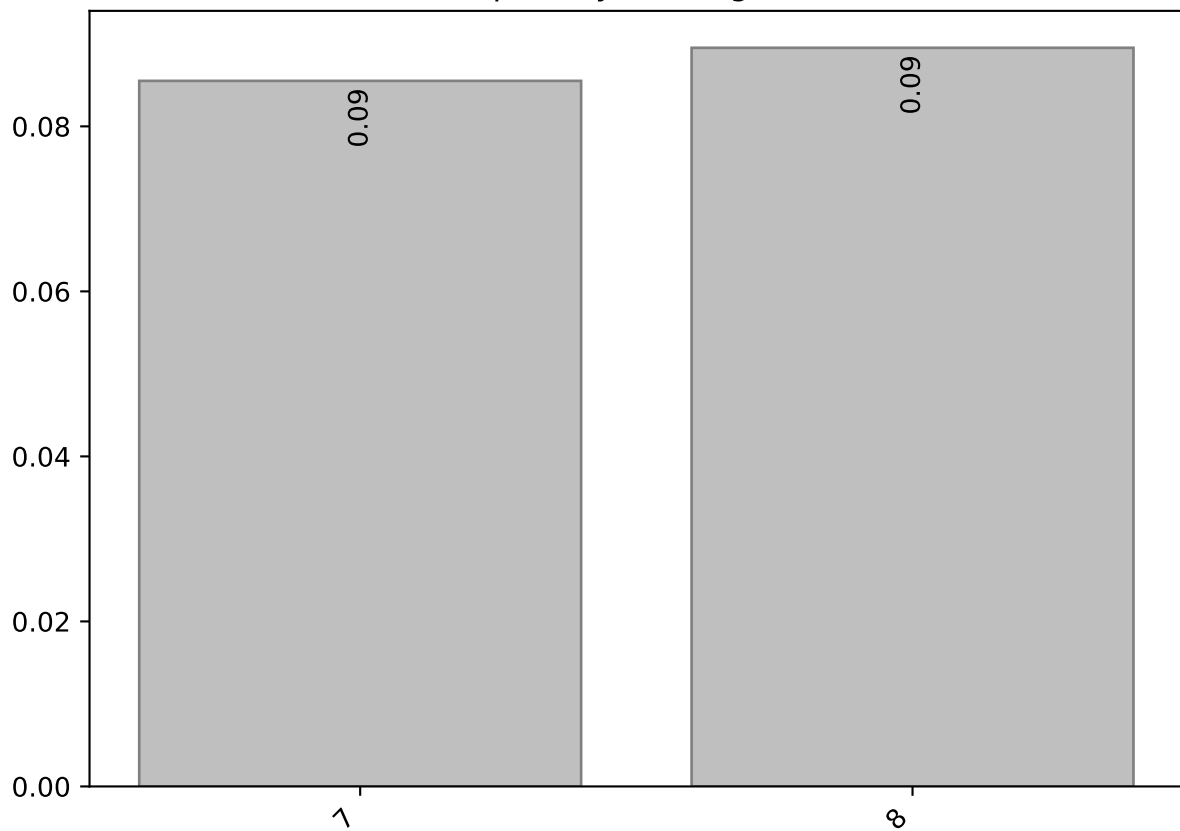
MS1 signal



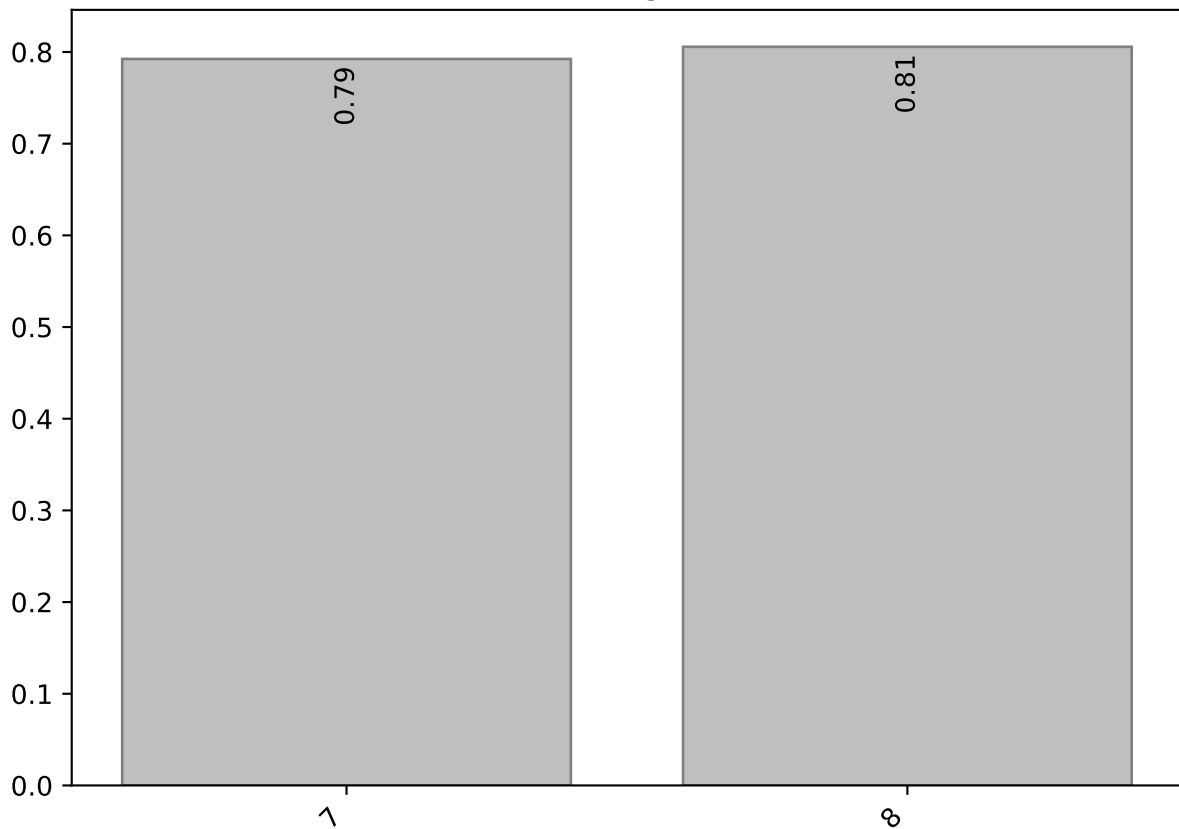
MS2 signal



Total quantity/MS2 signal ratio

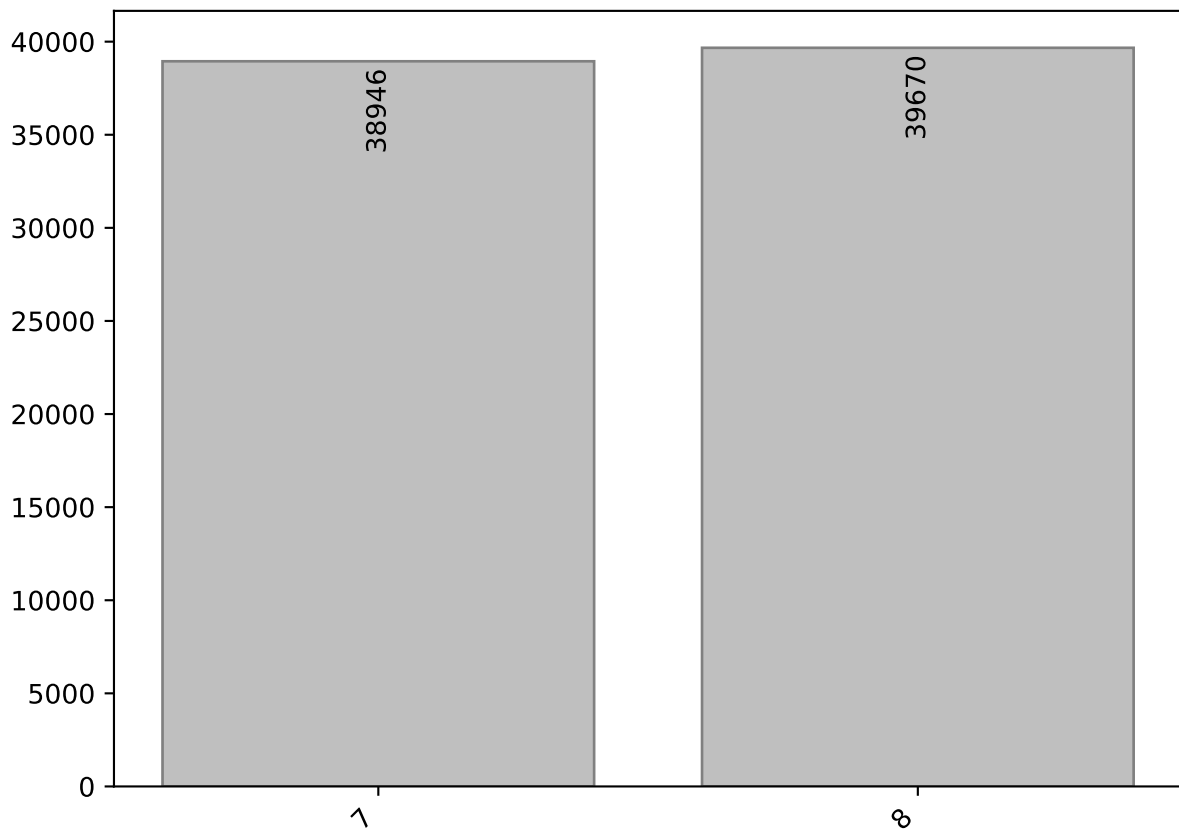


MS1/MS2 signal ratio

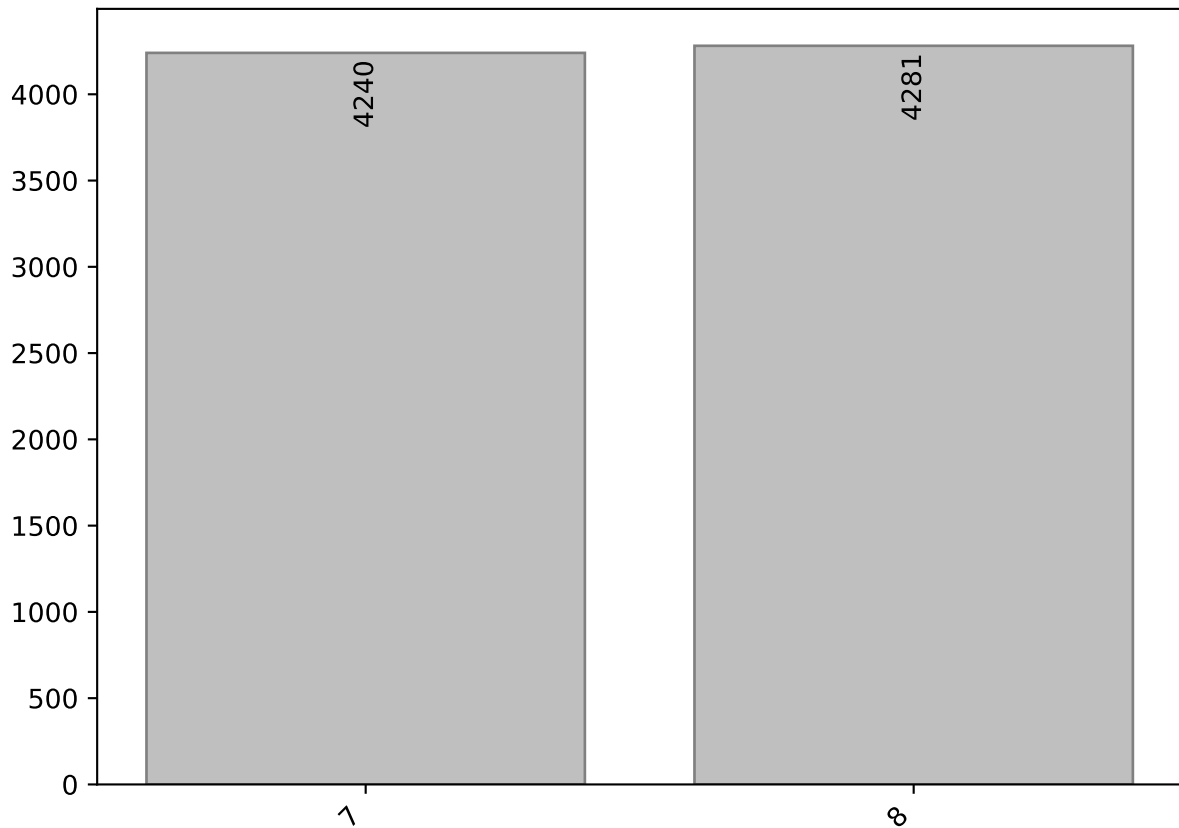




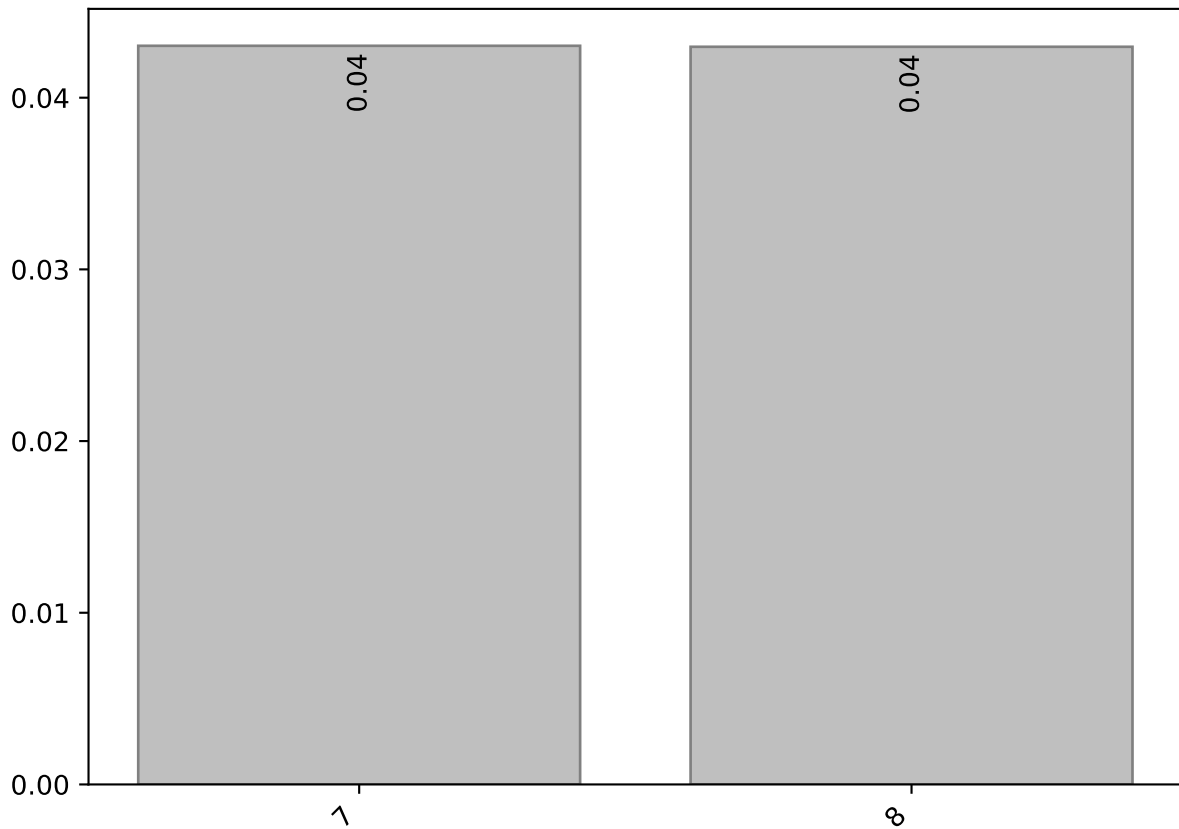
Precursors, 1% FDR



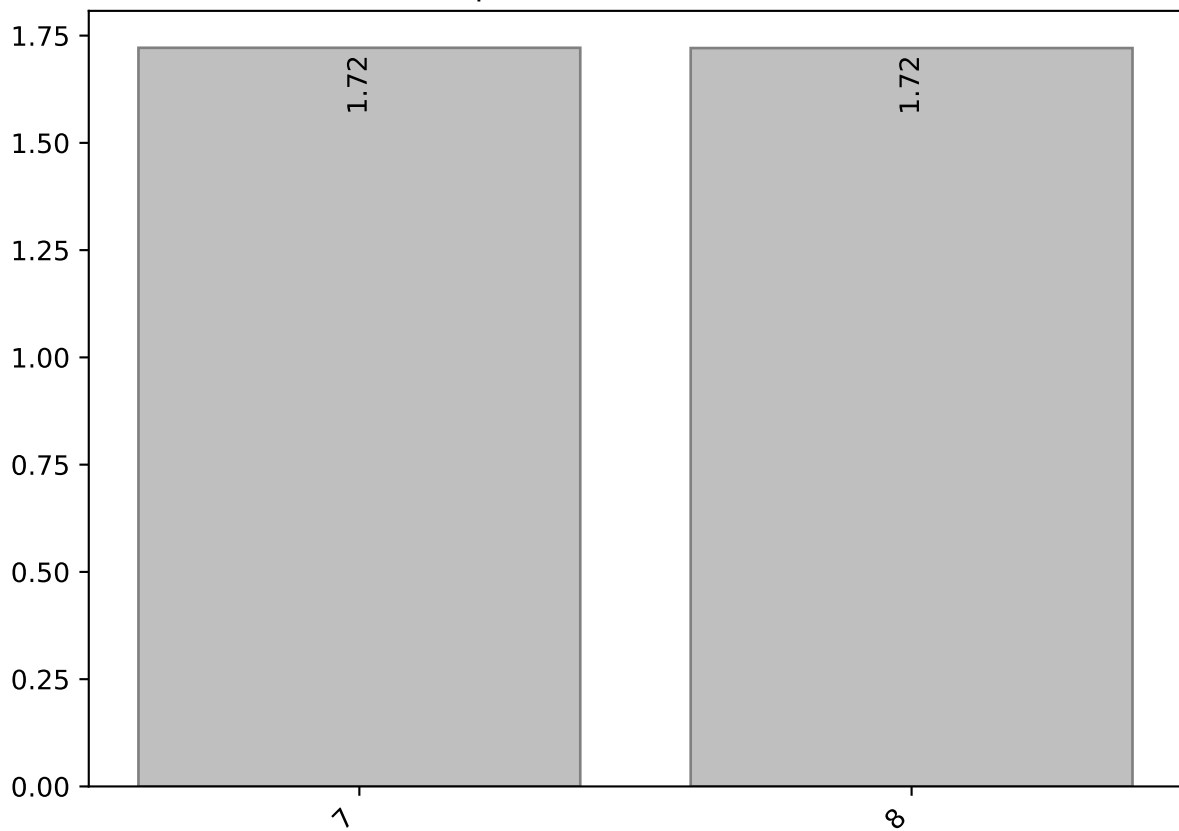
Unique proteins, 1% protein-level FDR



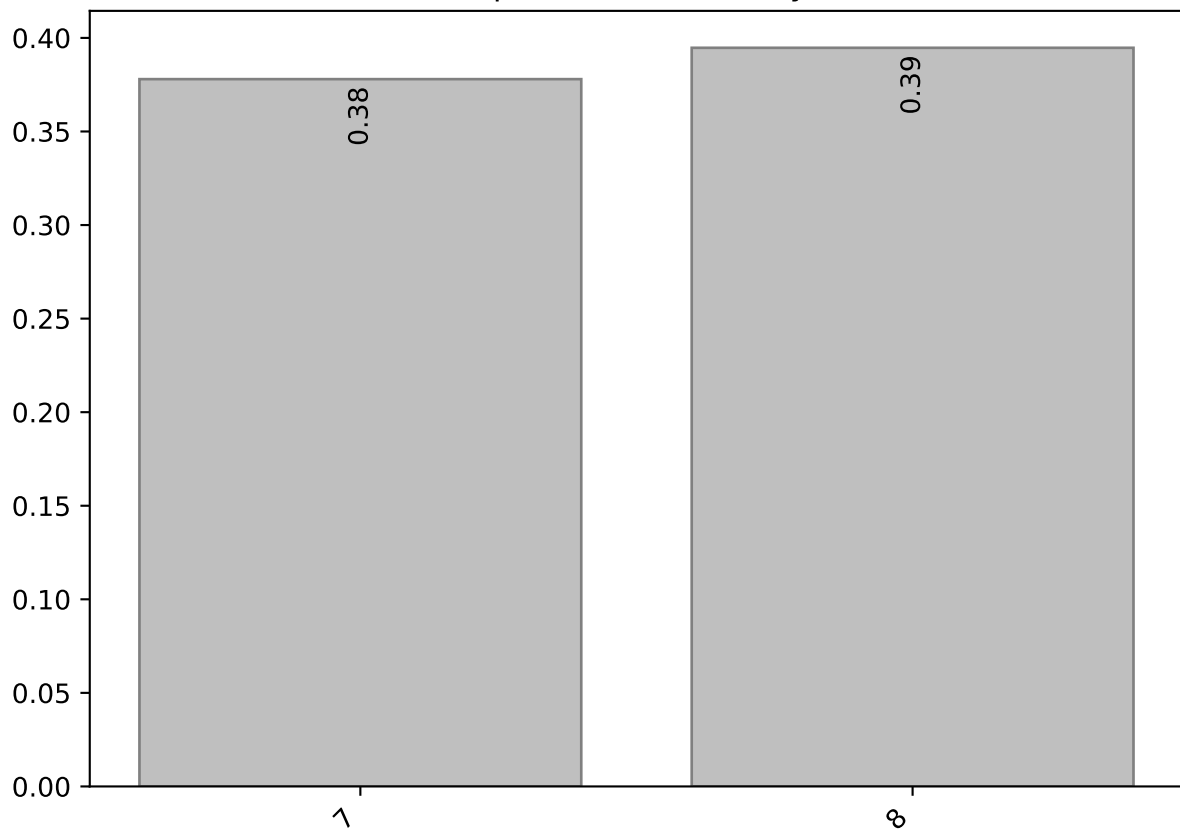
Mean peak FWHM, in minutes



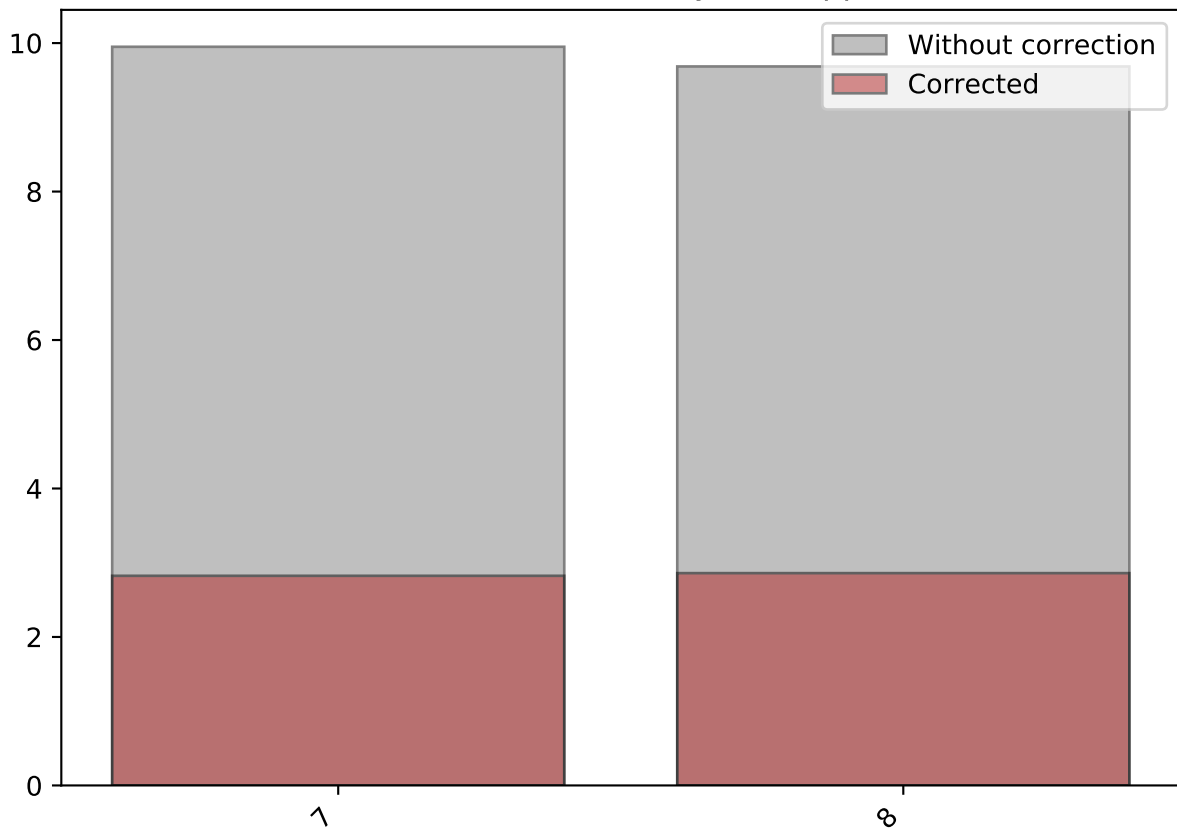
Mean peak FWHM, in MS2 scans



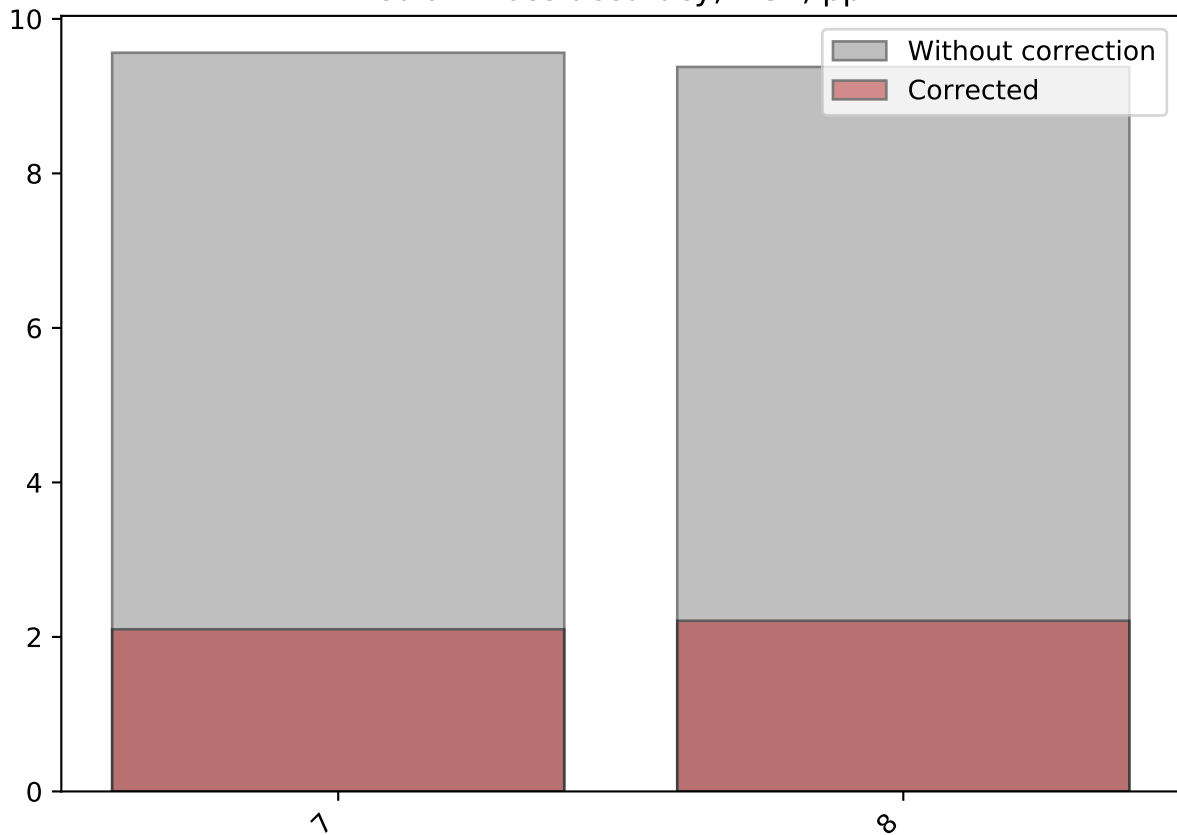
Median RT prediction accuracy, minutes



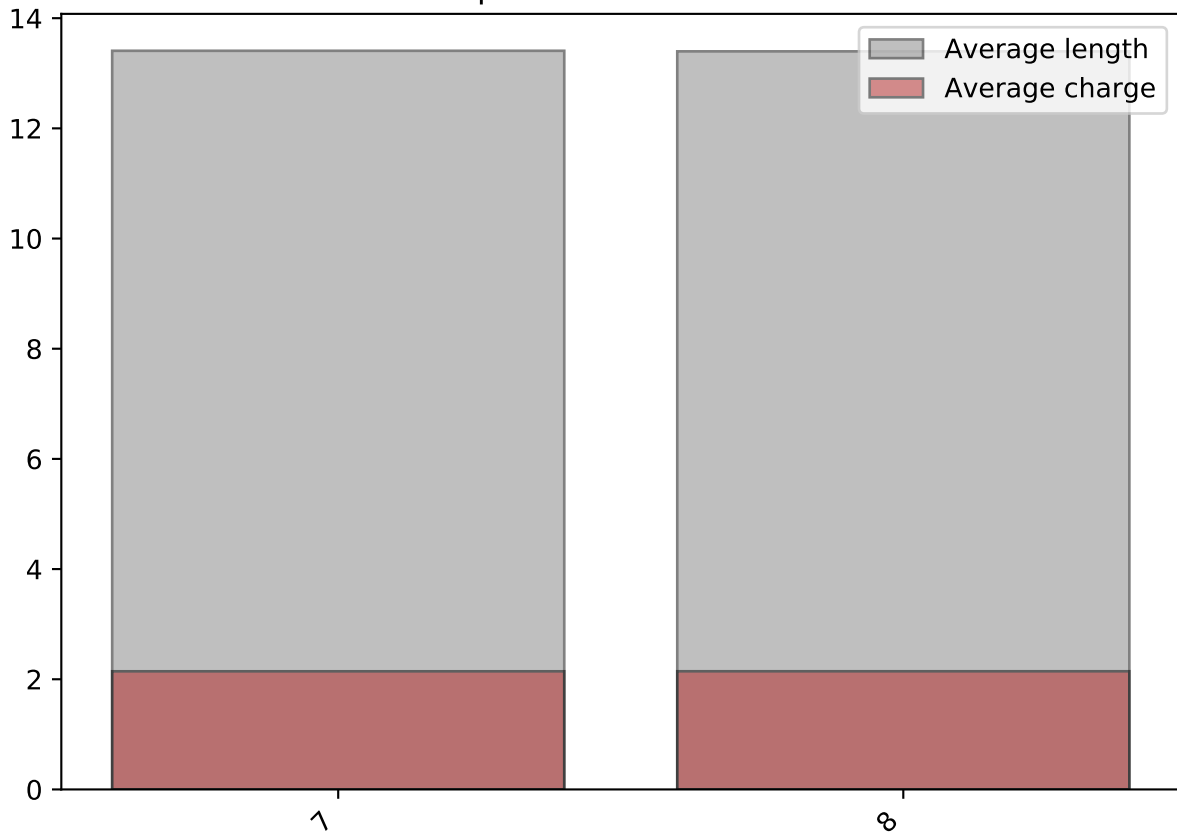
Median mass accuracy, MS2, ppm



Median mass accuracy, MS1, ppm

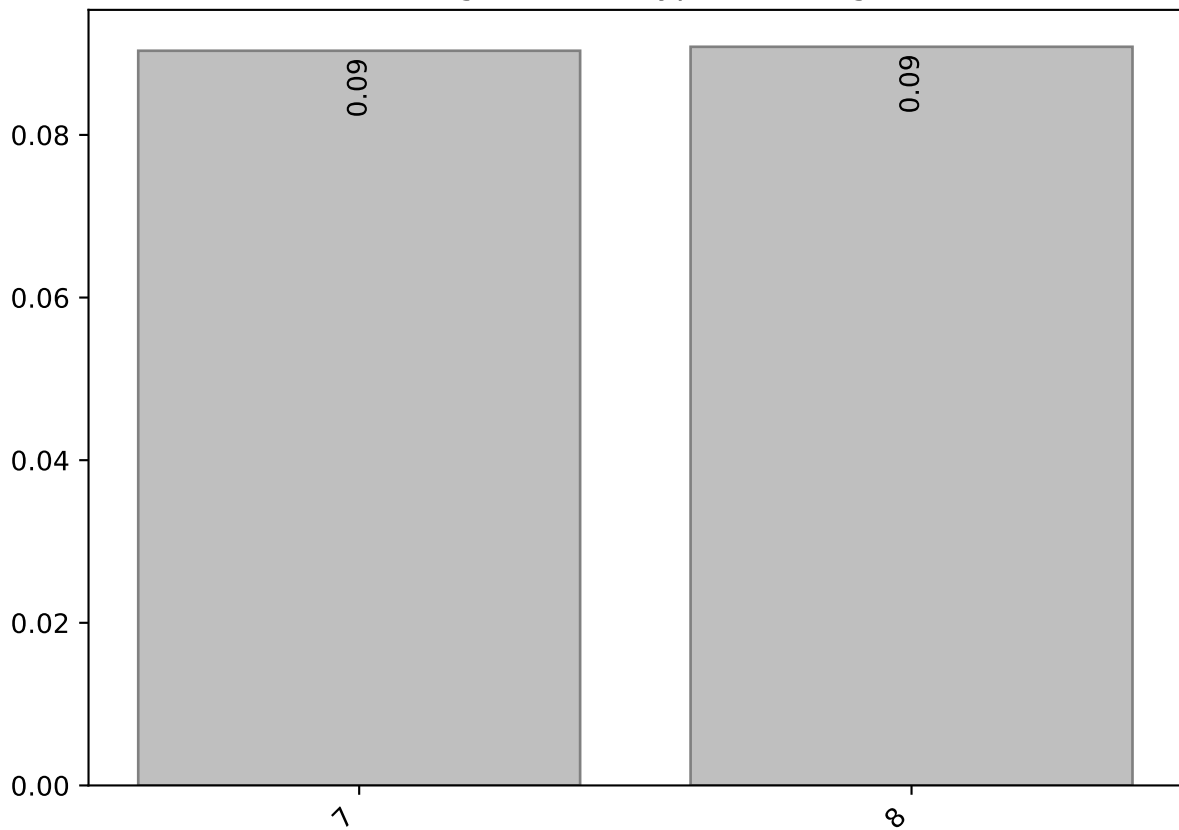


Peptide characteristics

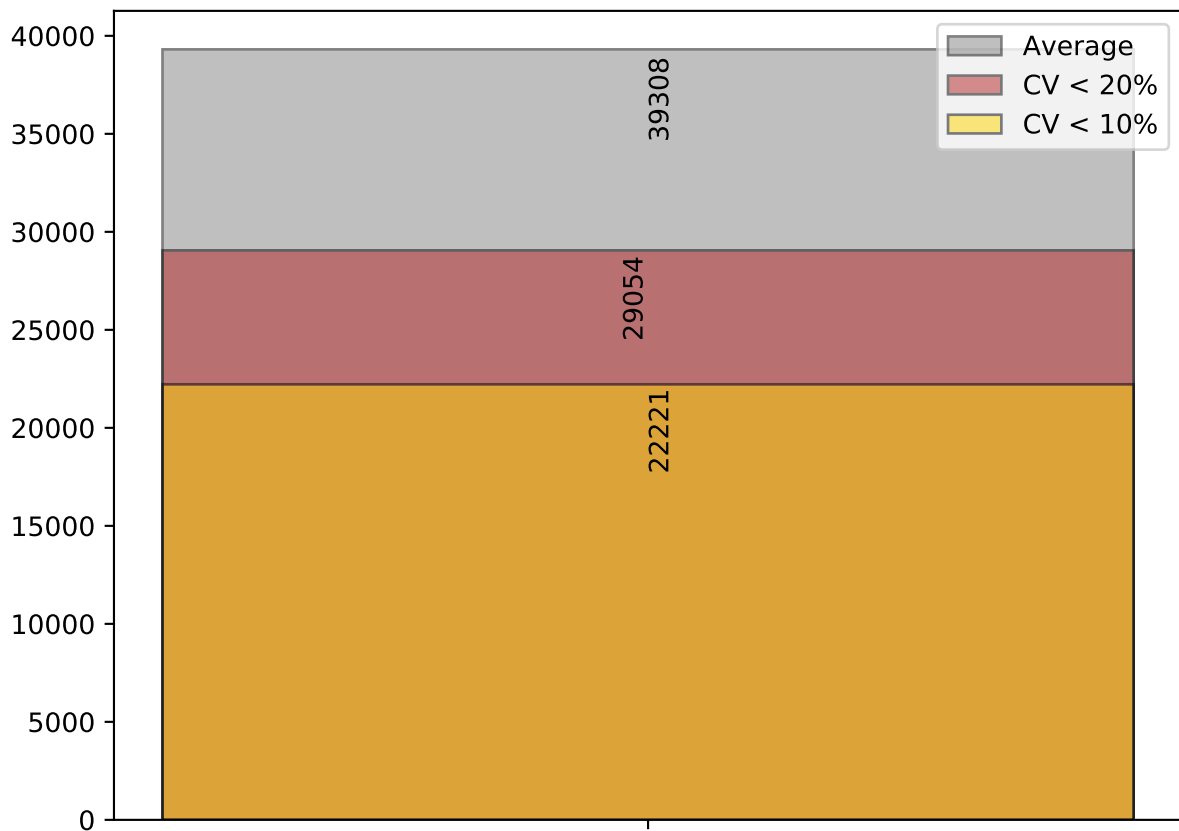




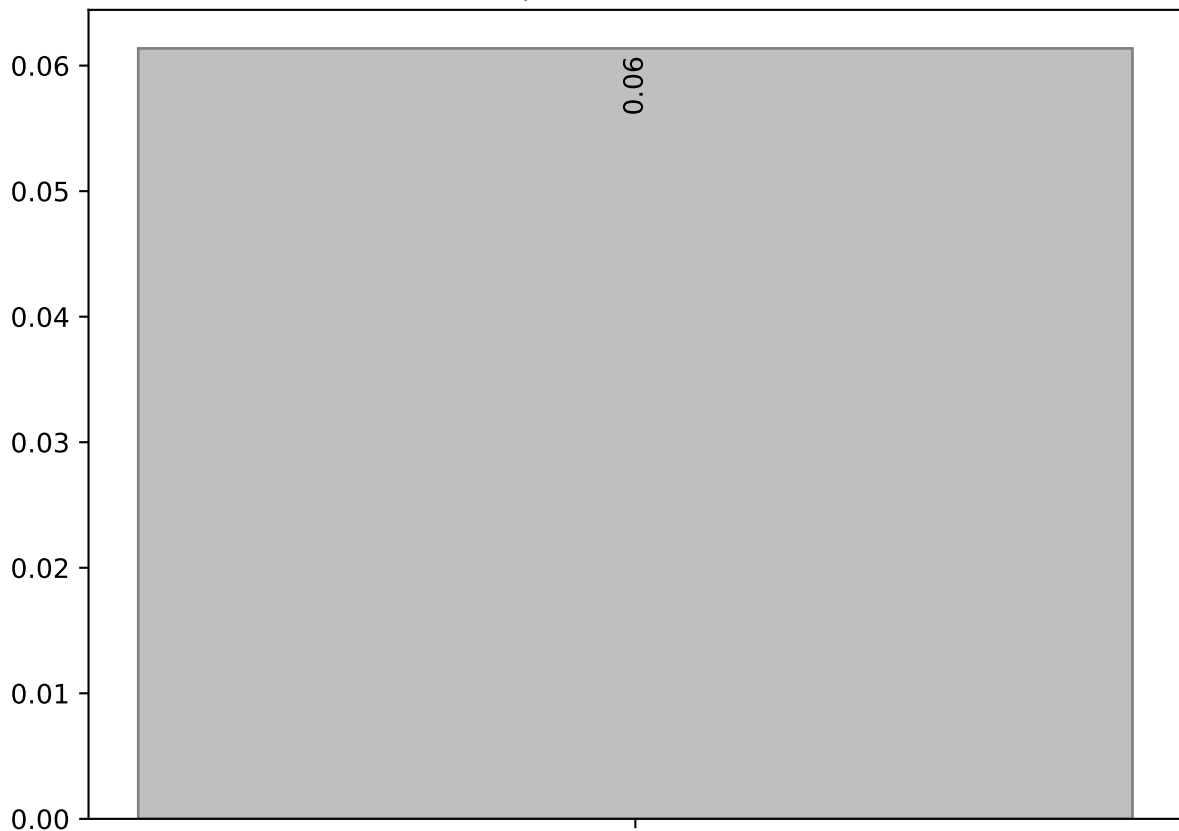
Average missed tryptic cleavages



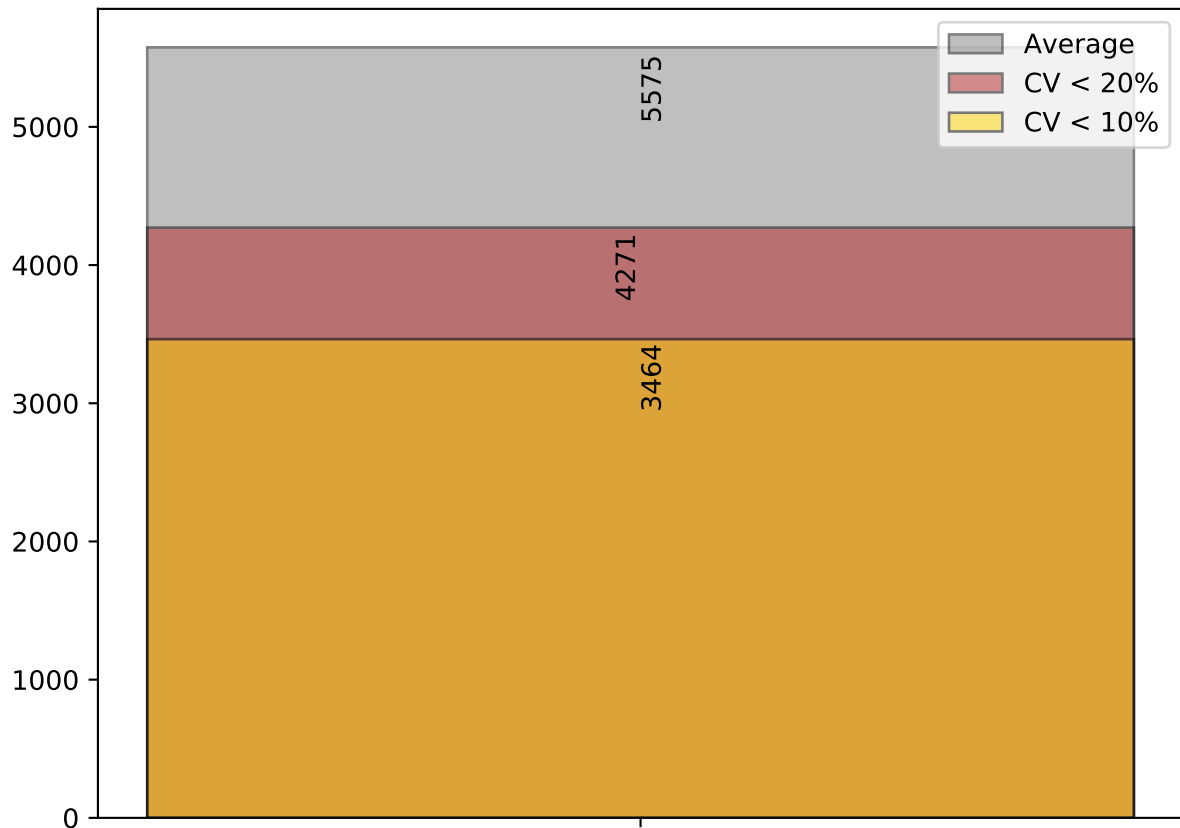
# Precursors, 1% FDR



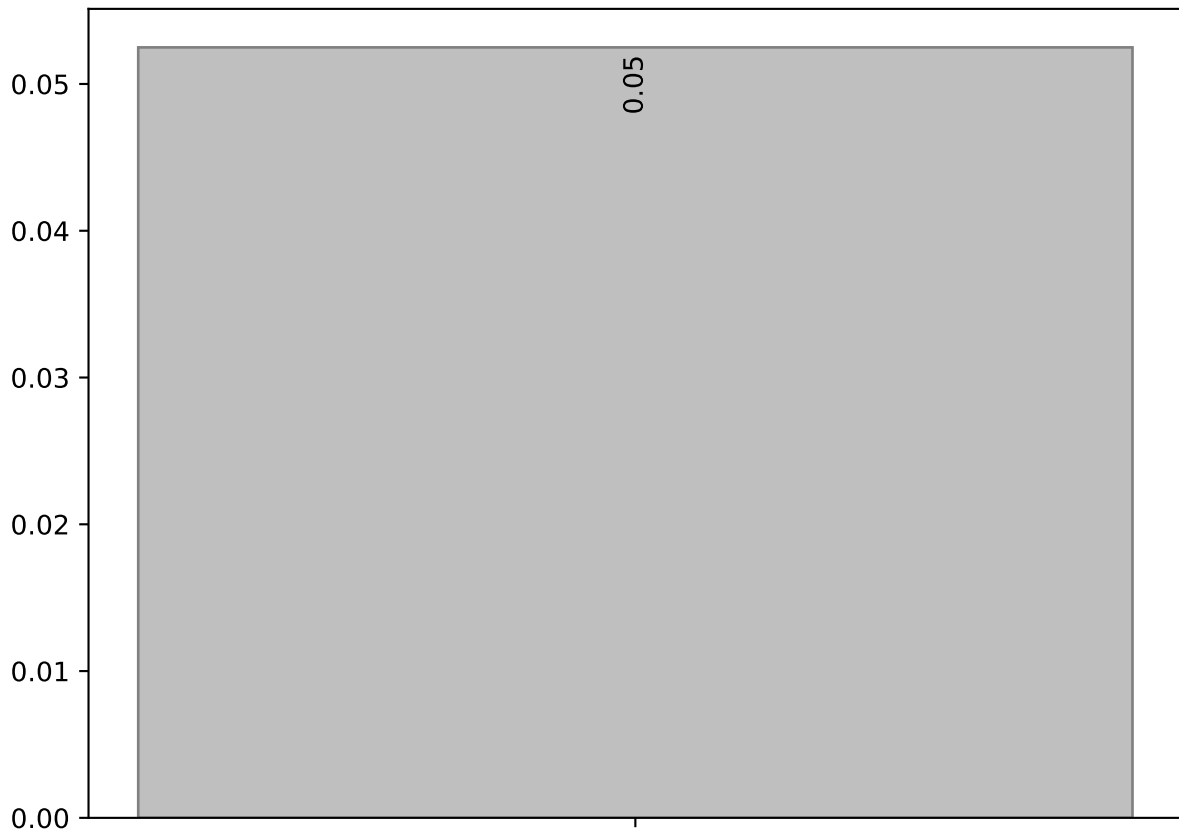
Median precursor CV, 1% FDR



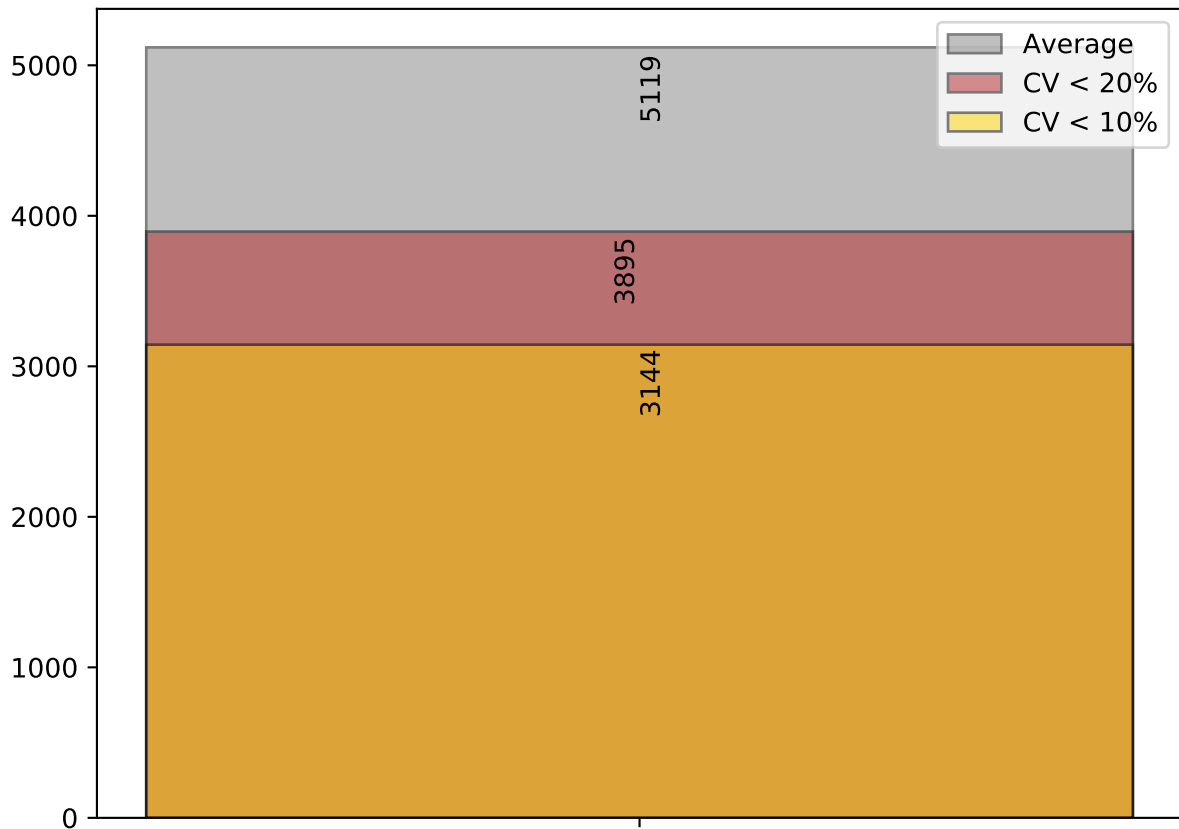
Protein groups, 1% precursor-level FDR



Median protein group CV, 1% precursor-level FDR



Unqie genes, 1% precursor-level FDR



Median gene CV, 1% precursor-level FDR

