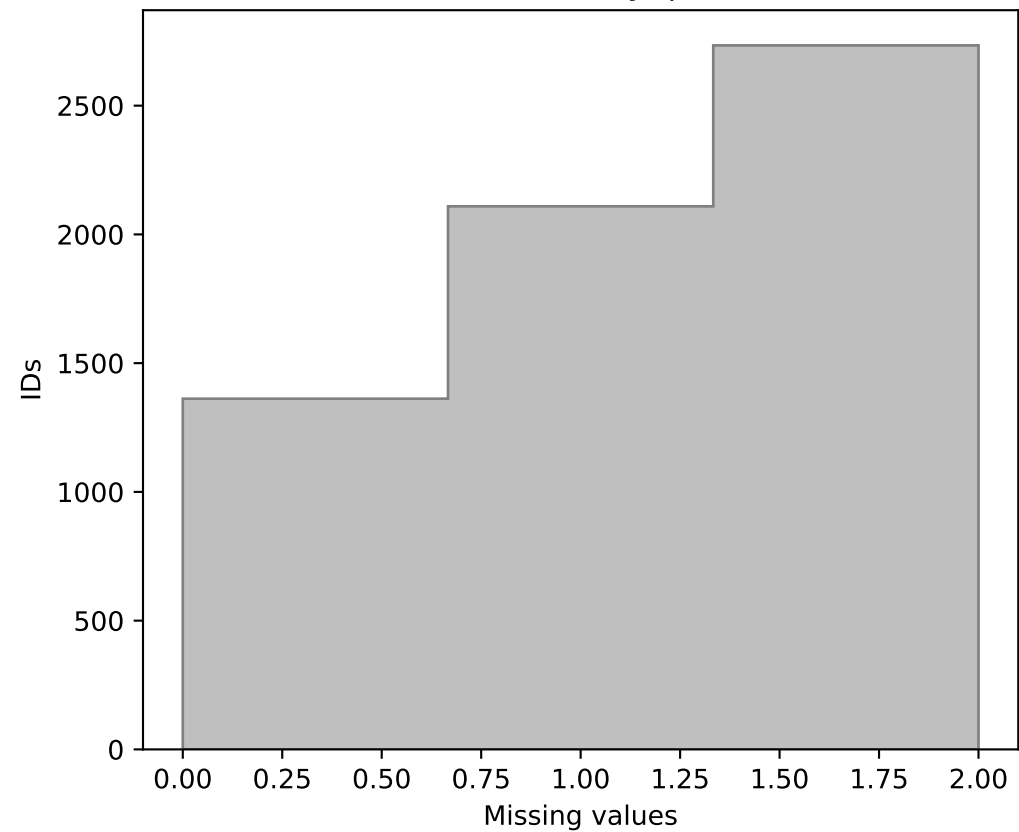
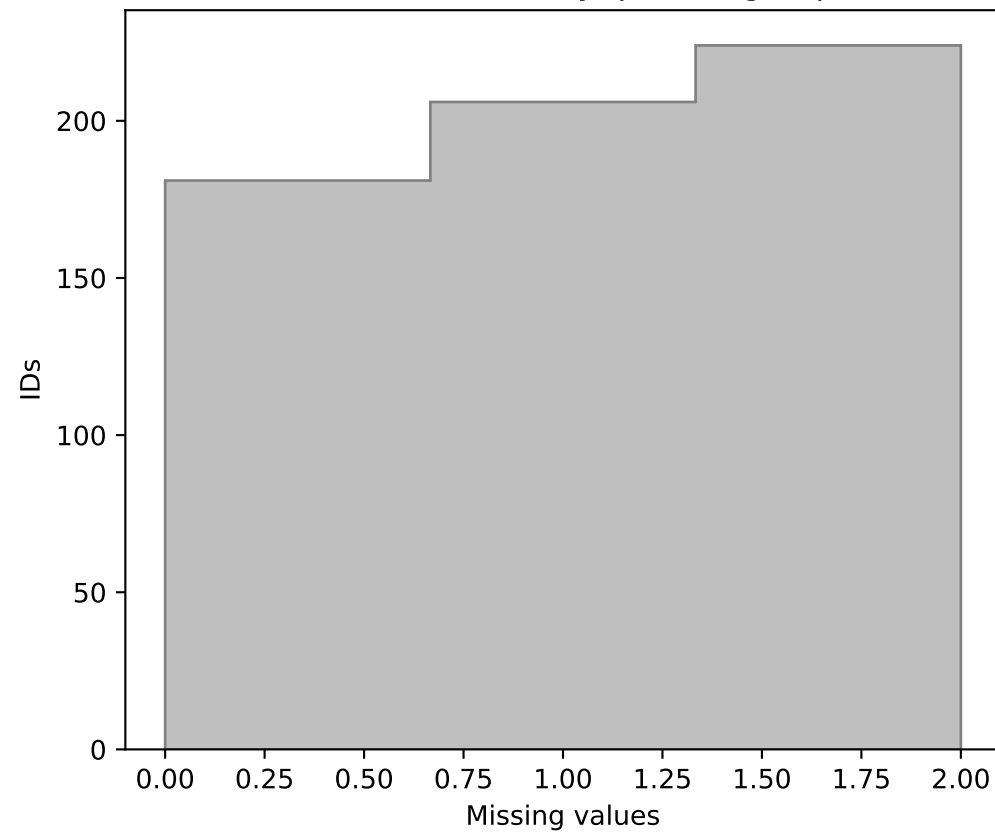


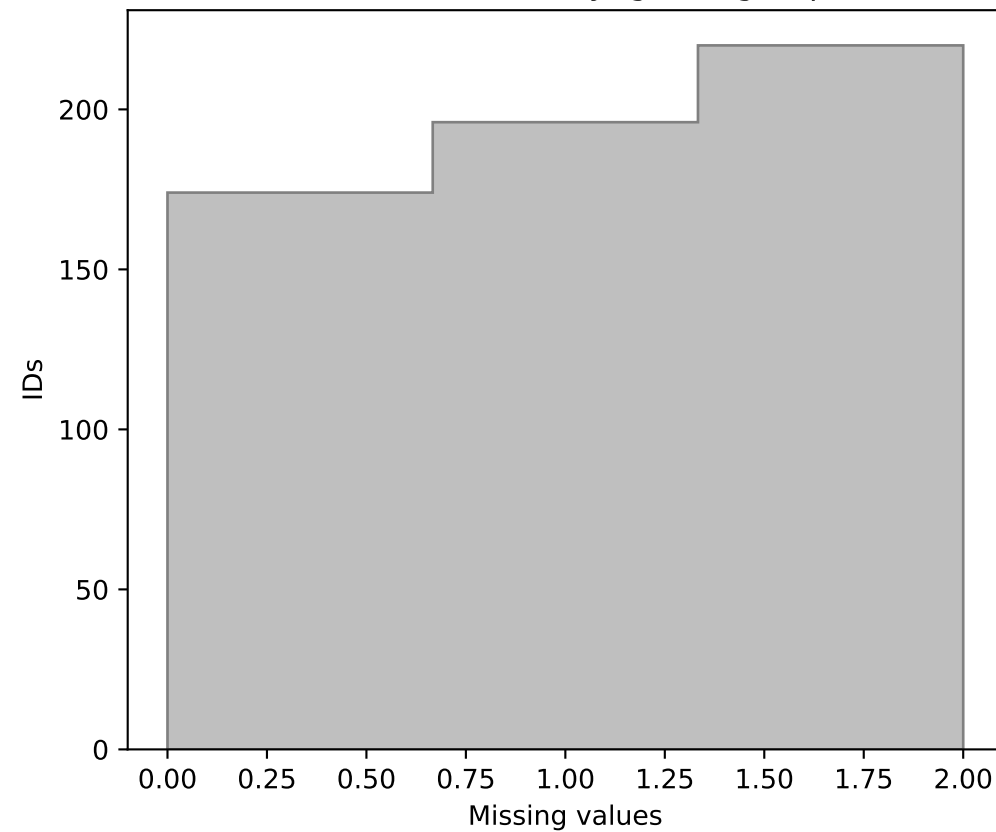
Identification consistency: precursors, CDF



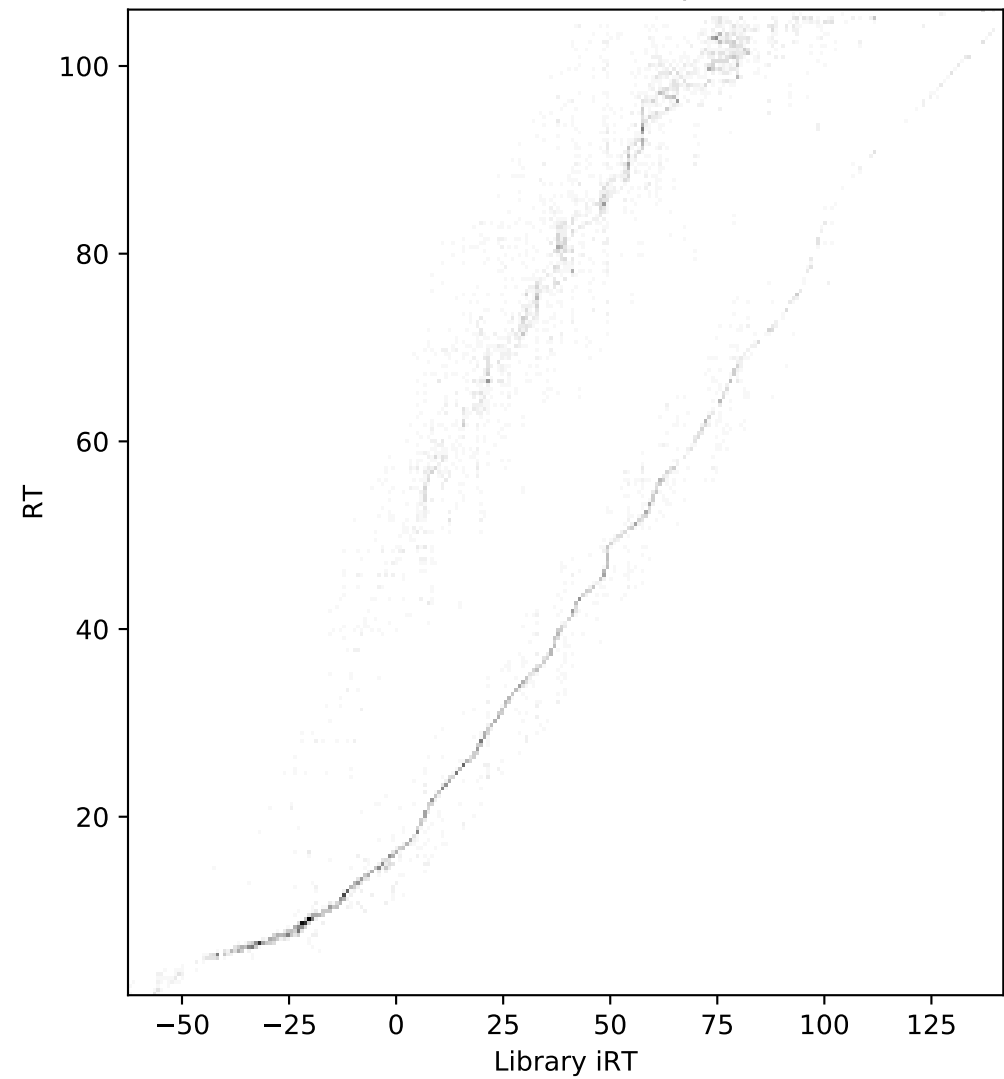
Identification consistency: protein groups, CDF



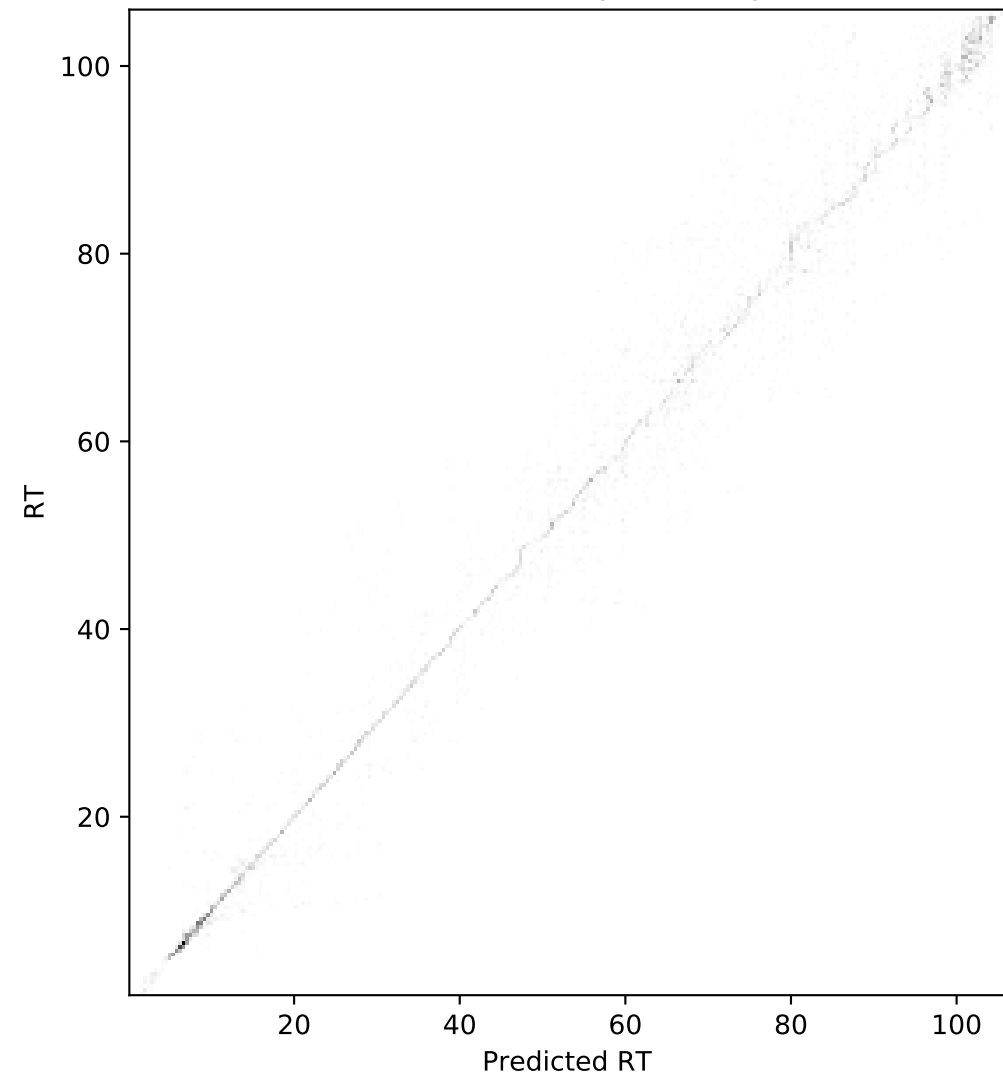
Identification consistency: genes groups, CDF



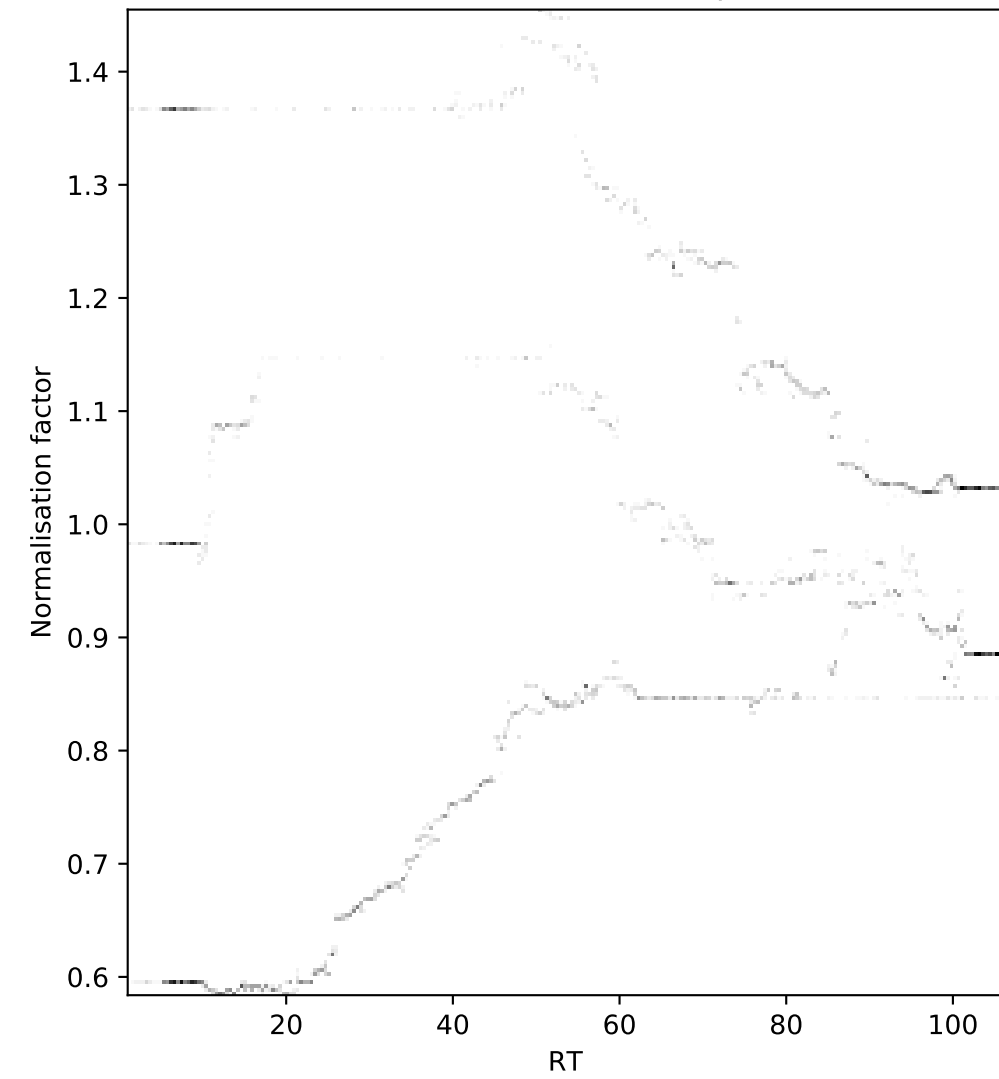
Retention times heatmap, all runs

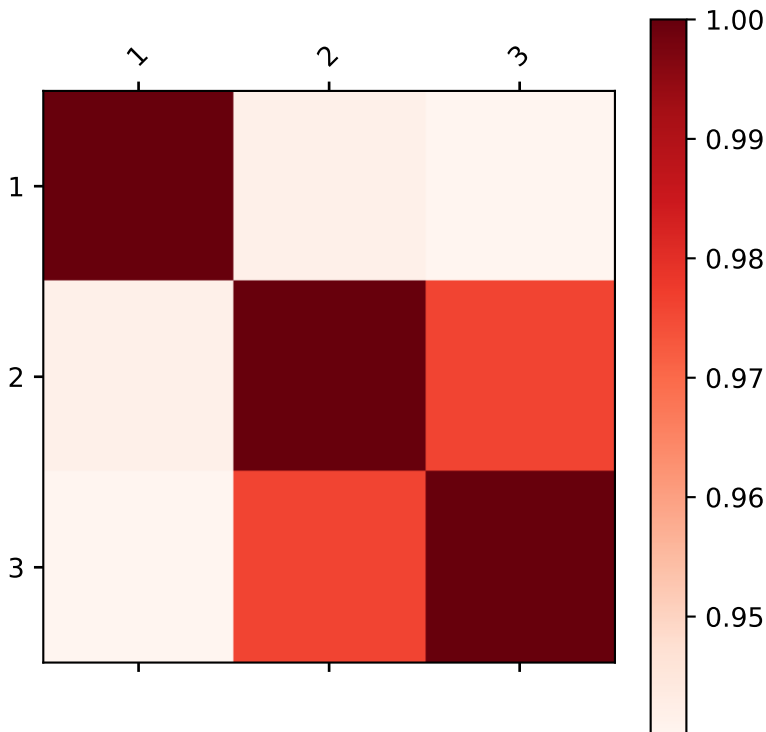


Retention time accuracy heatmap, all runs

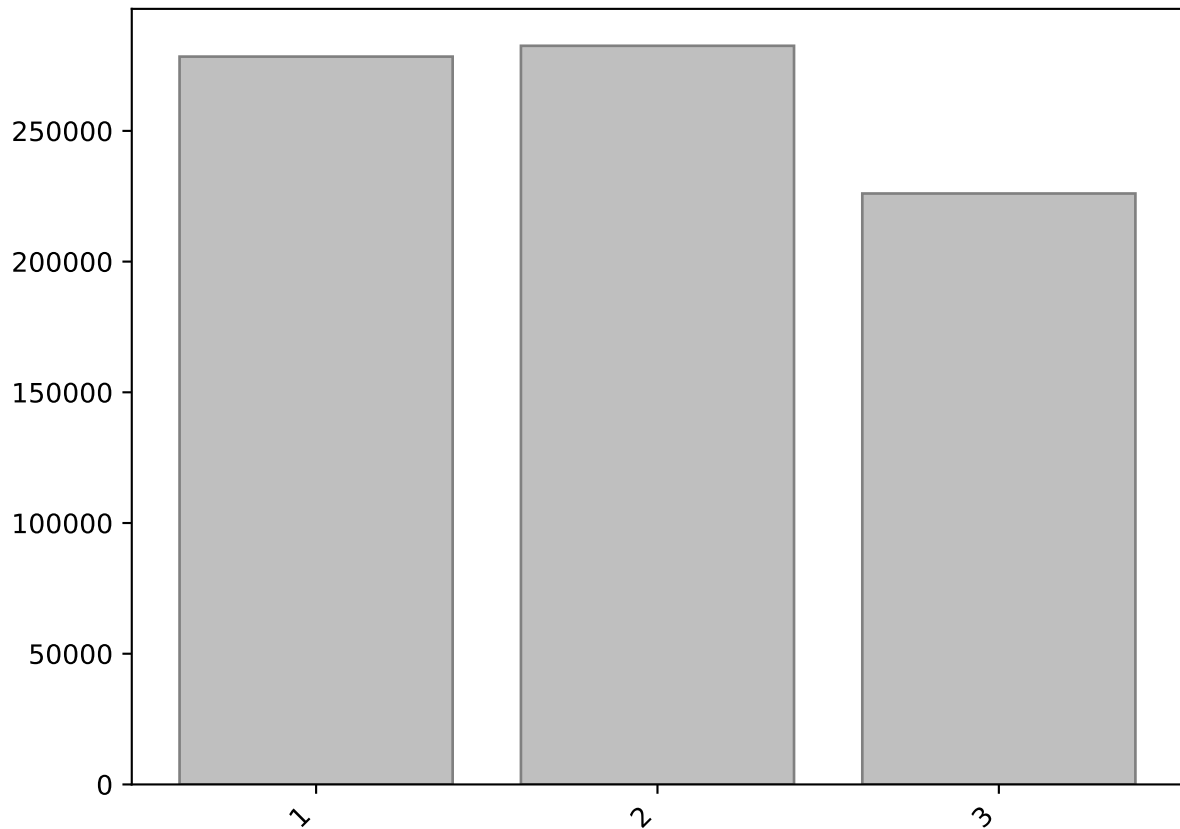


Normalisation factor heatmap, all runs

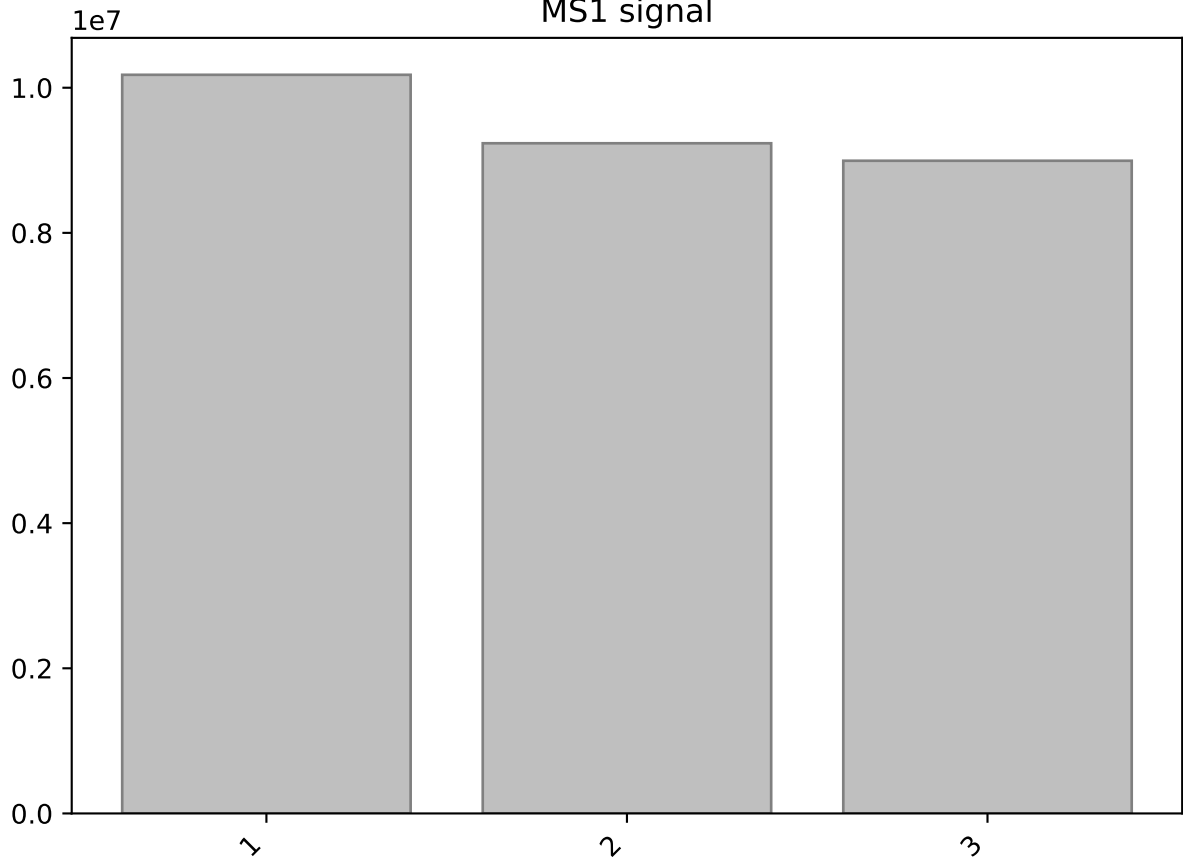




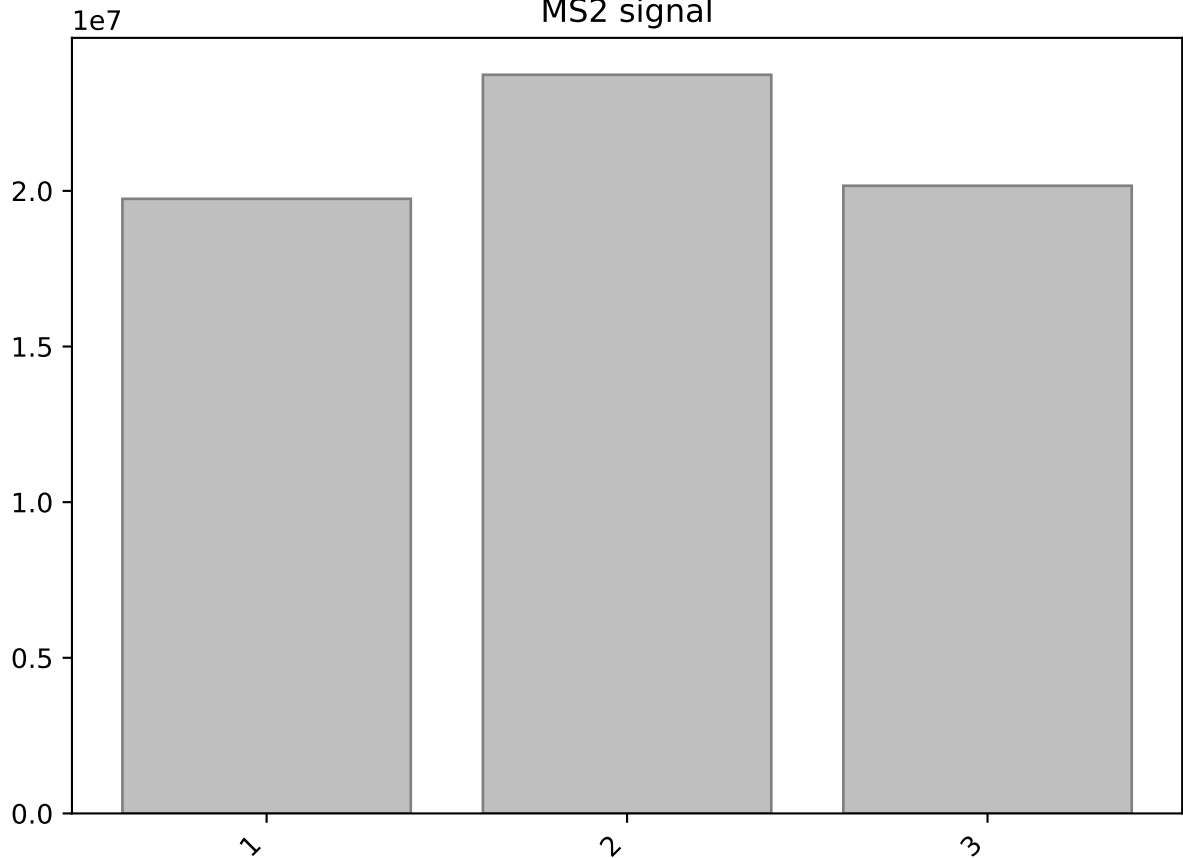
Total quantity, 1% FDR



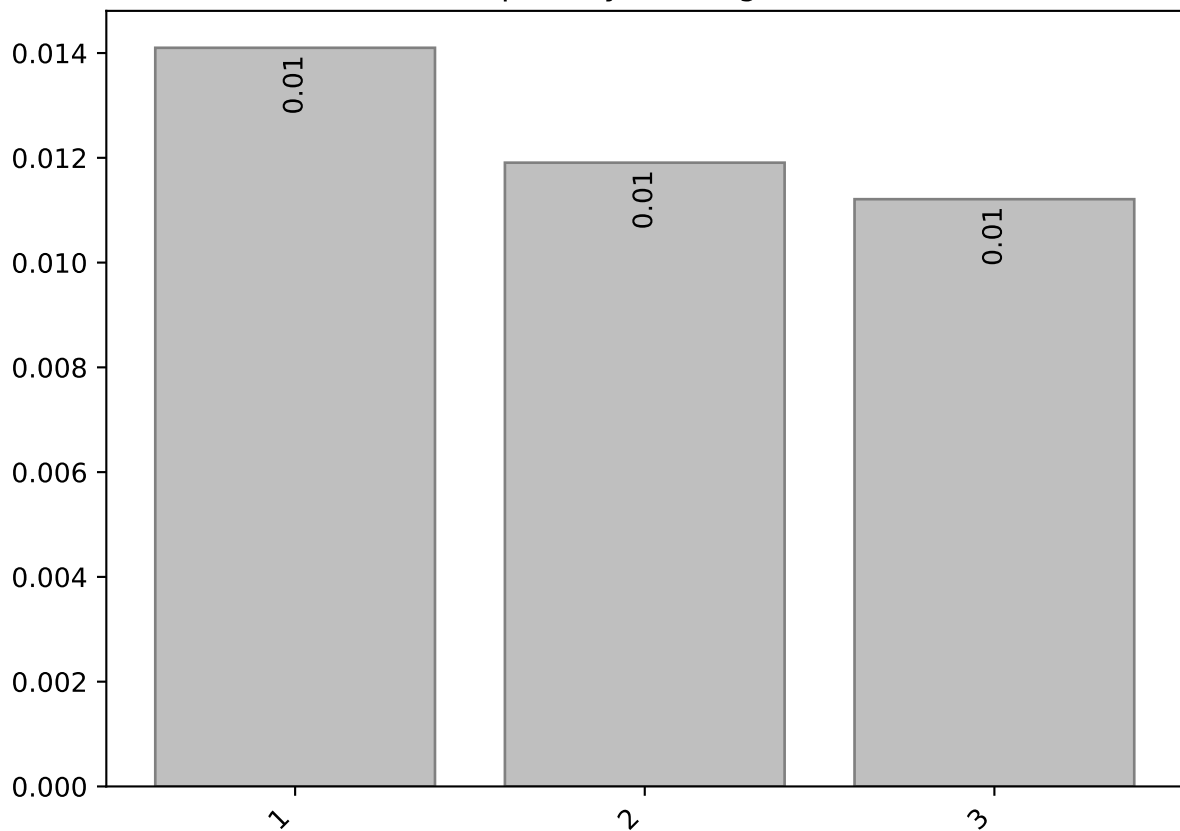
MS1 signal



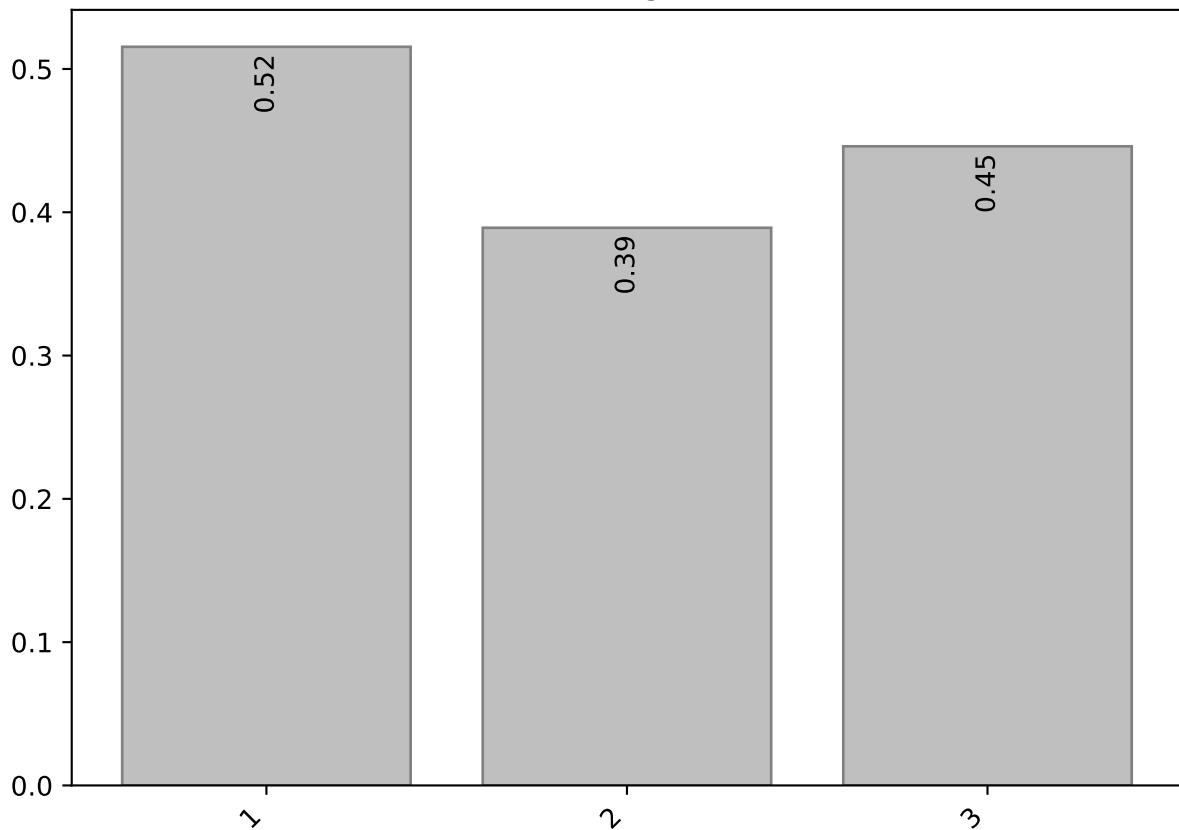
MS2 signal



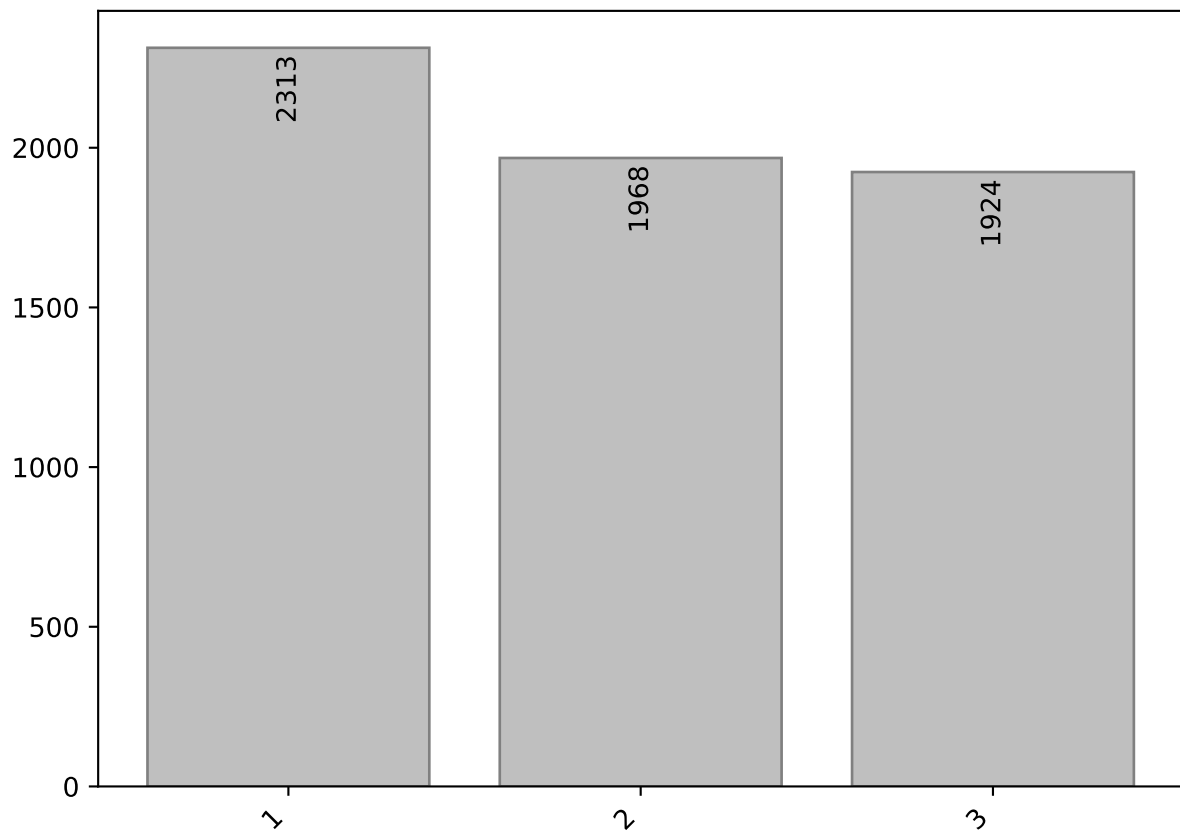
Total quantity/MS2 signal ratio



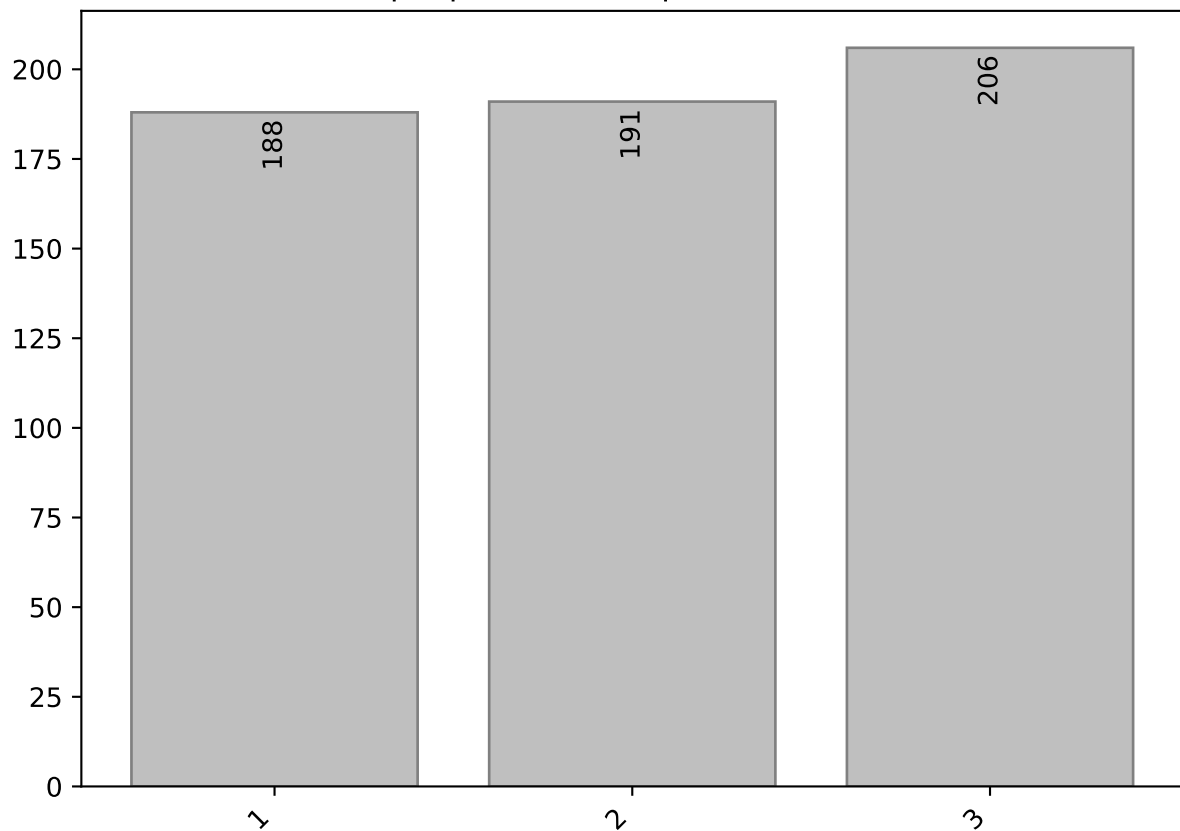
MS1/MS2 signal ratio



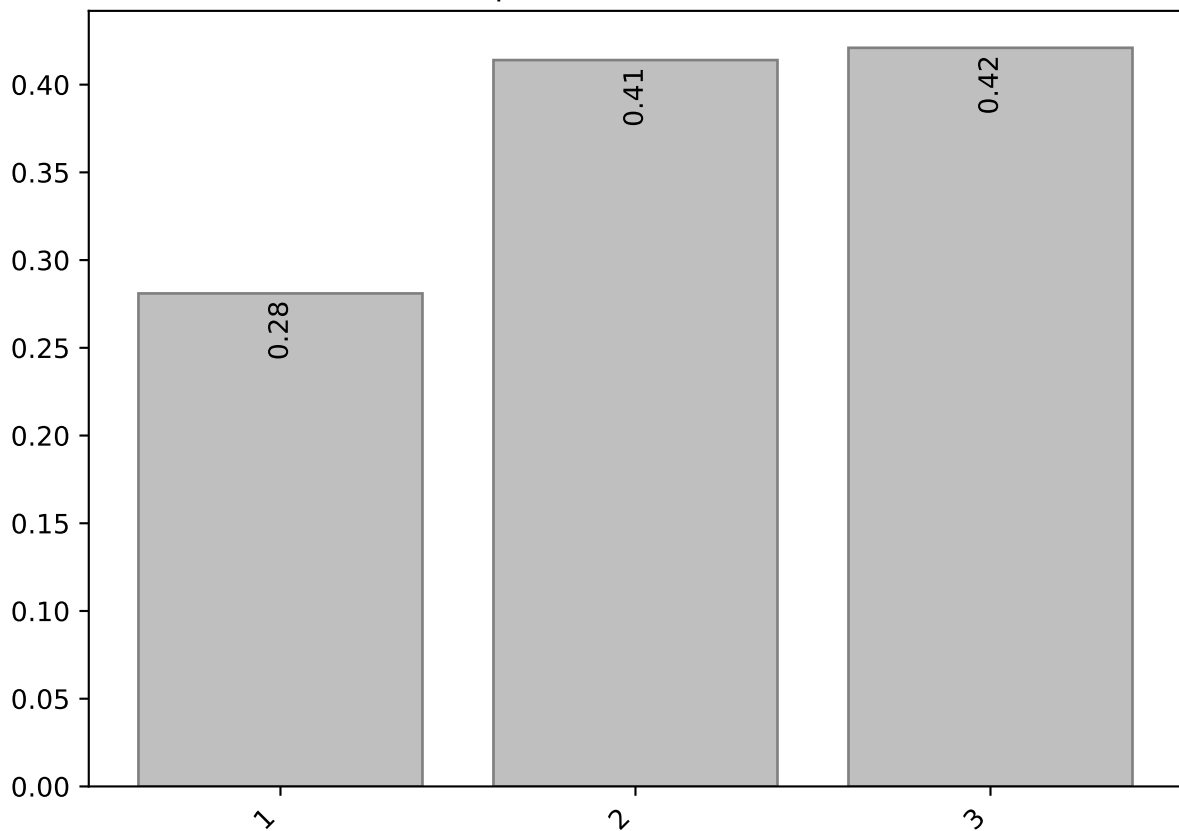
Precursors, 1% FDR



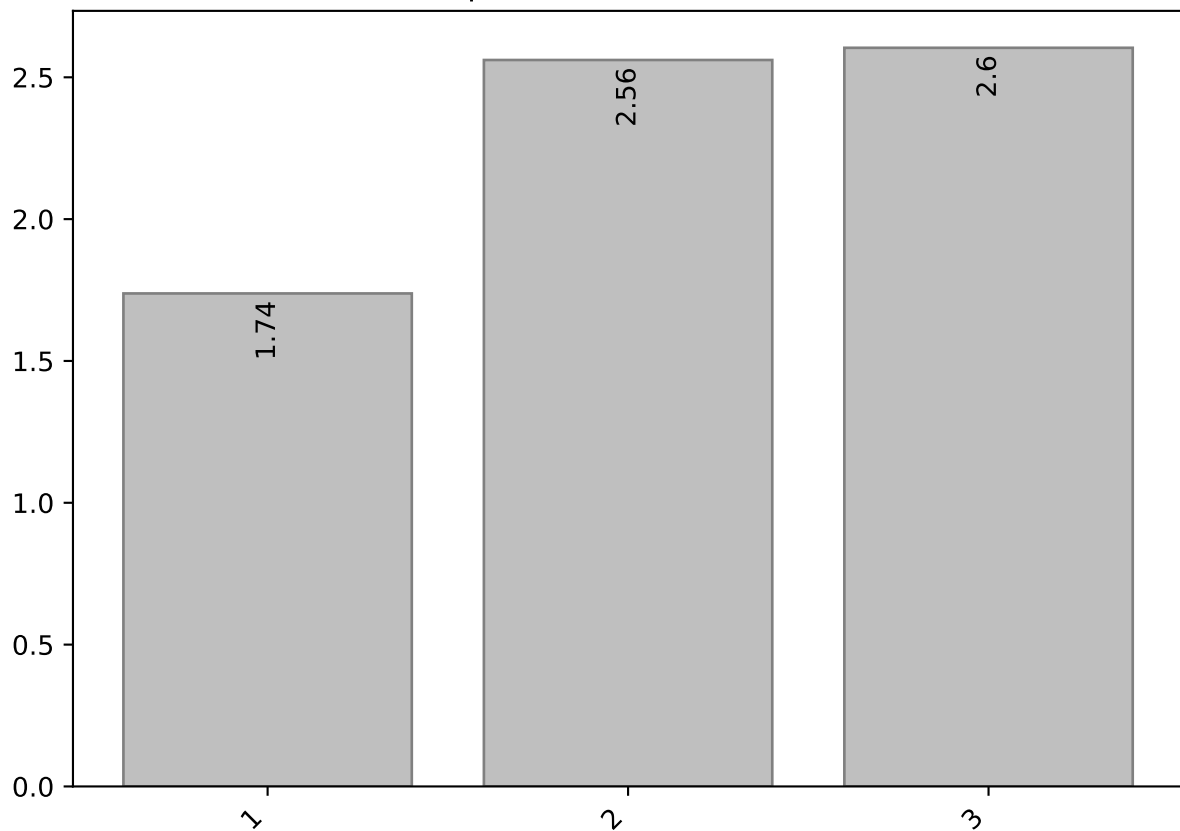
Unique proteins, 1% protein-level FDR



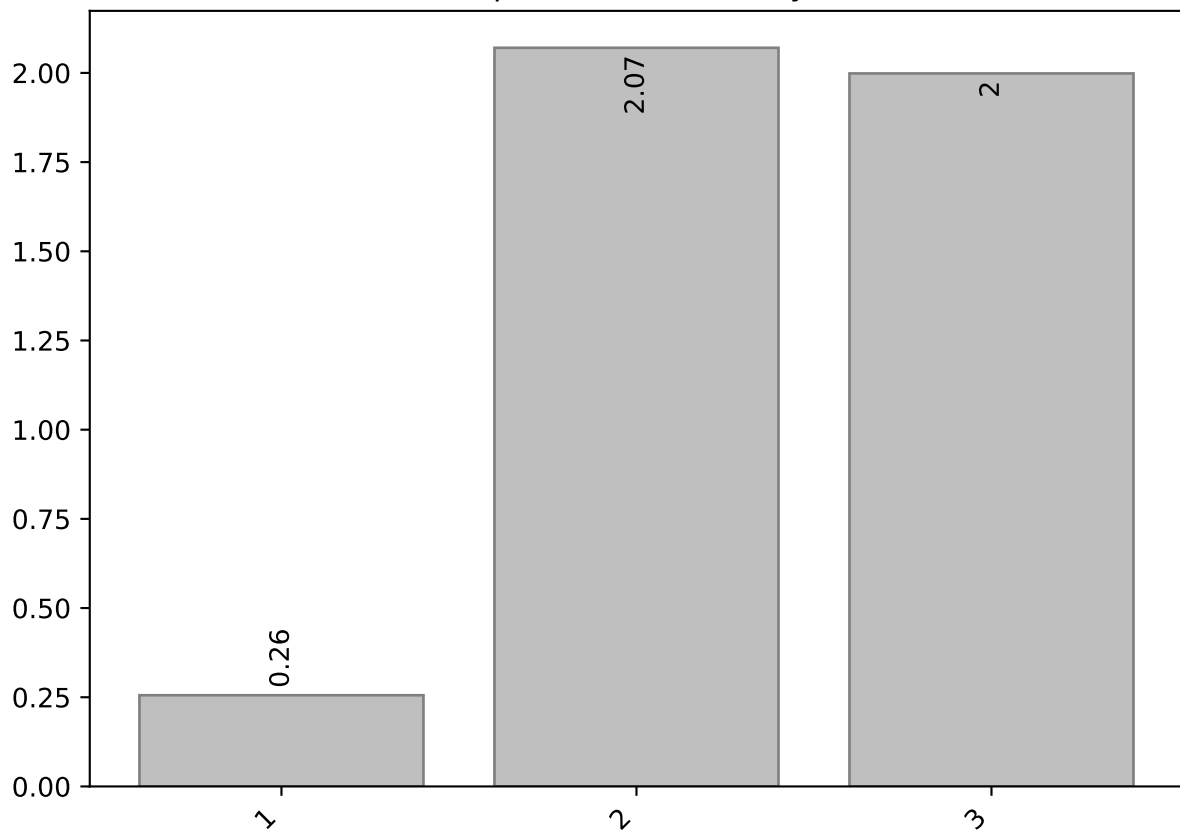
Mean peak FWHM, in minutes



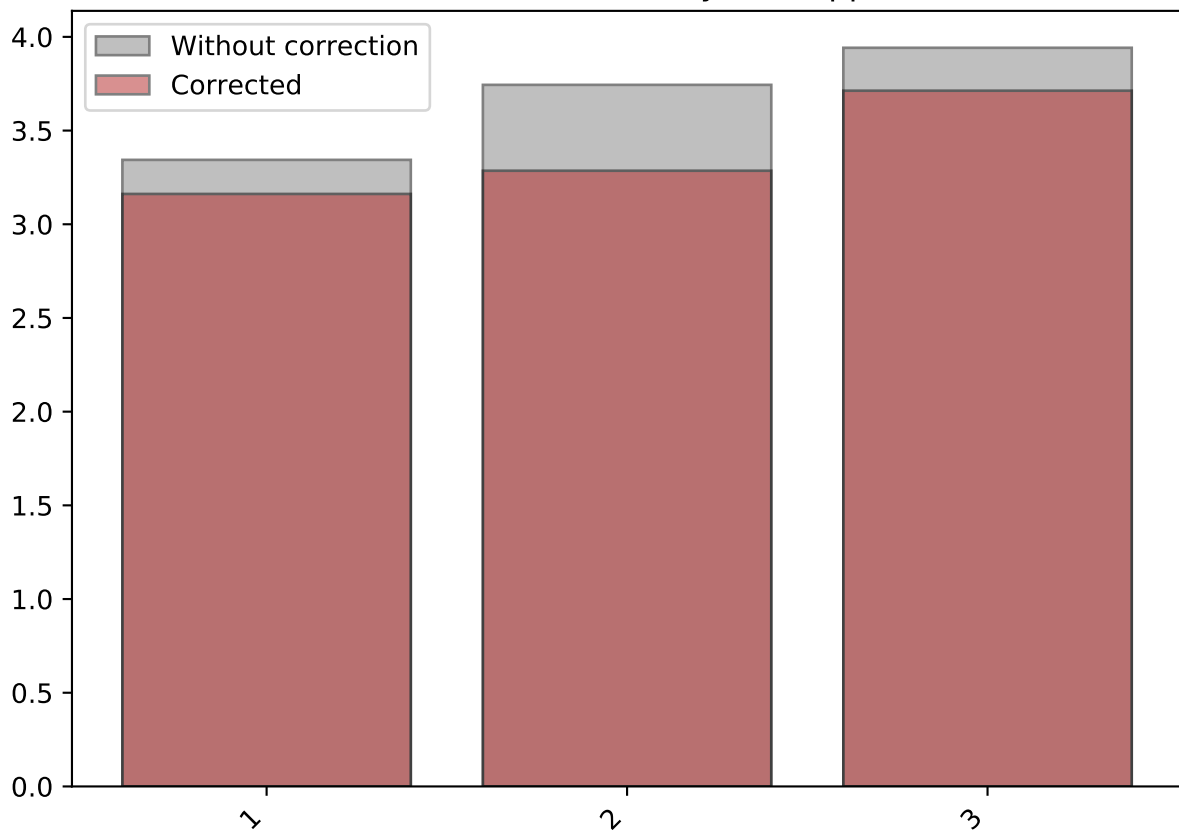
Mean peak FWHM, in MS2 scans



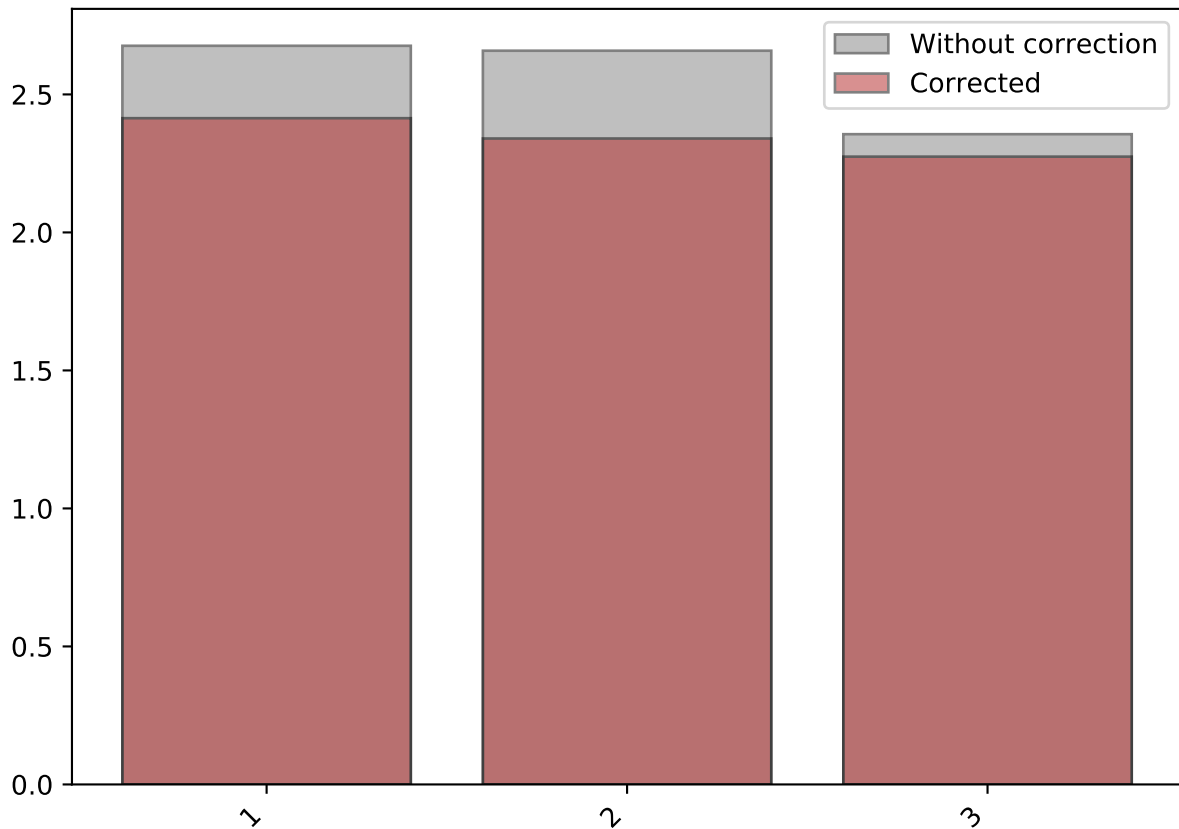
Median RT prediction accuracy, minutes



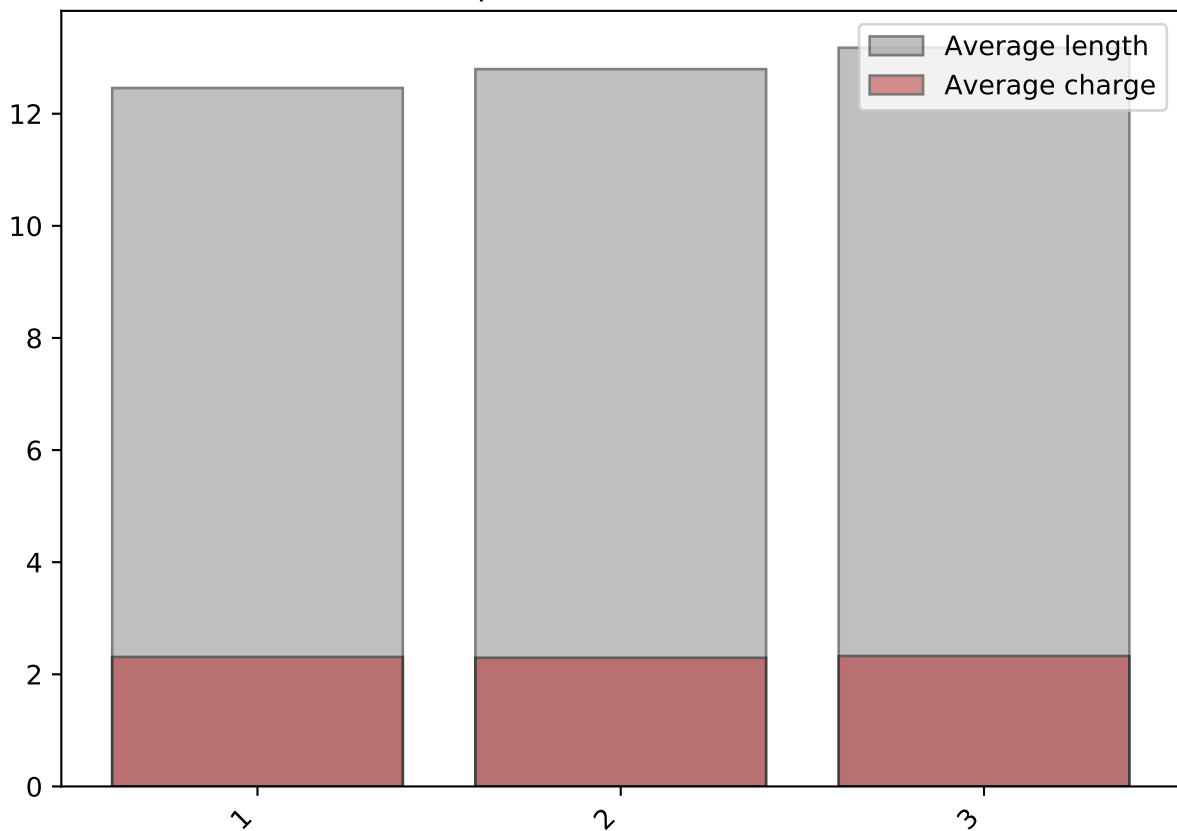
Median mass accuracy, MS2, ppm



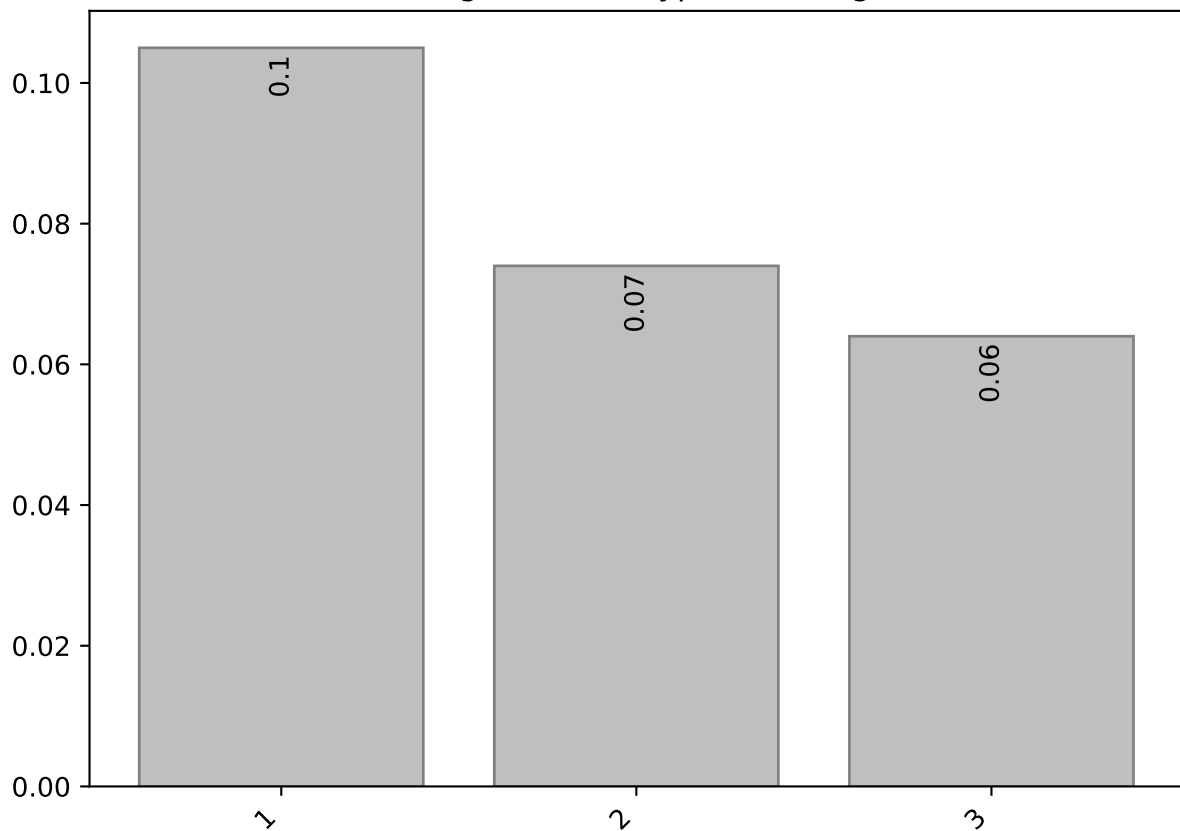
Median mass accuracy, MS1, ppm



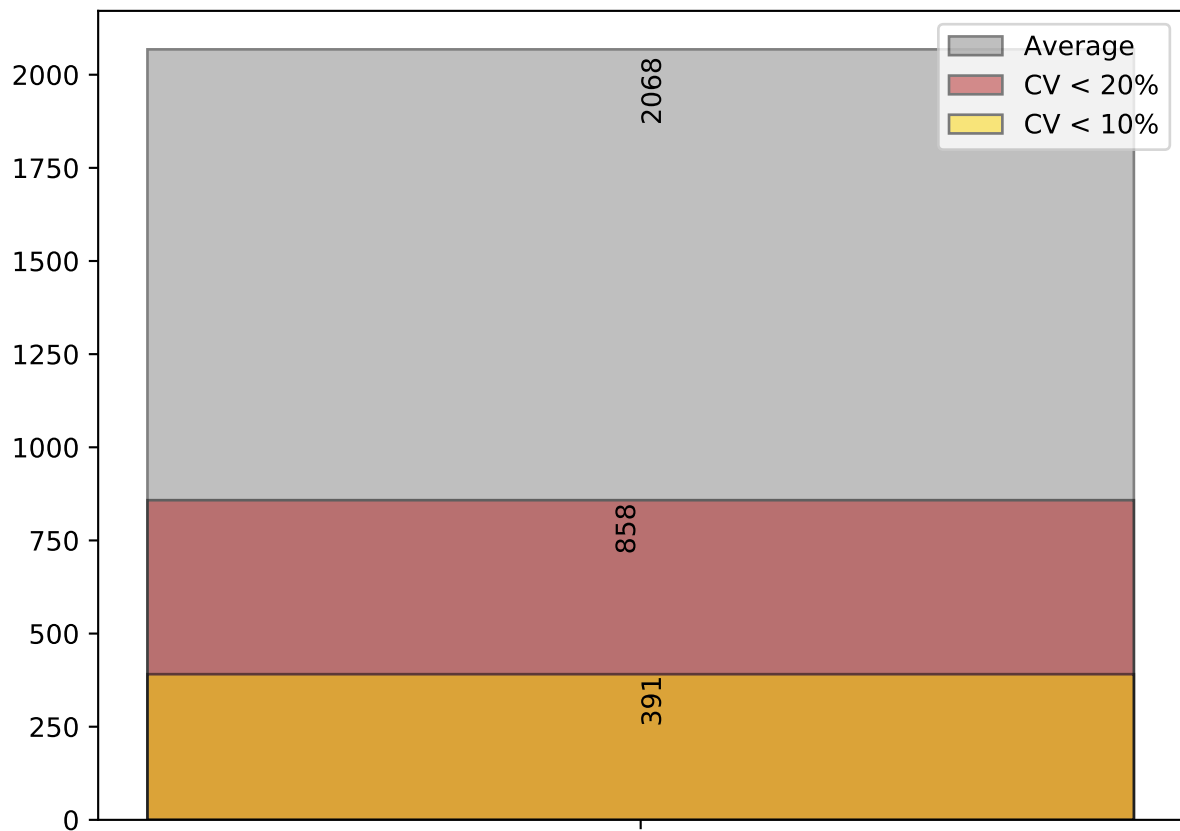
Peptide characteristics



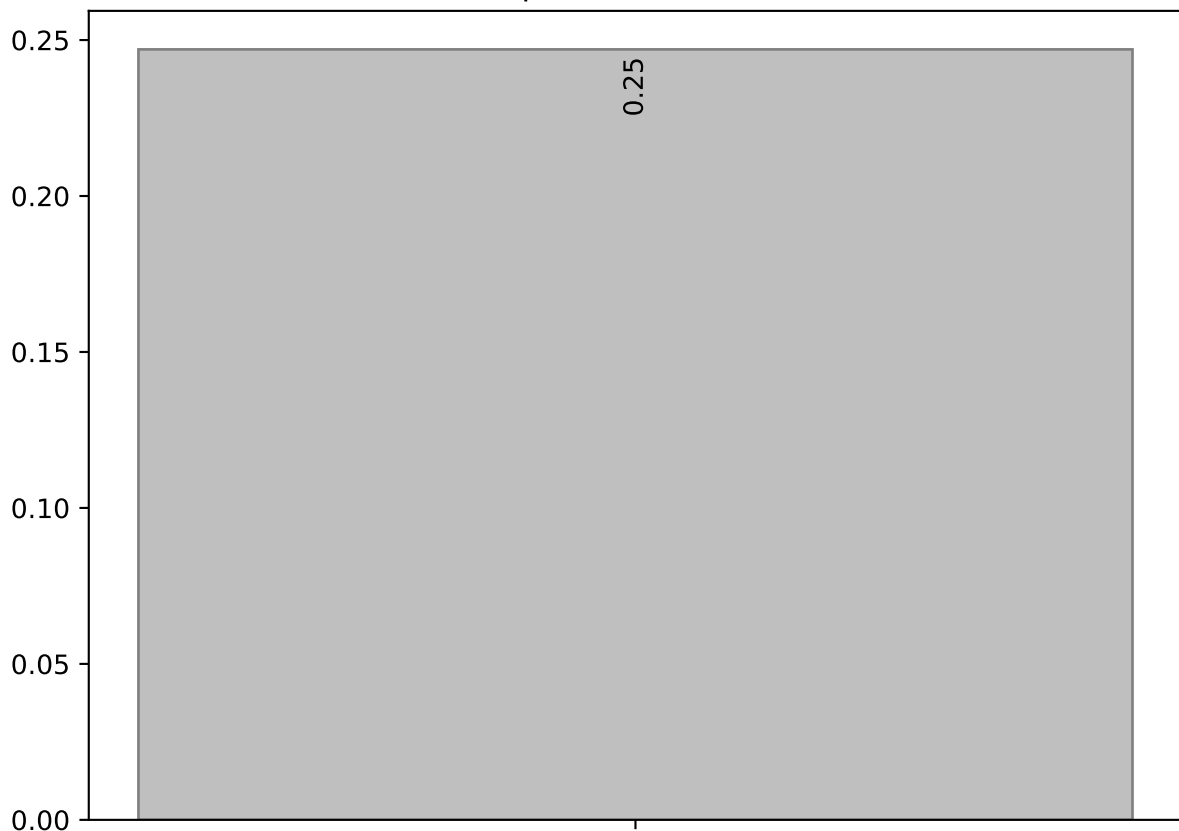
Average missed tryptic cleavages



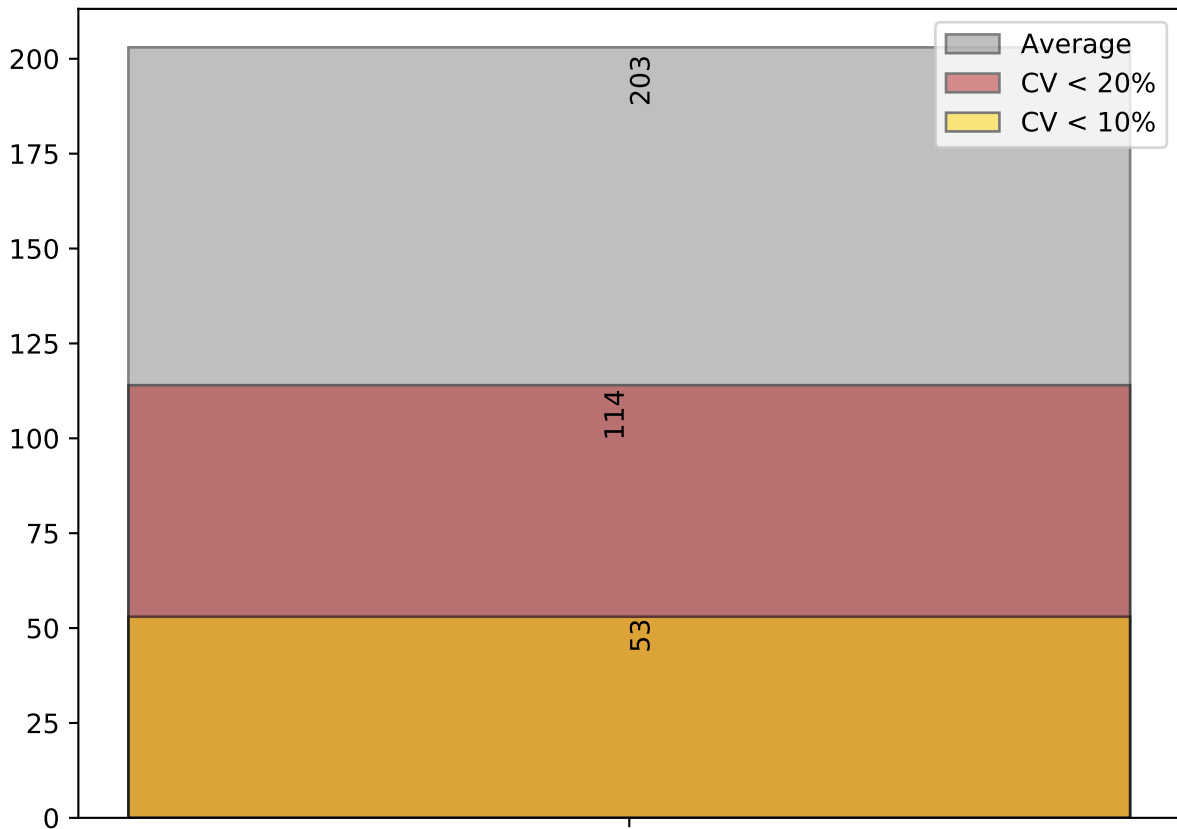
Precursors, 1% FDR



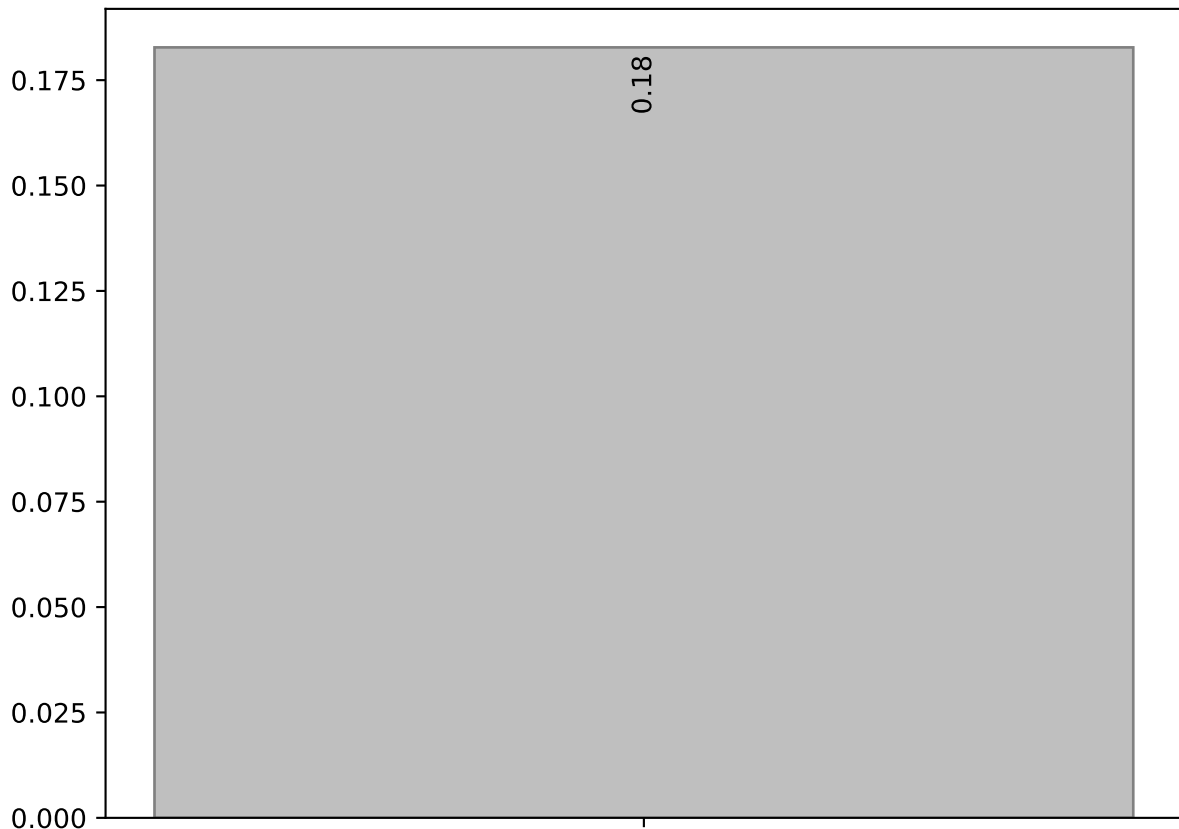
Median precursor CV, 1% FDR



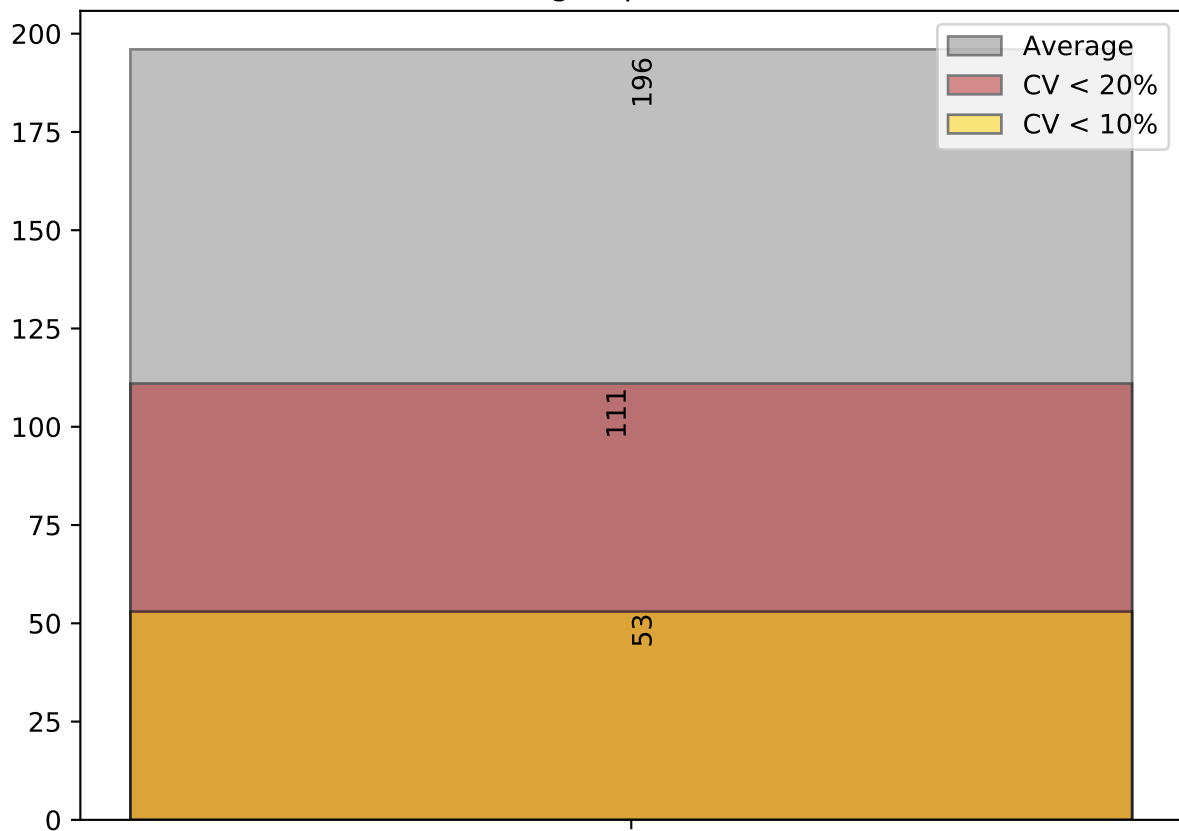
Protein groups, 1% FDR



Median protein group CV, 1% FDR



Gene groups, 1% FDR



Median gene group CV, 1% FDR

