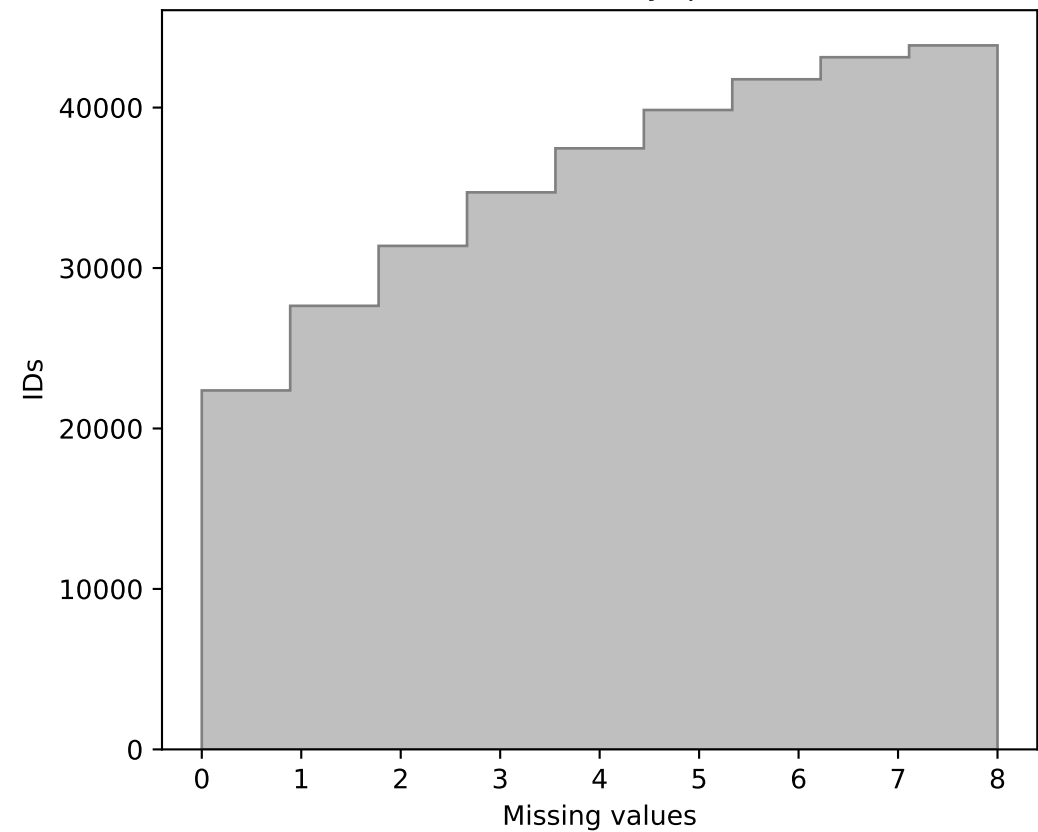
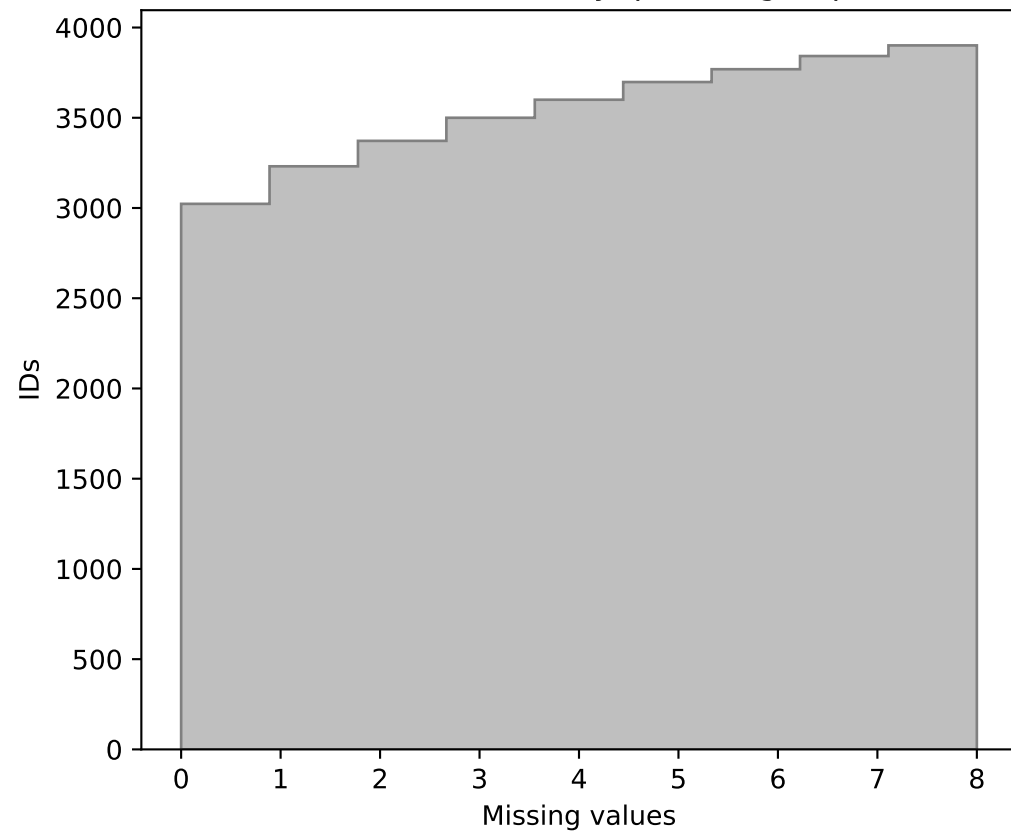


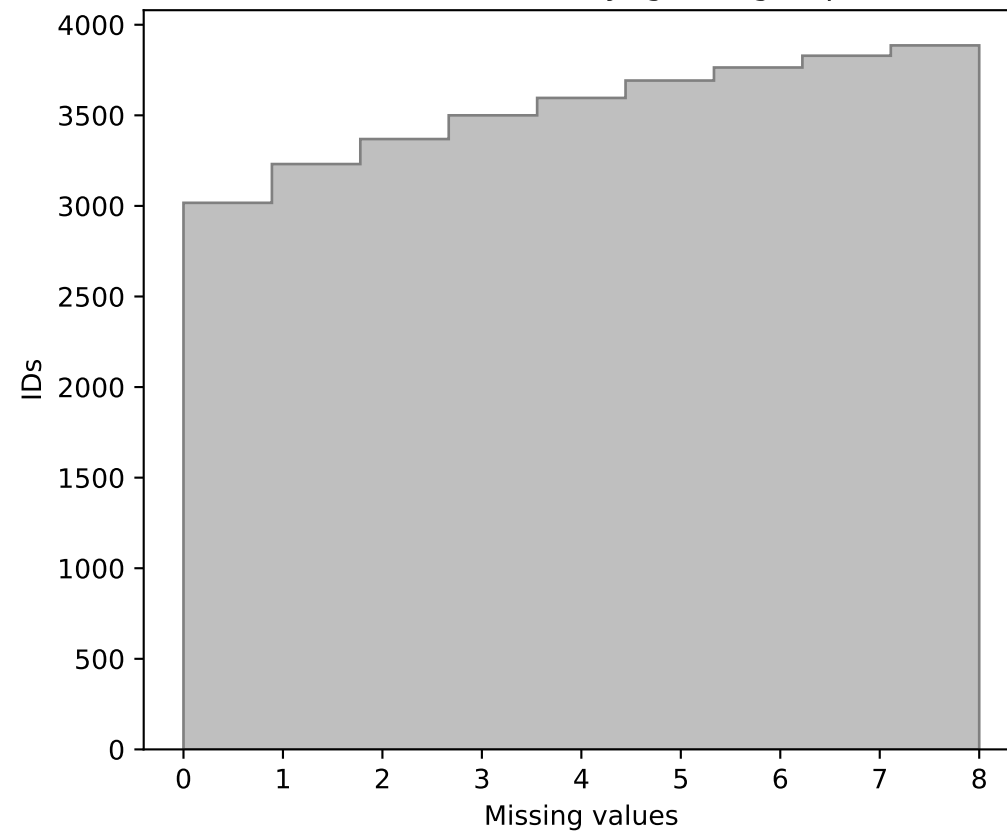
Identification consistency: precursors, CDF



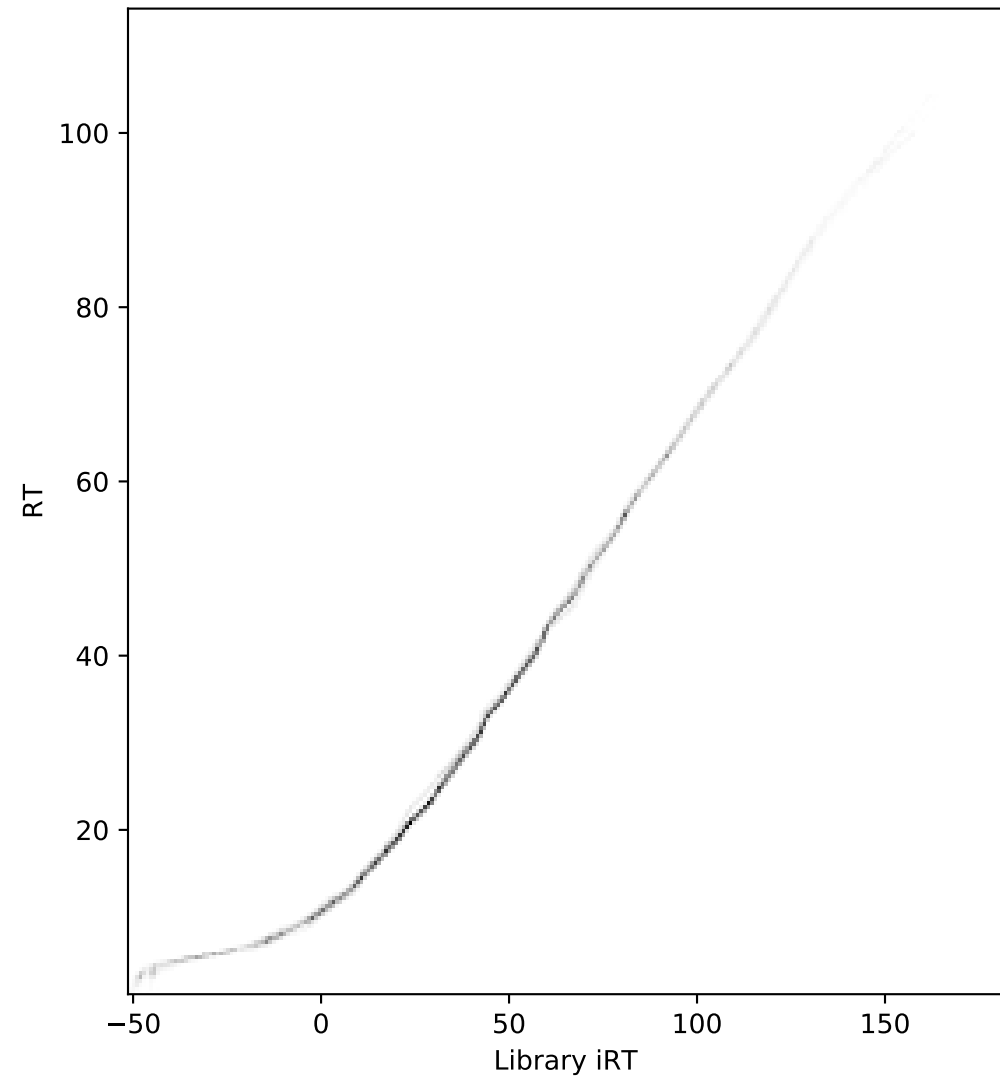
Identification consistency: protein groups, CDF



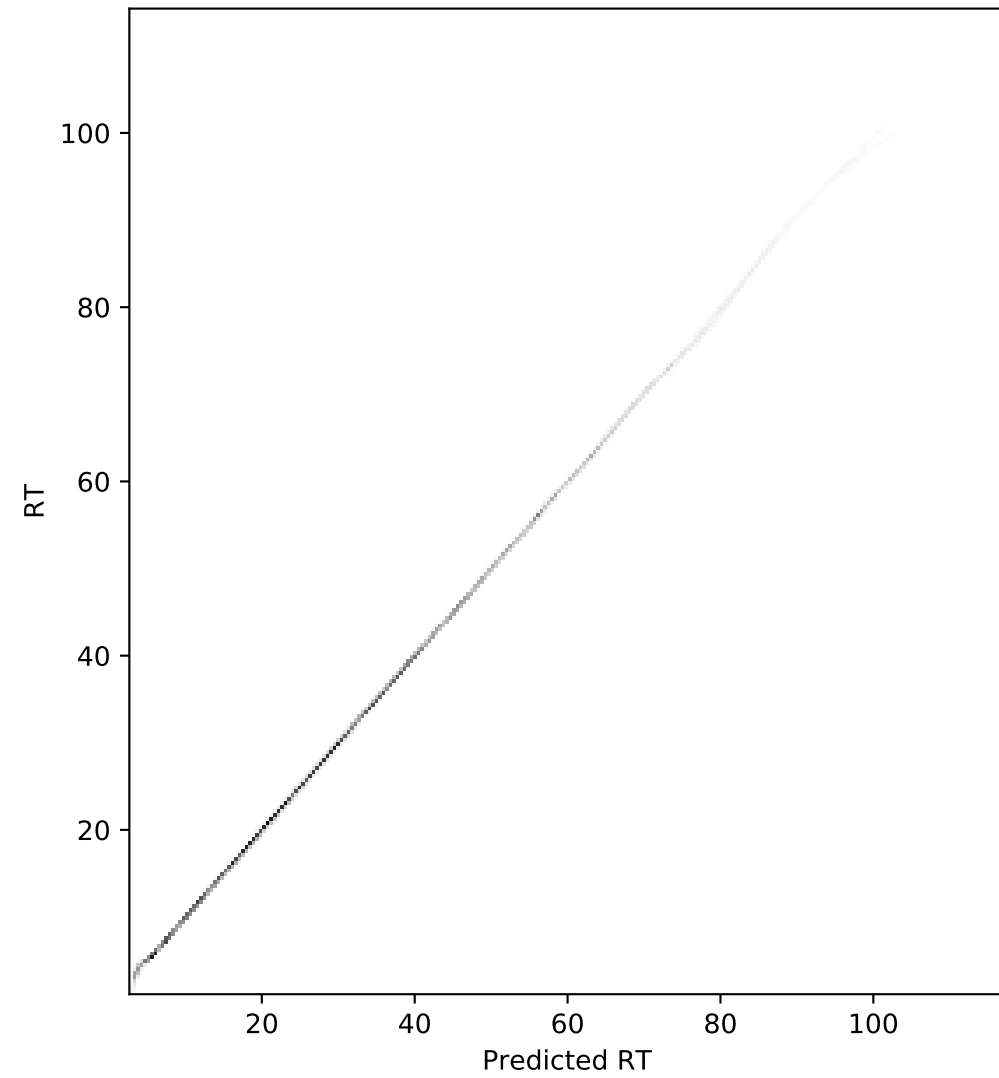
Identification consistency: genes groups, CDF



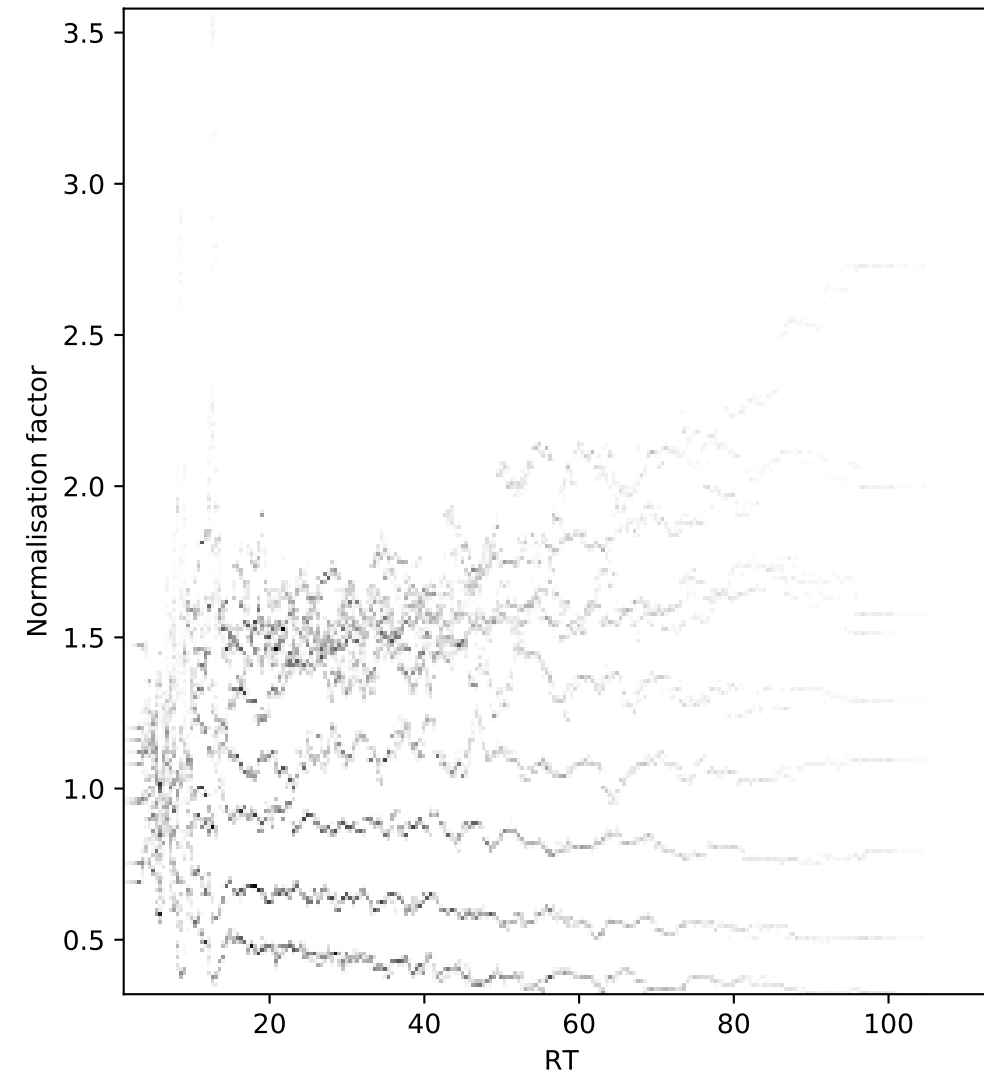
Retention times heatmap, all runs



Retention time accuracy heatmap, all runs

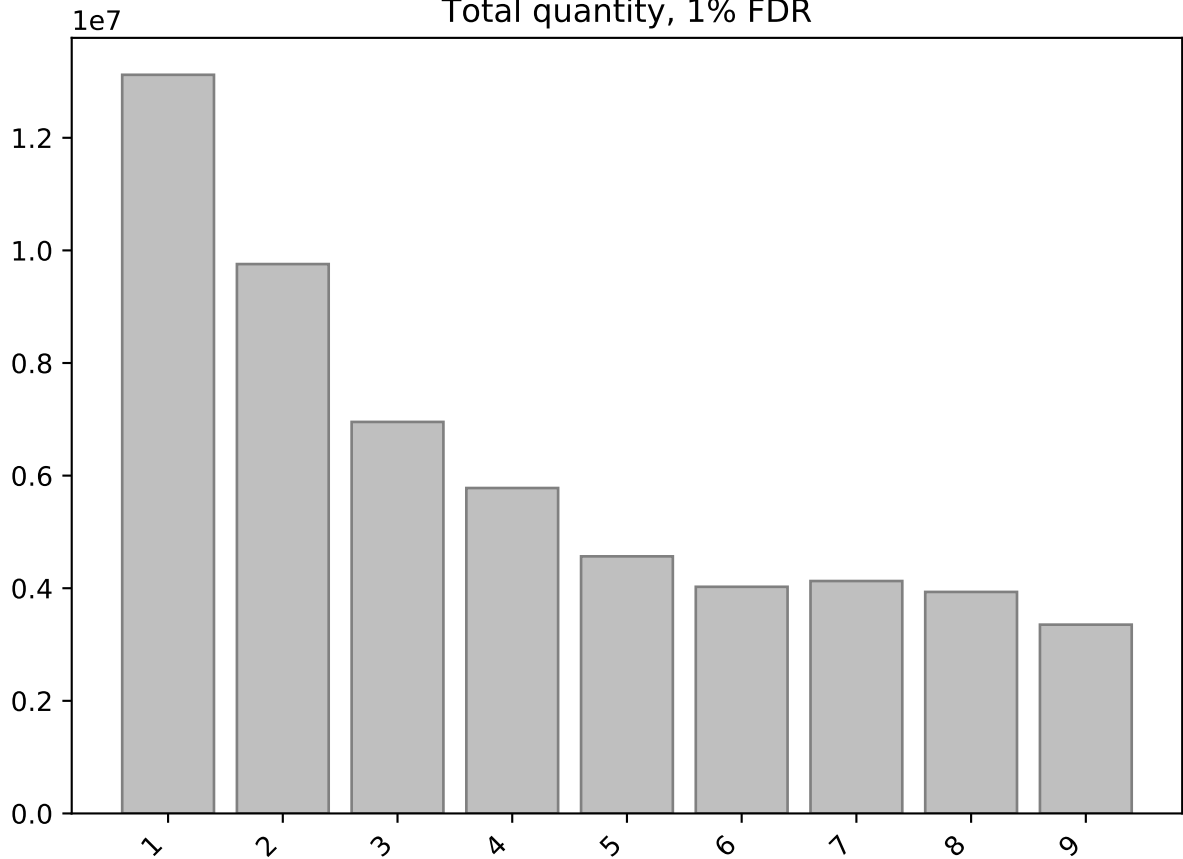


Normalisation factor heatmap, all runs

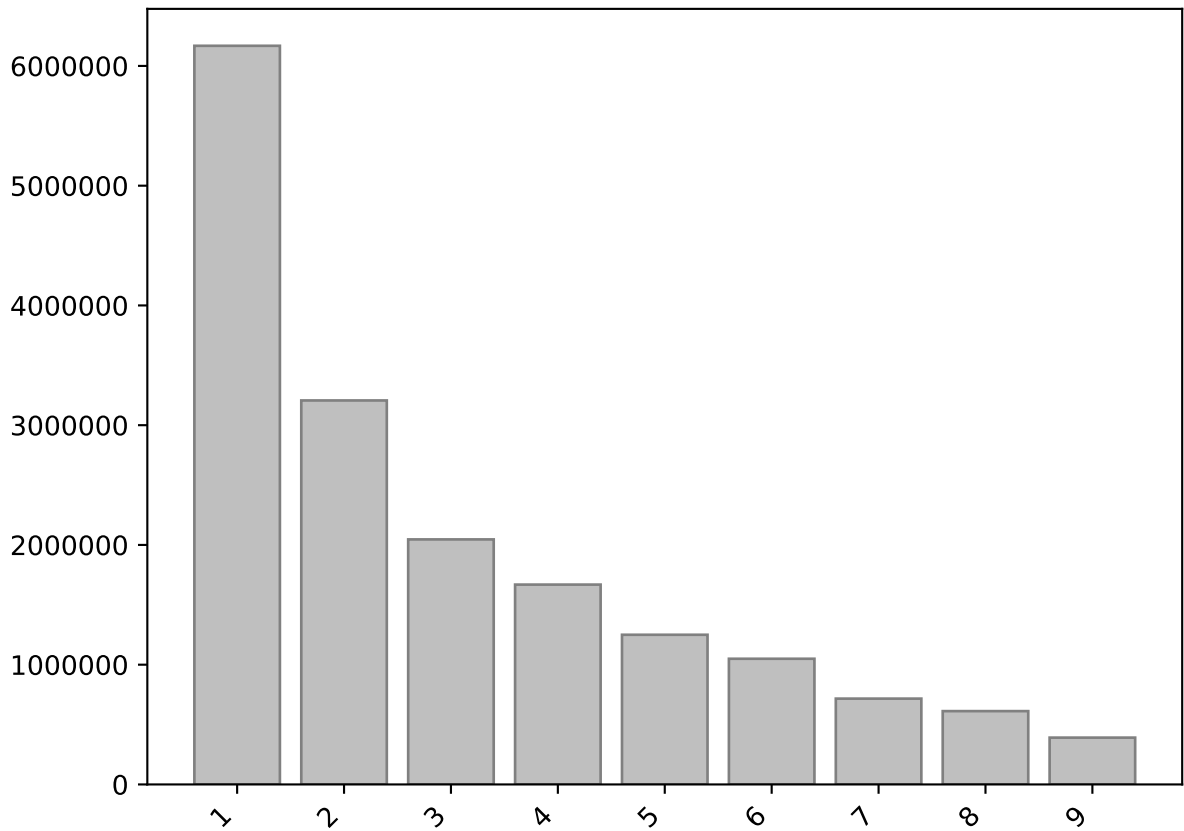




Total quantity, 1% FDR

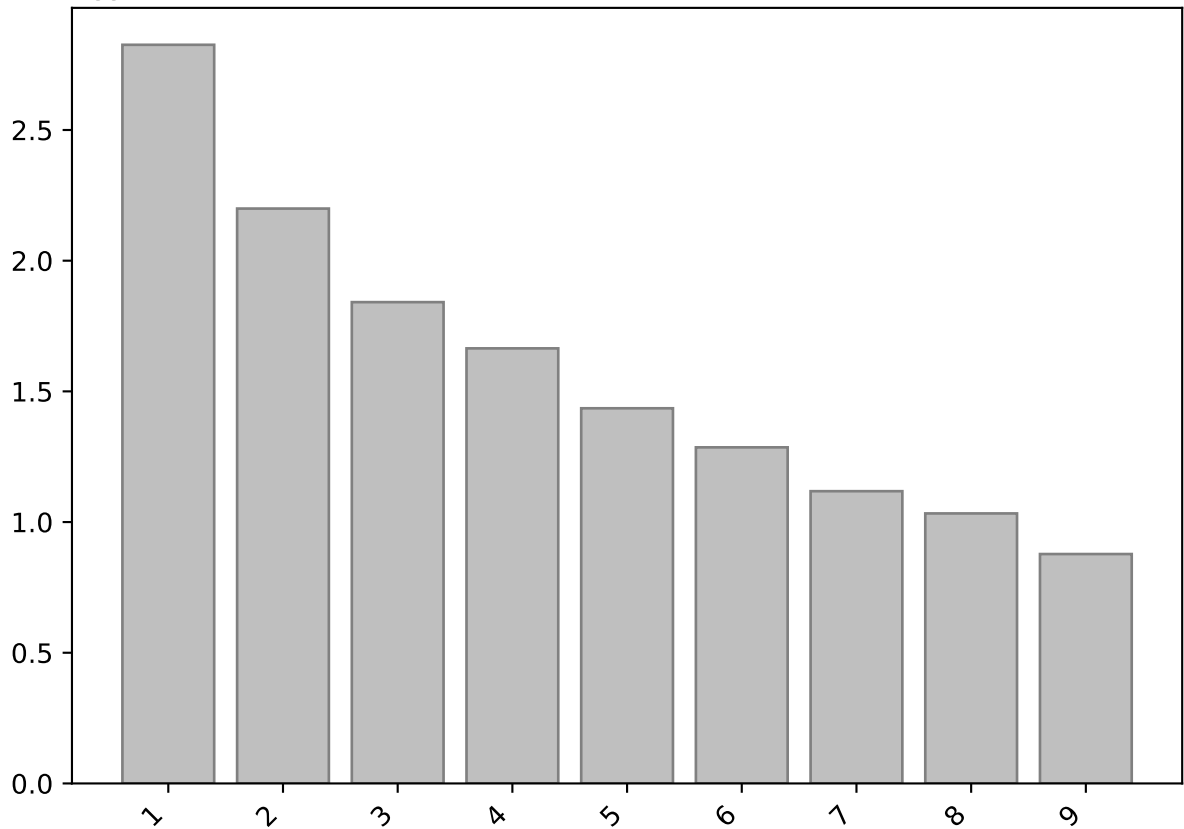


MS1 signal

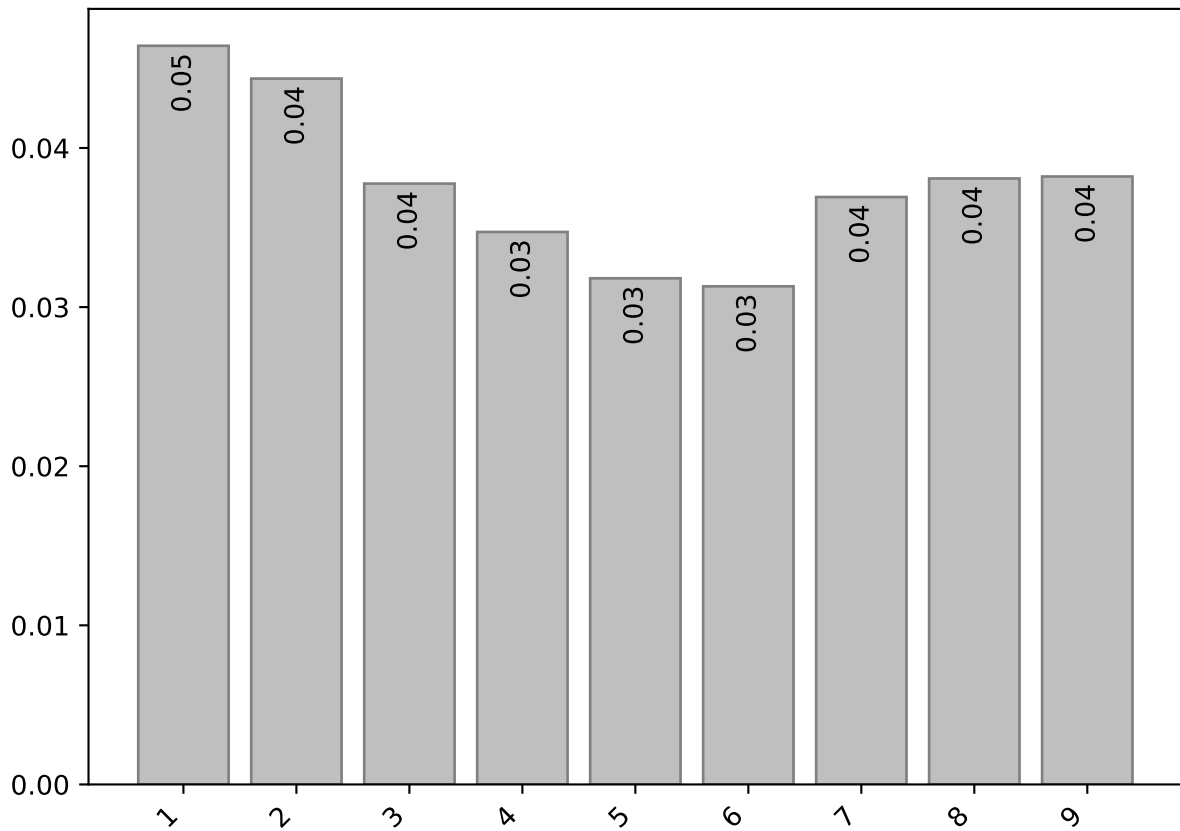


# MS2 signal

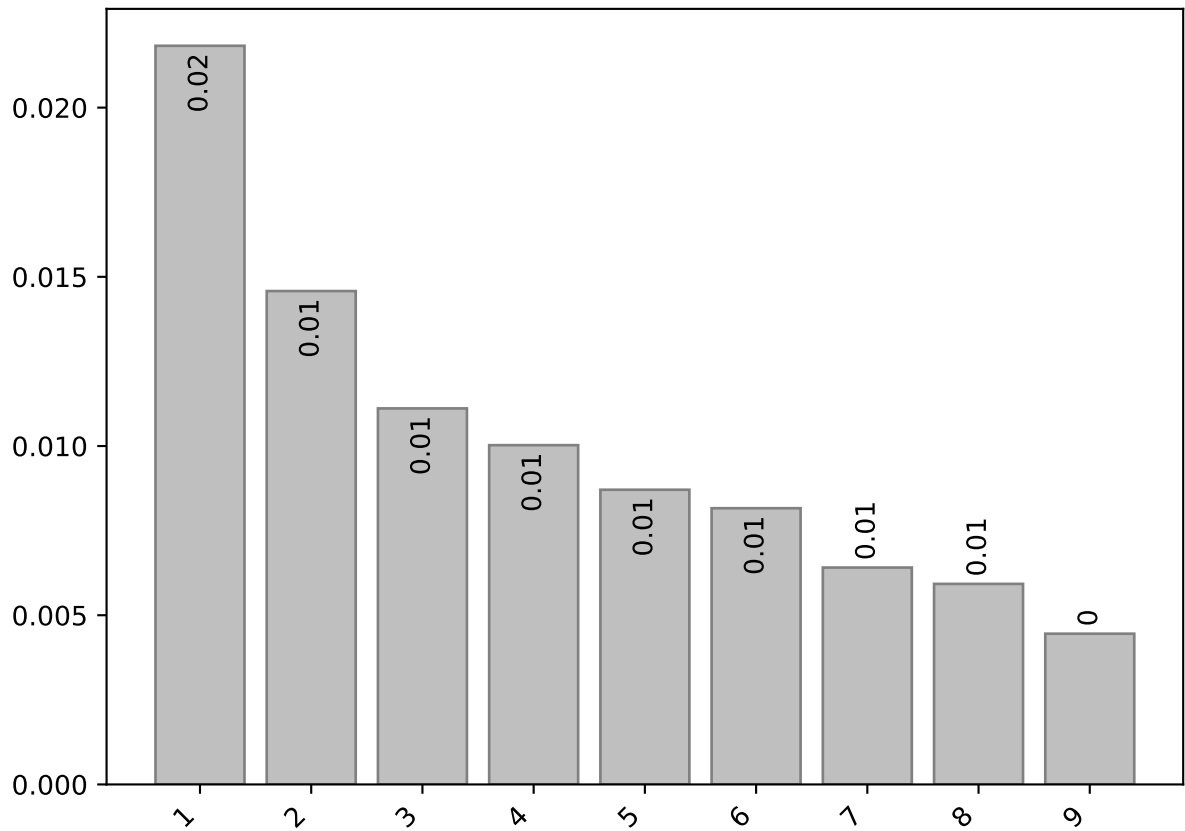
1e8



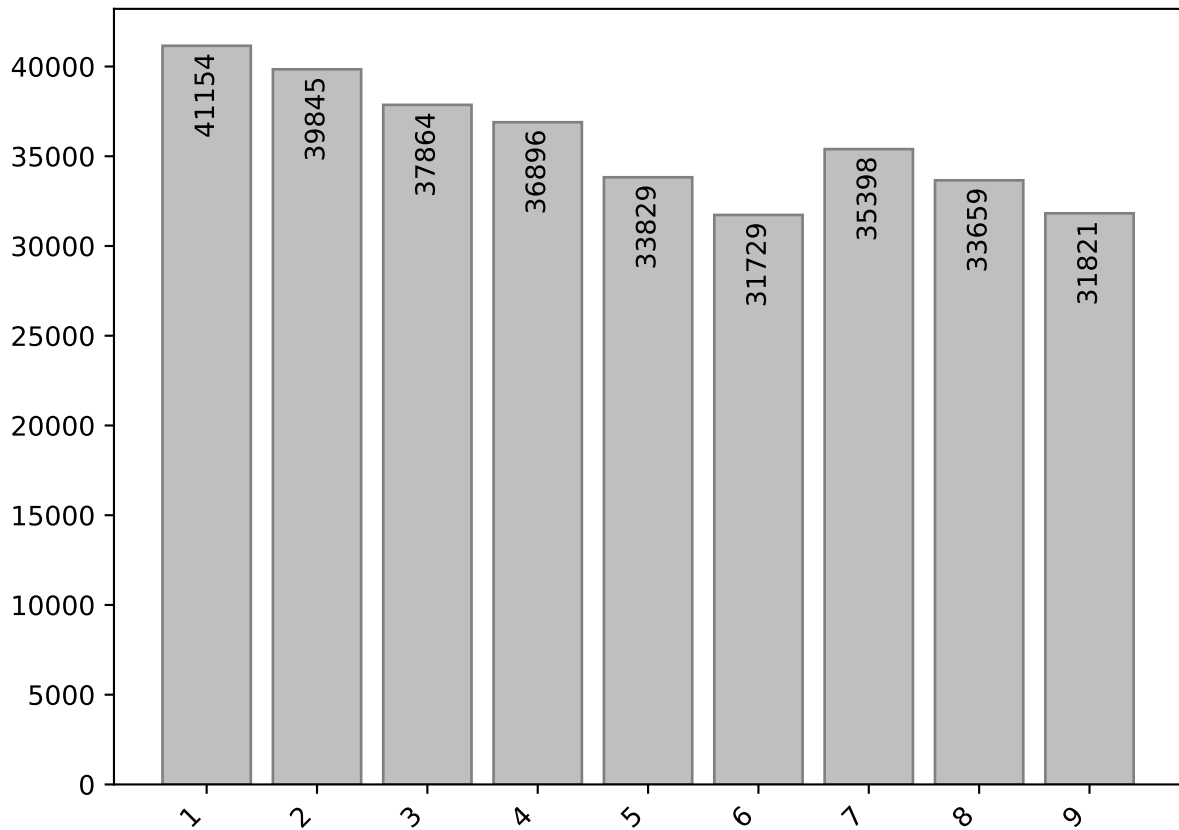
Total quantity/MS2 signal ratio



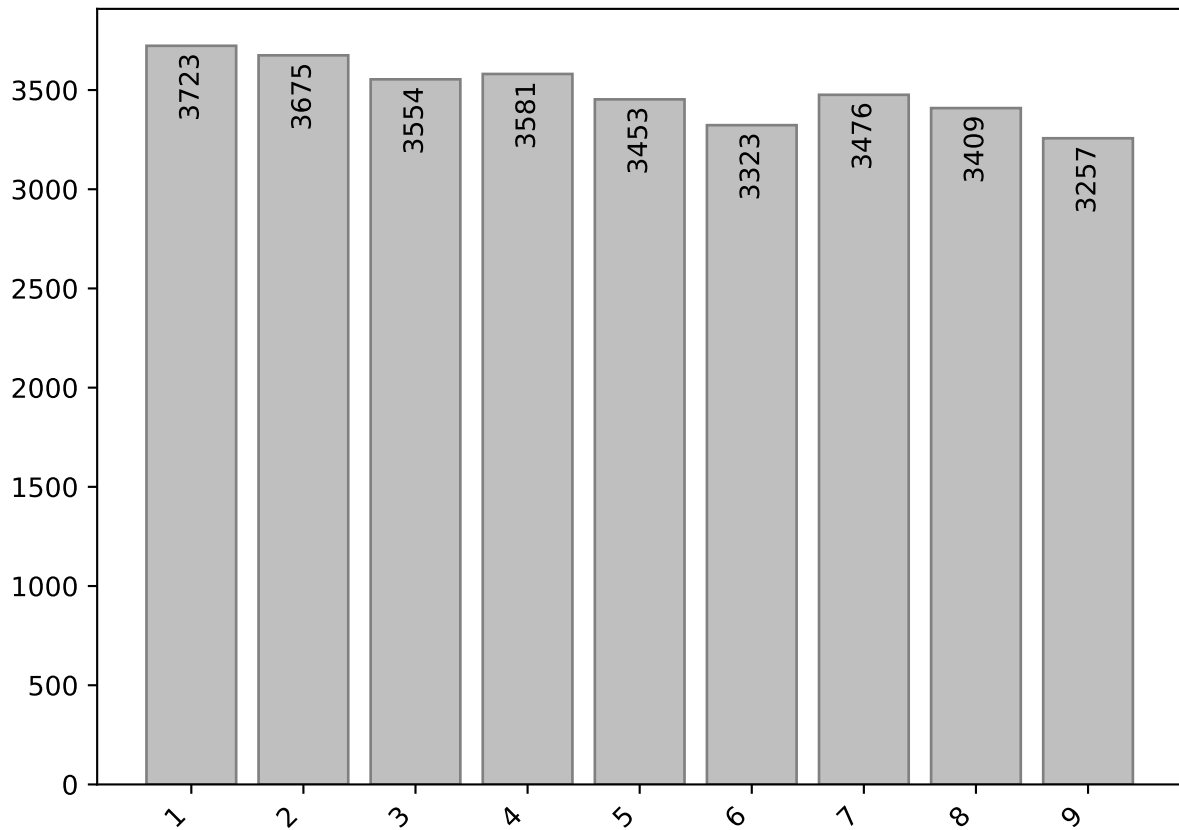
MS1/MS2 signal ratio



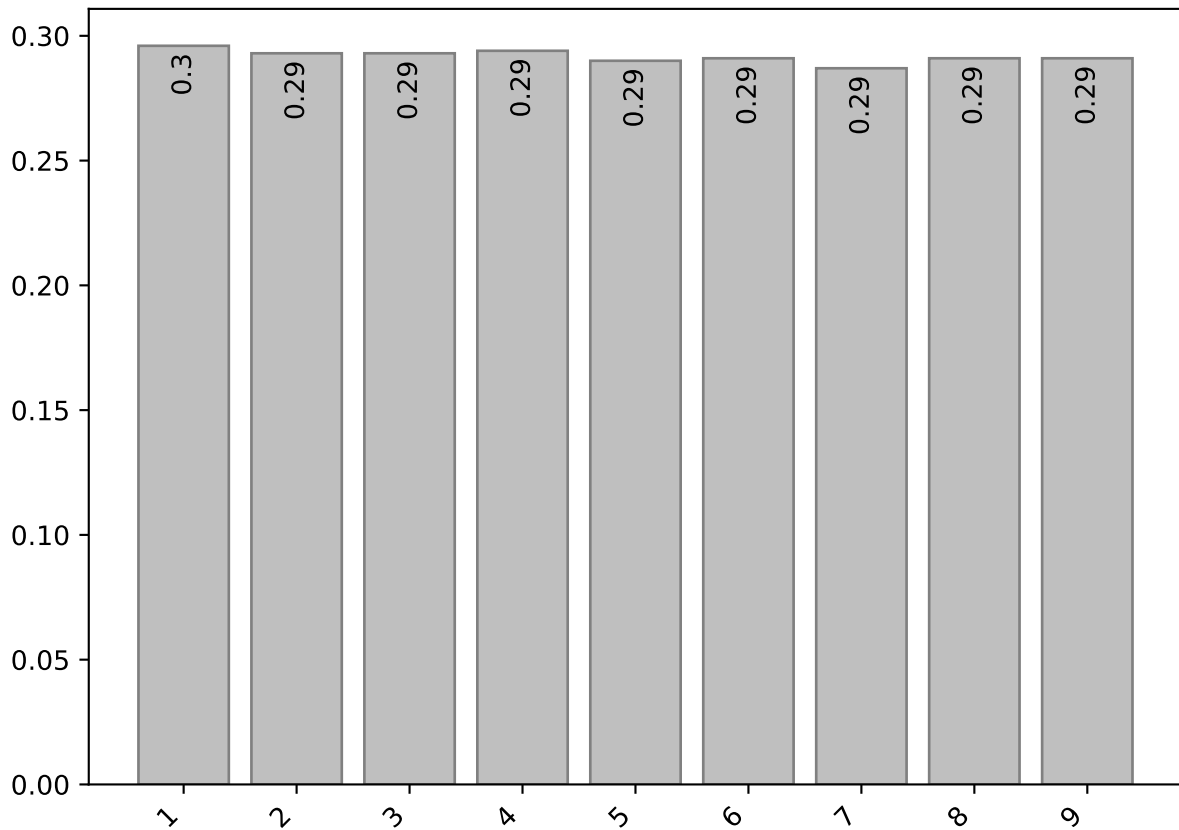
Precursors, 1% FDR



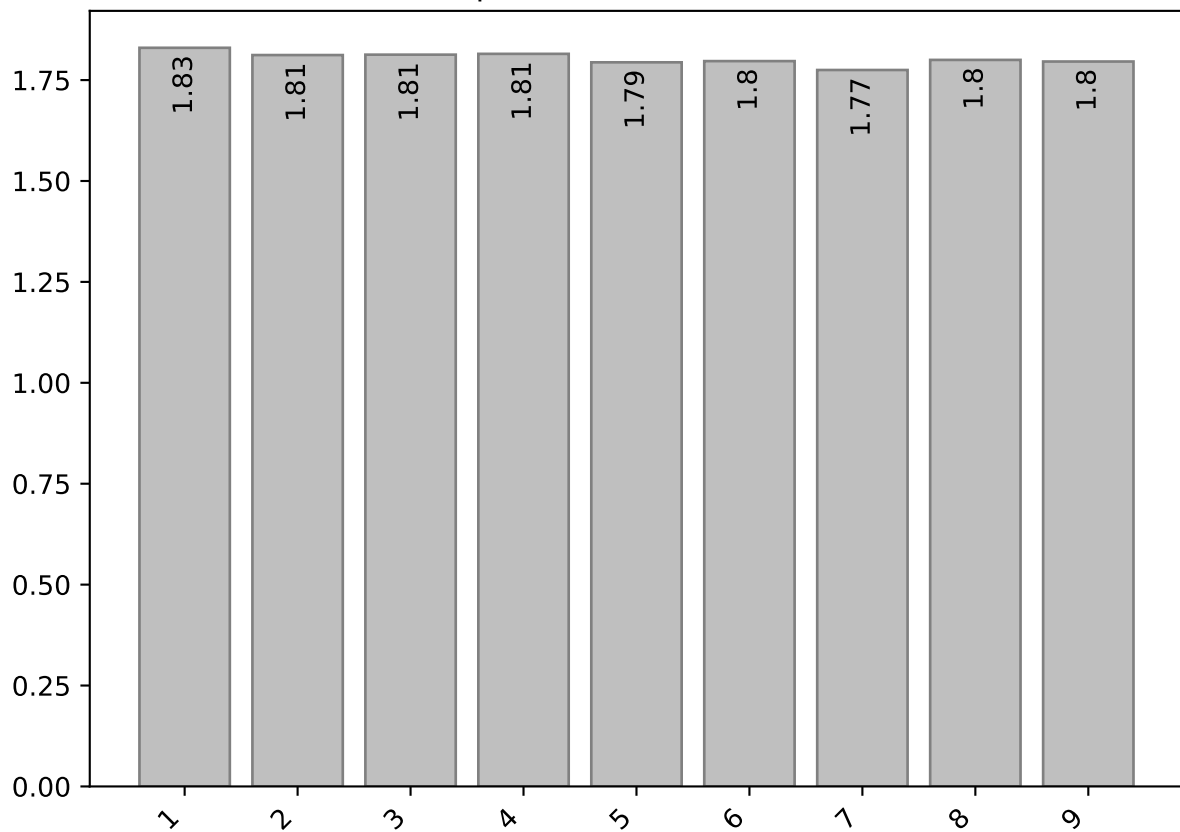
Unique proteins, 1% protein-level FDR



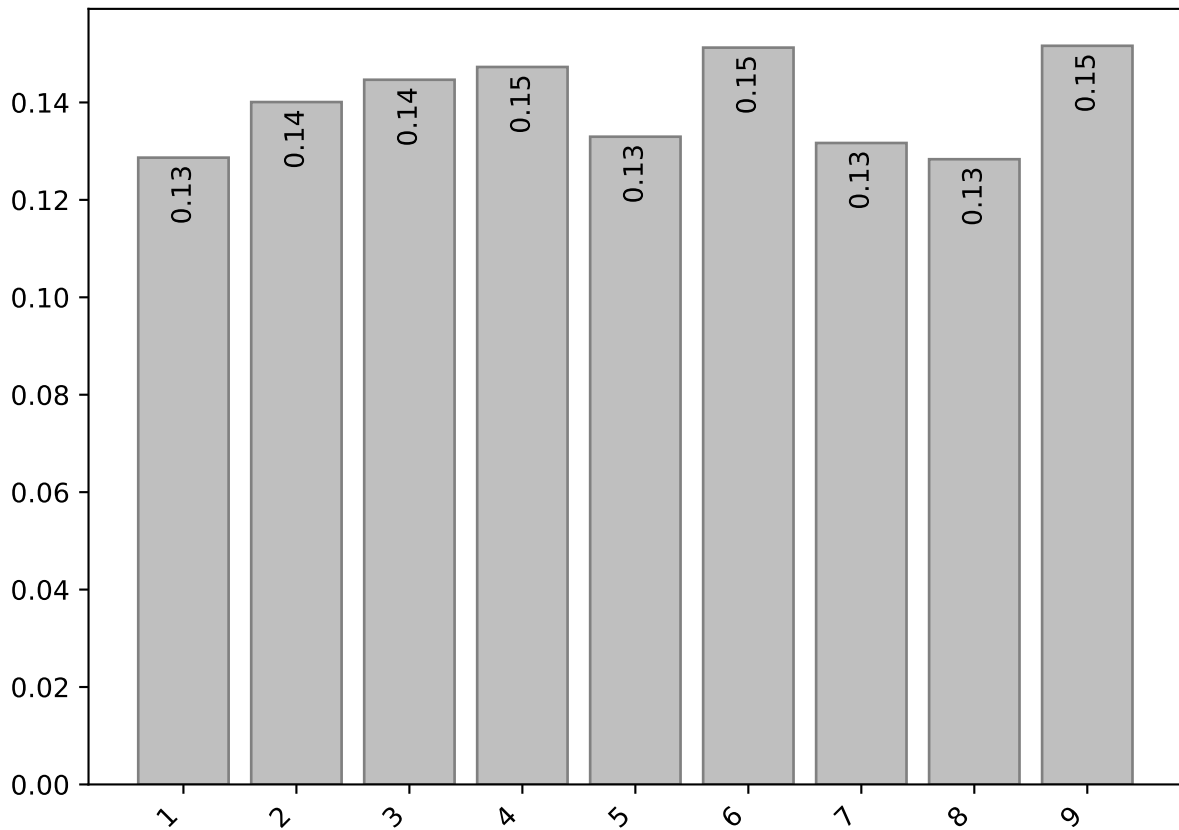
Mean peak FWHM, in minutes



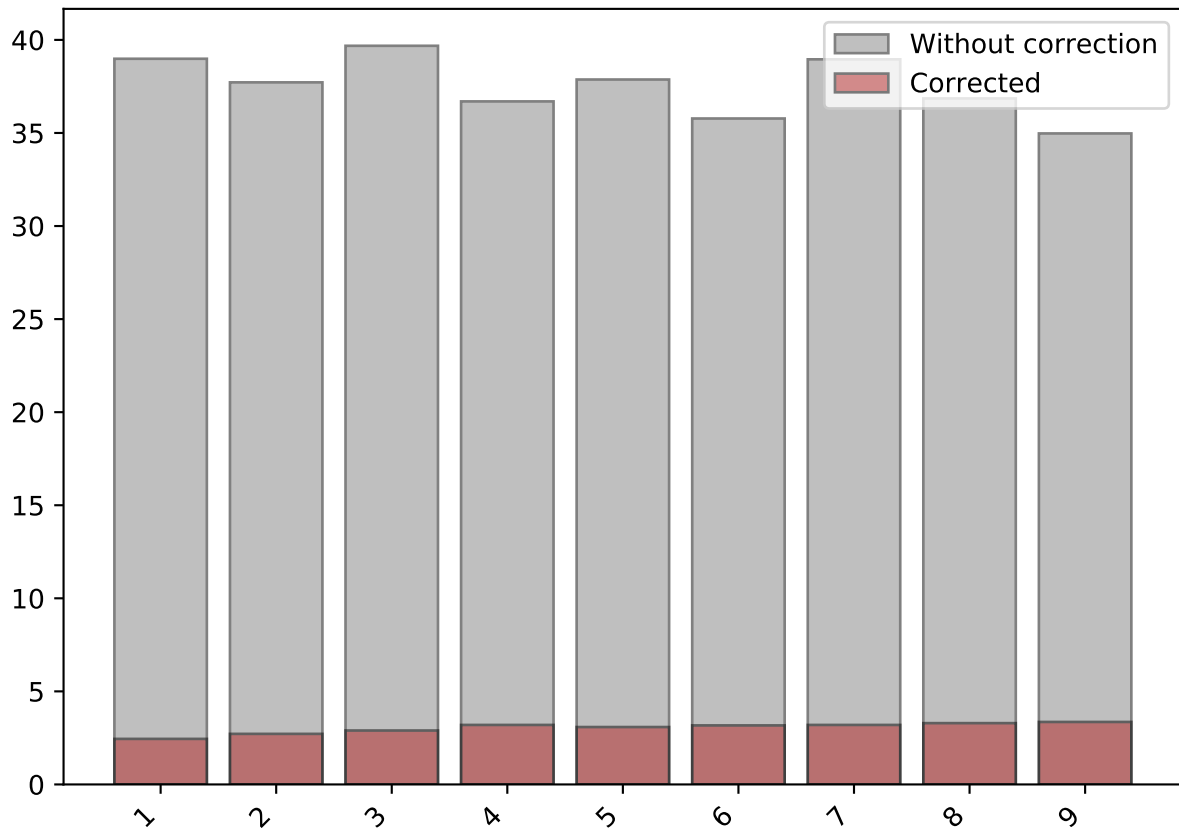
Mean peak FWHM, in MS2 scans



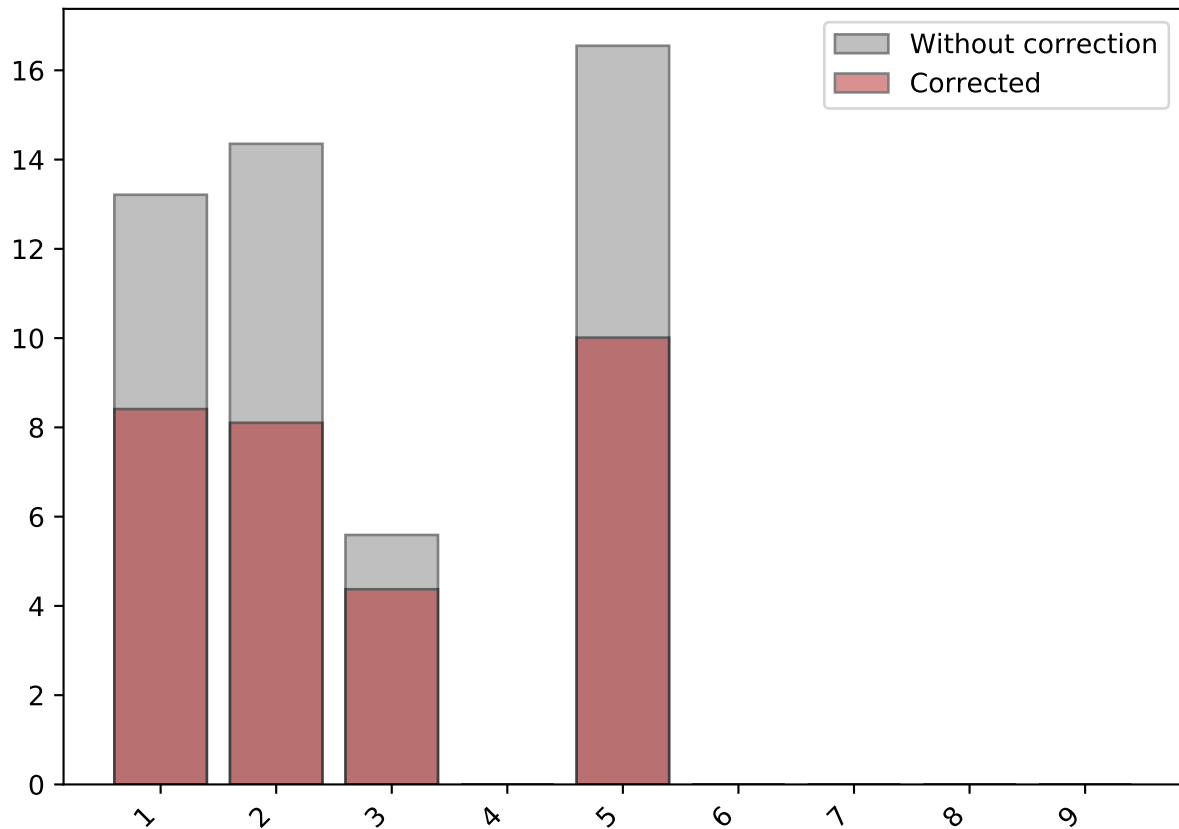
Median RT prediction accuracy, minutes



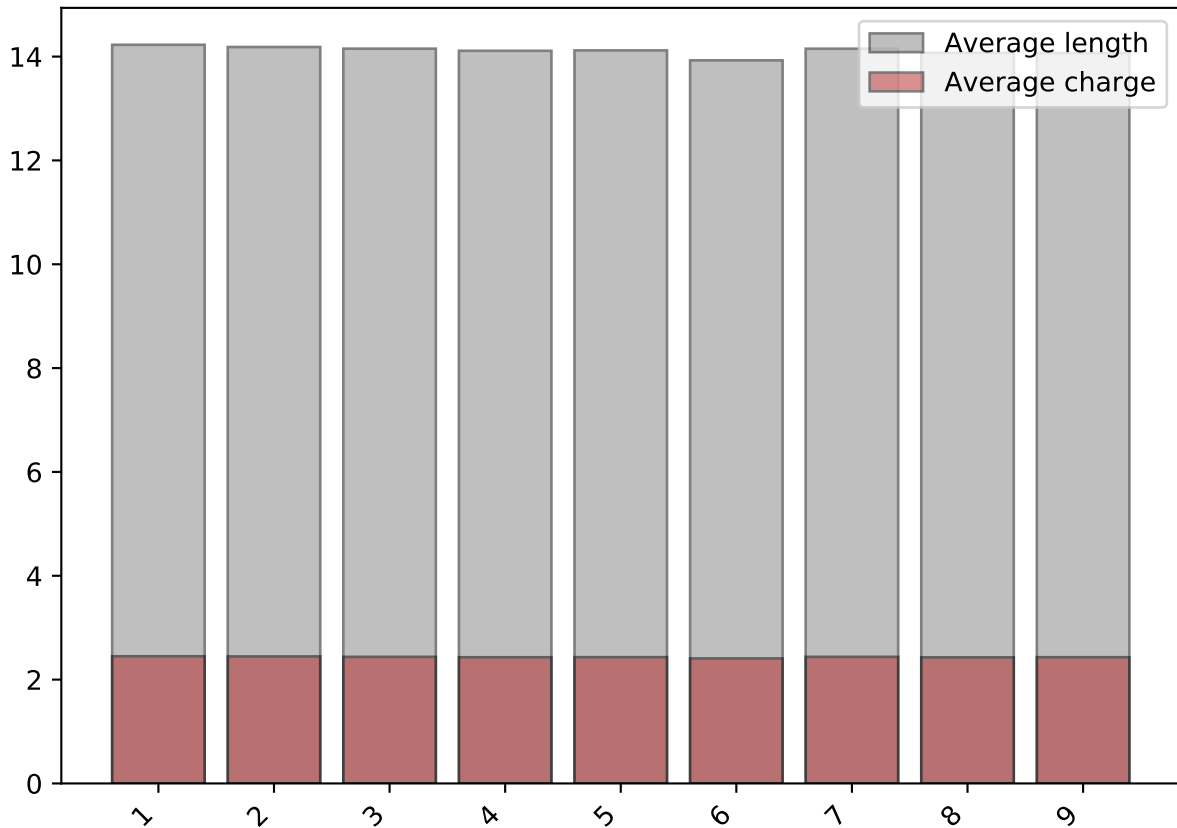
Median mass accuracy, MS2, ppm



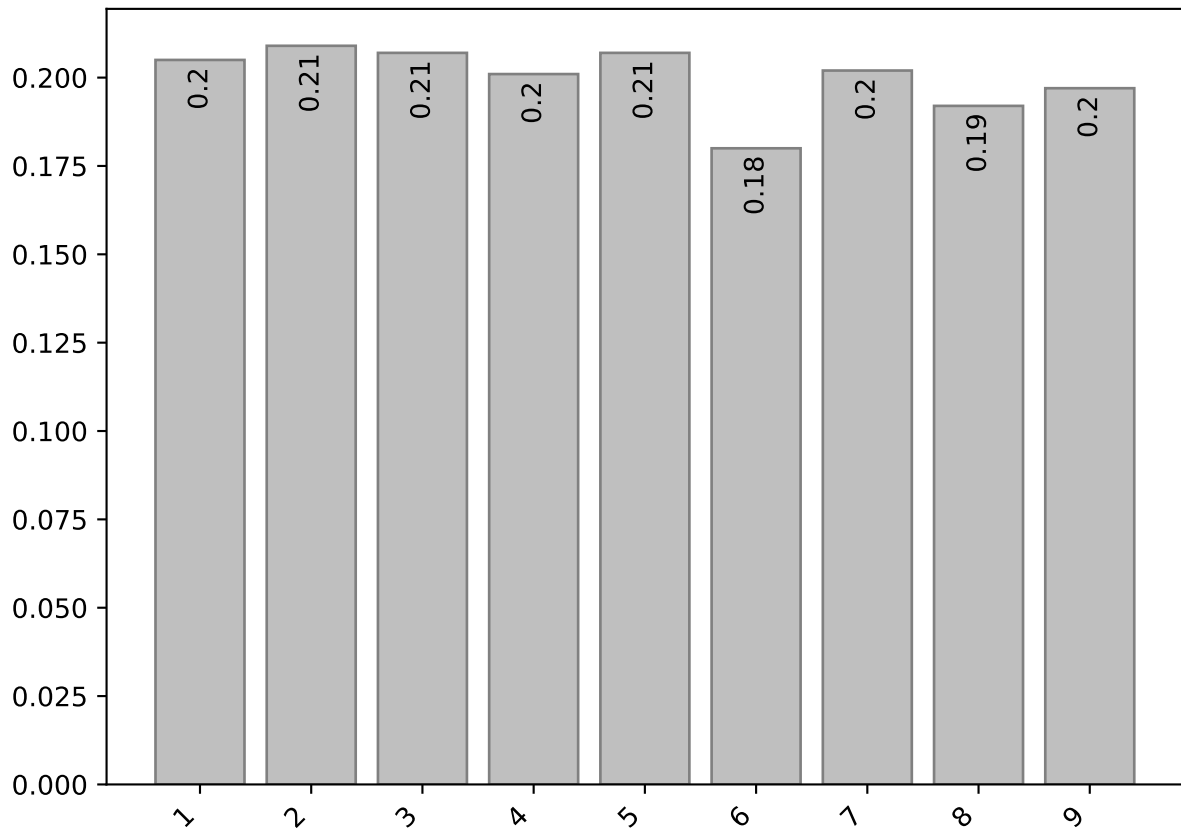
Median mass accuracy, MS1, ppm



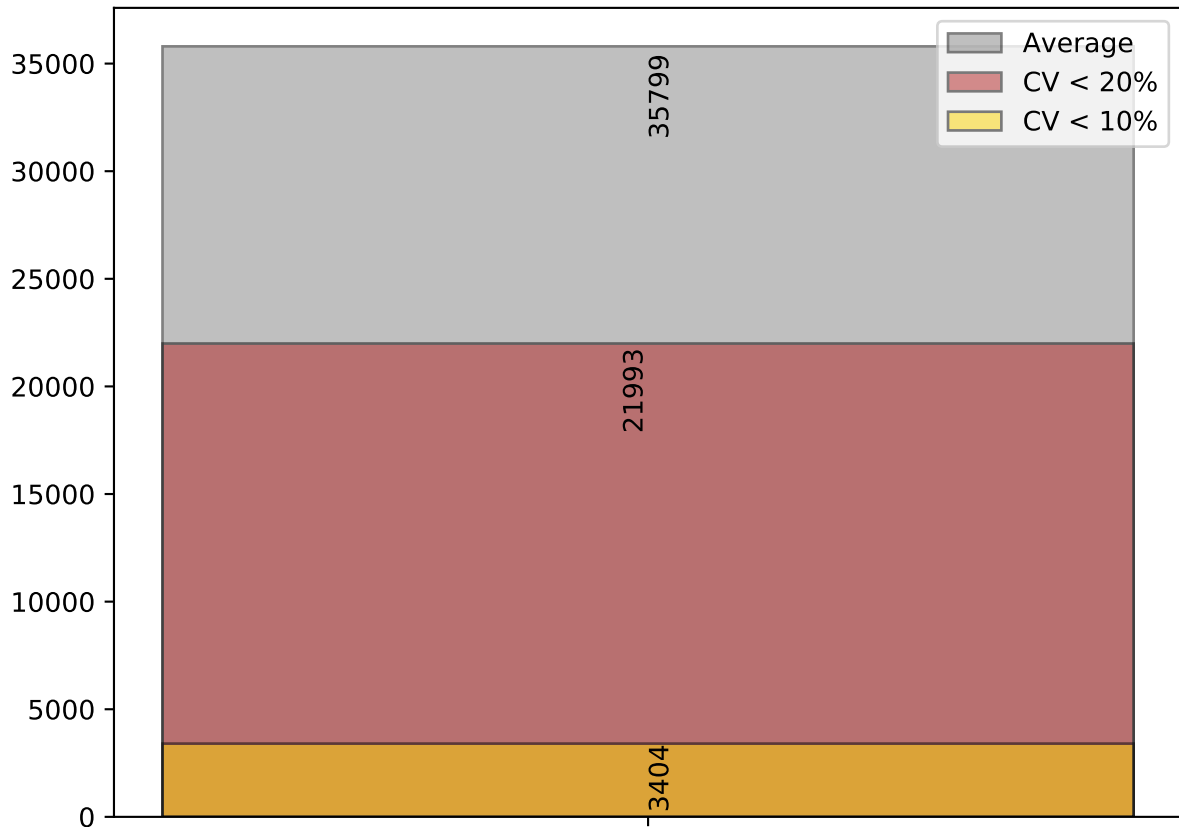
# Peptide characteristics



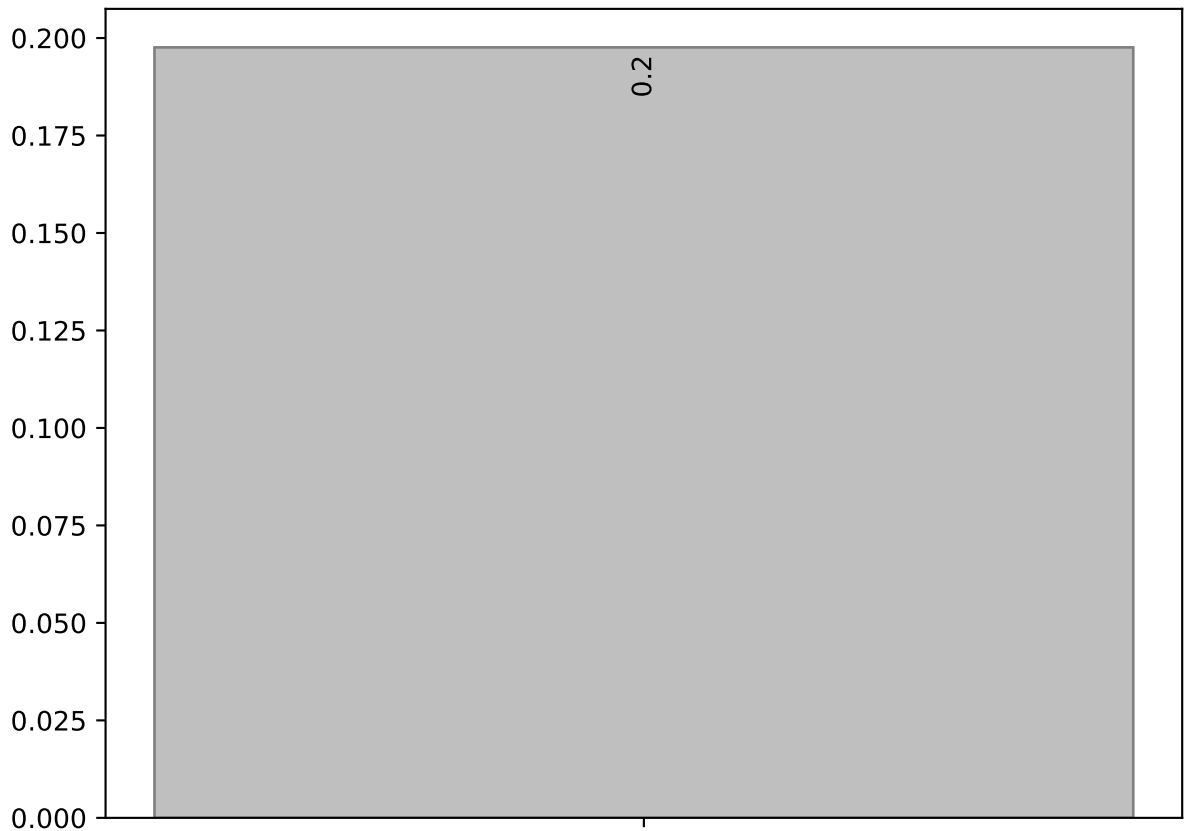
Average missed tryptic cleavages



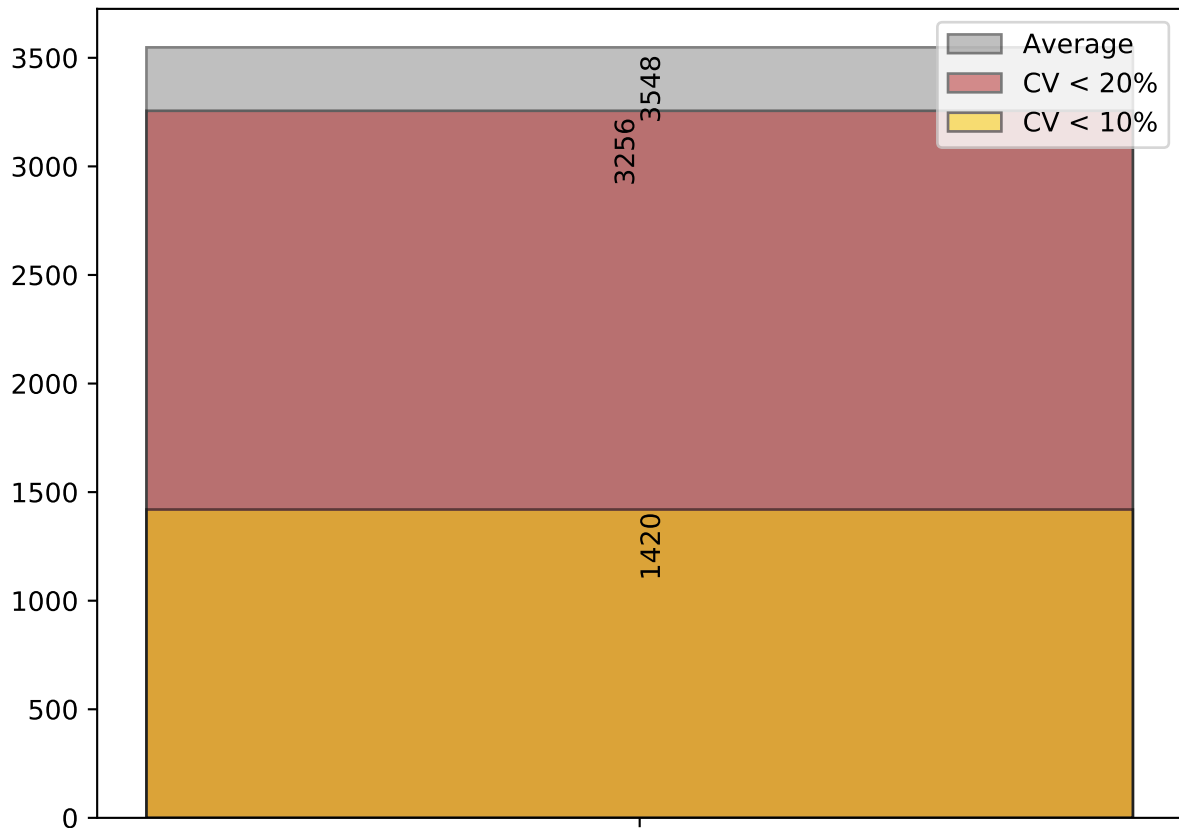
# Precursors, 1% FDR



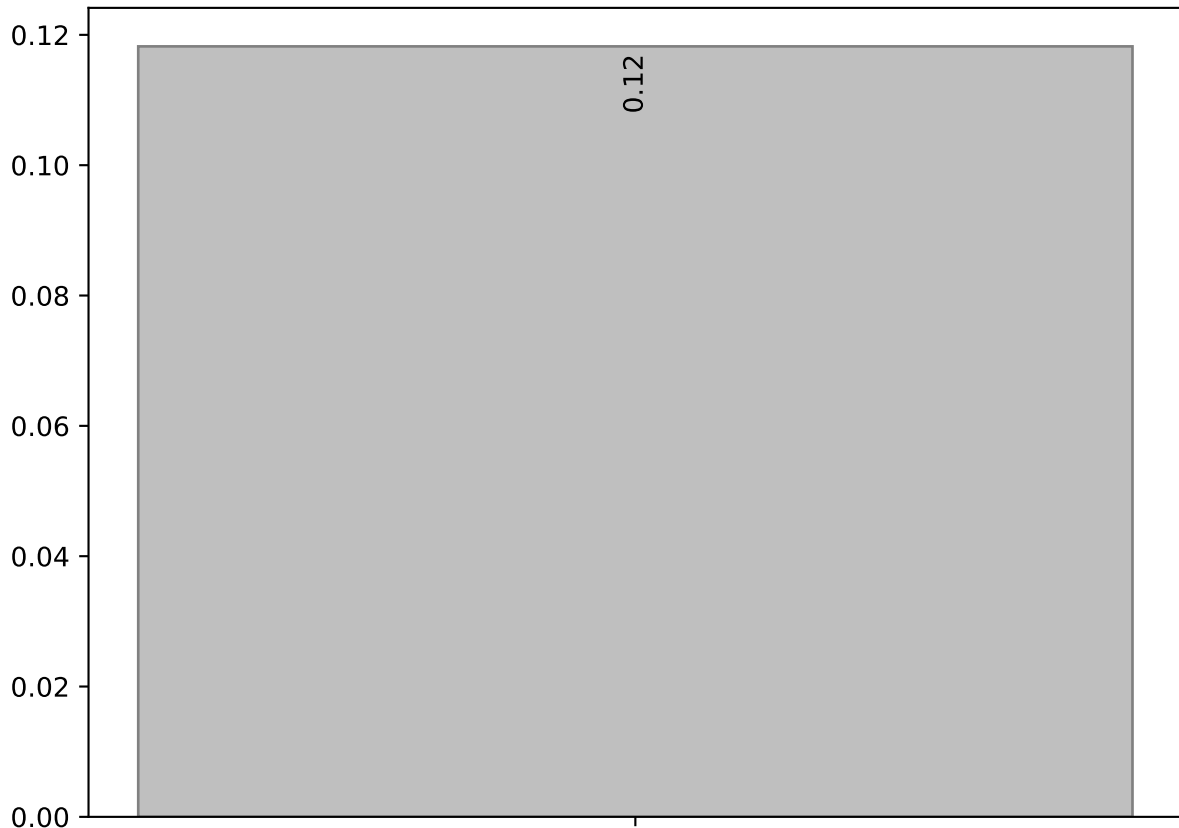
# Median precursor CV, 1% FDR



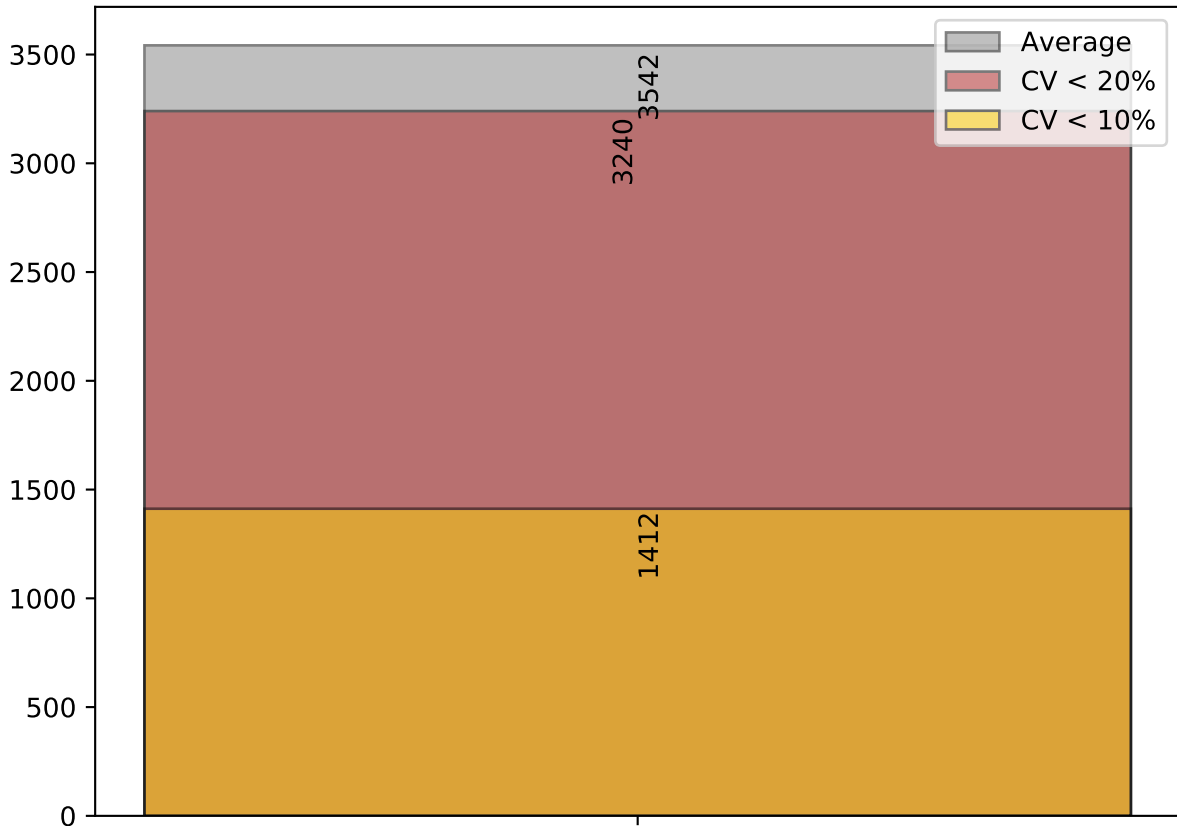
# Protein groups, 1% FDR



# Median protein group CV, 1% FDR



# Gene groups, 1% FDR



# Median gene group CV, 1% FDR

