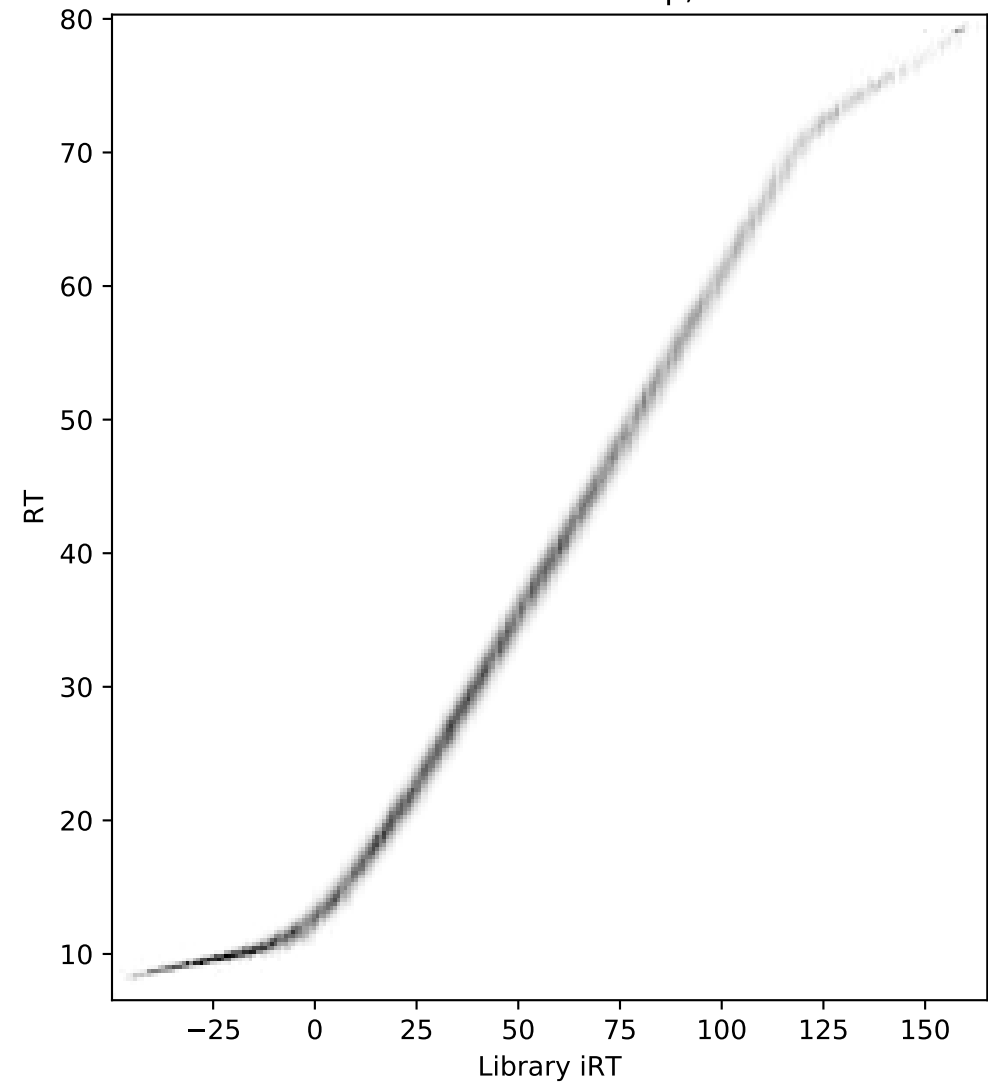
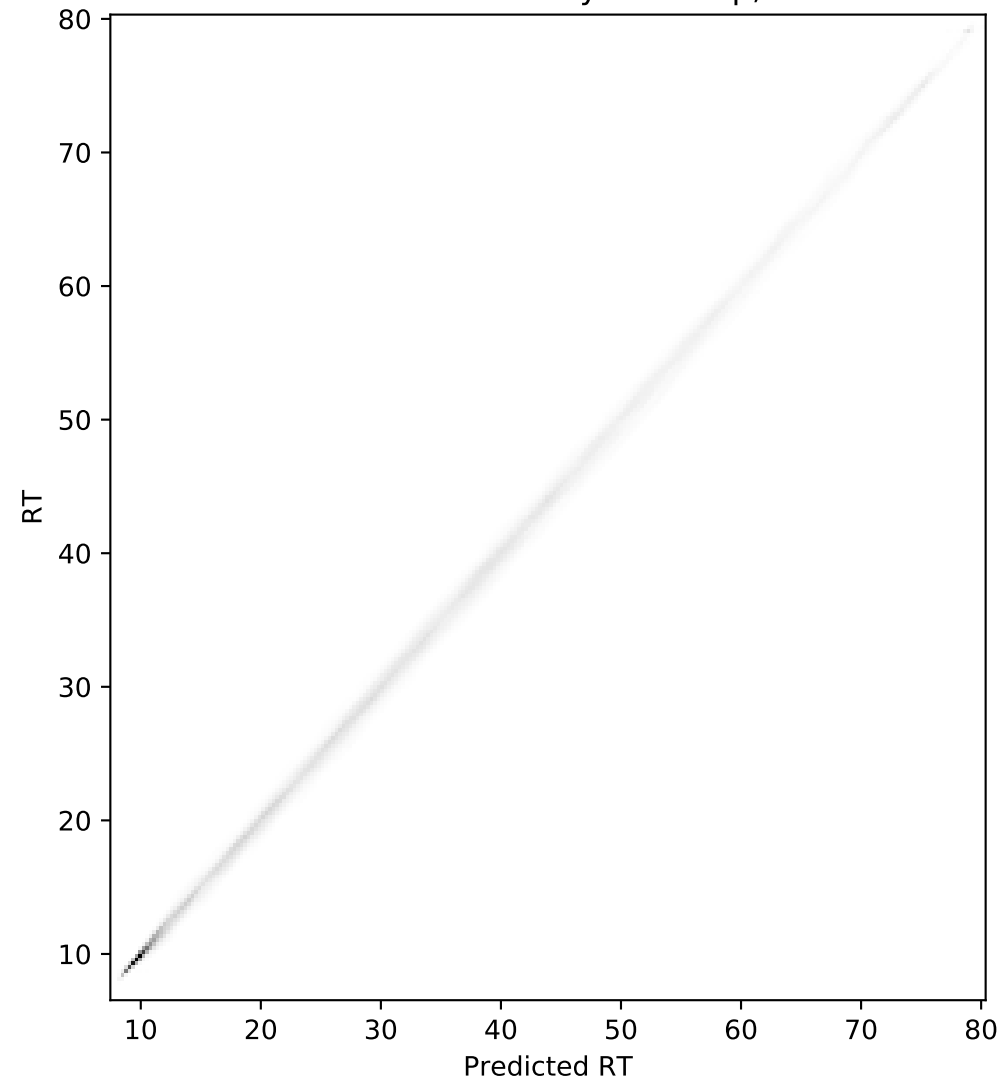


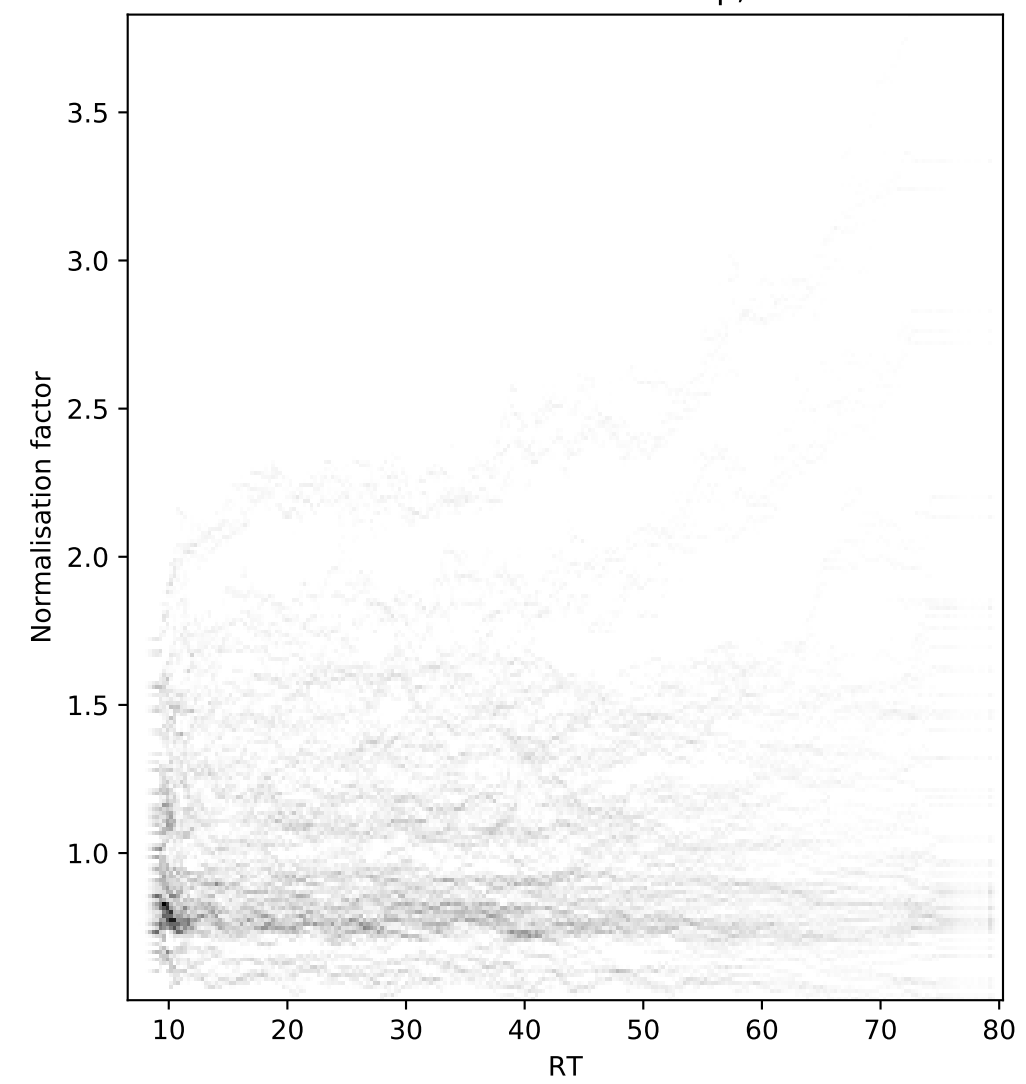
Retention times heatmap, all runs



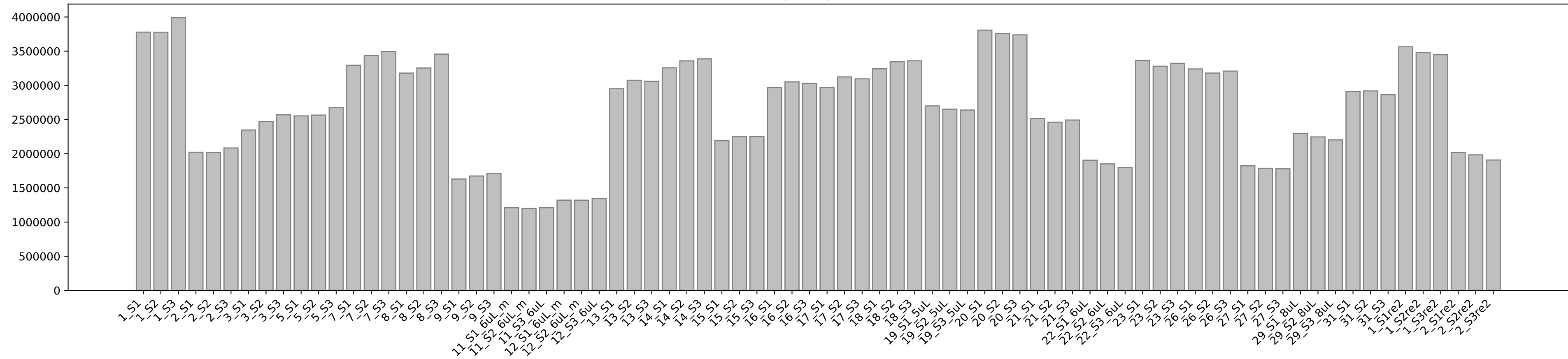
Retention time accuracy heatmap, all runs



Normalisation factor heatmap, all runs

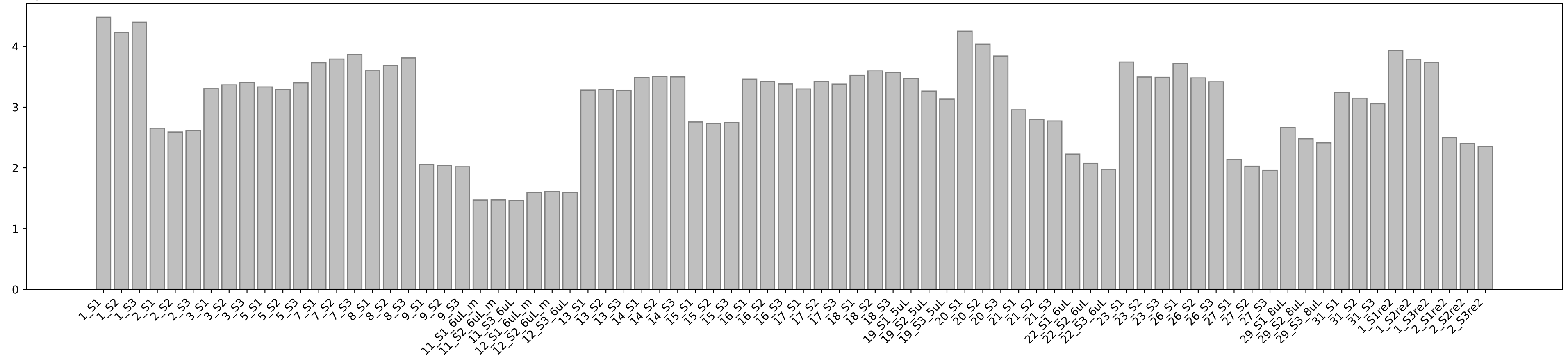


Total quantity, 1% FDR



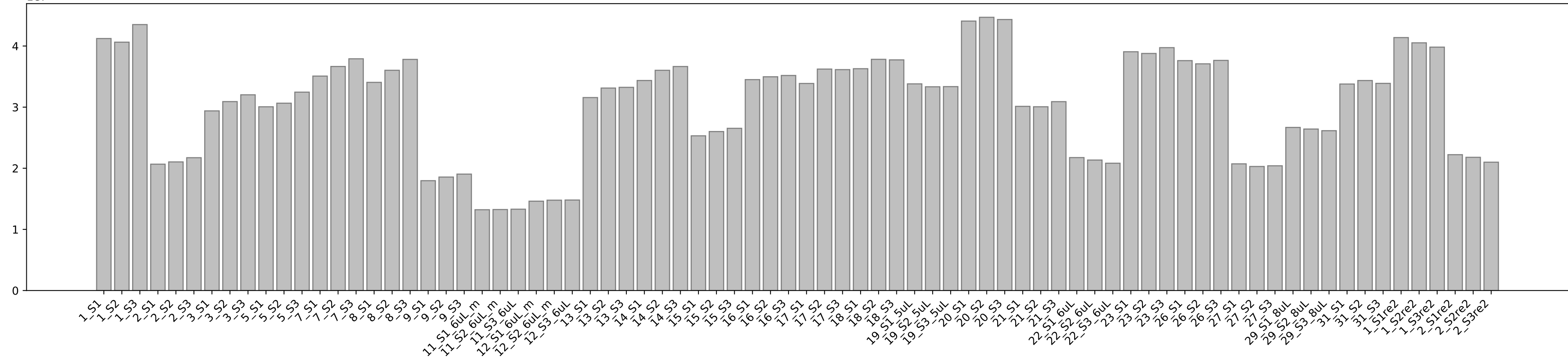
MS1 signal

1e7

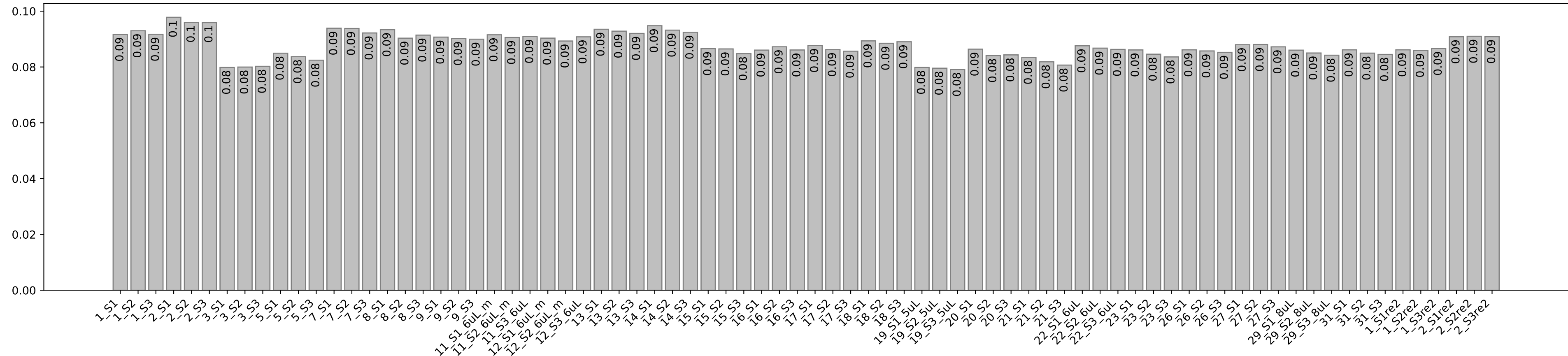


MS2 signal

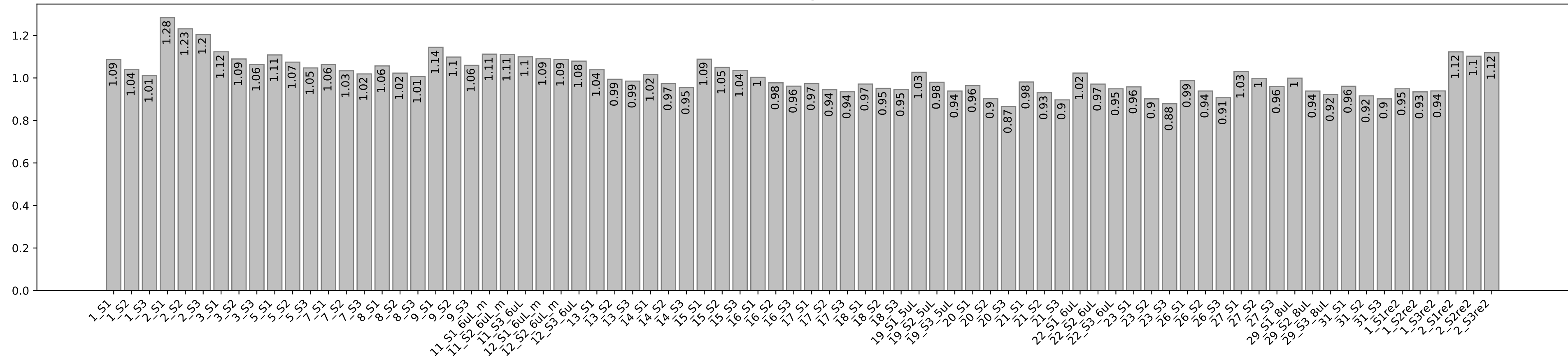
1e7



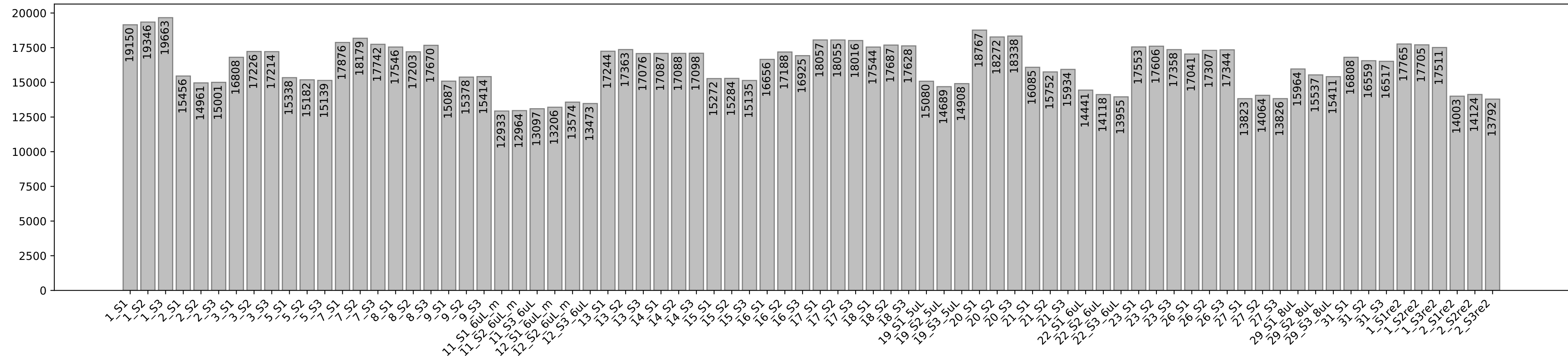
Total quantity/MS2 signal ratio



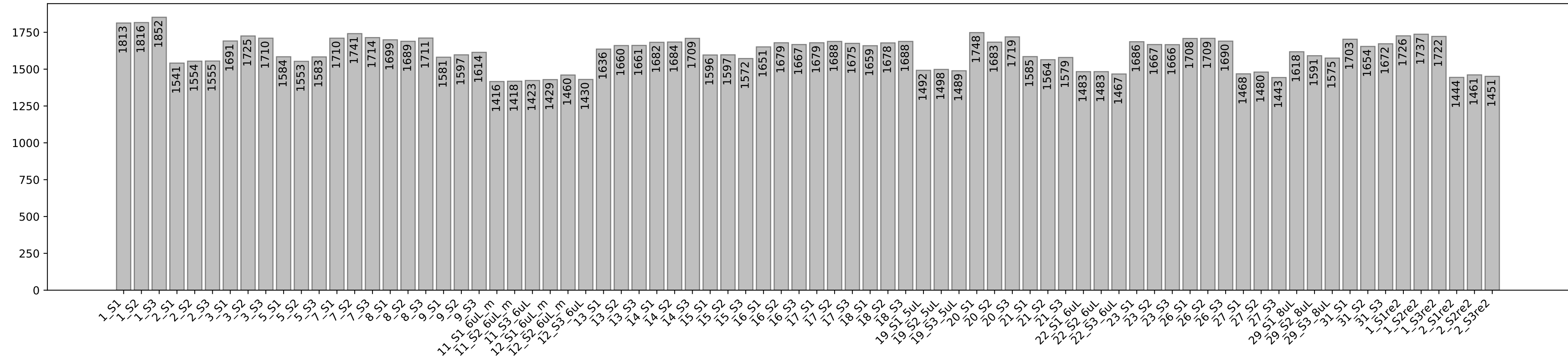
MS1/MS2 signal ratio



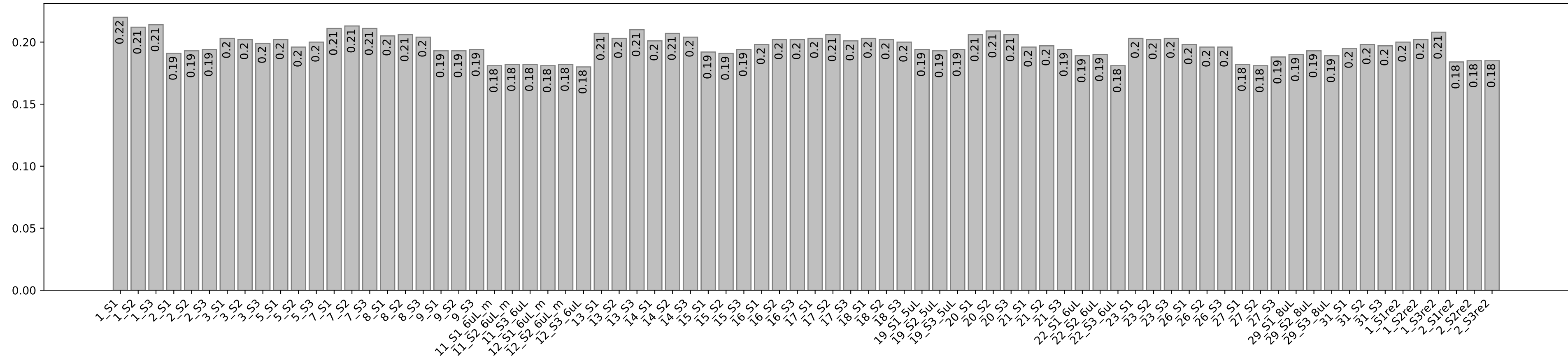
Precursors, 1% FDR



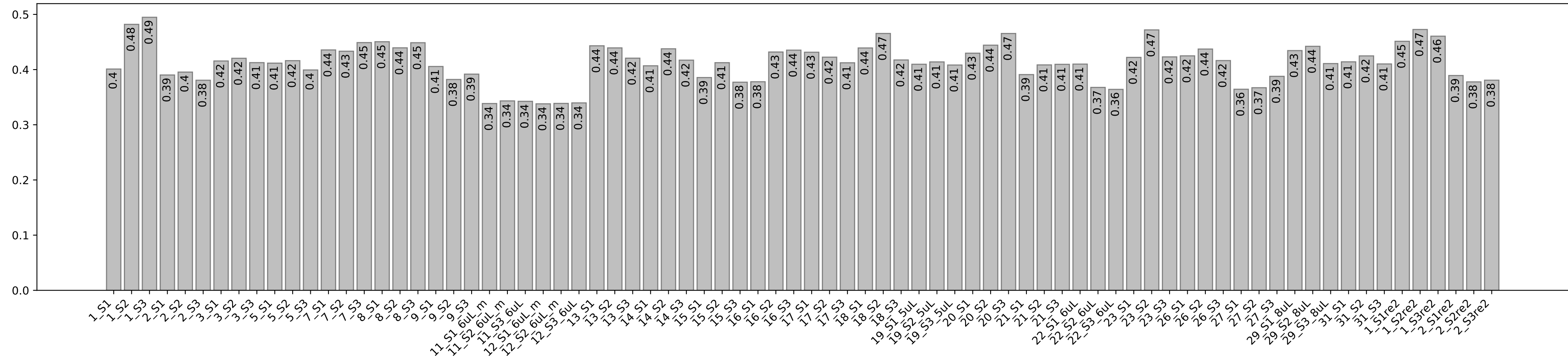
Unique proteins, 1% protein-level FDR



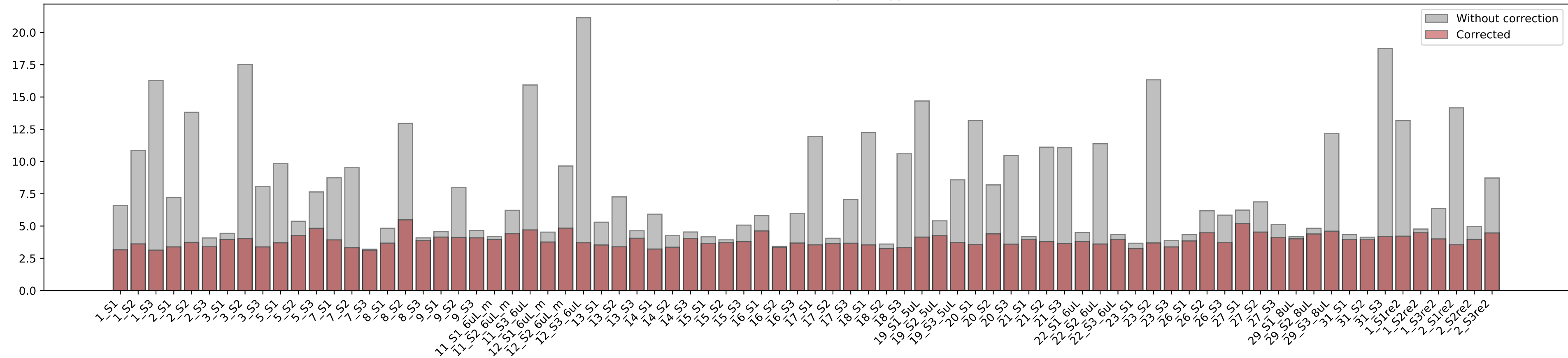
Mean peak FWHM, in minutes



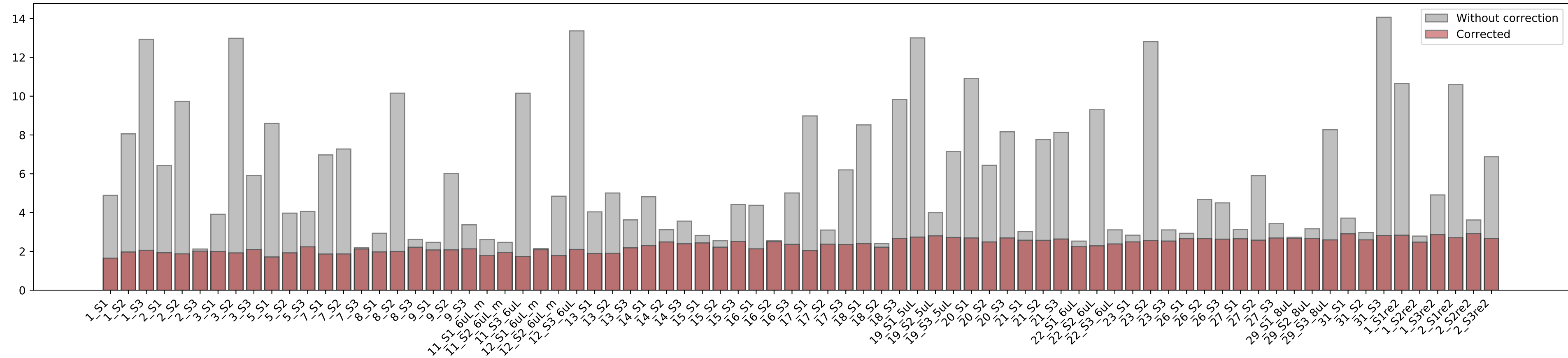
Median RT prediction accuracy, minutes



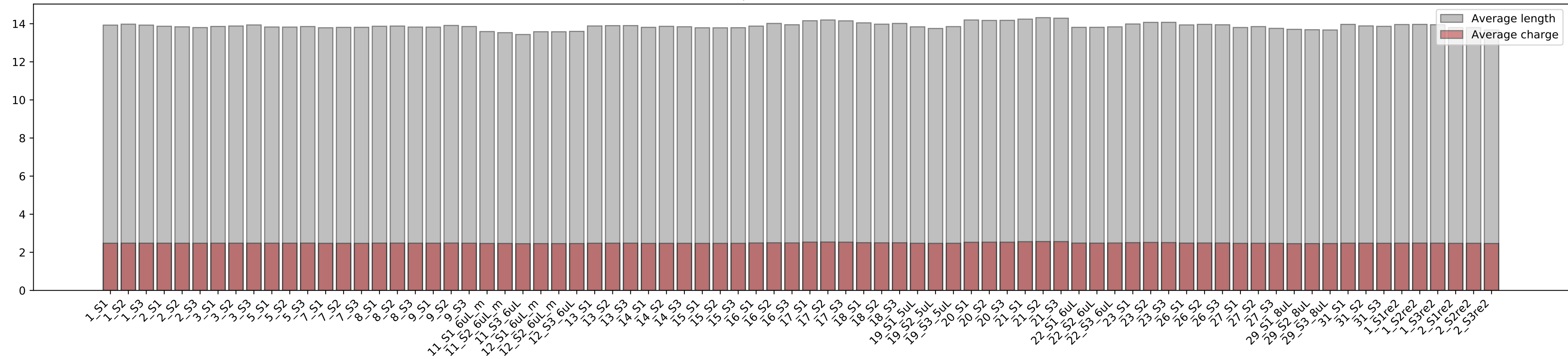
Median mass accuracy, MS2, ppm



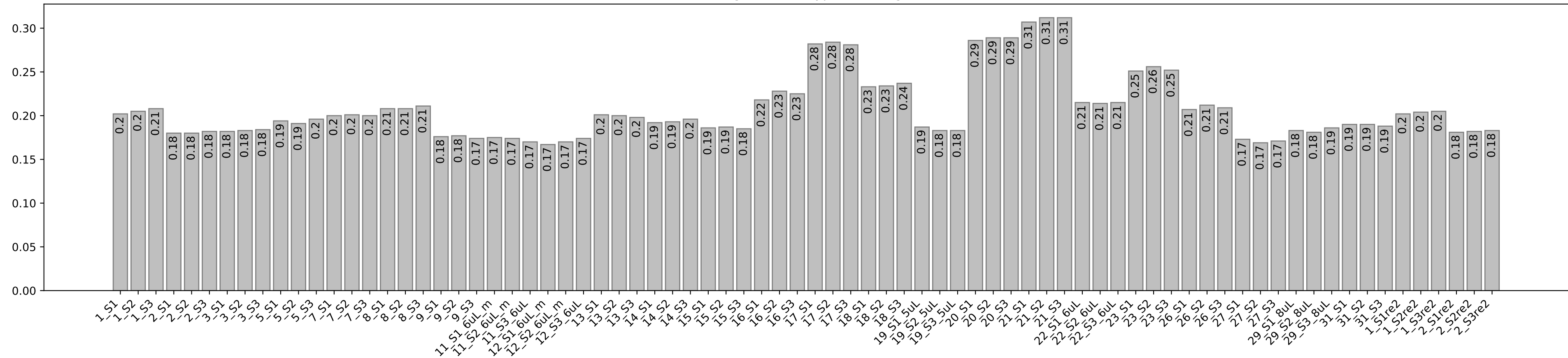
Median mass accuracy, MS1, ppm



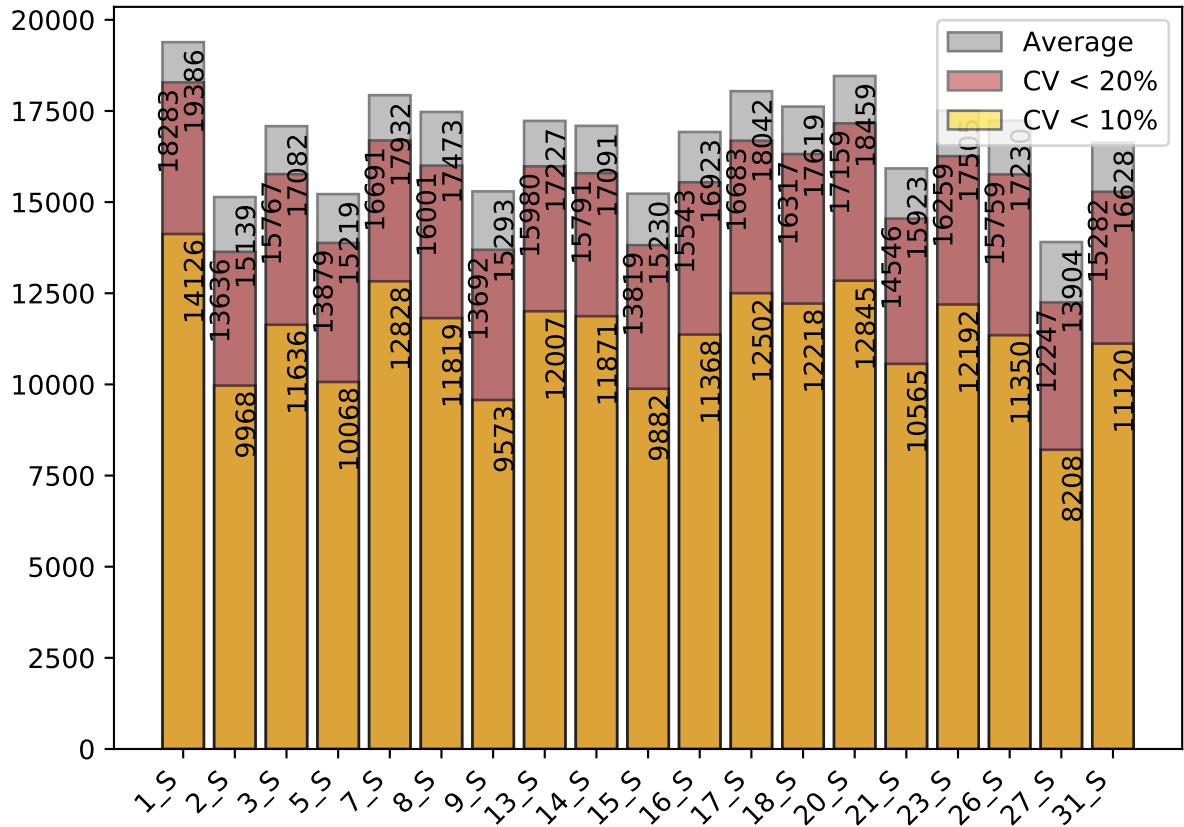
Peptide characteristics



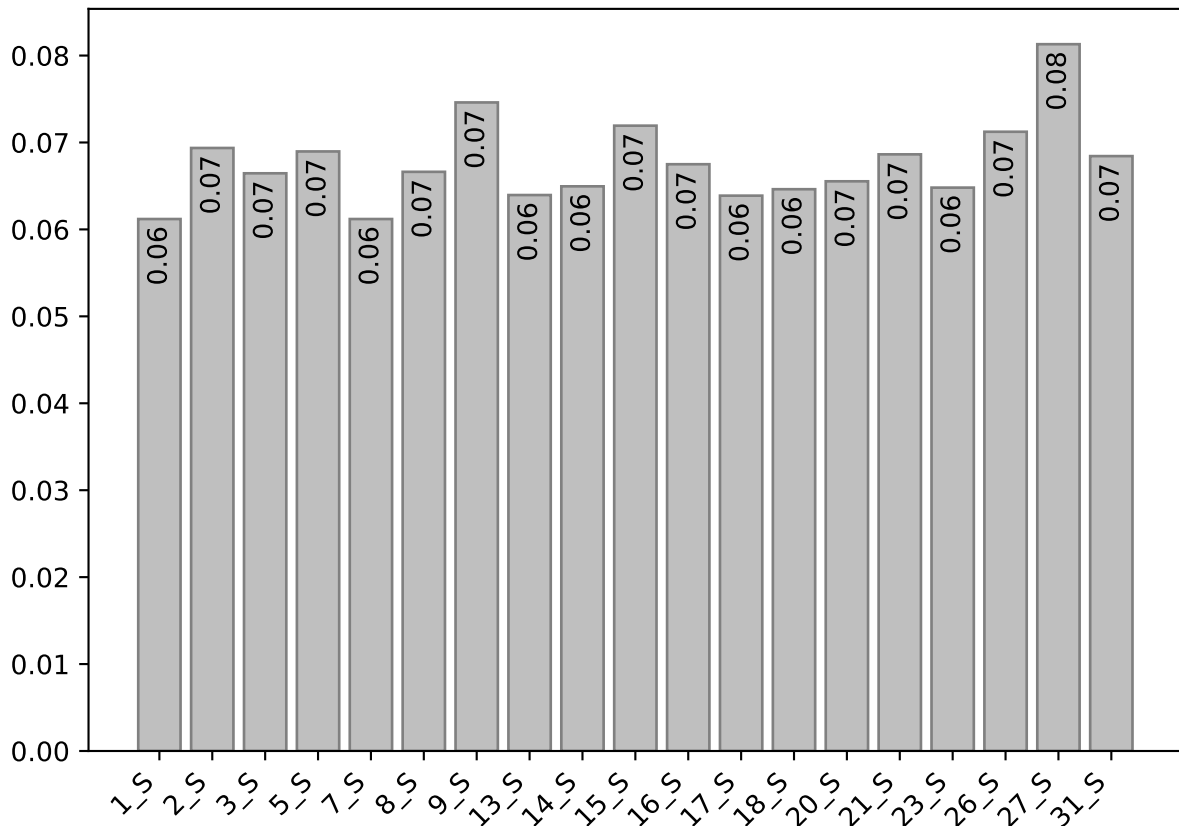
Average missed tryptic cleavages



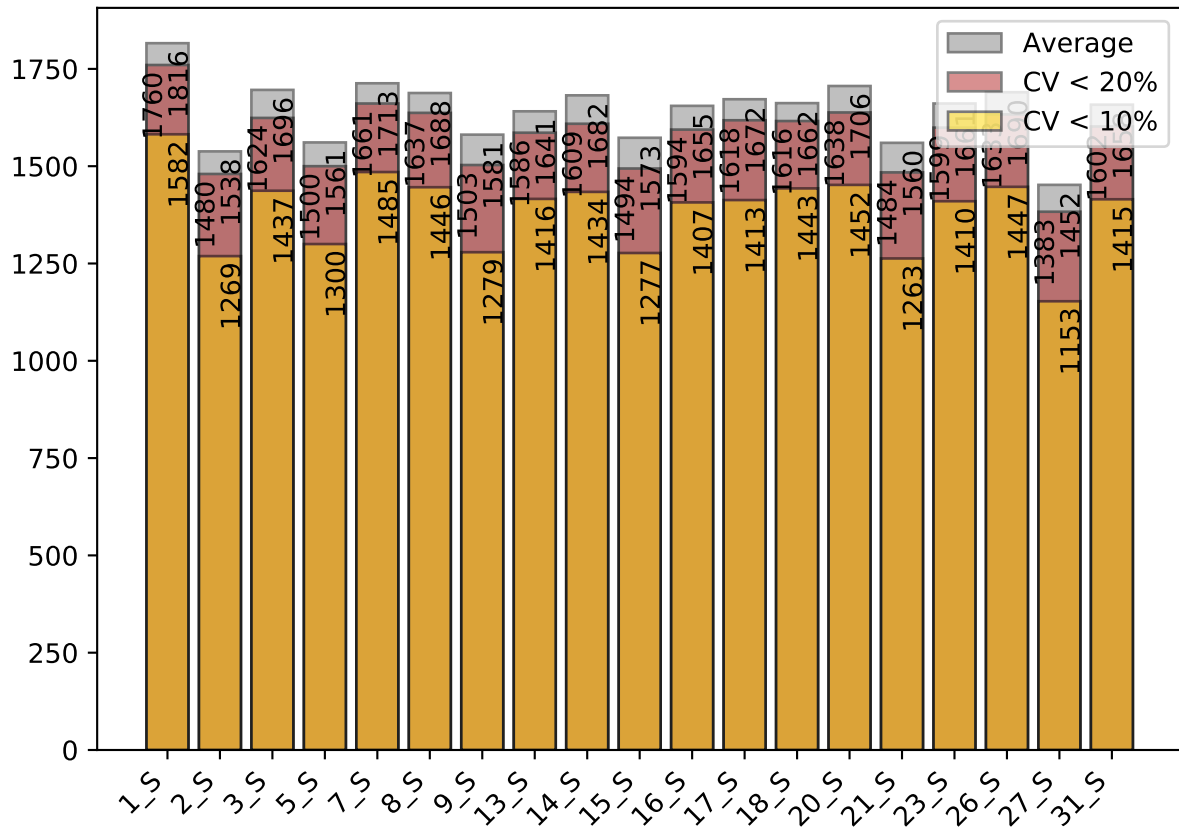
Precursors, 1% FDR



Median precursor CV, 1% FDR



Protein groups, 1% FDR



Median protein group CV, 1% FDR

