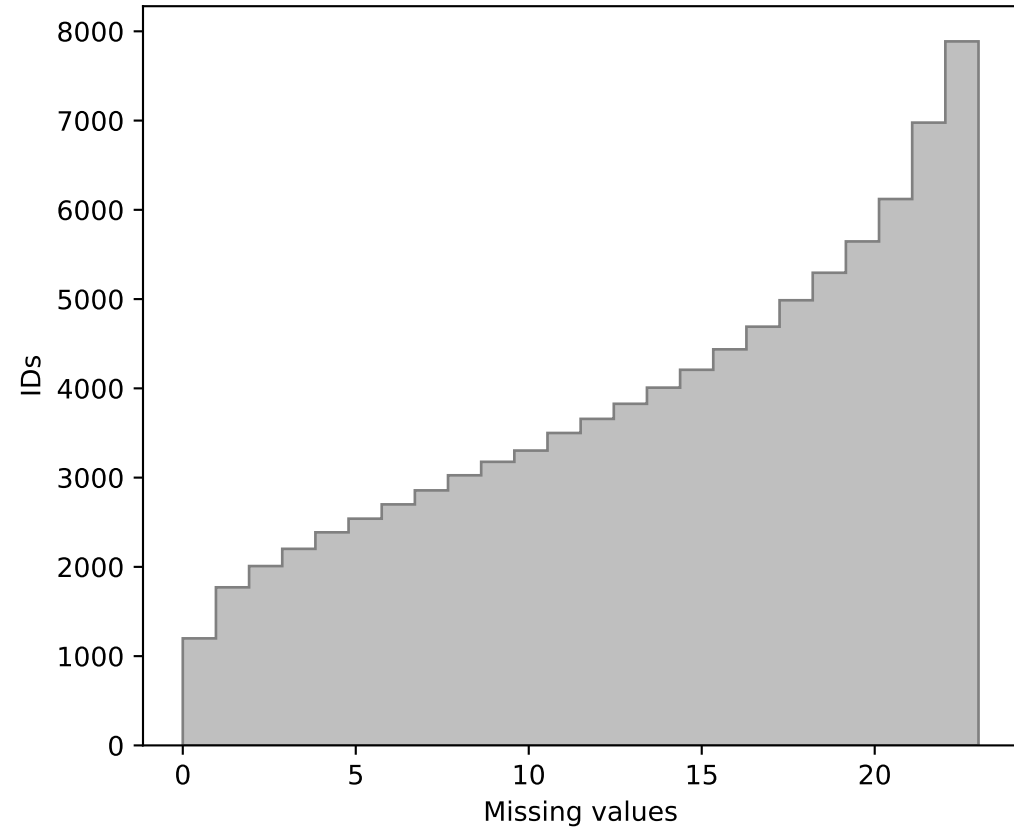
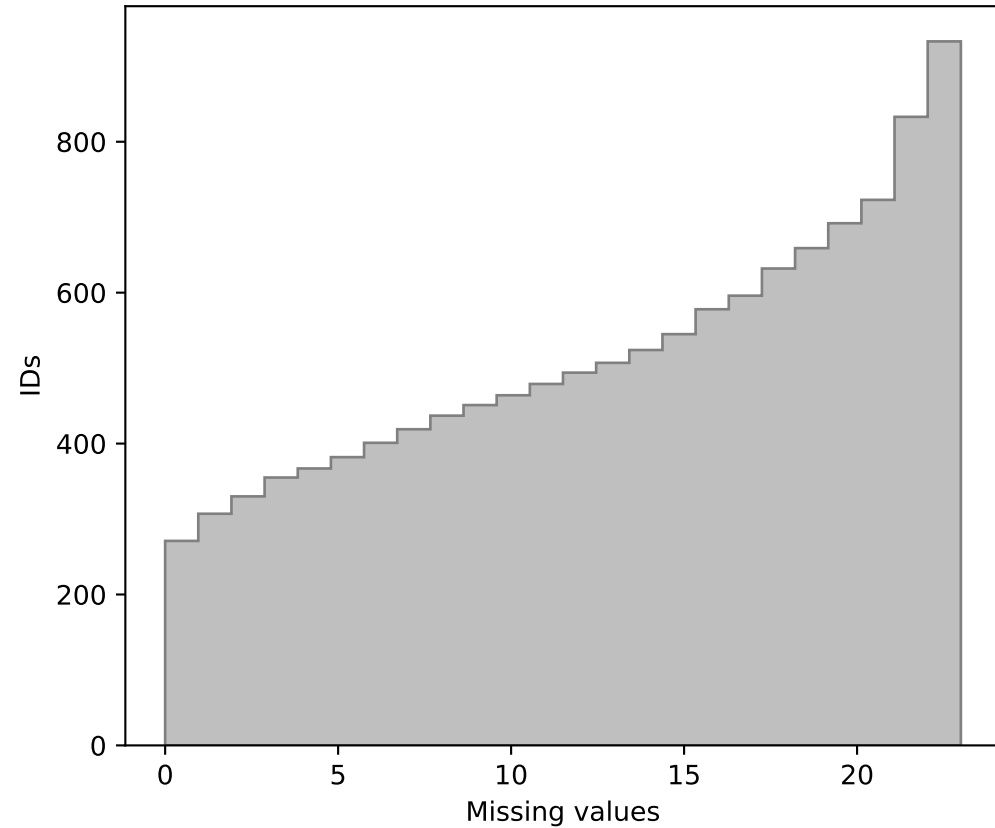


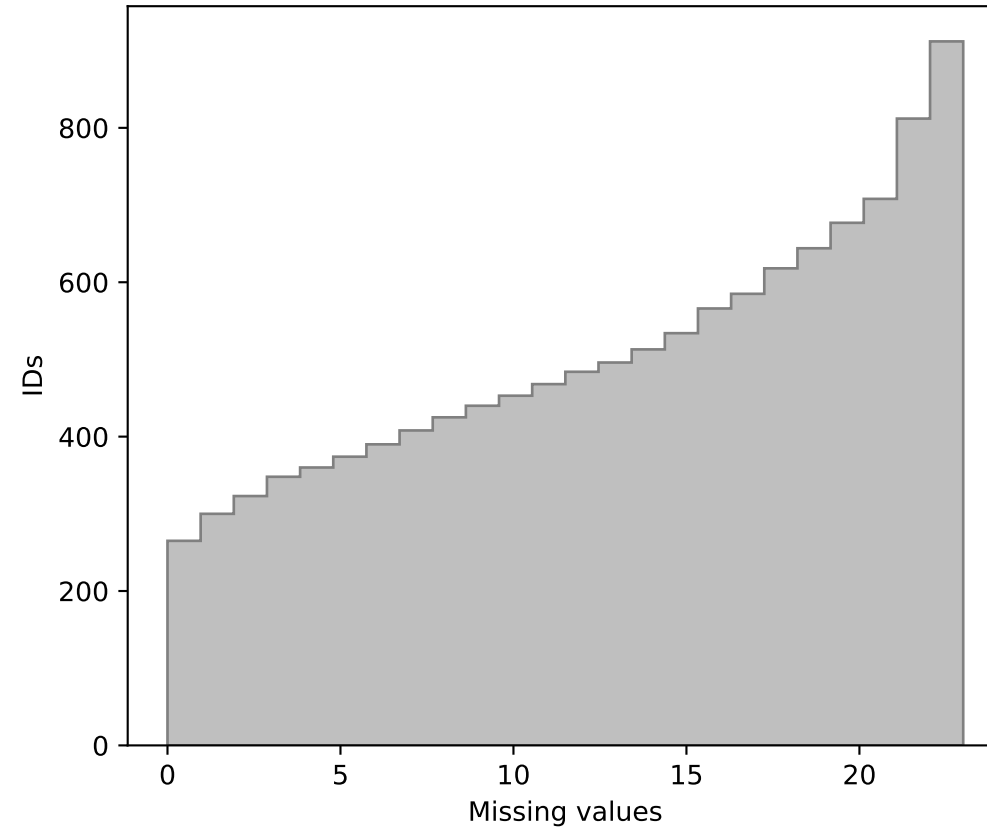
Identification consistency: precursors, CDF



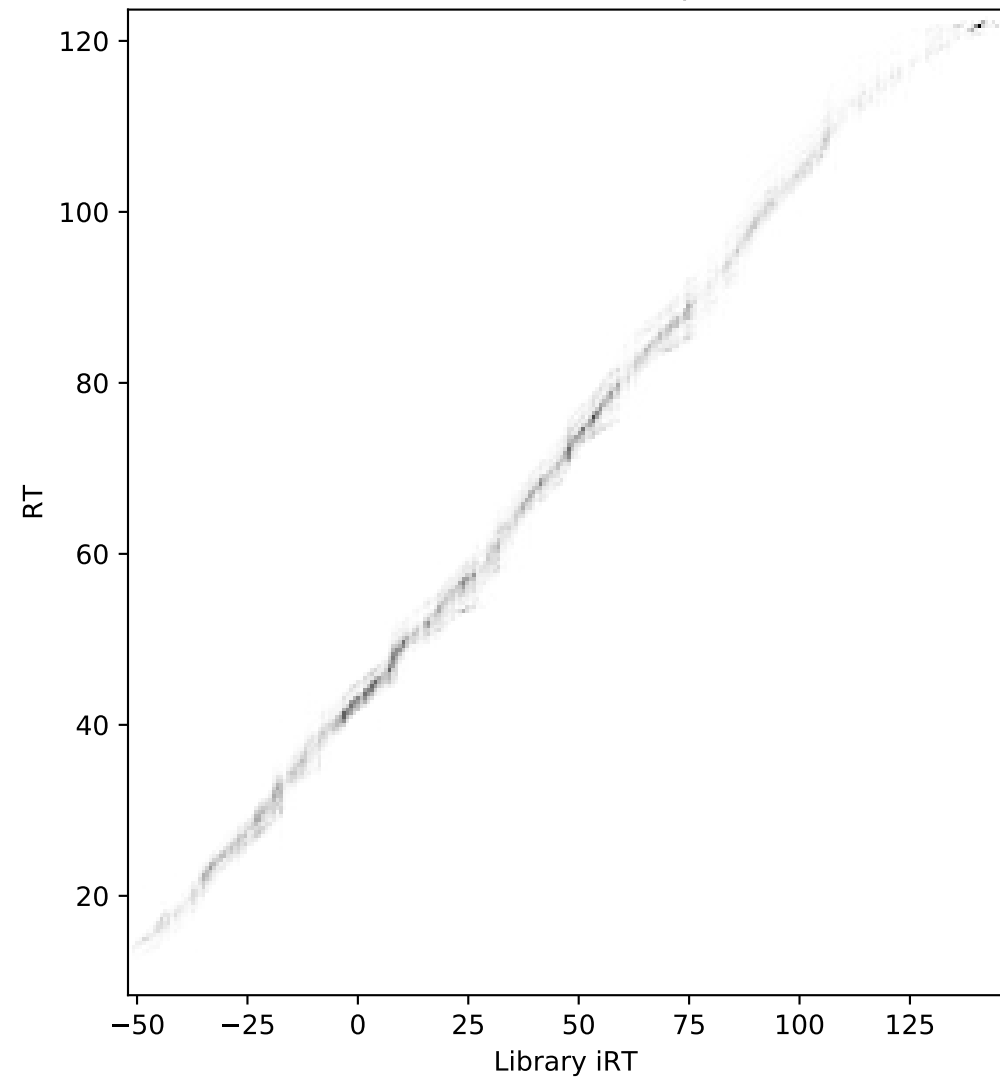
Identification consistency: protein groups, CDF



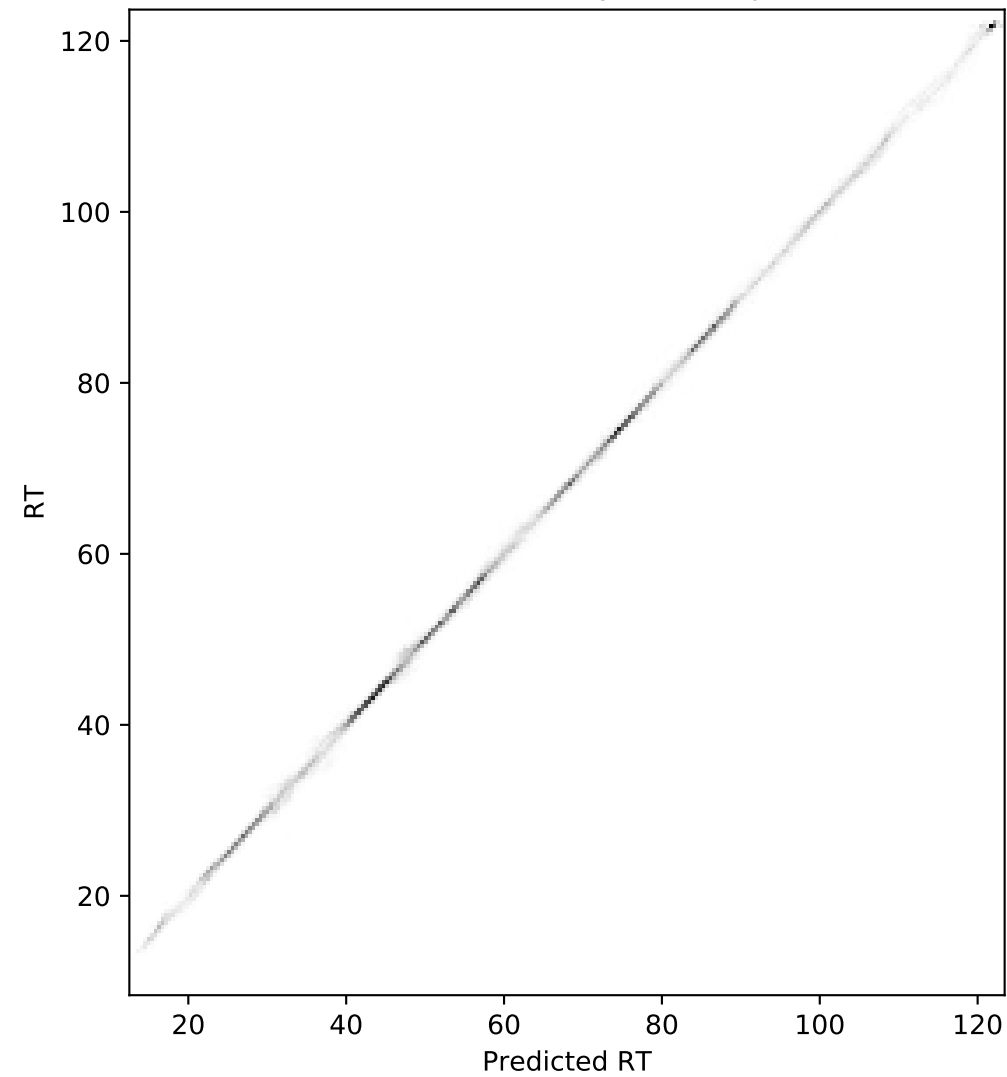
Identification consistency: genes groups, CDF



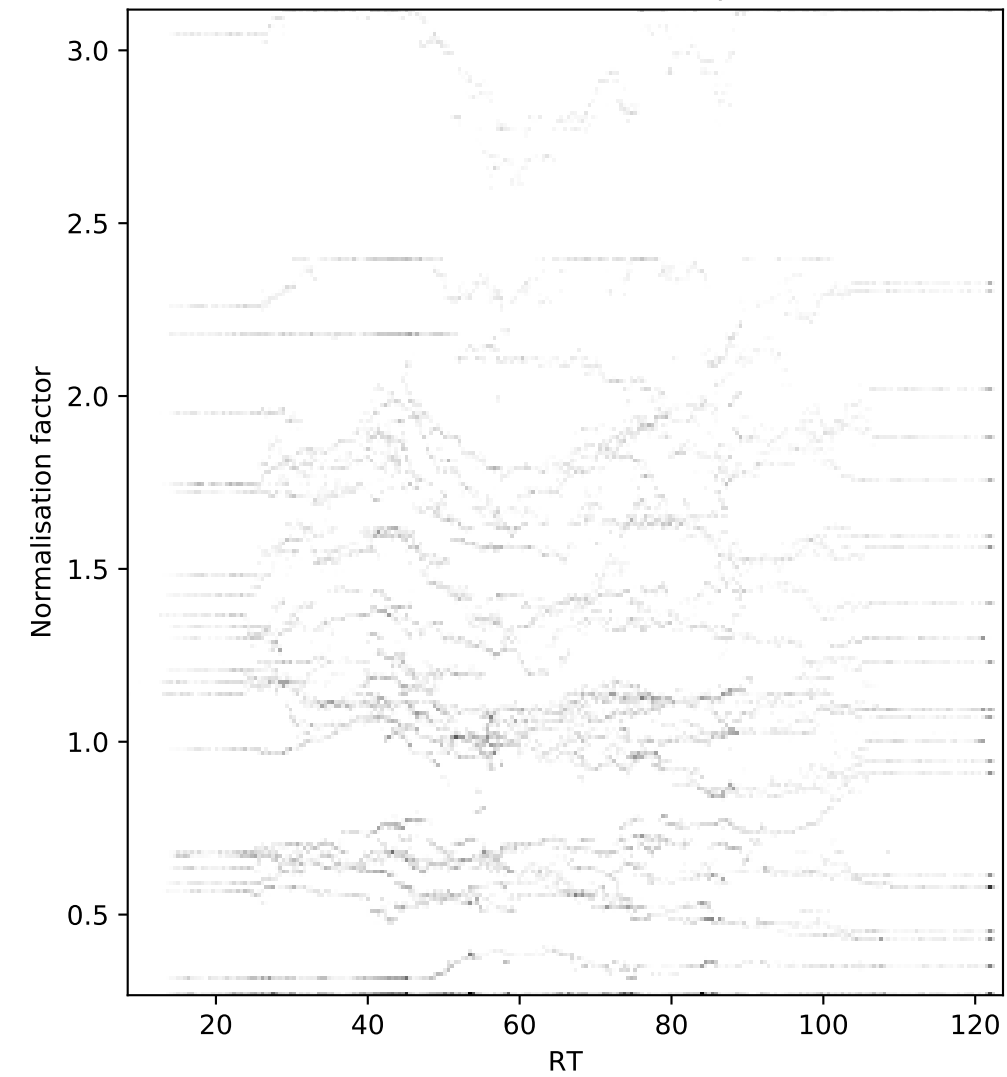
Retention times heatmap, all runs

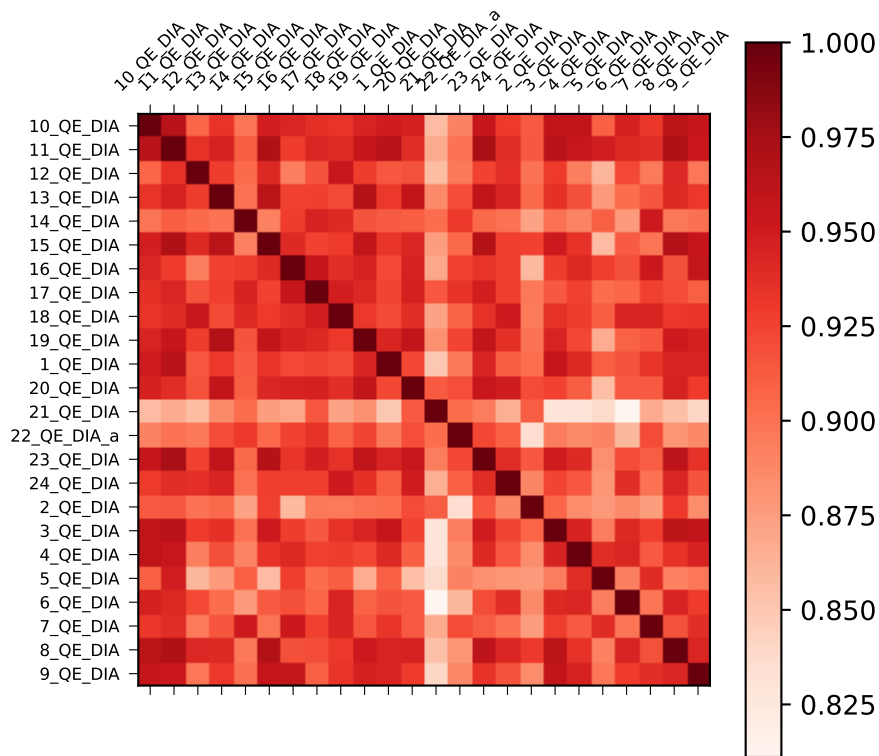


Retention time accuracy heatmap, all runs



Normalisation factor heatmap, all runs



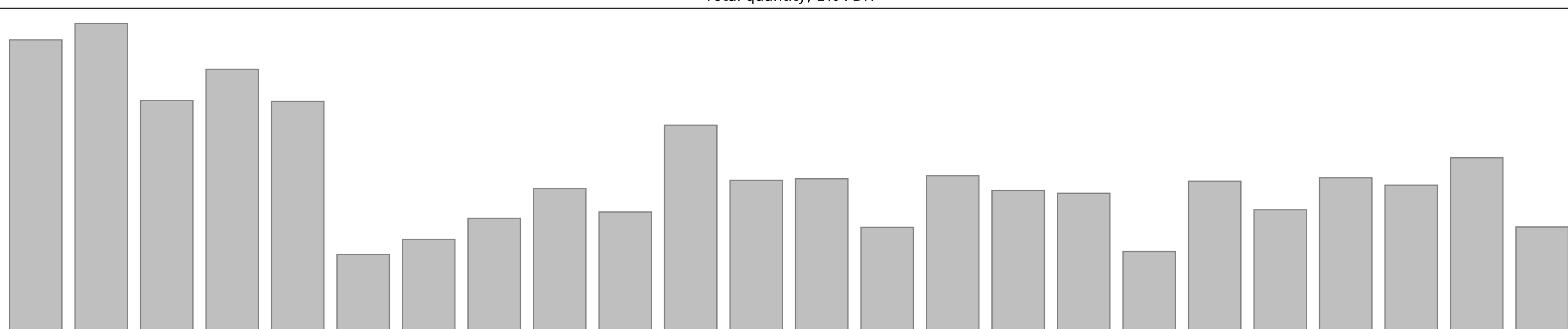


Total quantity, 1% FDR

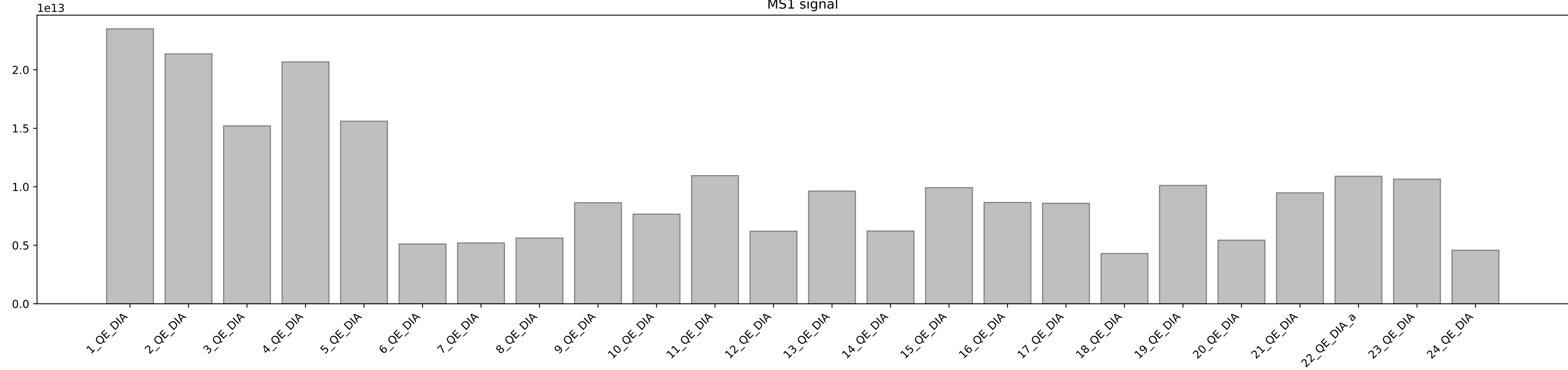
1e11

6
5
4
3
2
1
0

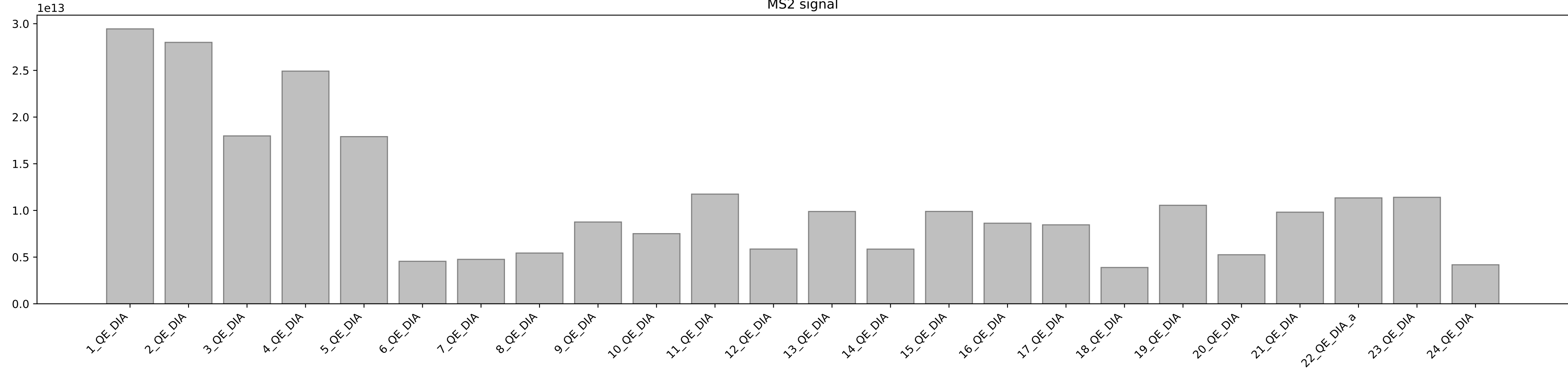
1_QE_DIA 2_QE_DIA 3_QE_DIA 4_QE_DIA 5_QE_DIA 6_QE_DIA 7_QE_DIA 8_QE_DIA 9_QE_DIA 10_QE_DIA 11_QE_DIA 12_QE_DIA 13_QE_DIA 14_QE_DIA 15_QE_DIA 16_QE_DIA 17_QE_DIA 18_QE_DIA 19_QE_DIA 20_QE_DIA 21_QE_DIA 22_QE_DIA_a 23_QE_DIA 24_QE_DIA



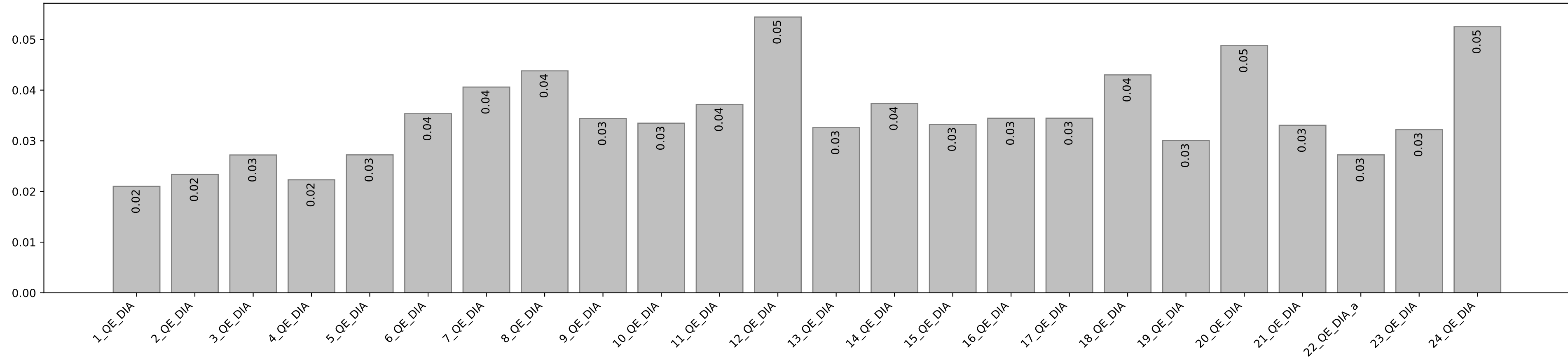
MS1 signal



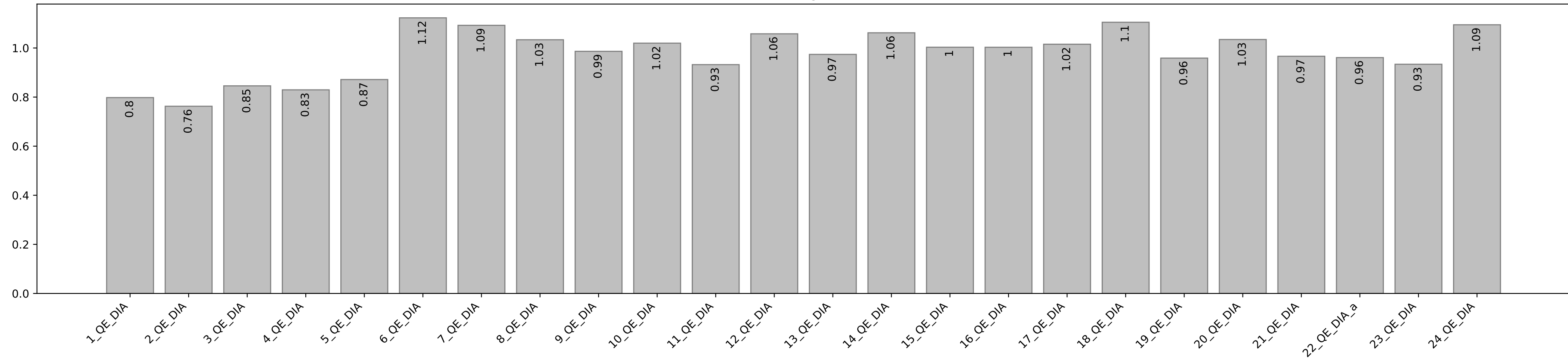
MS2 signal



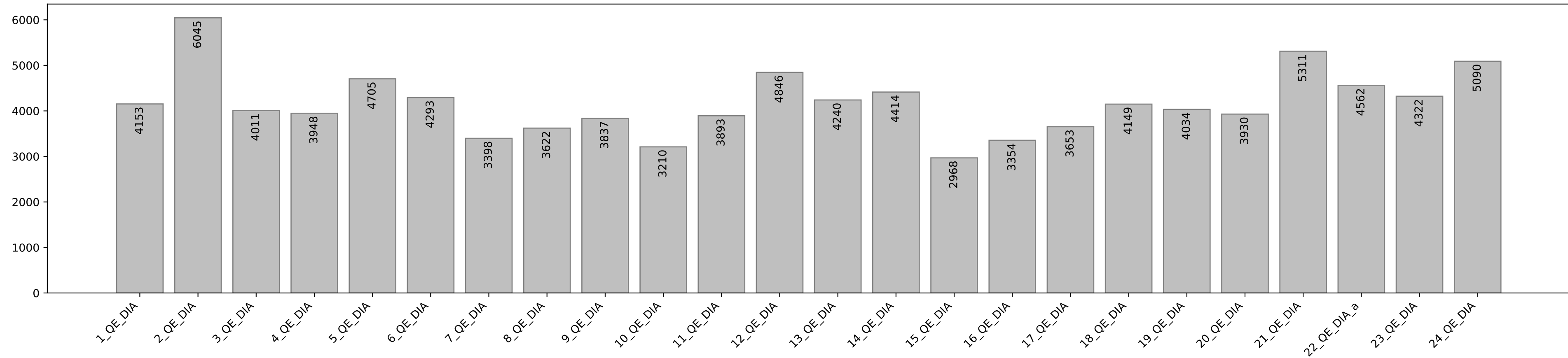
Total quantity/MS2 signal ratio



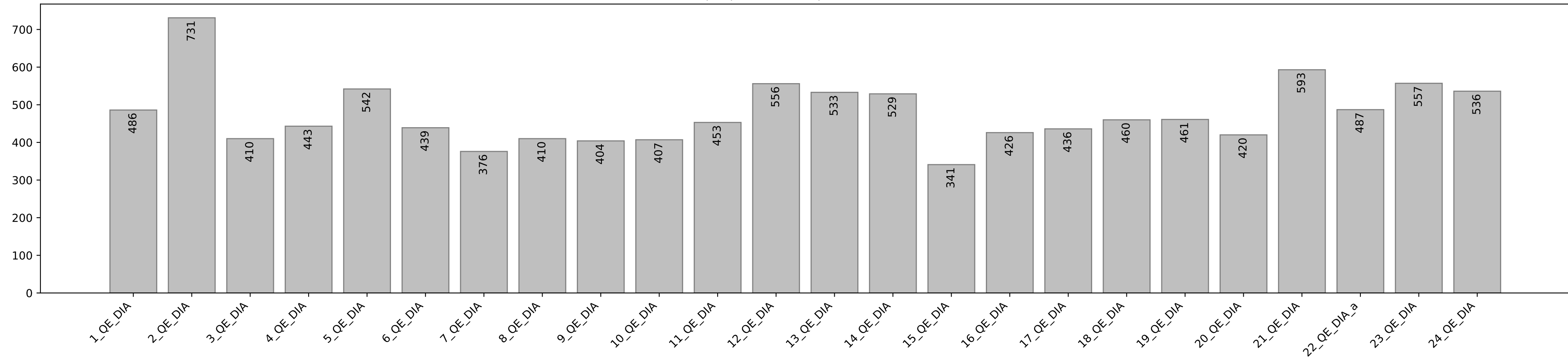
MS1/MS2 signal ratio



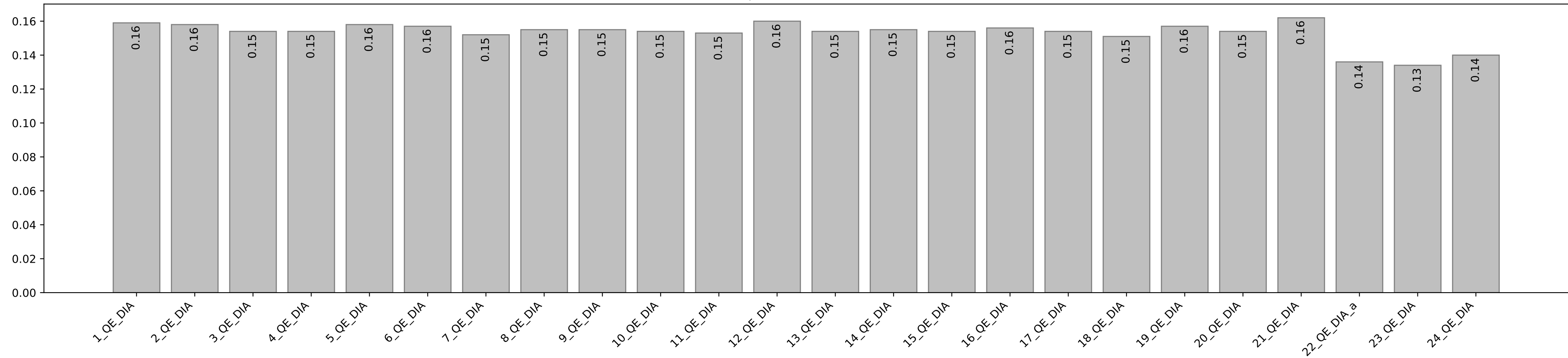
Precursors, 1% FDR



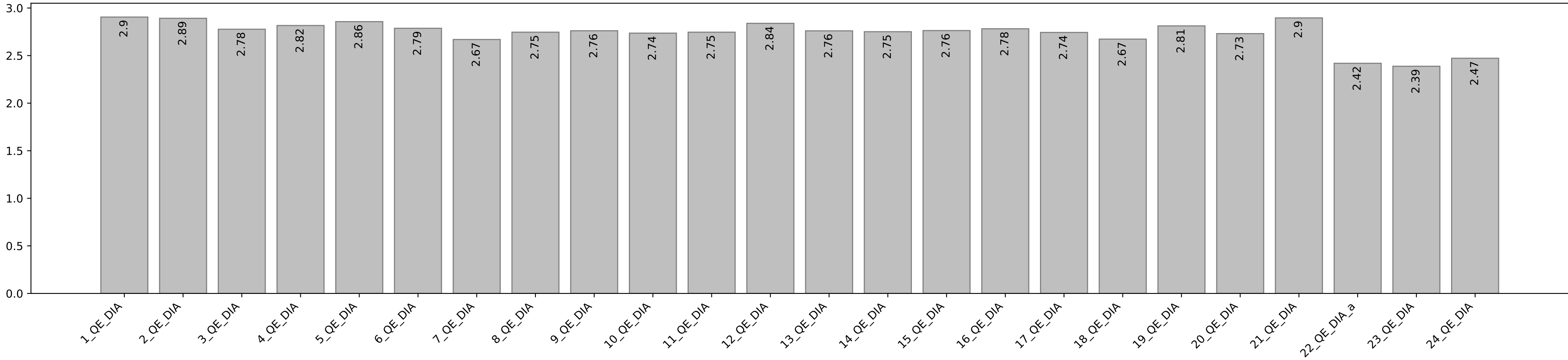
Unique proteins, 1% protein-level FDR



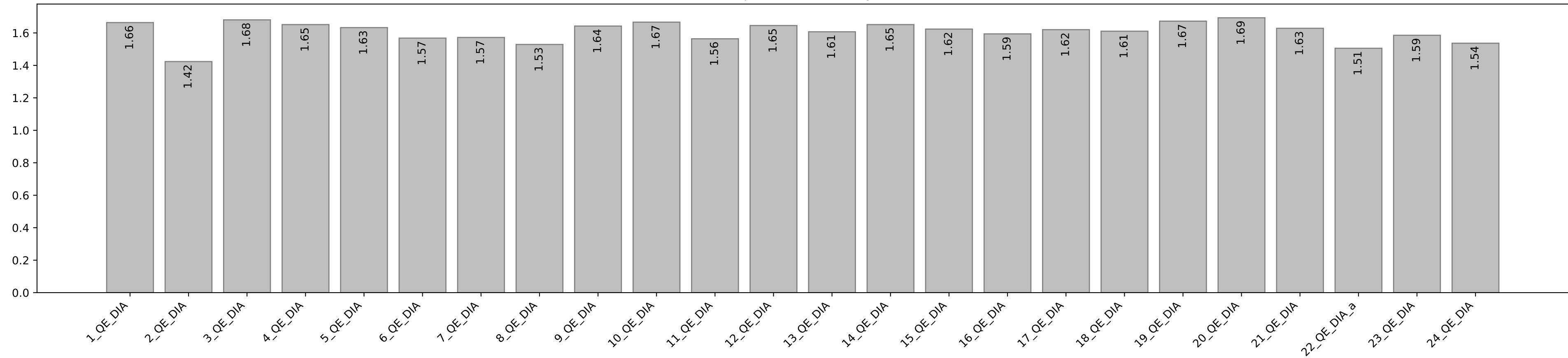
Mean peak FWHM, in minutes



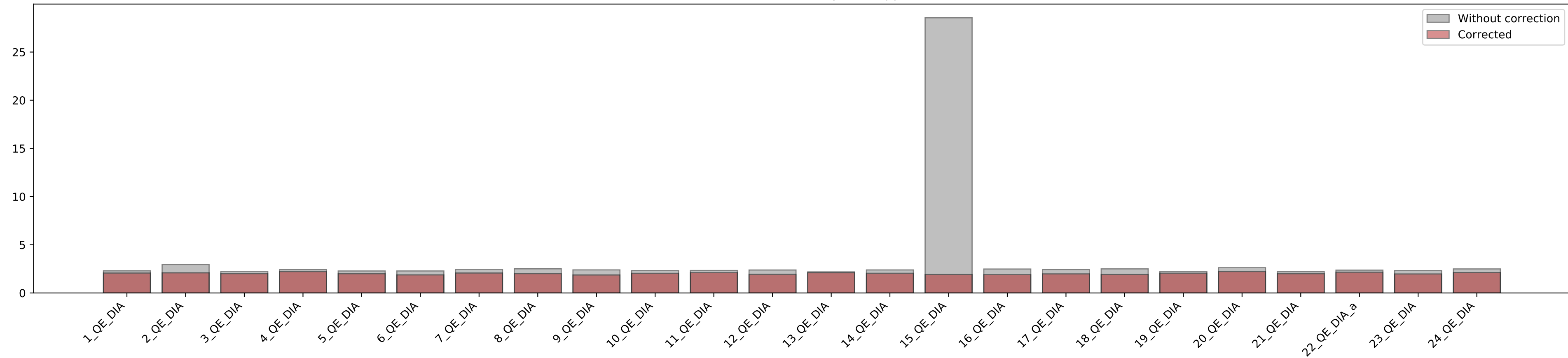
Mean peak FWHM, in MS2 scans



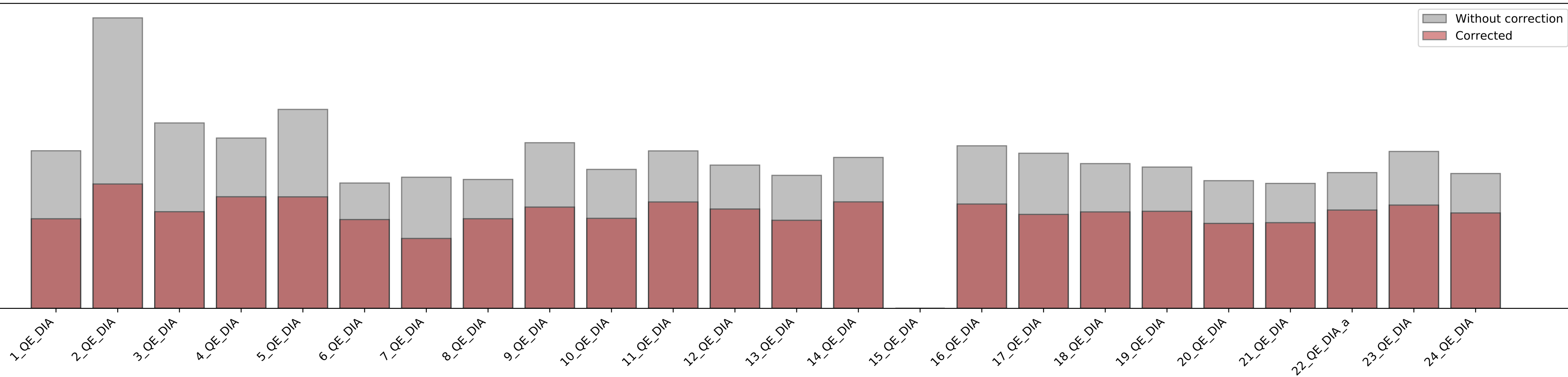
Median RT prediction accuracy, minutes



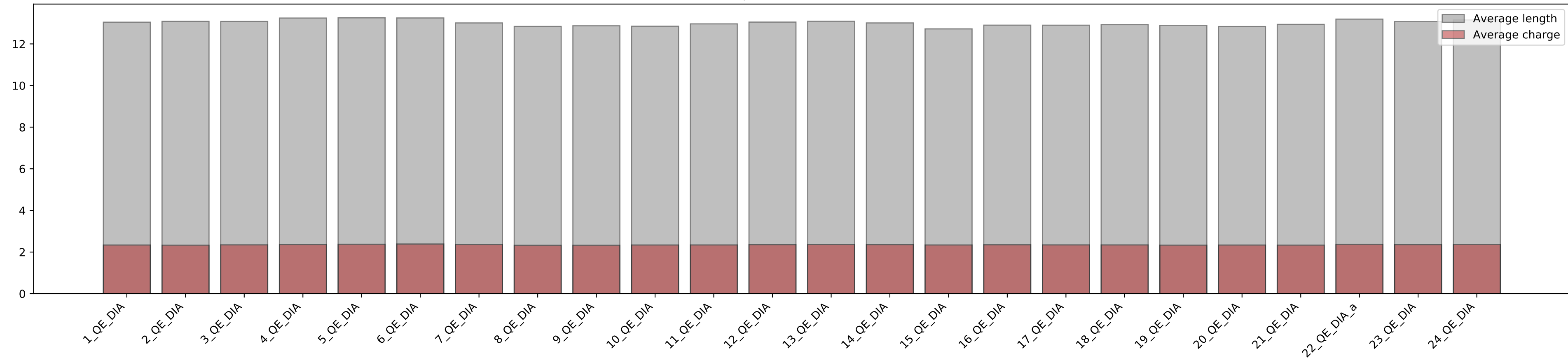
Median mass accuracy, MS2, ppm



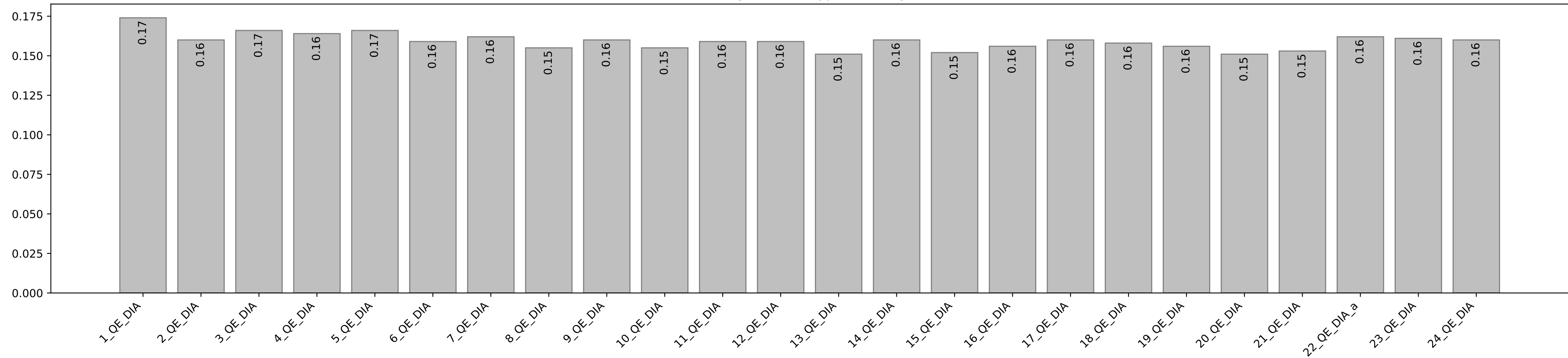
Median mass accuracy, MS1, ppm



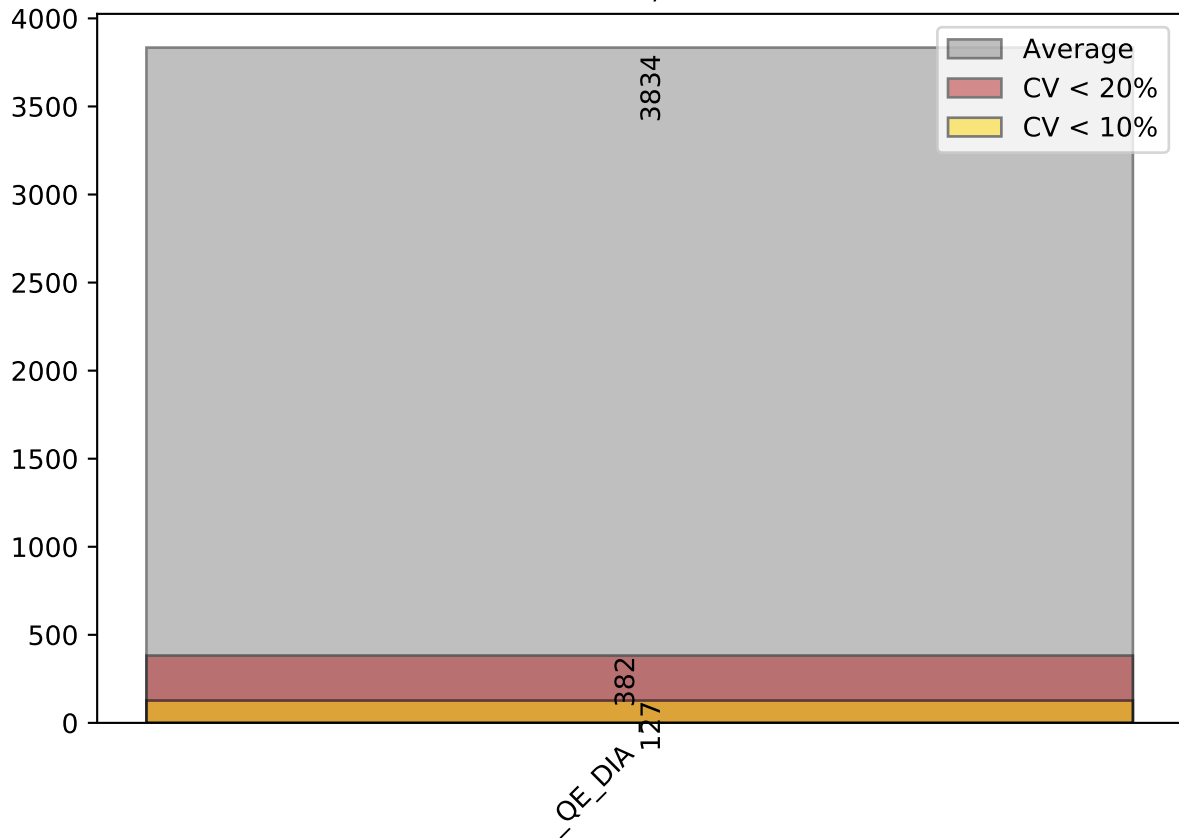
Peptide characteristics



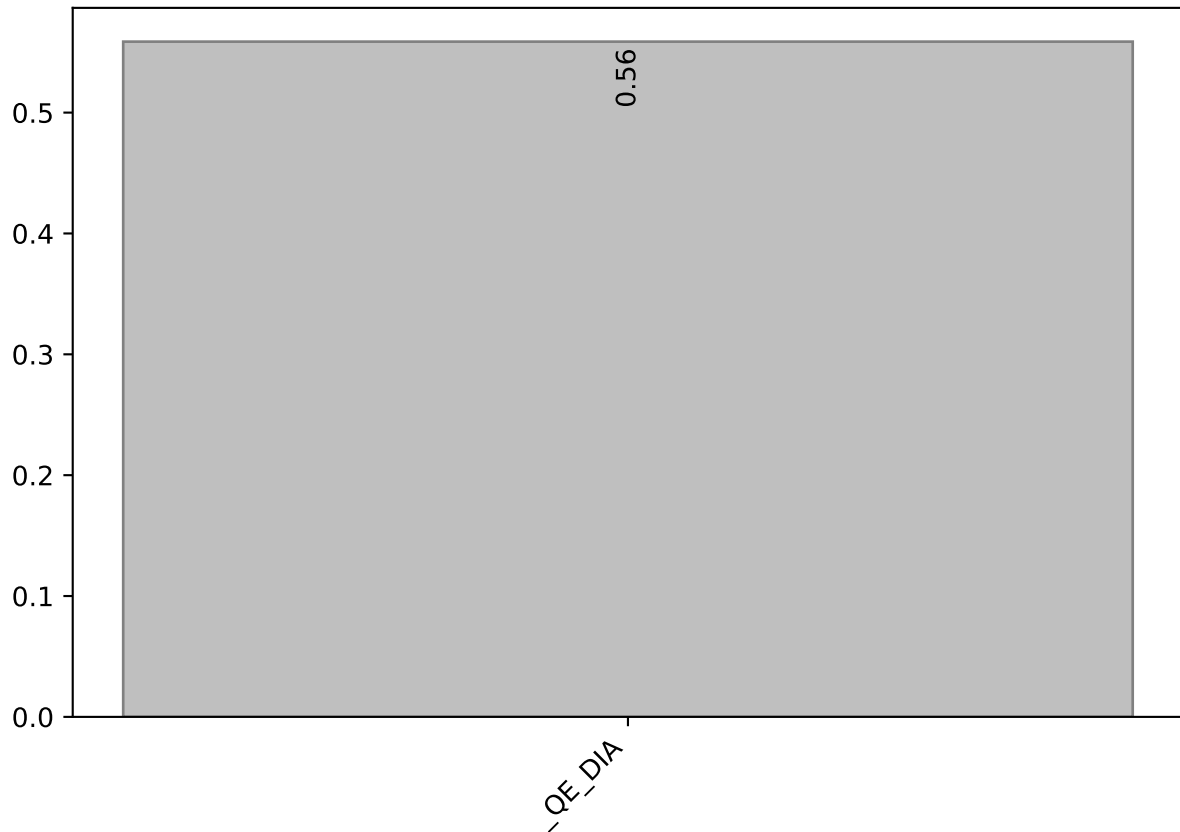
Average missed tryptic cleavages



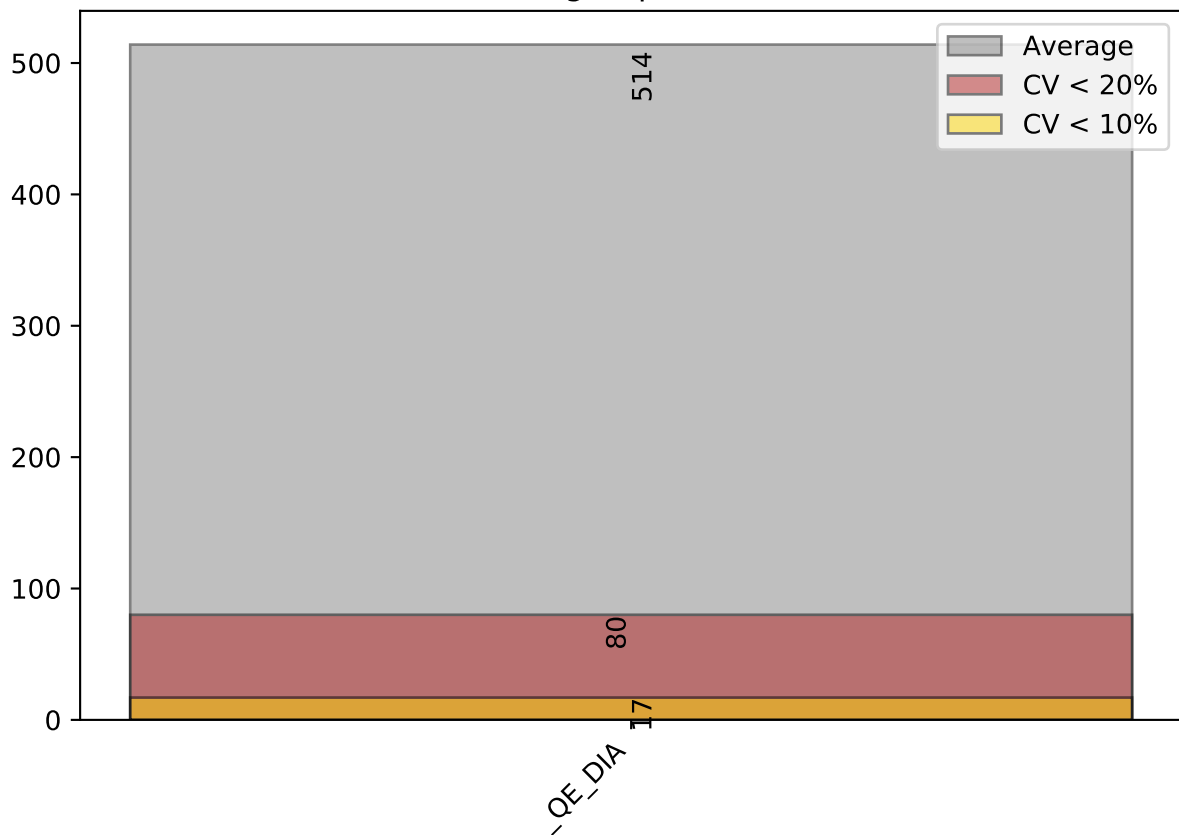
Precursors, 1% FDR



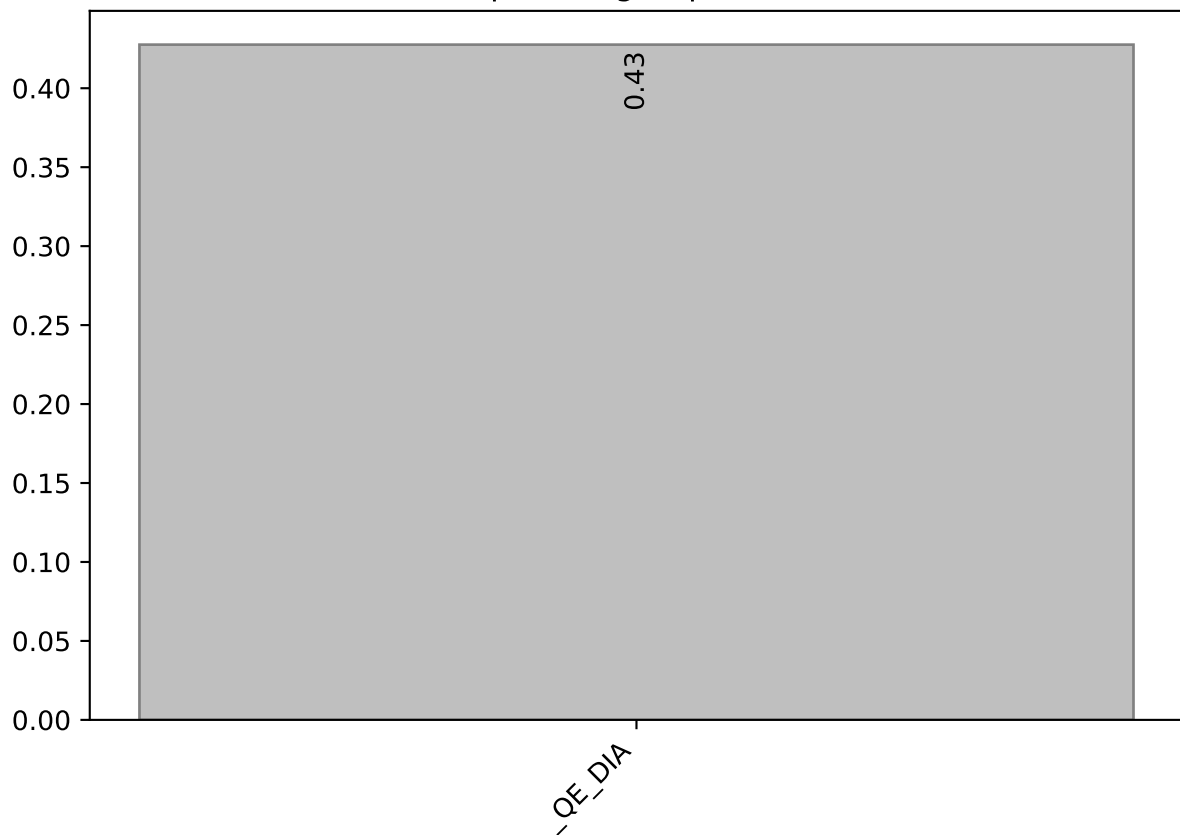
Median precursor CV, 1% FDR



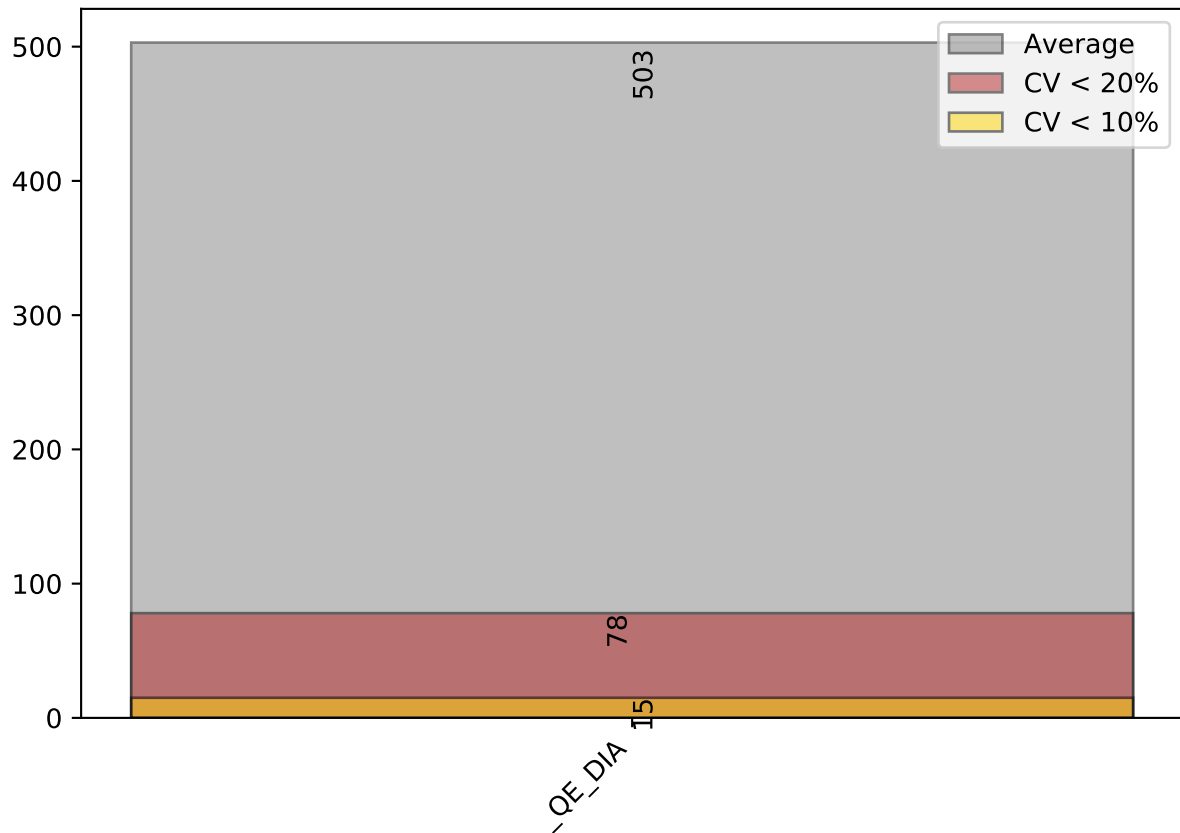
Protein groups, 1% FDR



Median protein group CV, 1% FDR



Gene groups, 1% FDR



Median gene group CV, 1% FDR

