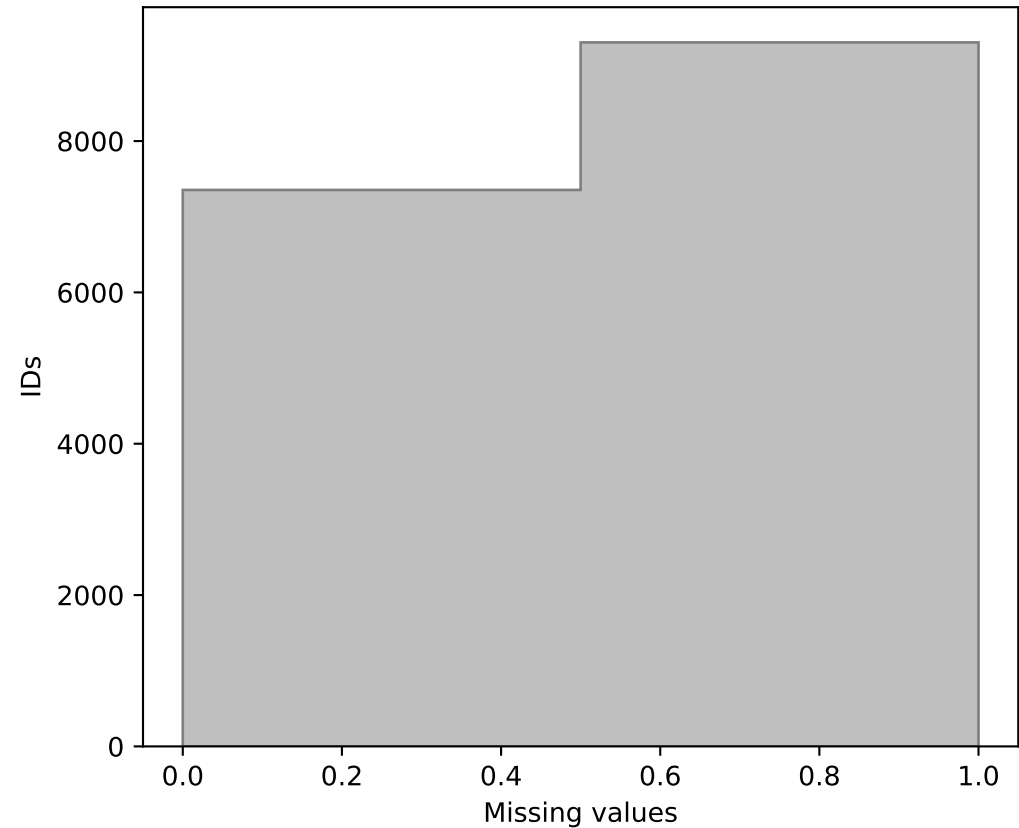
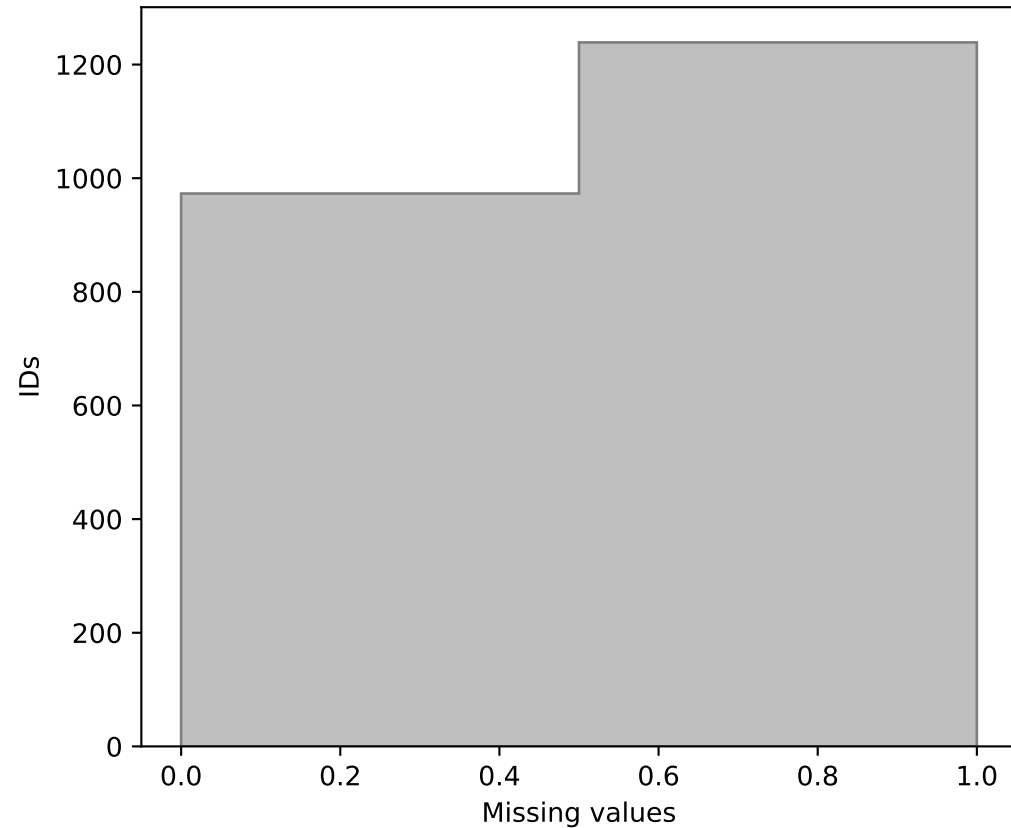


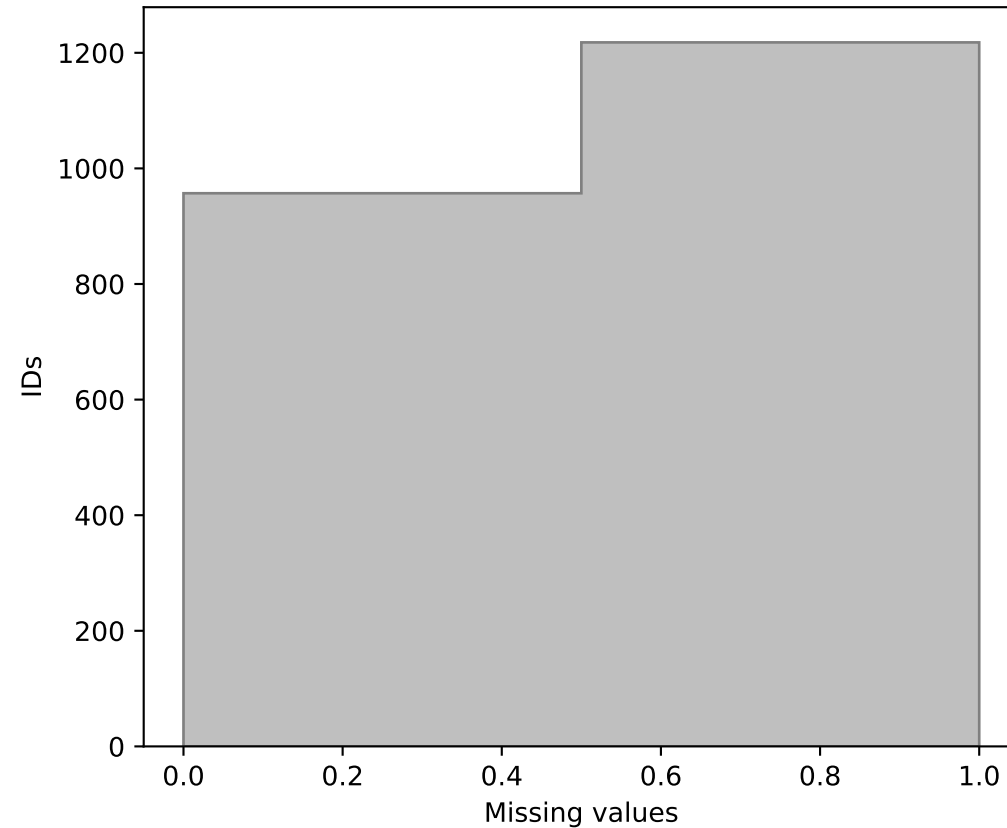
Identification consistency: precursors, CDF



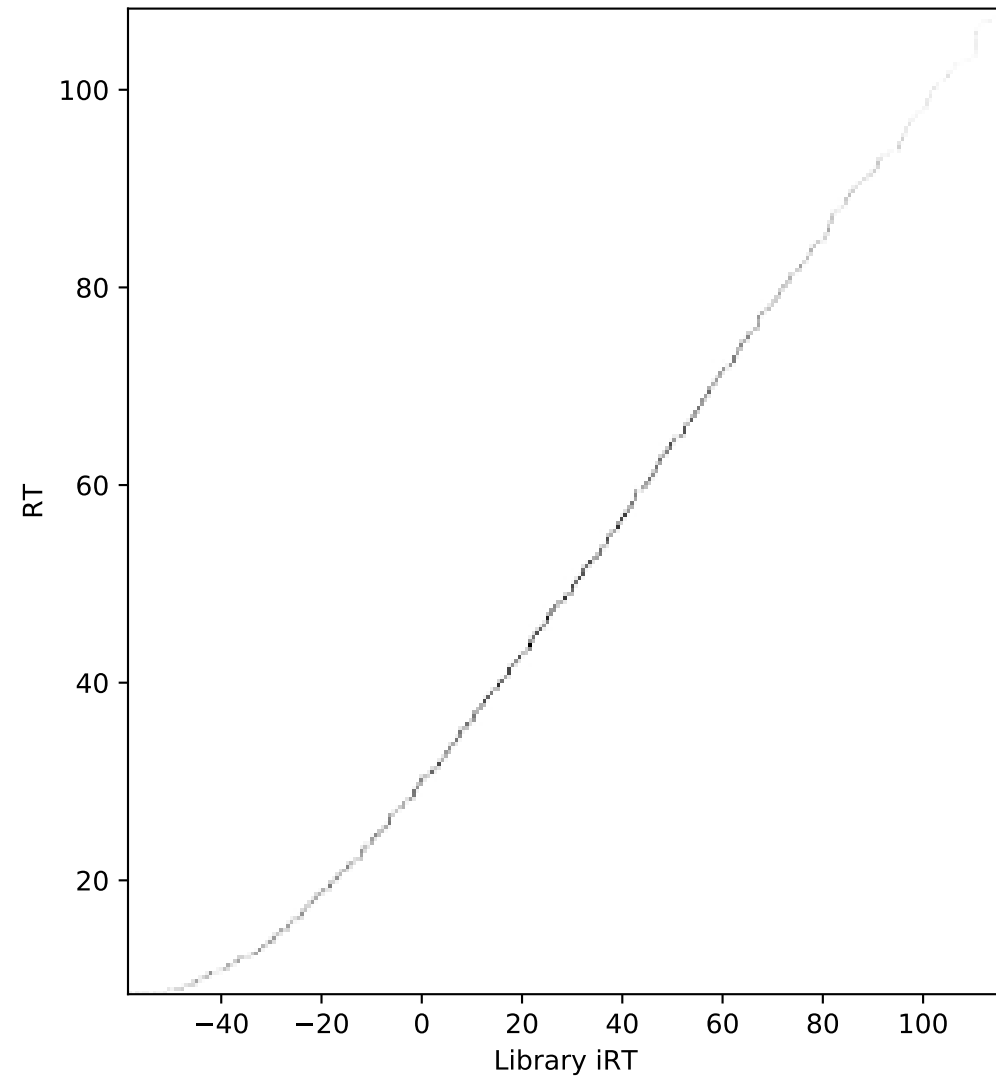
Identification consistency: protein groups, CDF



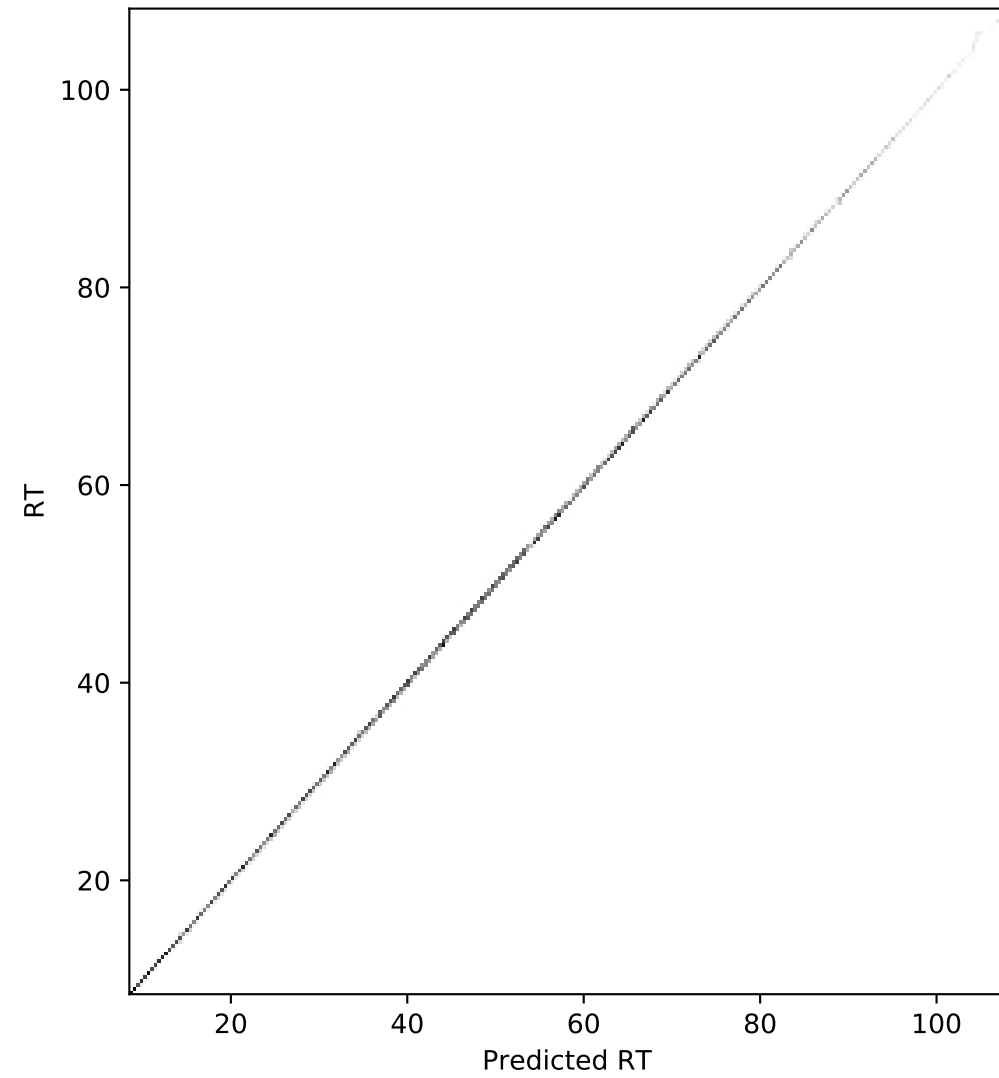
Identification consistency: genes groups, CDF



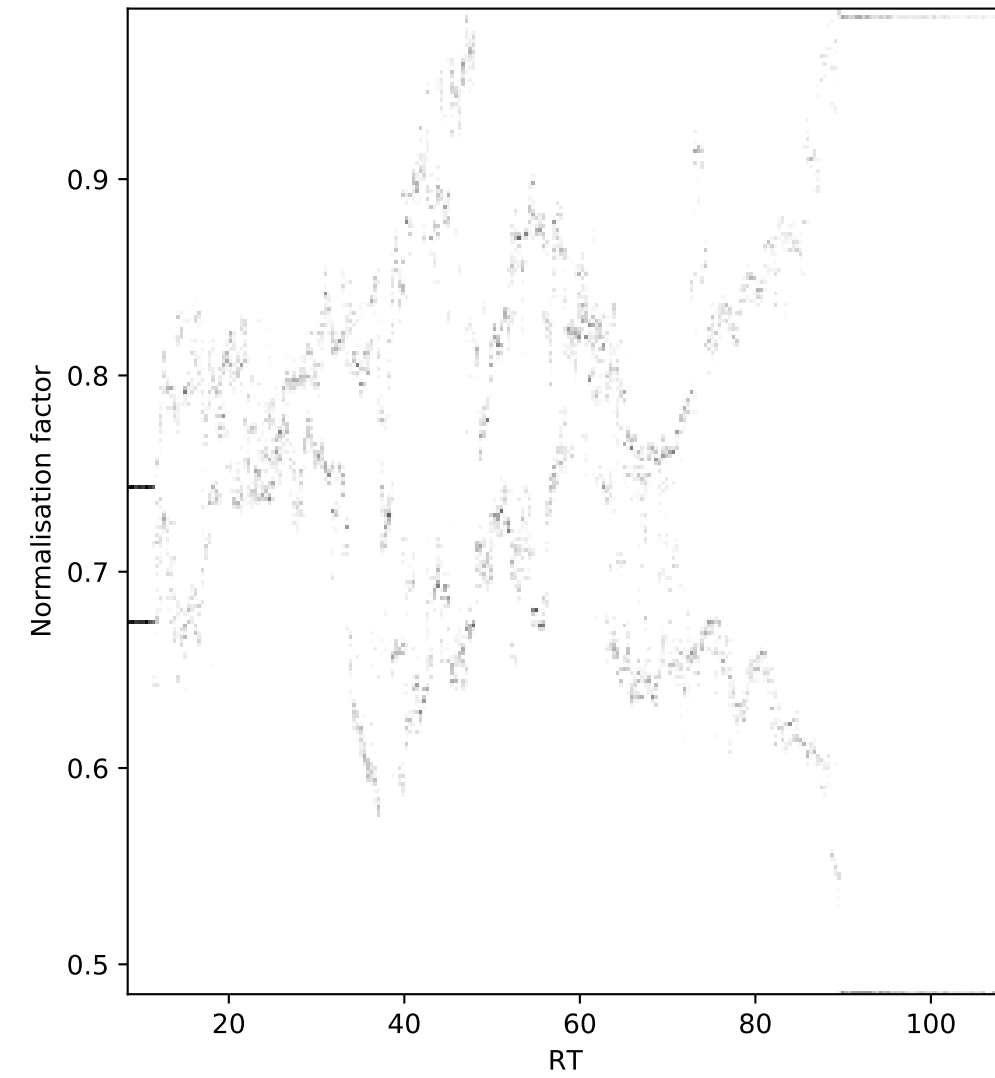
Retention times heatmap, all runs

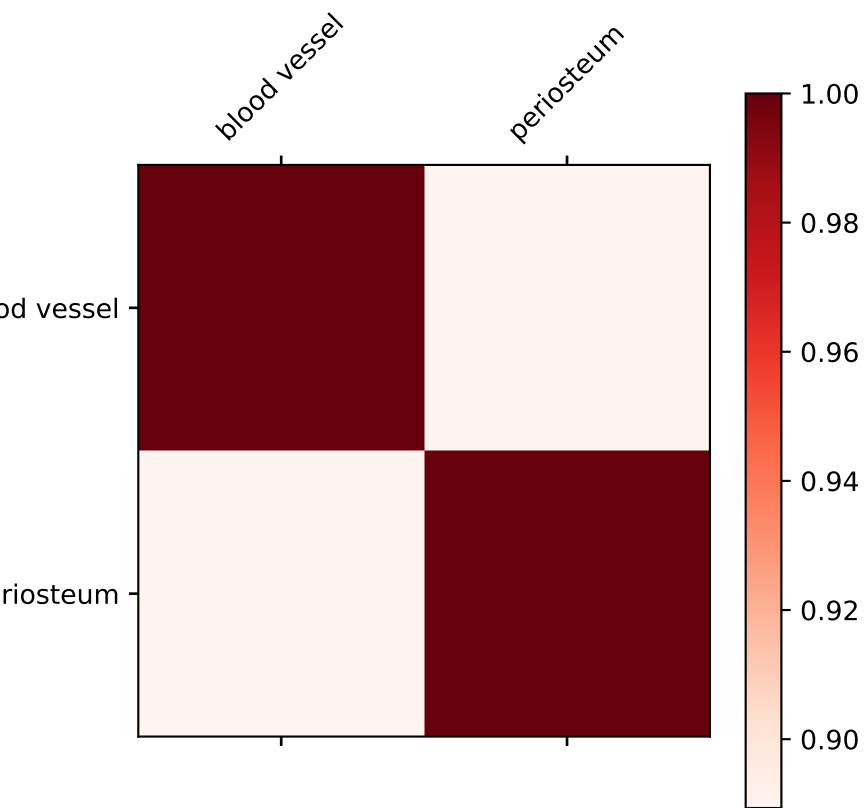


Retention time accuracy heatmap, all runs

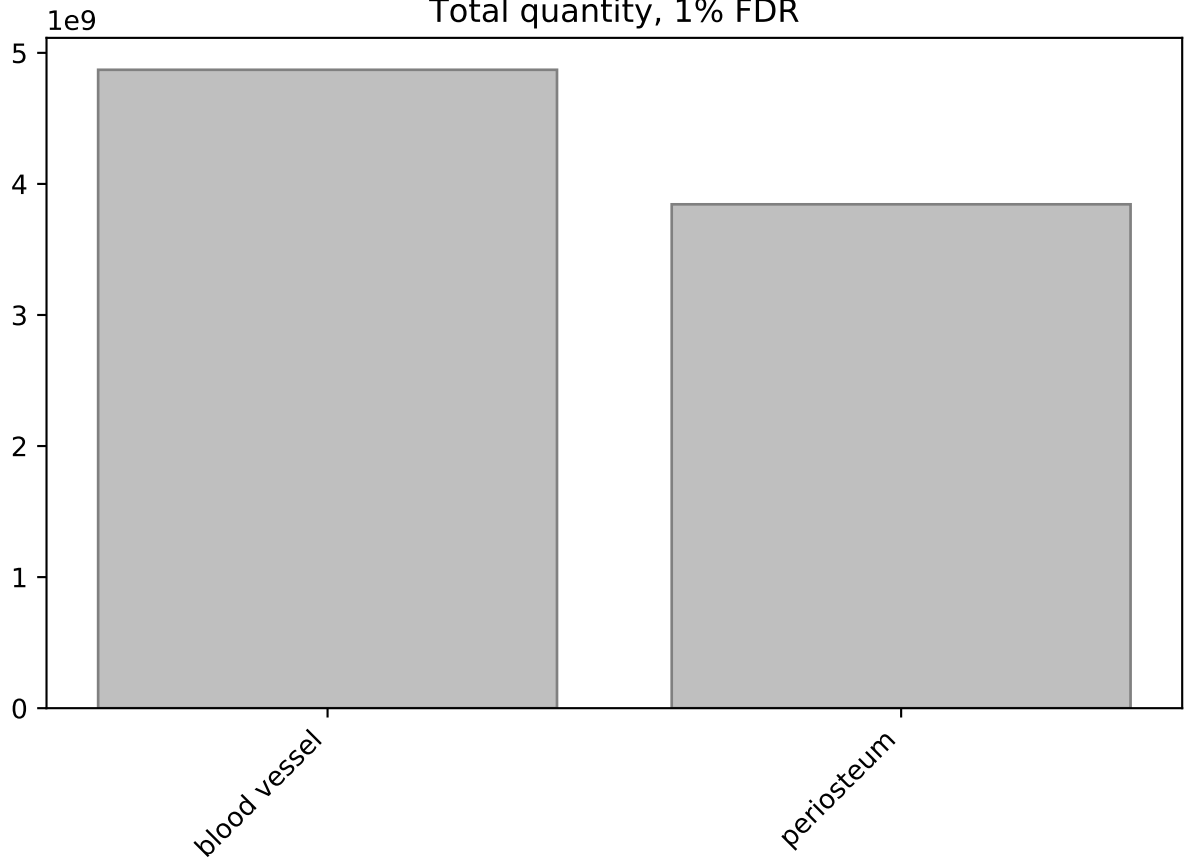


Normalisation factor heatmap, all runs





Total quantity, 1% FDR



MS1 signal

1e10

7

6

5

4

3

2

1

0

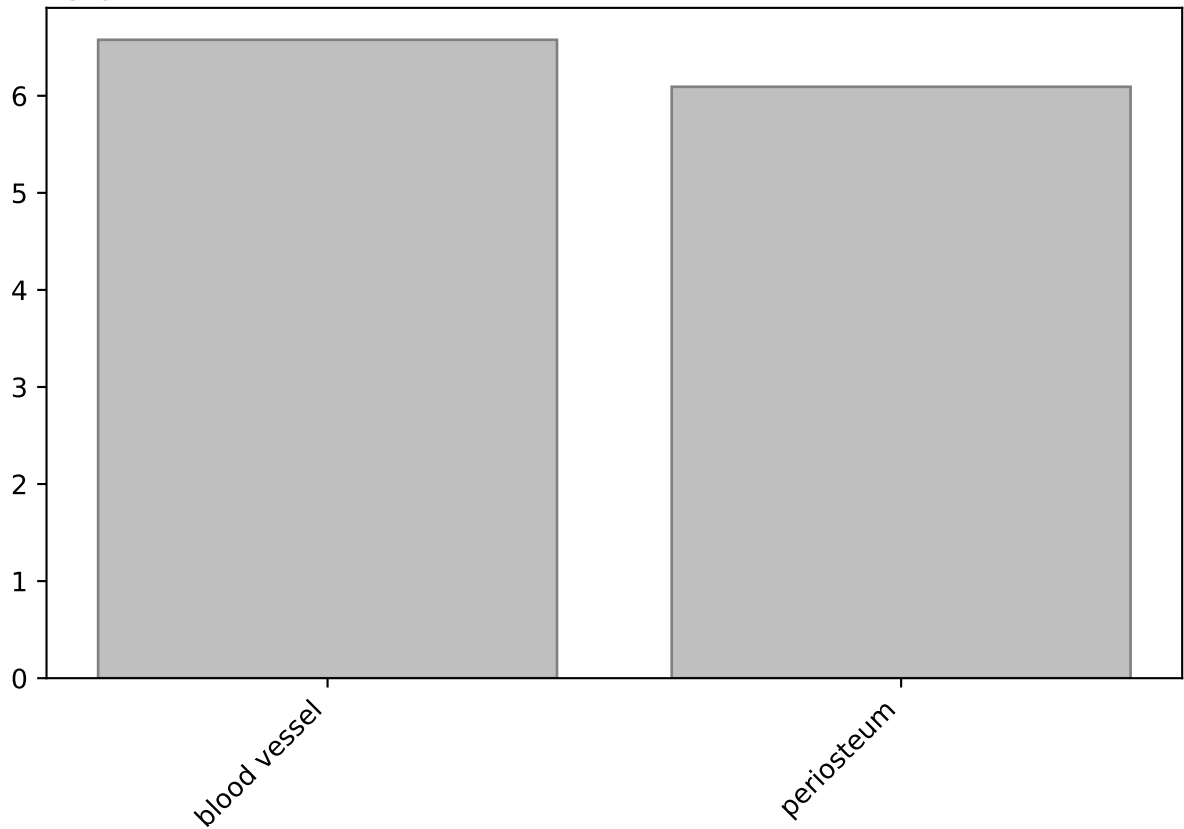
blood vessel

periosteum

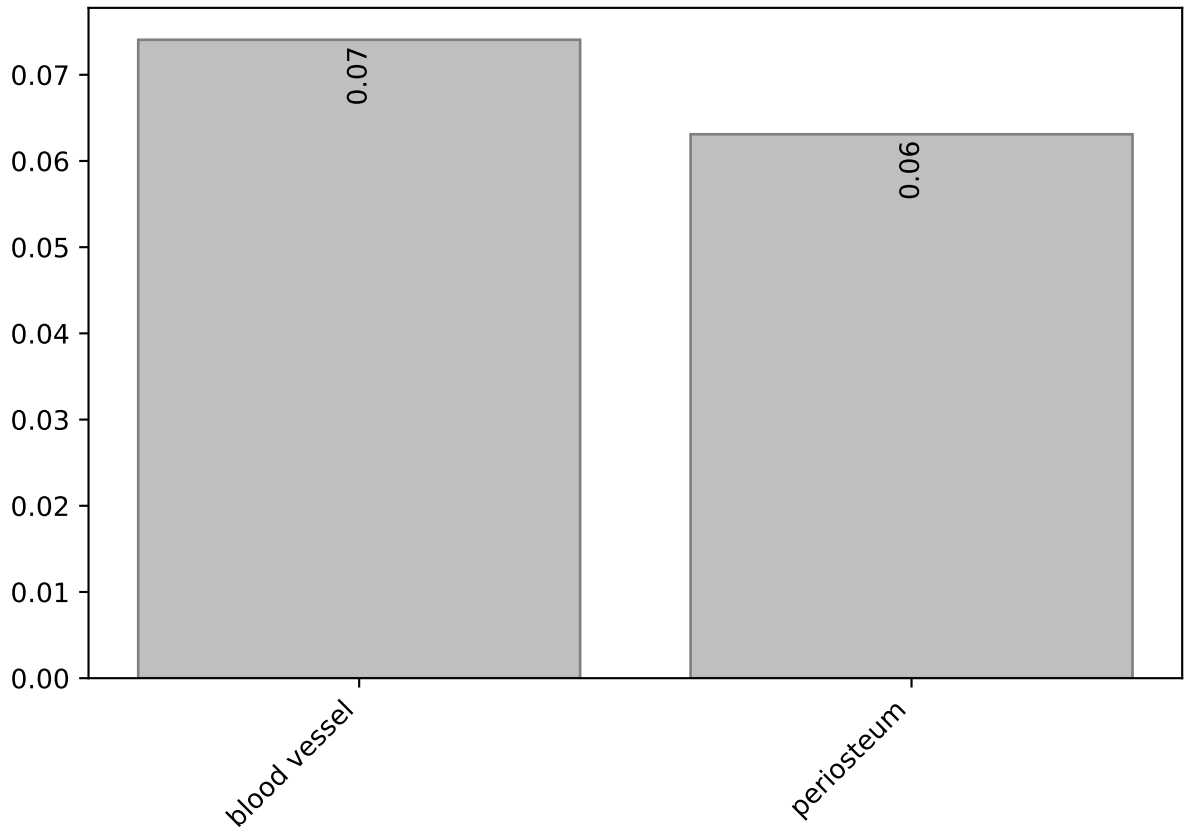


MS2 signal

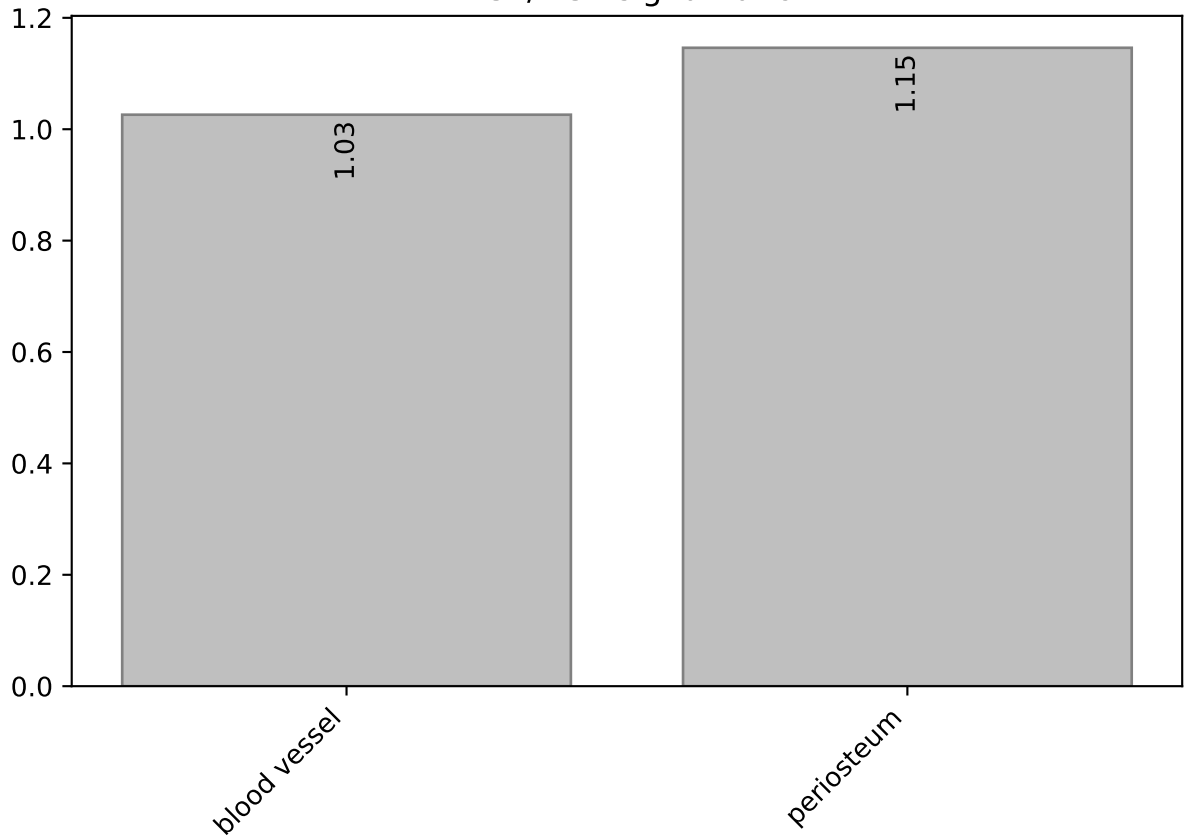
1e10



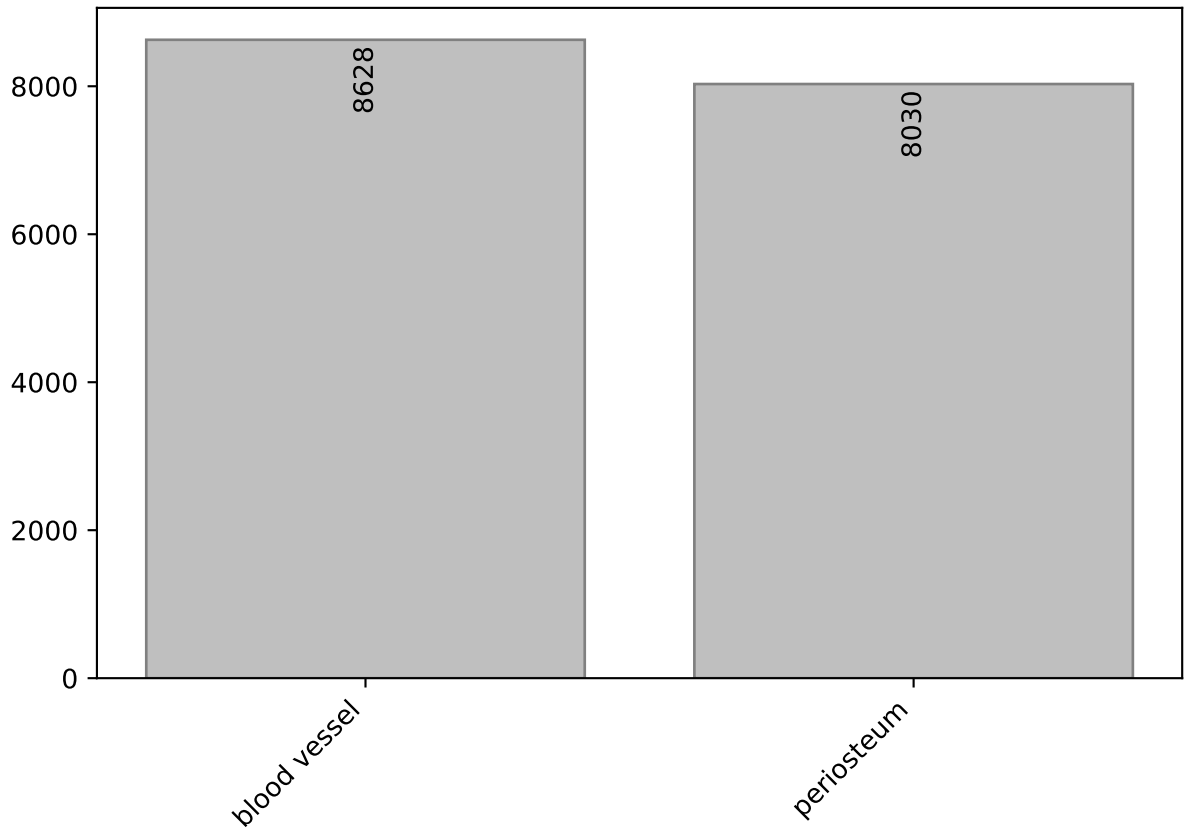
Total quantity/MS2 signal ratio



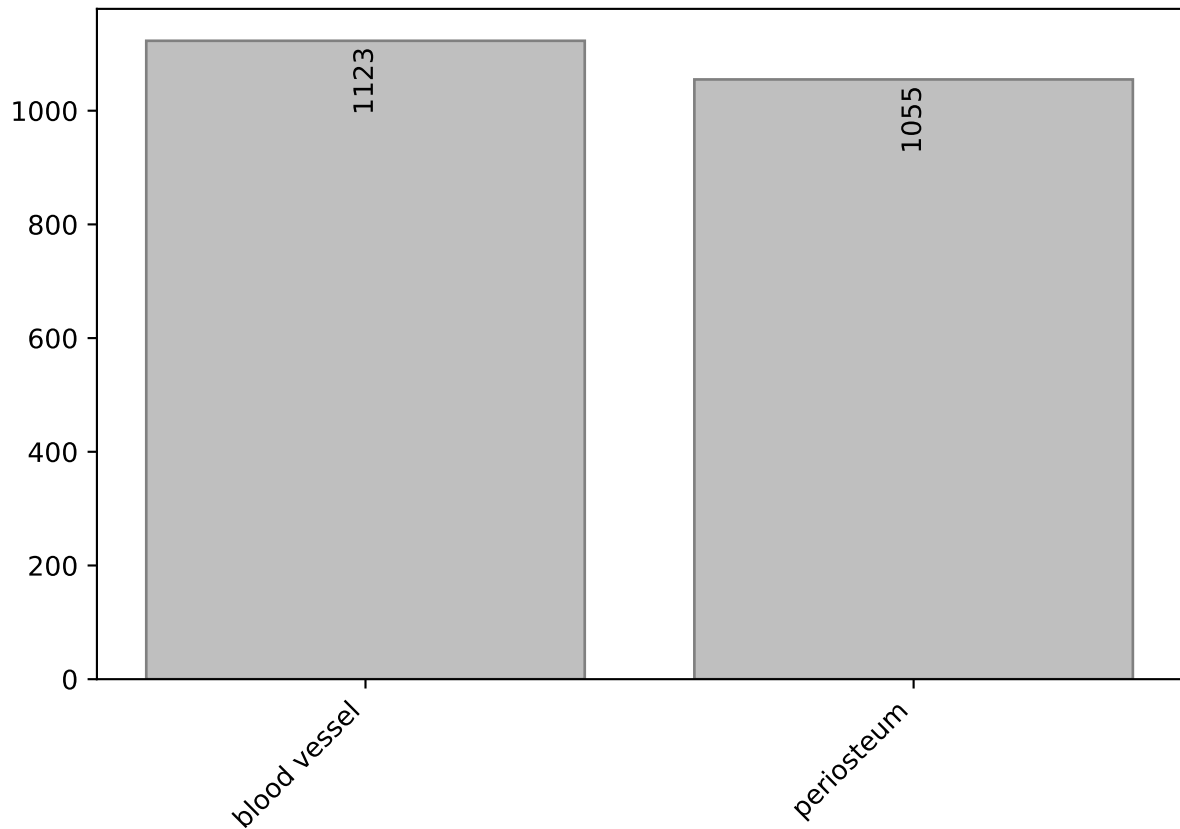
MS1/MS2 signal ratio



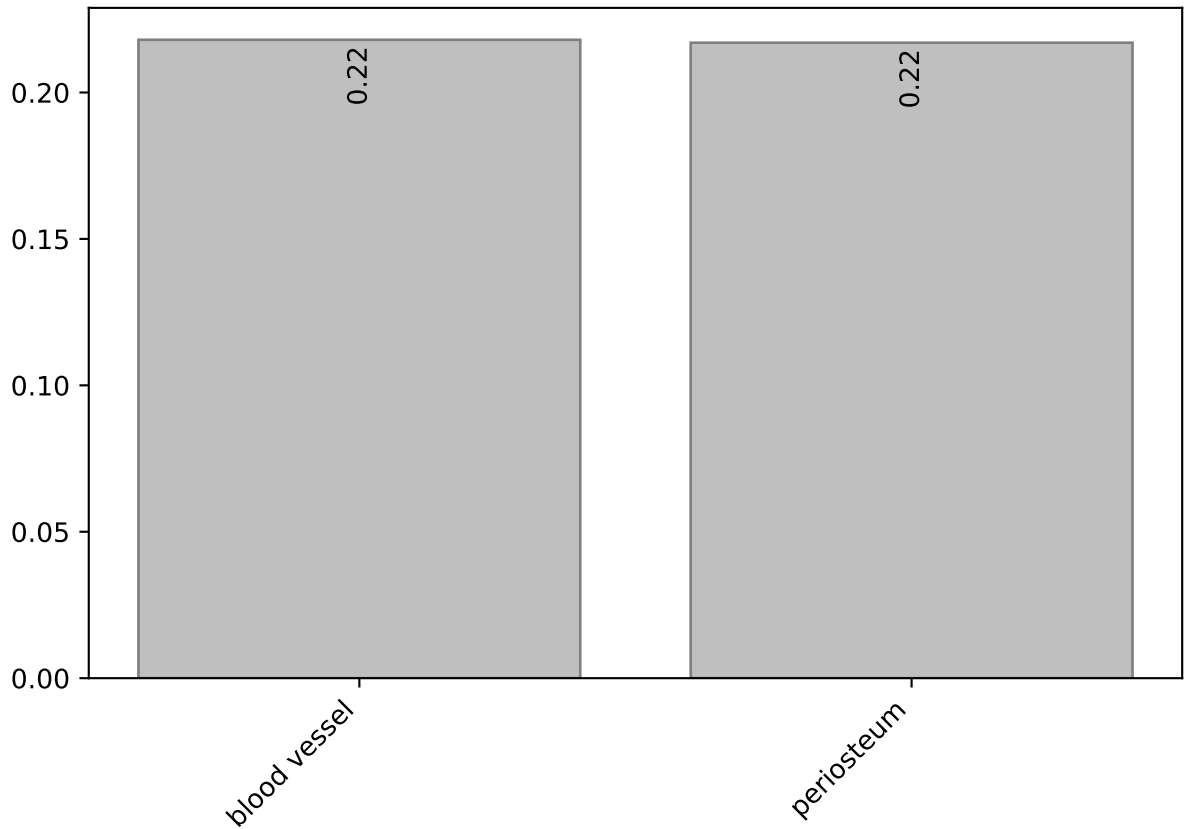
Precursors, 1% FDR



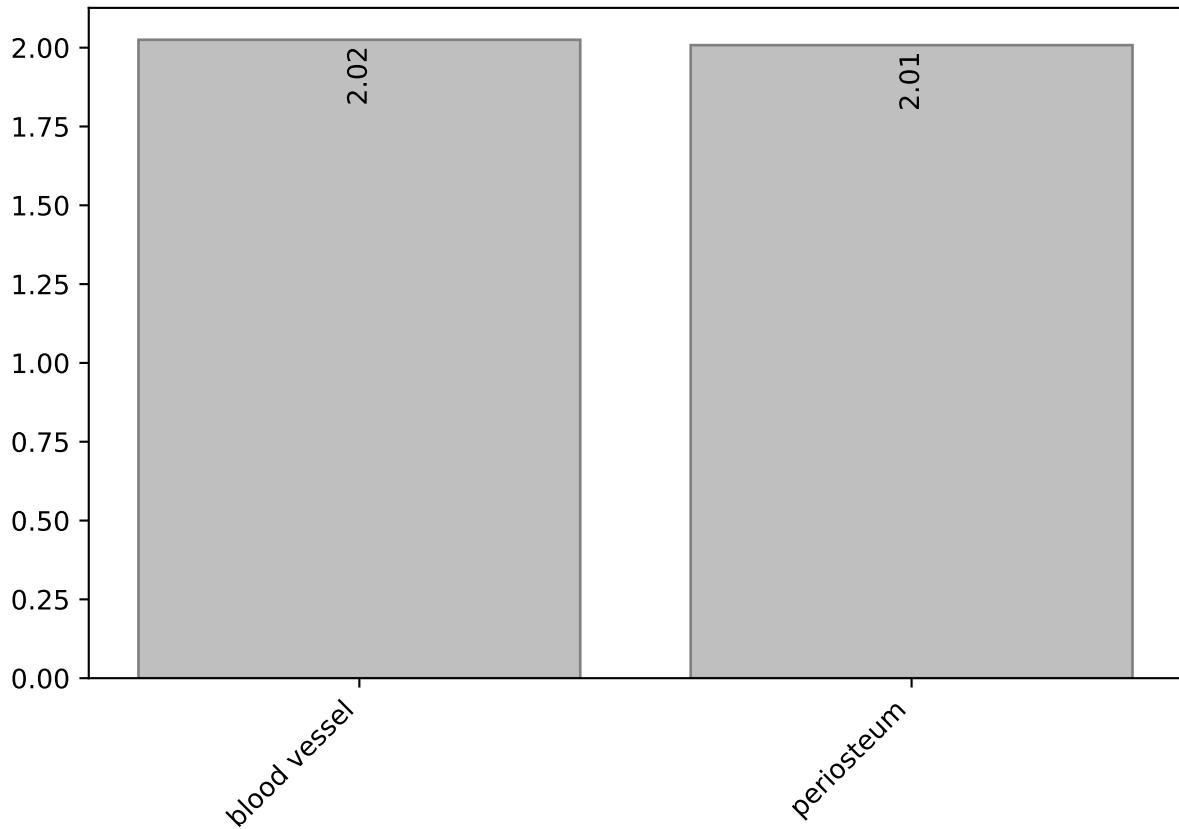
Unique proteins, 1% protein-level FDR



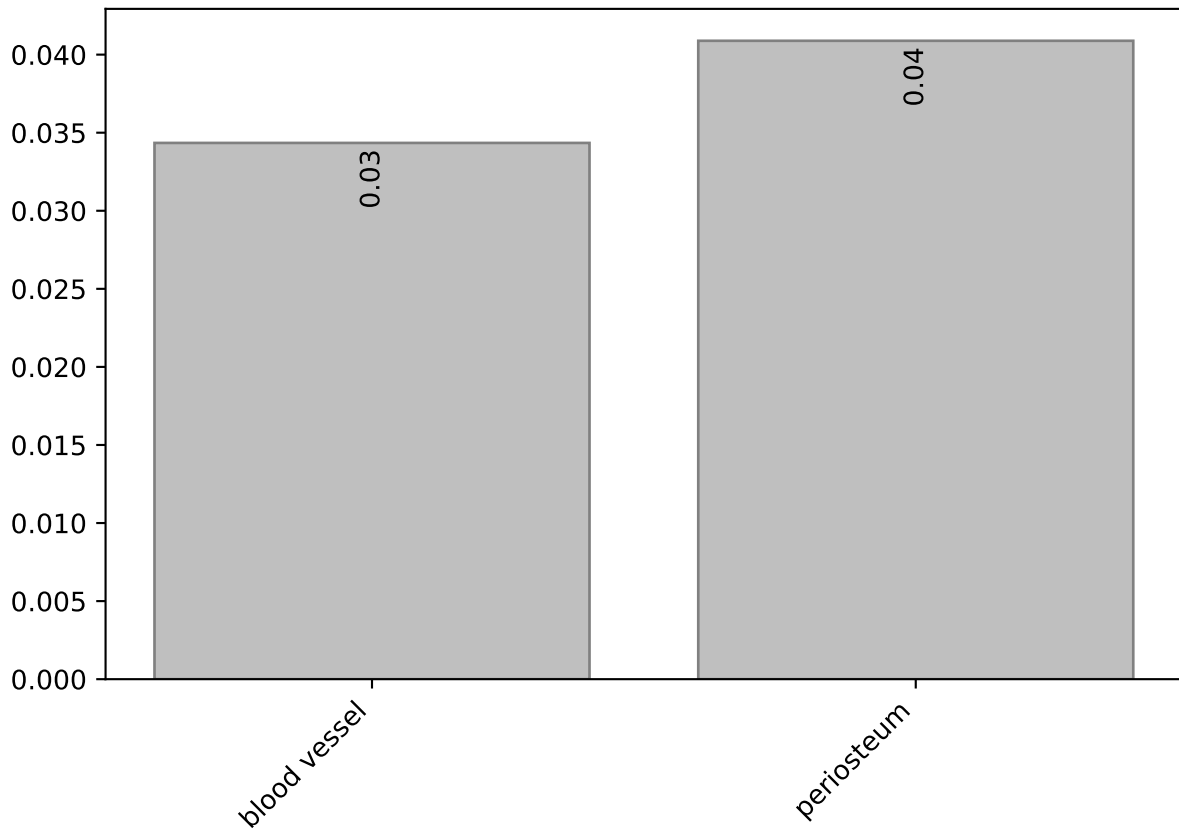
Mean peak FWHM, in minutes



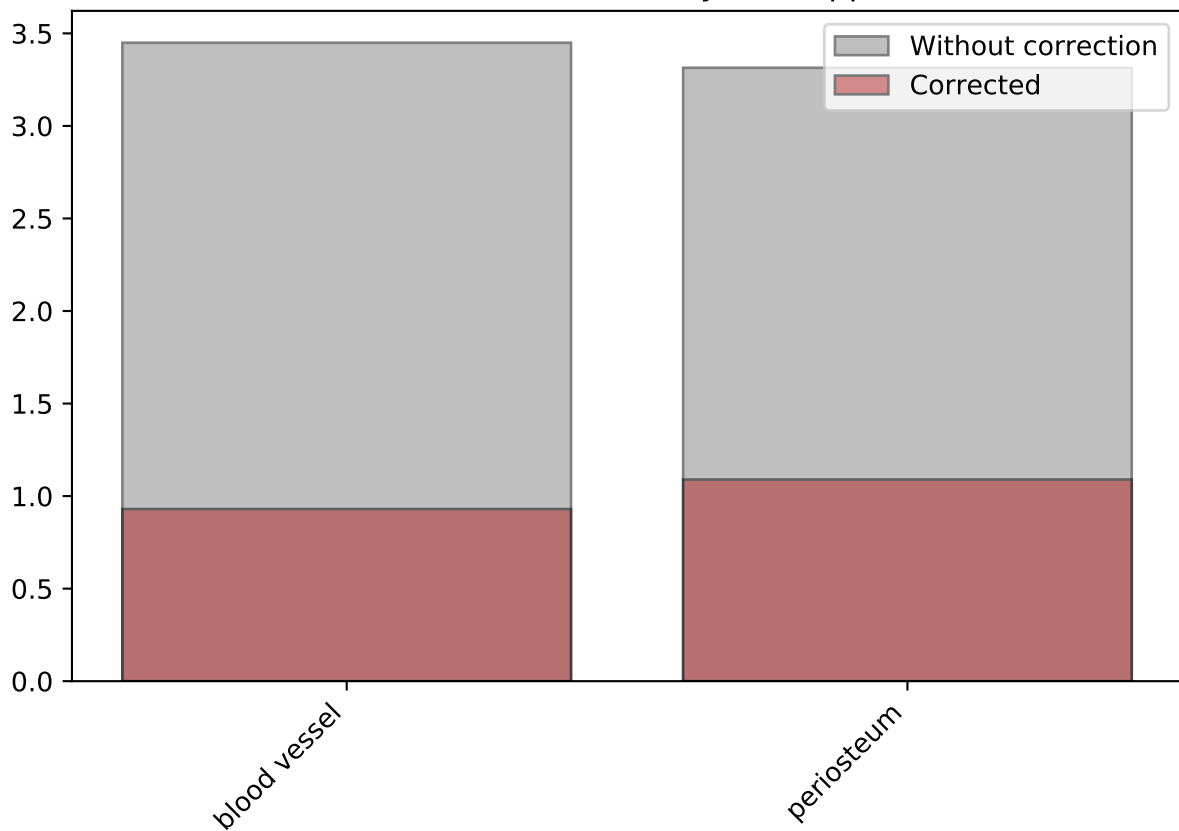
Mean peak FWHM, in MS2 scans



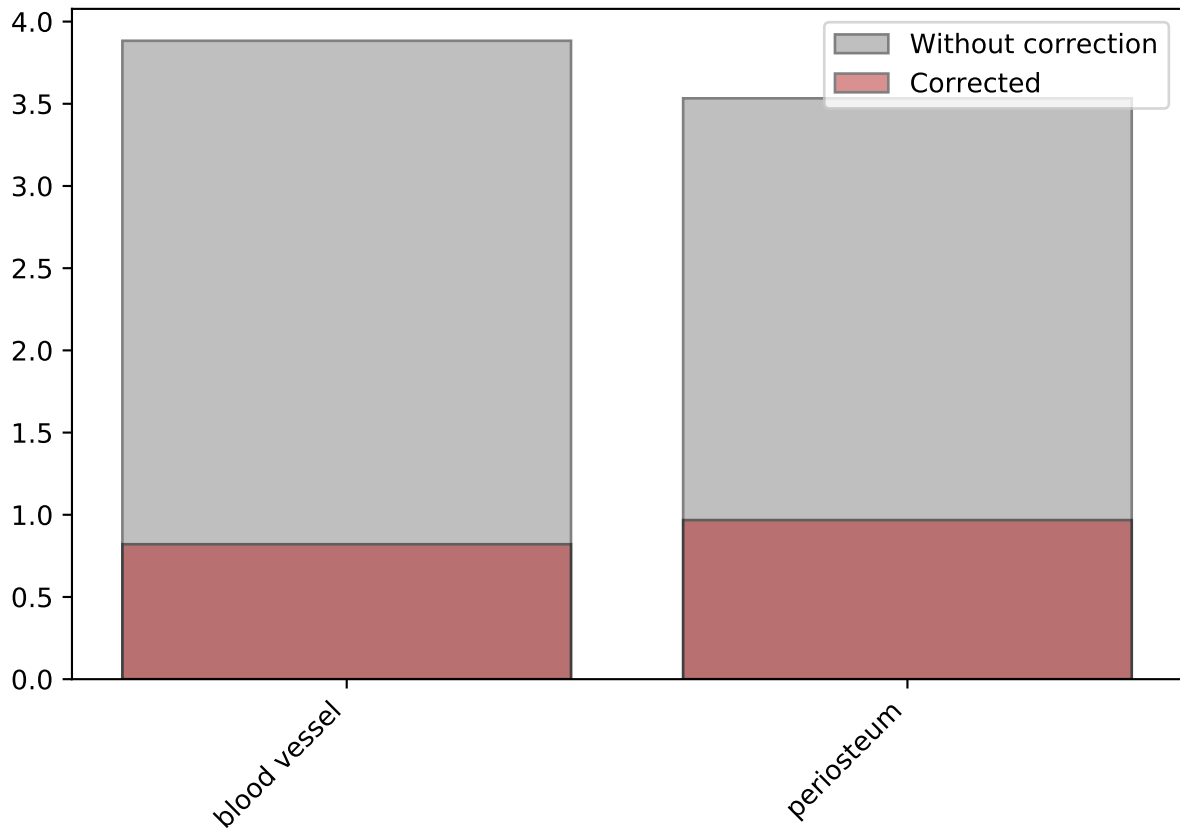
Median RT prediction accuracy, minutes



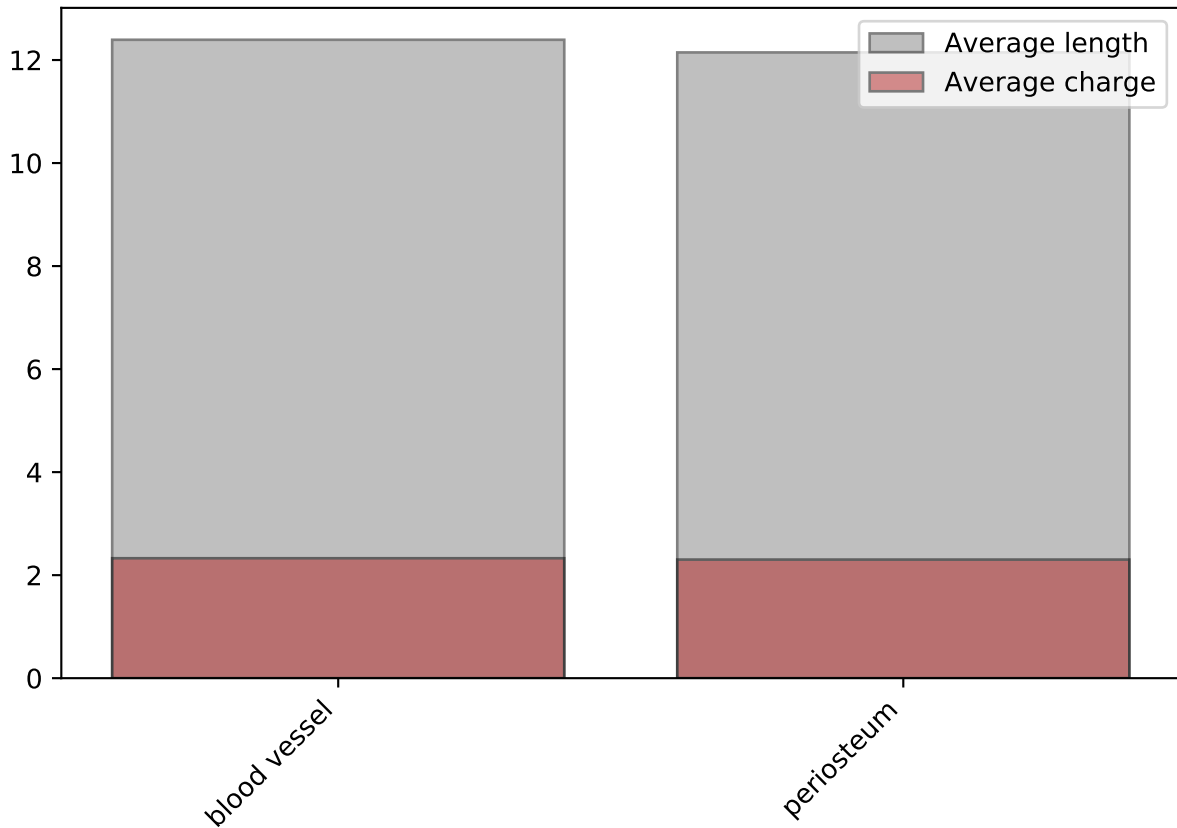
Median mass accuracy, MS2, ppm



Median mass accuracy, MS1, ppm



Peptide characteristics



Average missed tryptic cleavages

