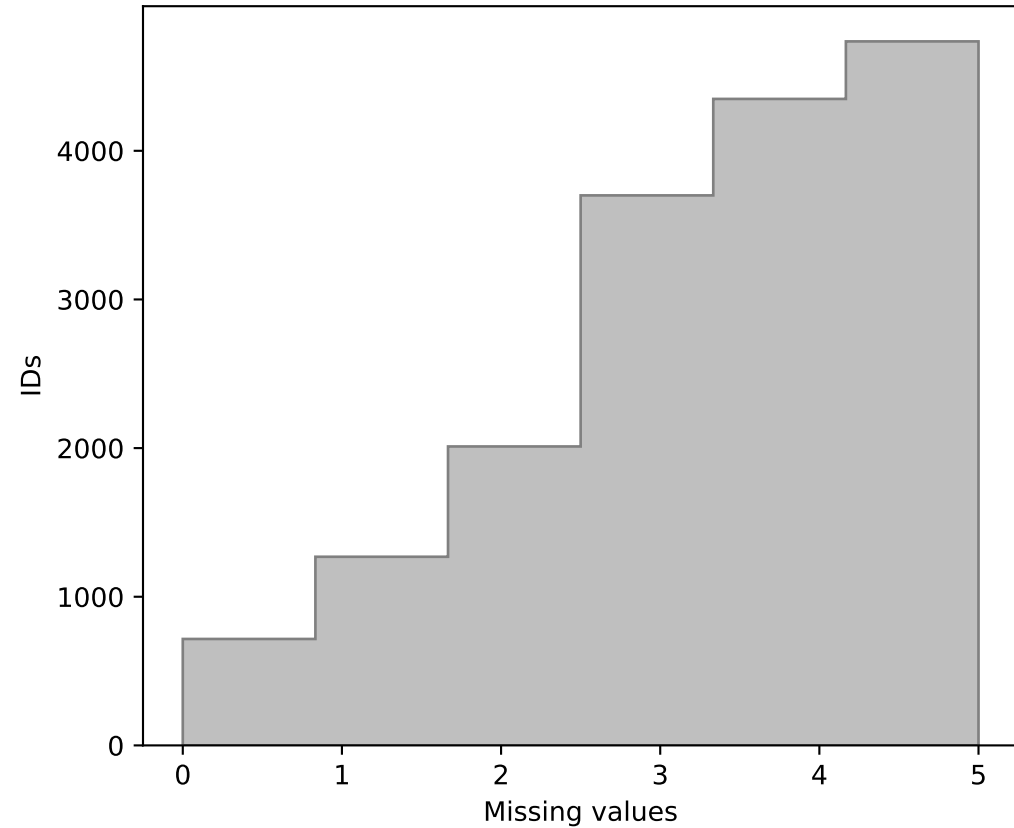
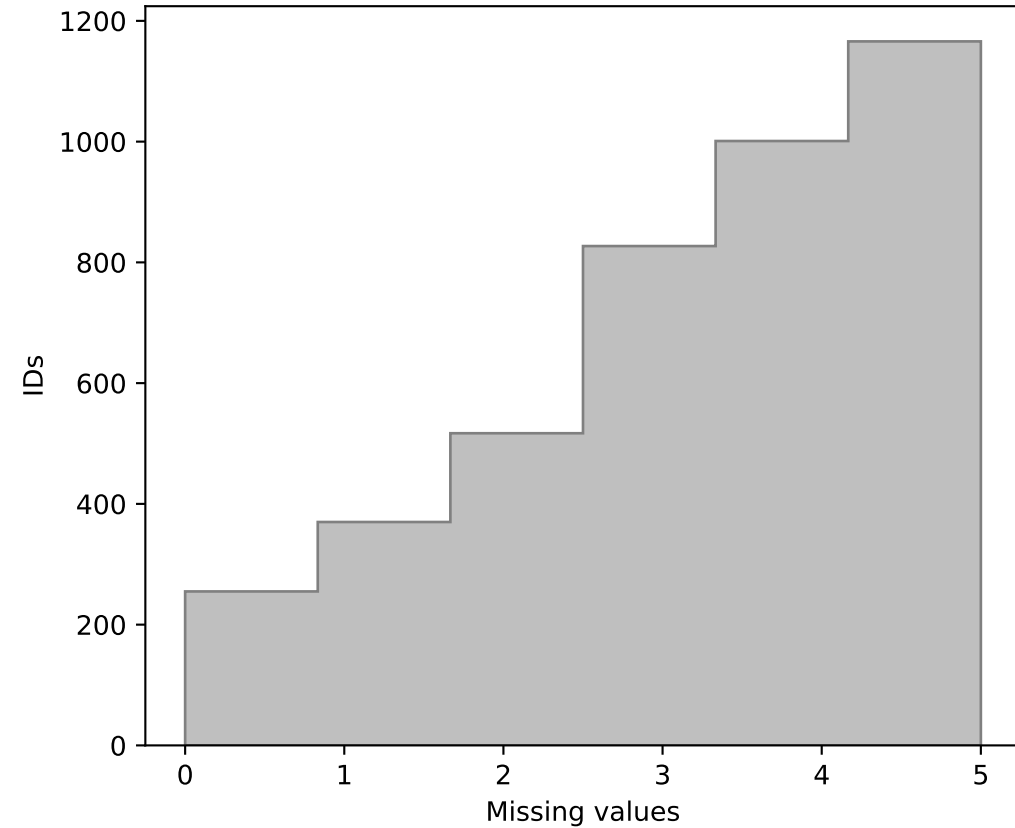


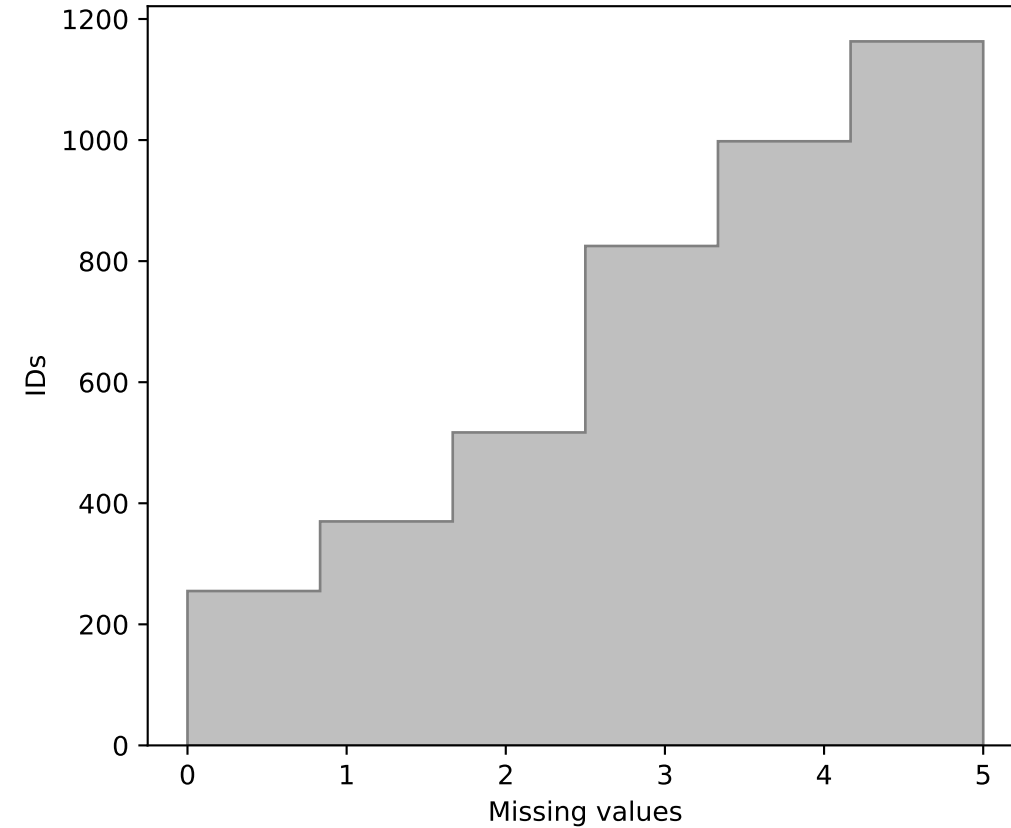
Identification consistency: precursors, CDF



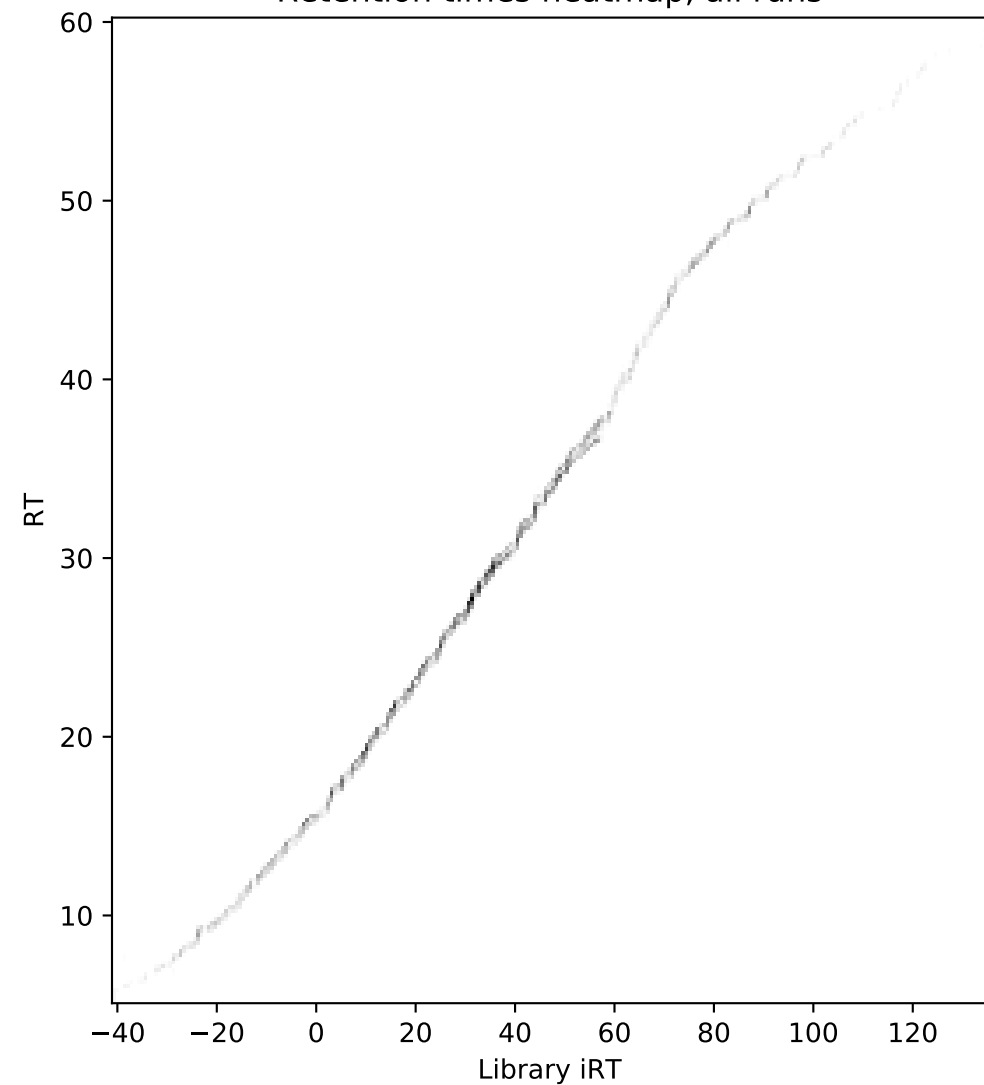
Identification consistency: protein groups, CDF



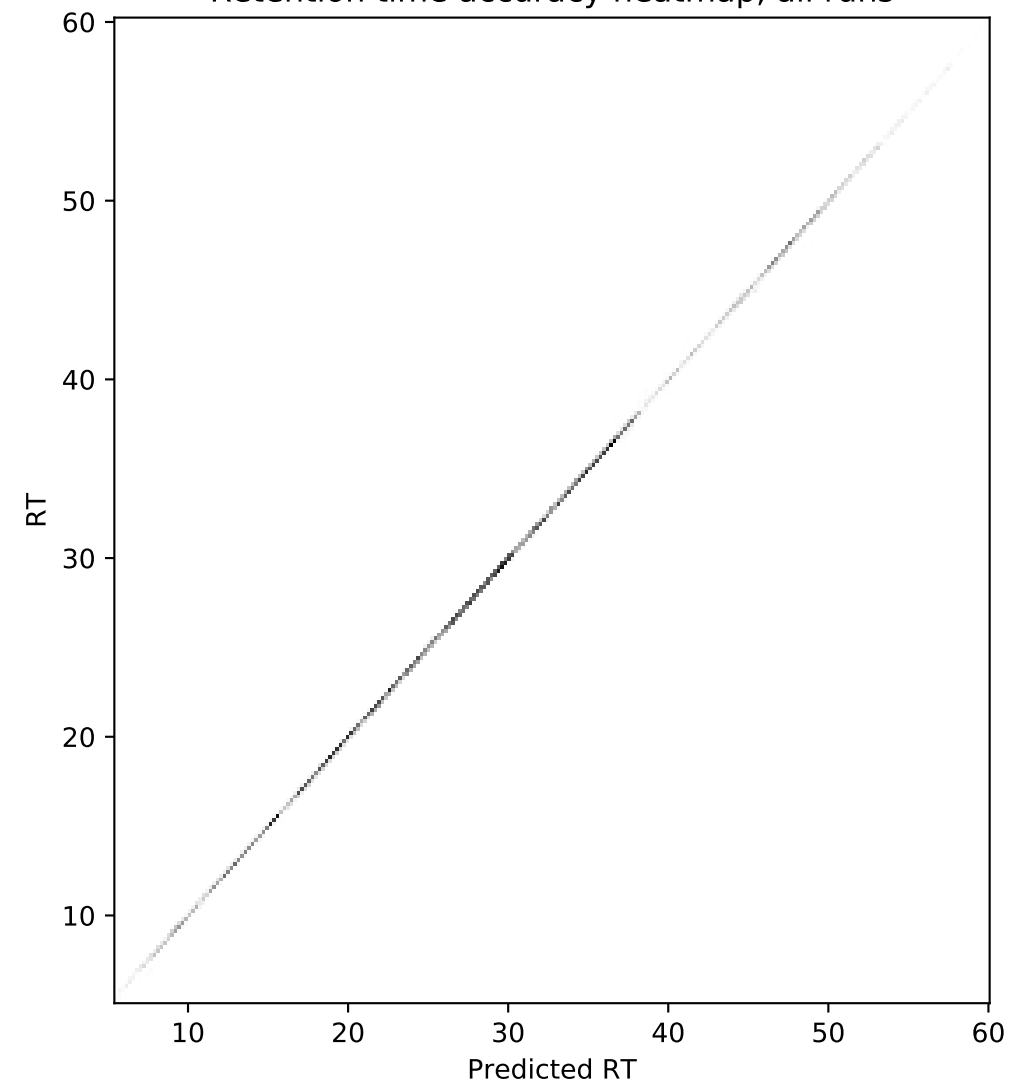
Identification consistency: genes groups, CDF



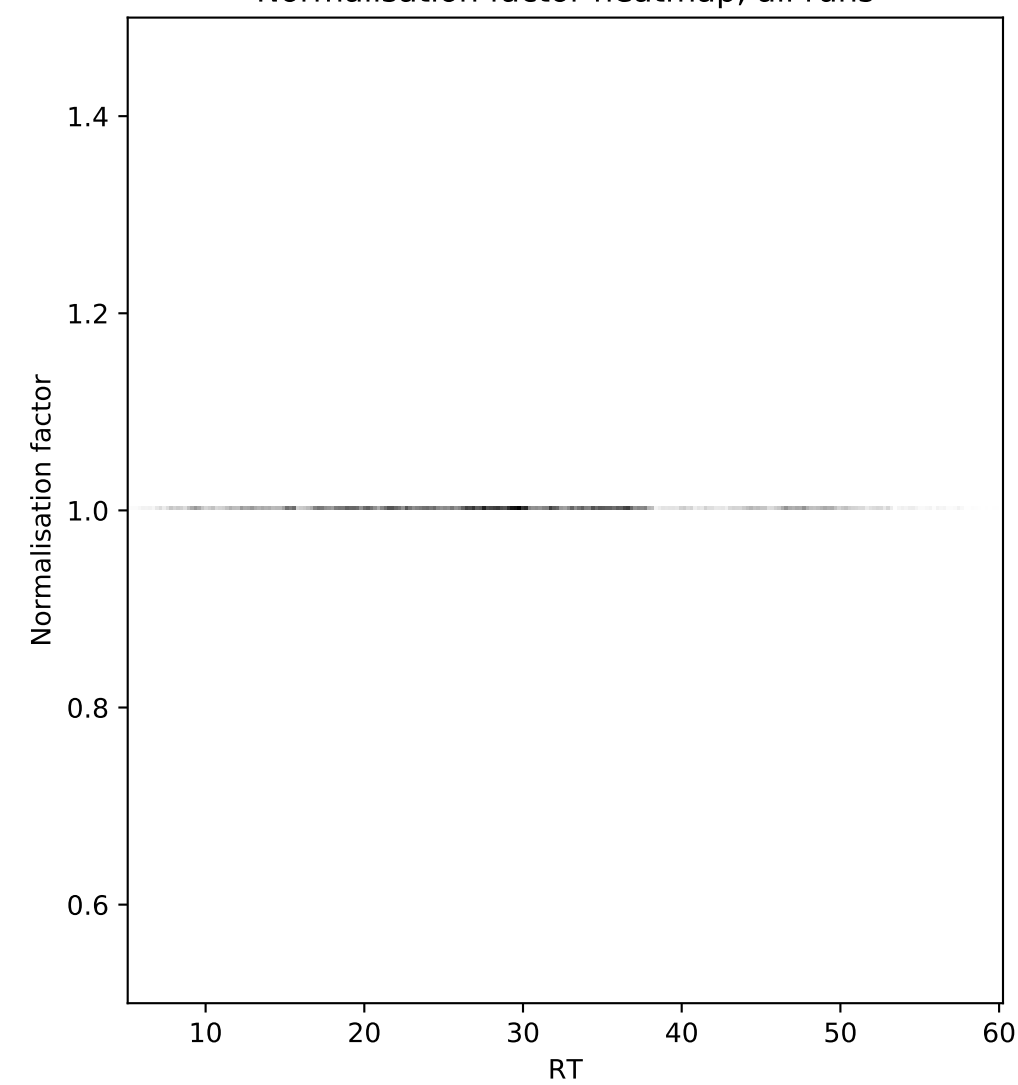
Retention times heatmap, all runs

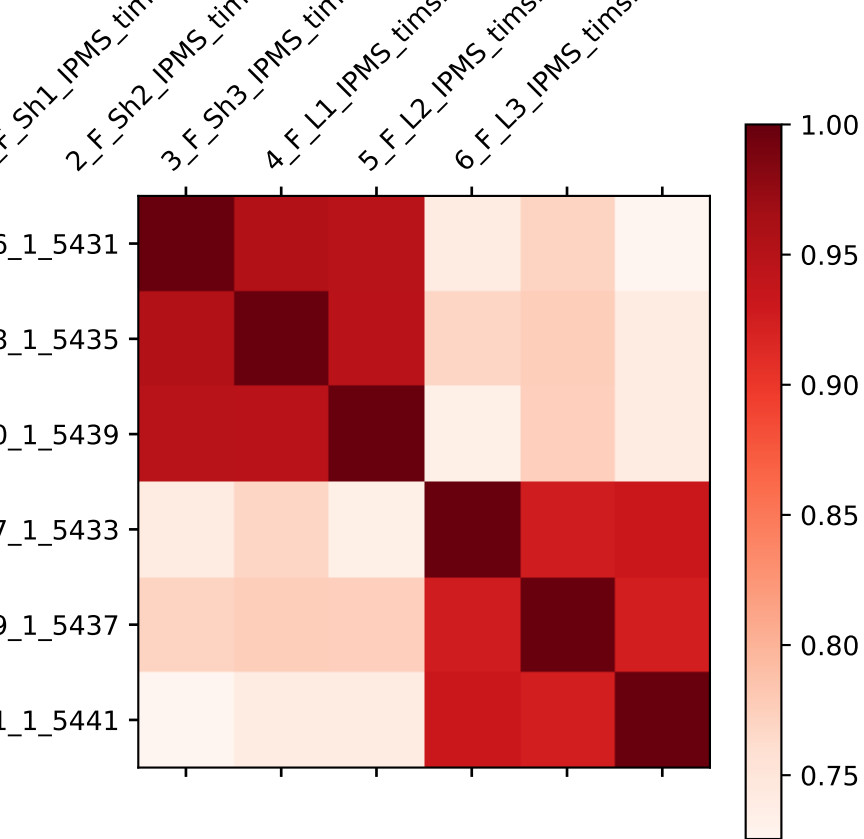


Retention time accuracy heatmap, all runs

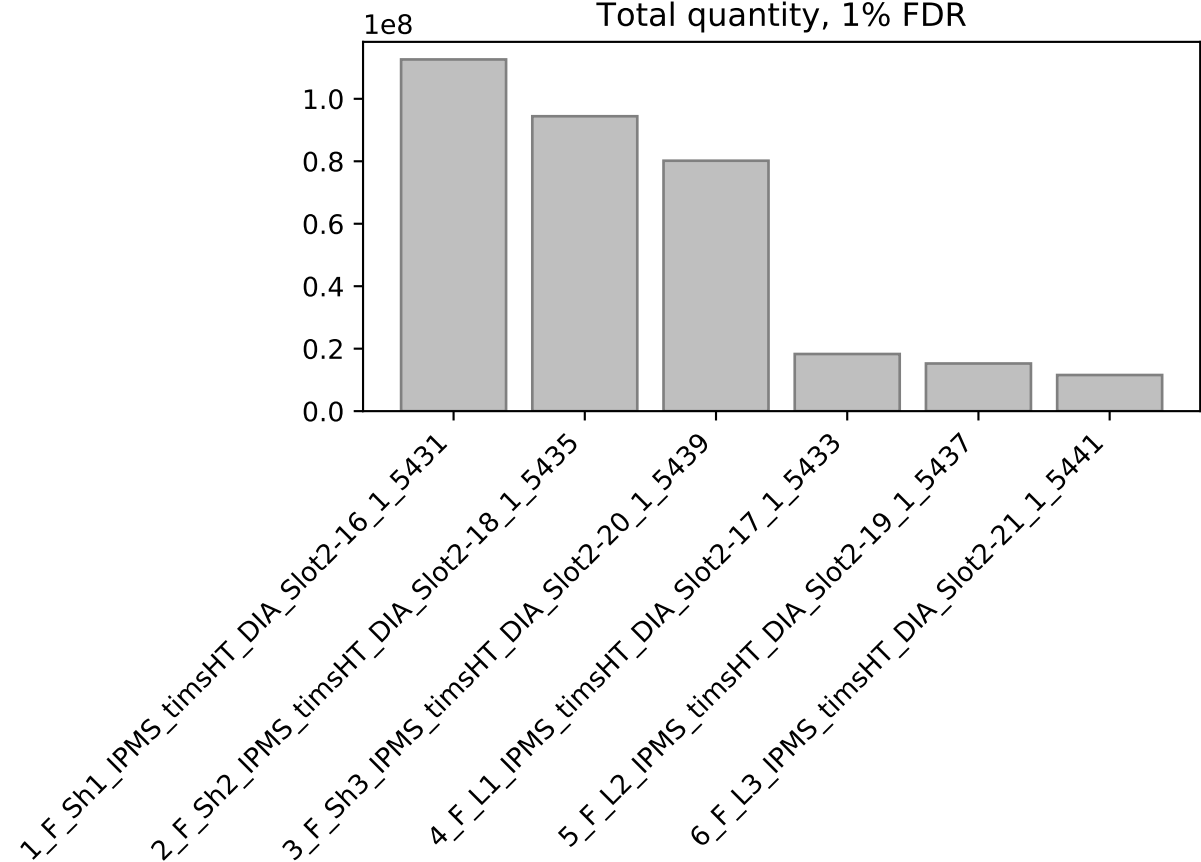


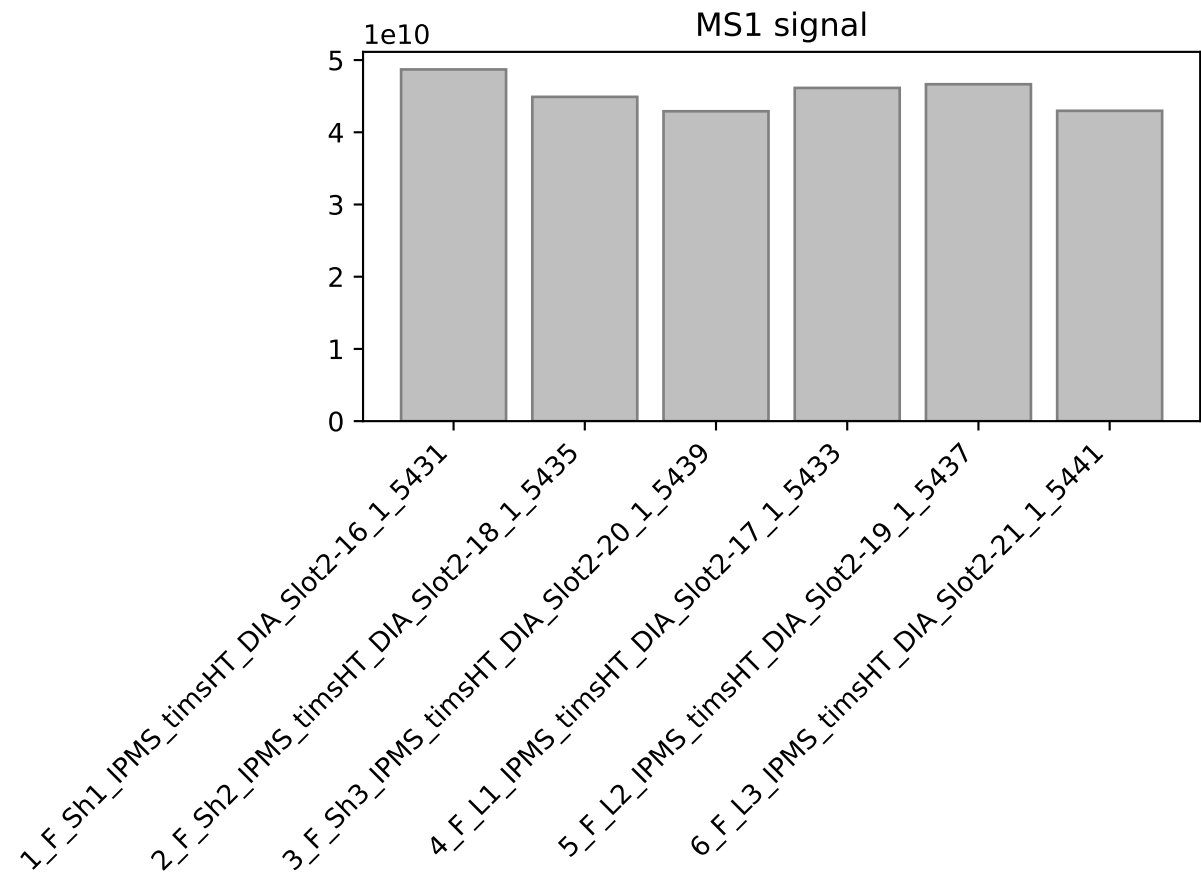
Normalisation factor heatmap, all runs



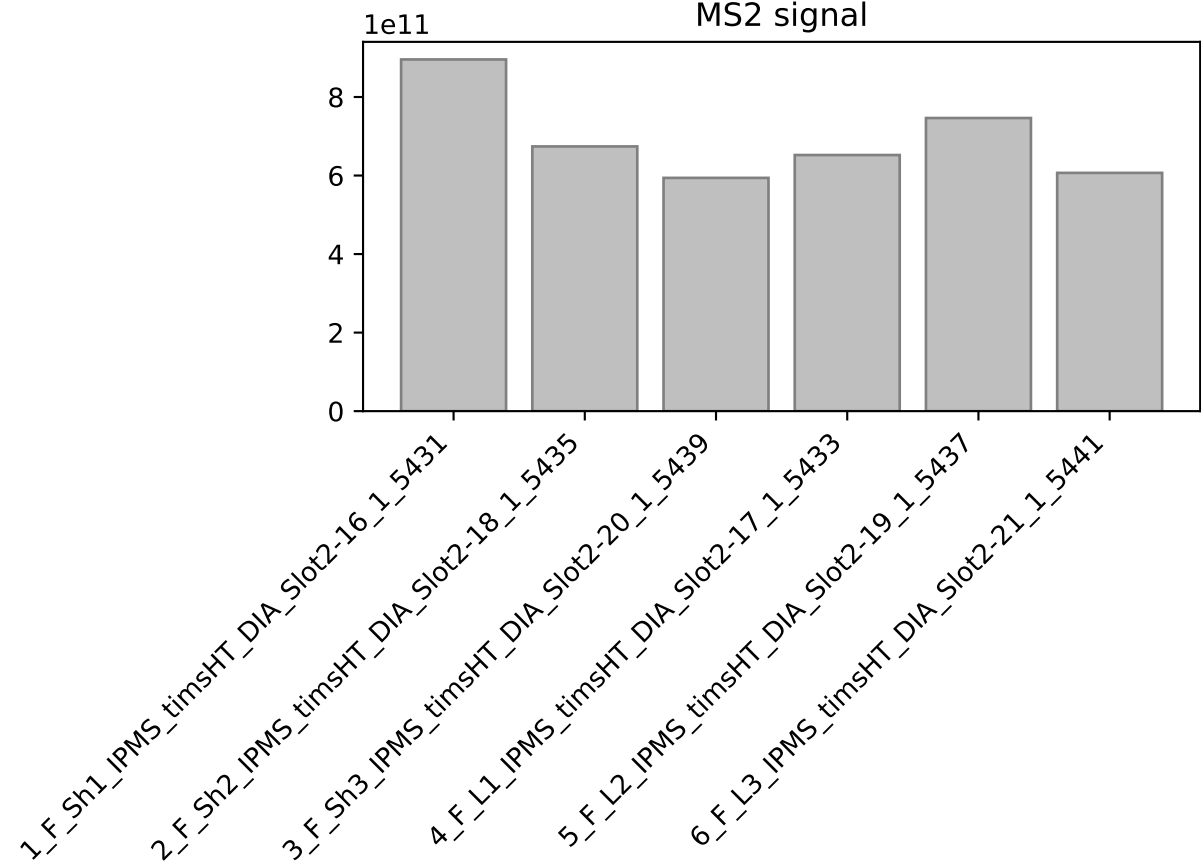


Total quantity, 1% FDR

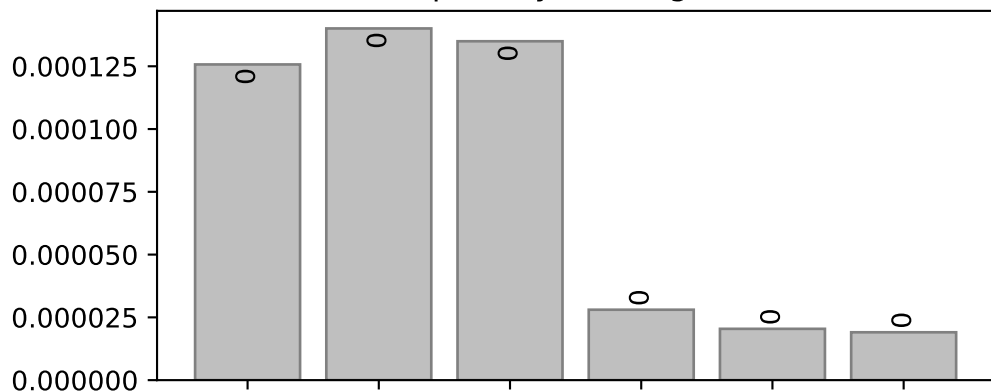




MS2 signal



Total quantity/MS2 signal ratio



1\_F\_Sh1\_IPMS\_timsHT\_DIA\_Slot2-16\_1\_5431

2\_F\_Sh2\_IPMS\_timsHT\_DIA\_Slot2-18\_1\_5435

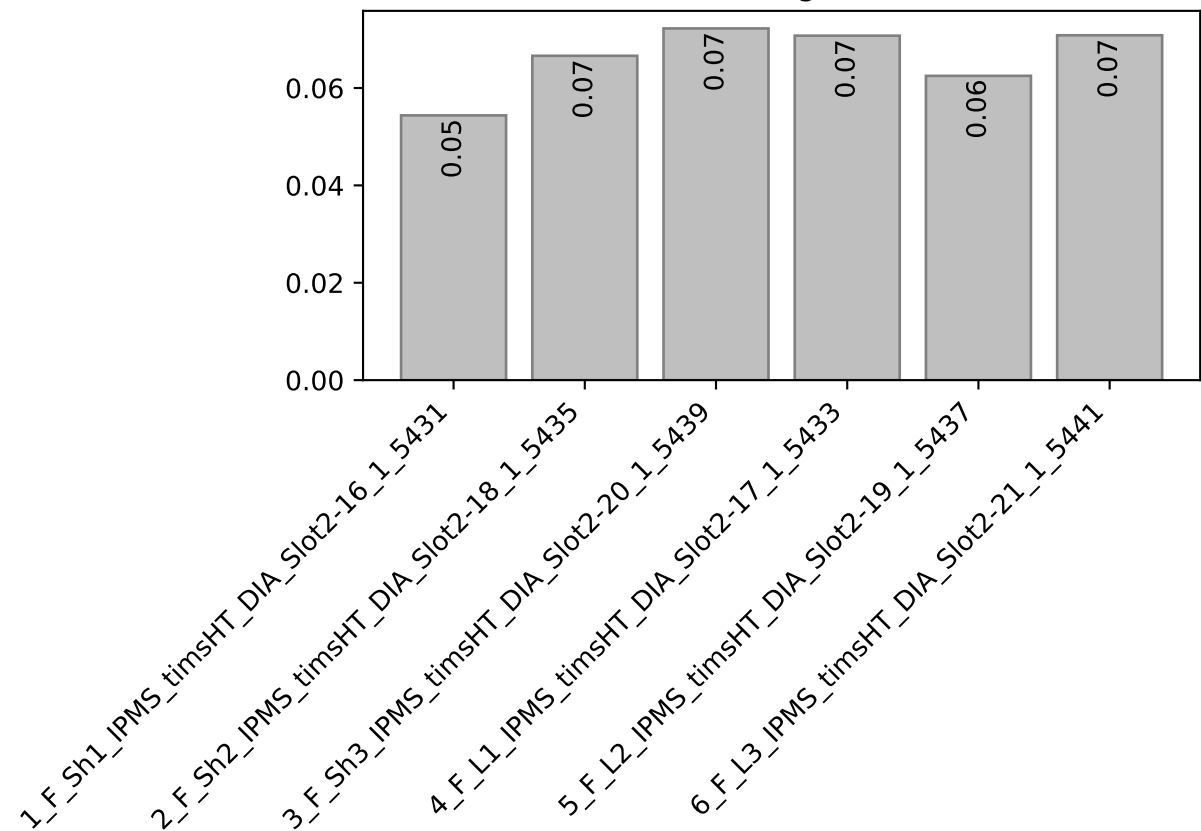
3\_F\_Sh3\_IPMS\_timsHT\_DIA\_Slot2-20\_1\_5439

4\_F\_L1\_IPMS\_timsHT\_DIA\_Slot2-17\_1\_5433

5\_F\_L2\_IPMS\_timsHT\_DIA\_Slot2-19\_1\_5437

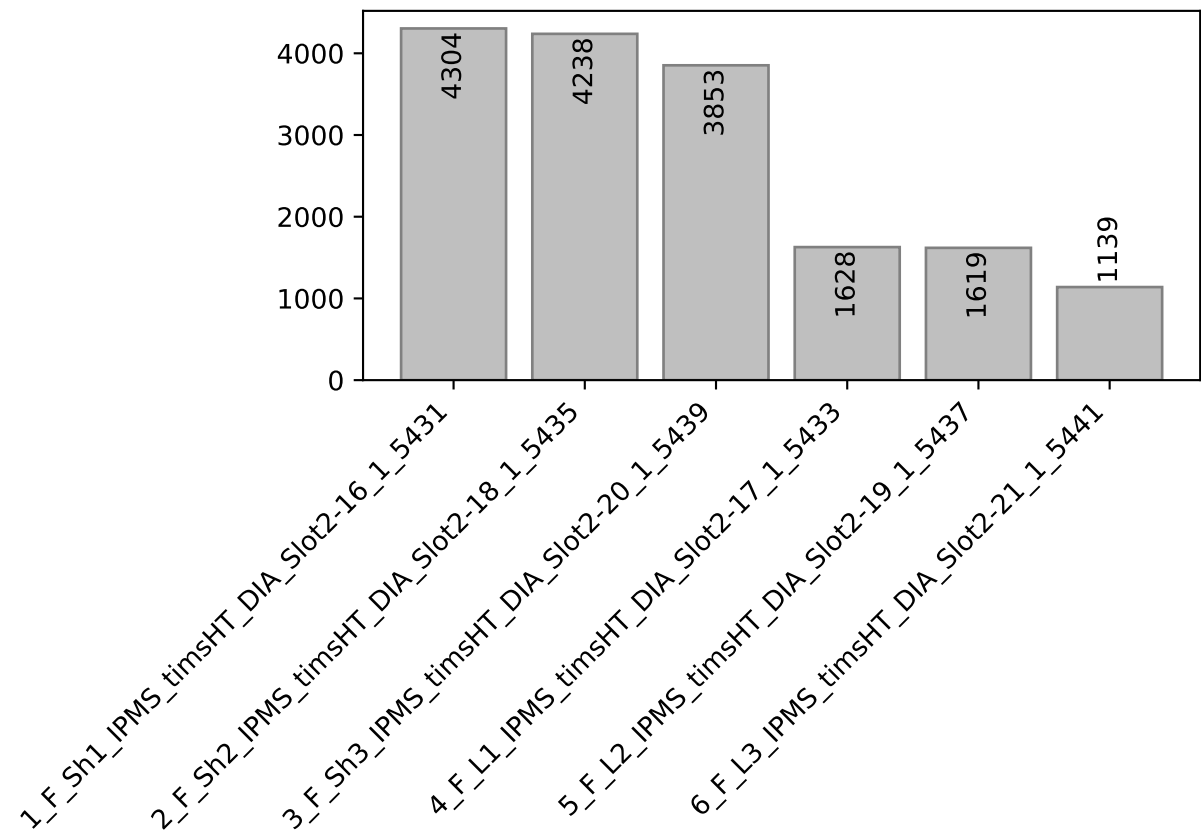
6\_F\_L3\_IPMS\_timsHT\_DIA\_Slot2-21\_1\_5441

MS1/MS2 signal ratio

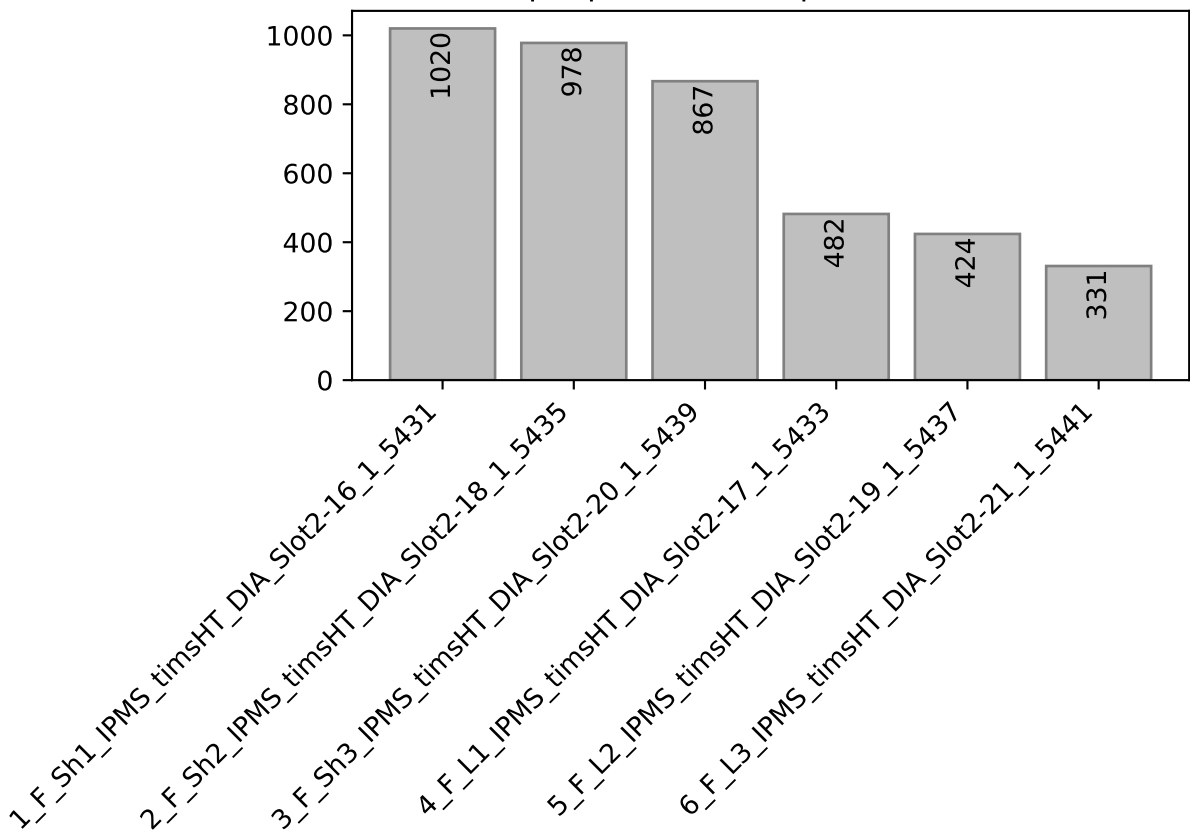




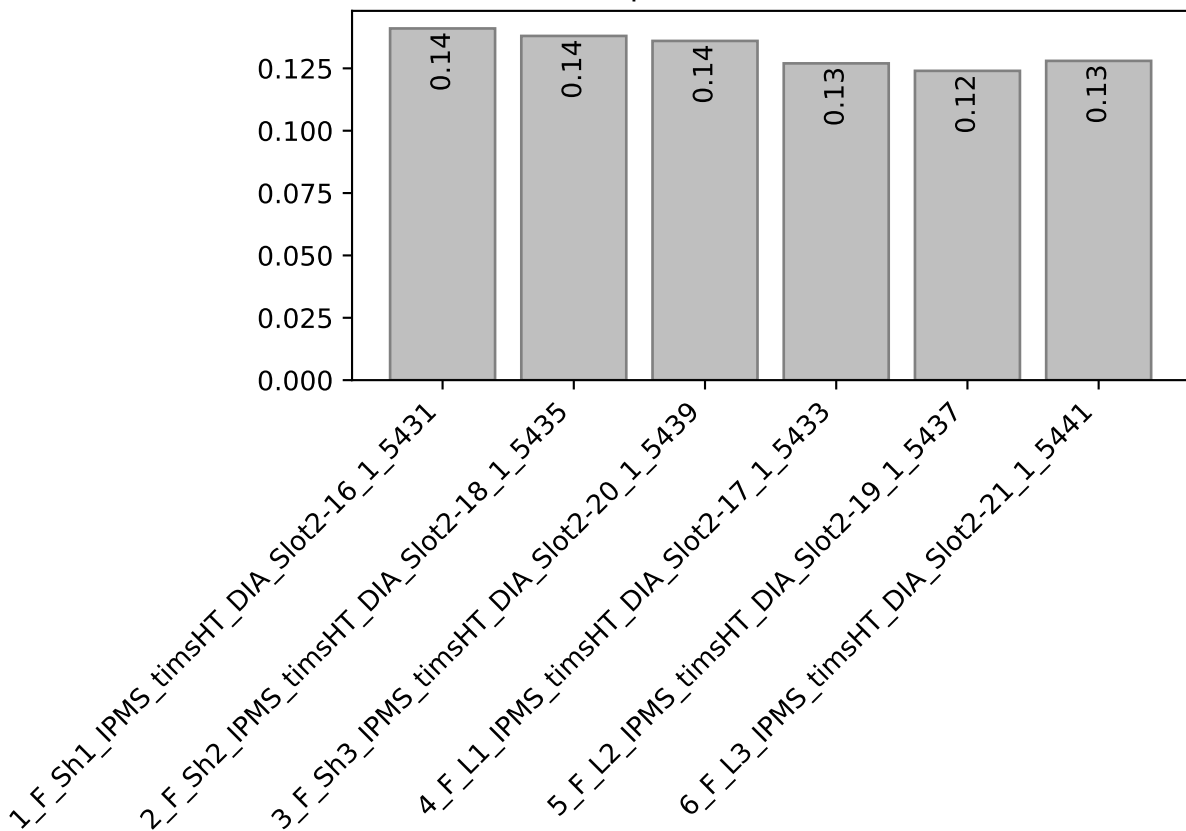
Precursors, 1% FDR



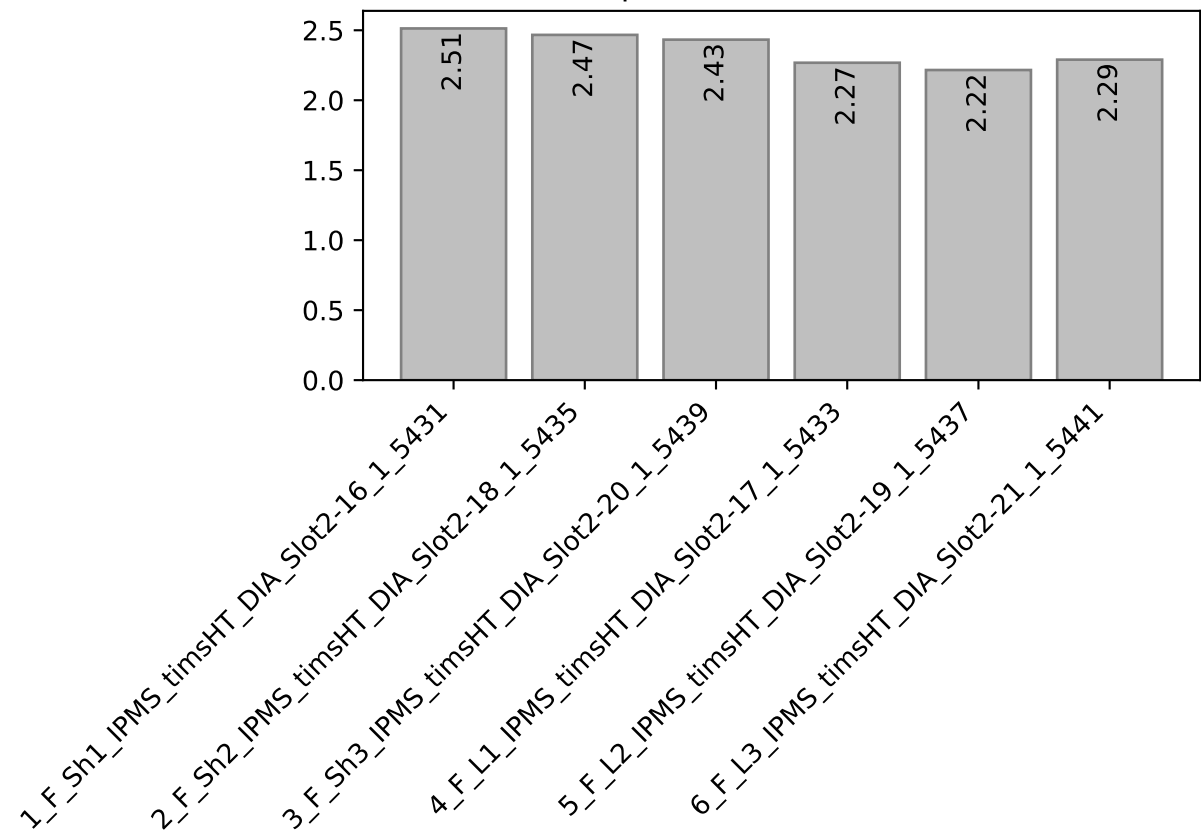
Unique proteins, 1% protein-level FDR



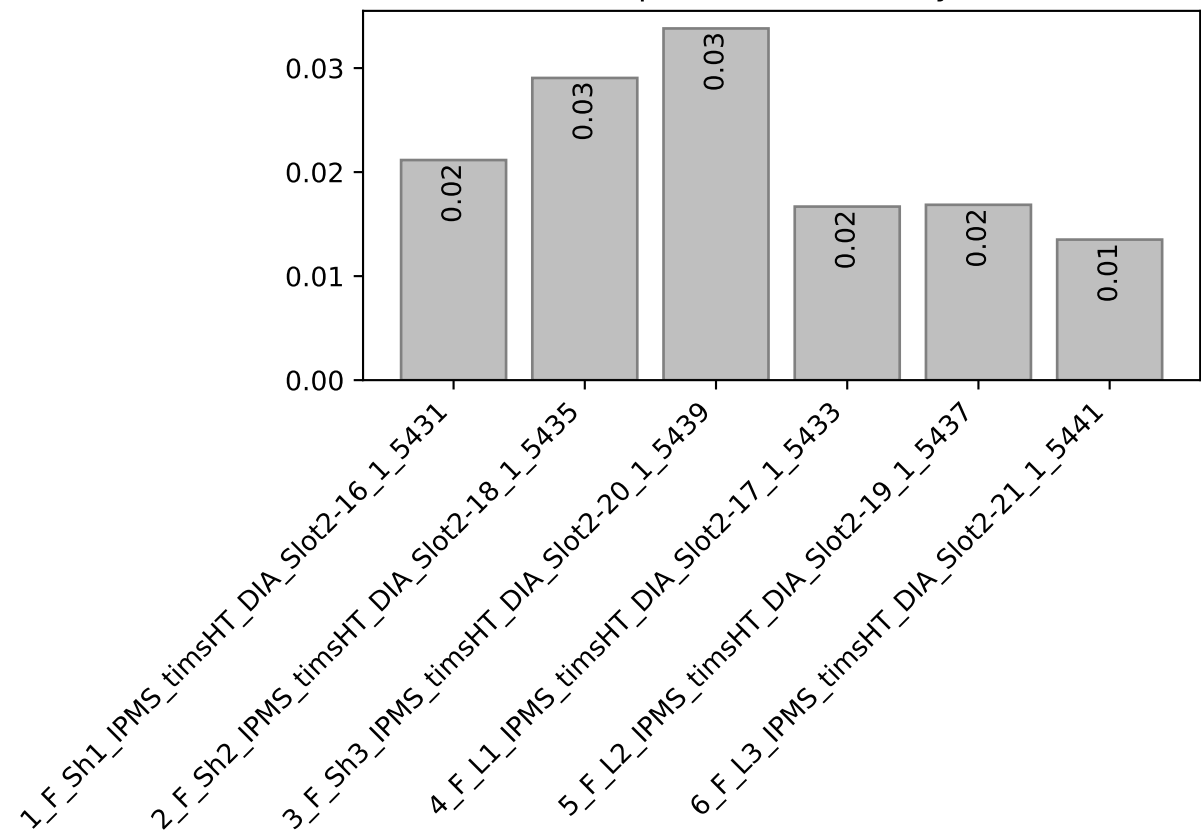
Mean peak FWHM, in minutes



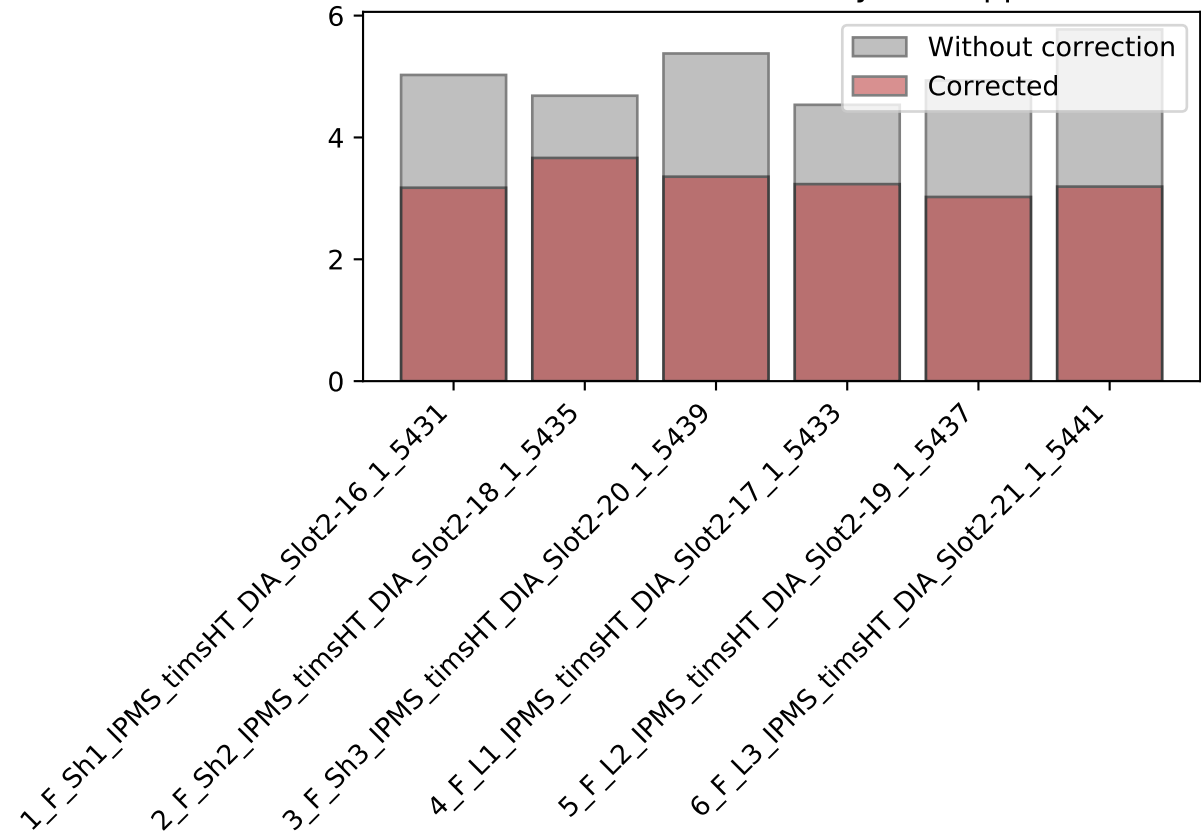
Mean peak FWHM, in MS2 scans



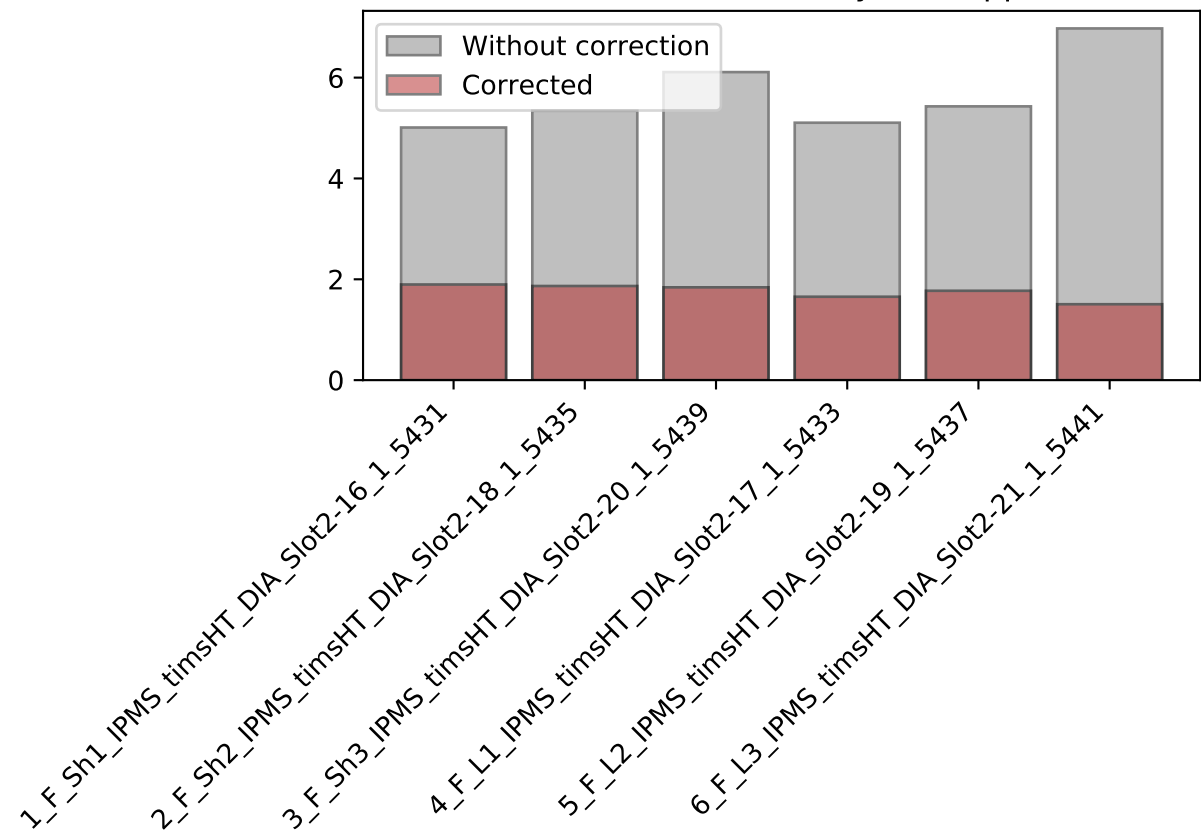
Median RT prediction accuracy, minutes



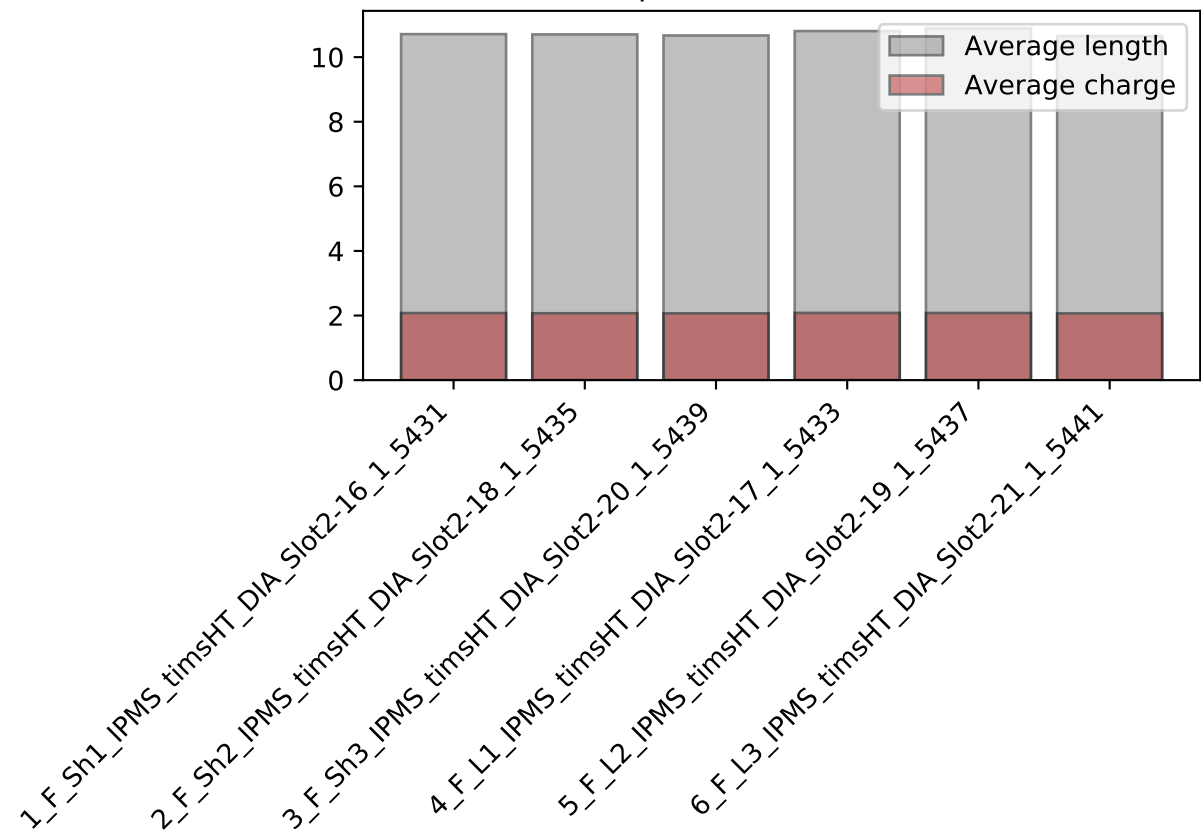
Median mass accuracy, MS2, ppm



Median mass accuracy, MS1, ppm



## Peptide characteristics





Average missed tryptic cleavages

