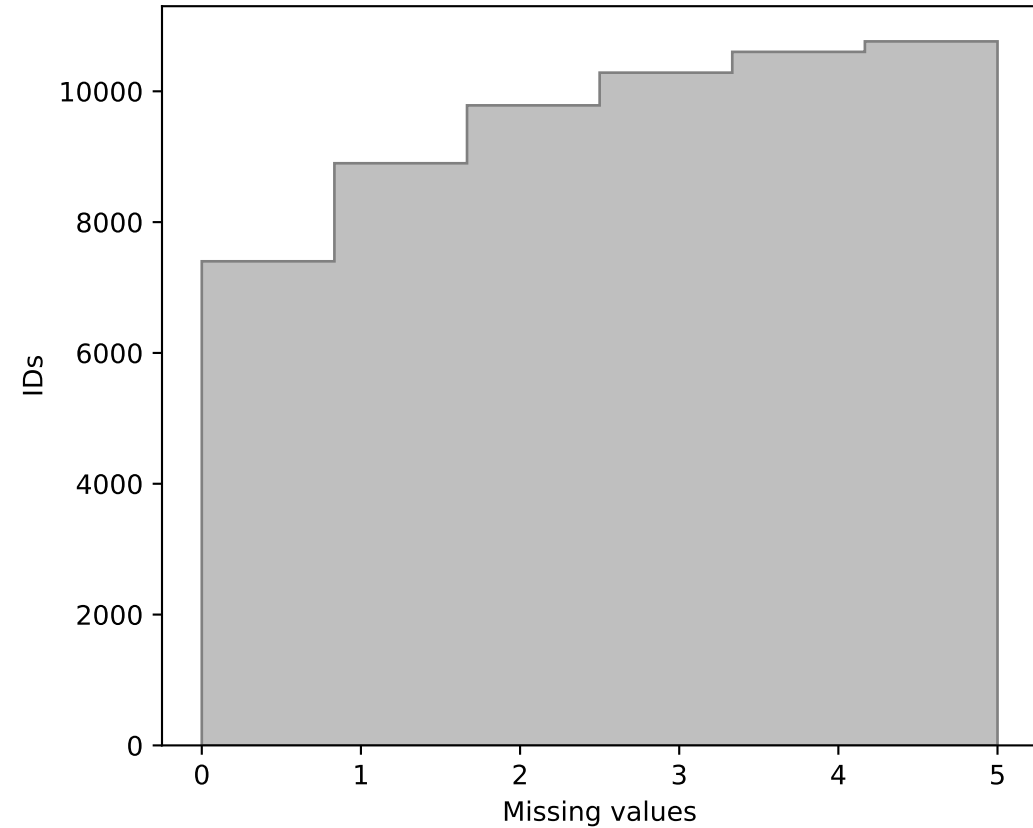
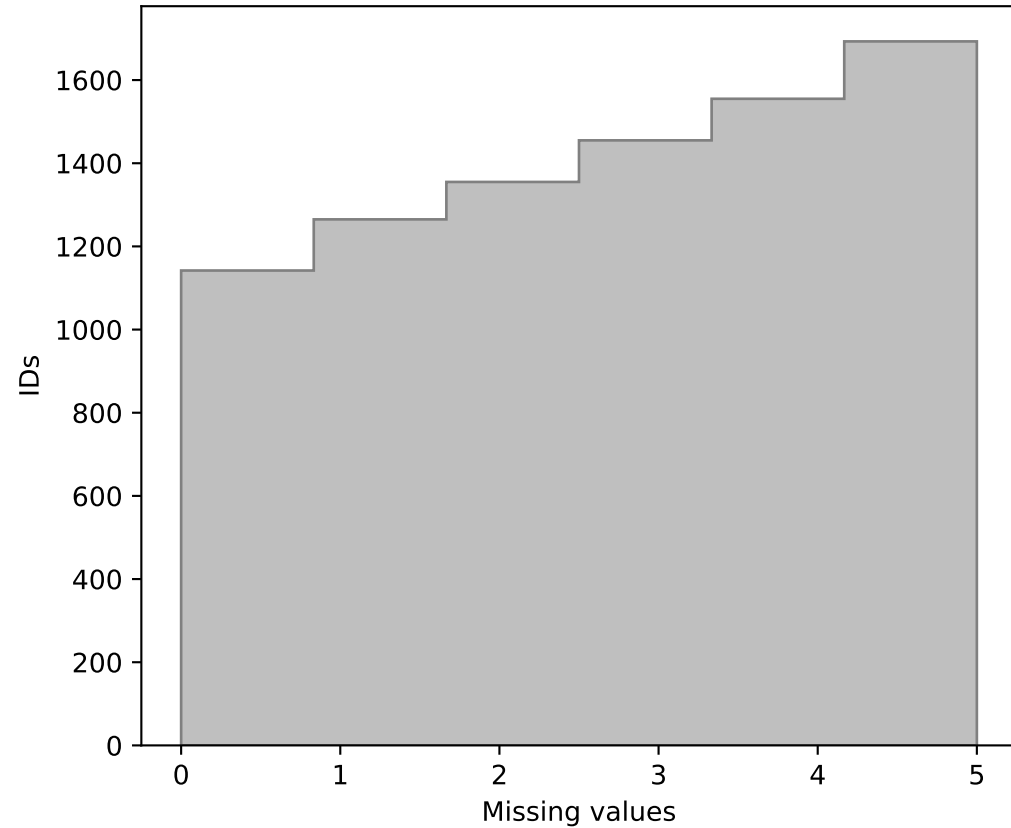


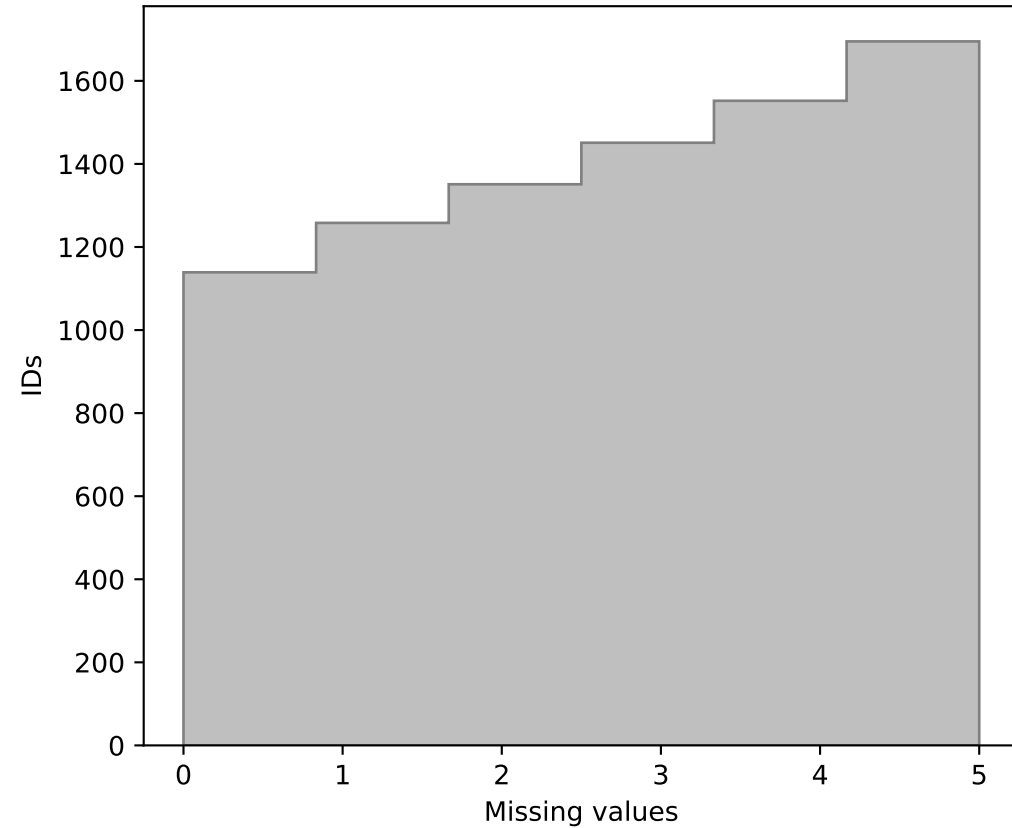
Identification consistency: precursors, CDF



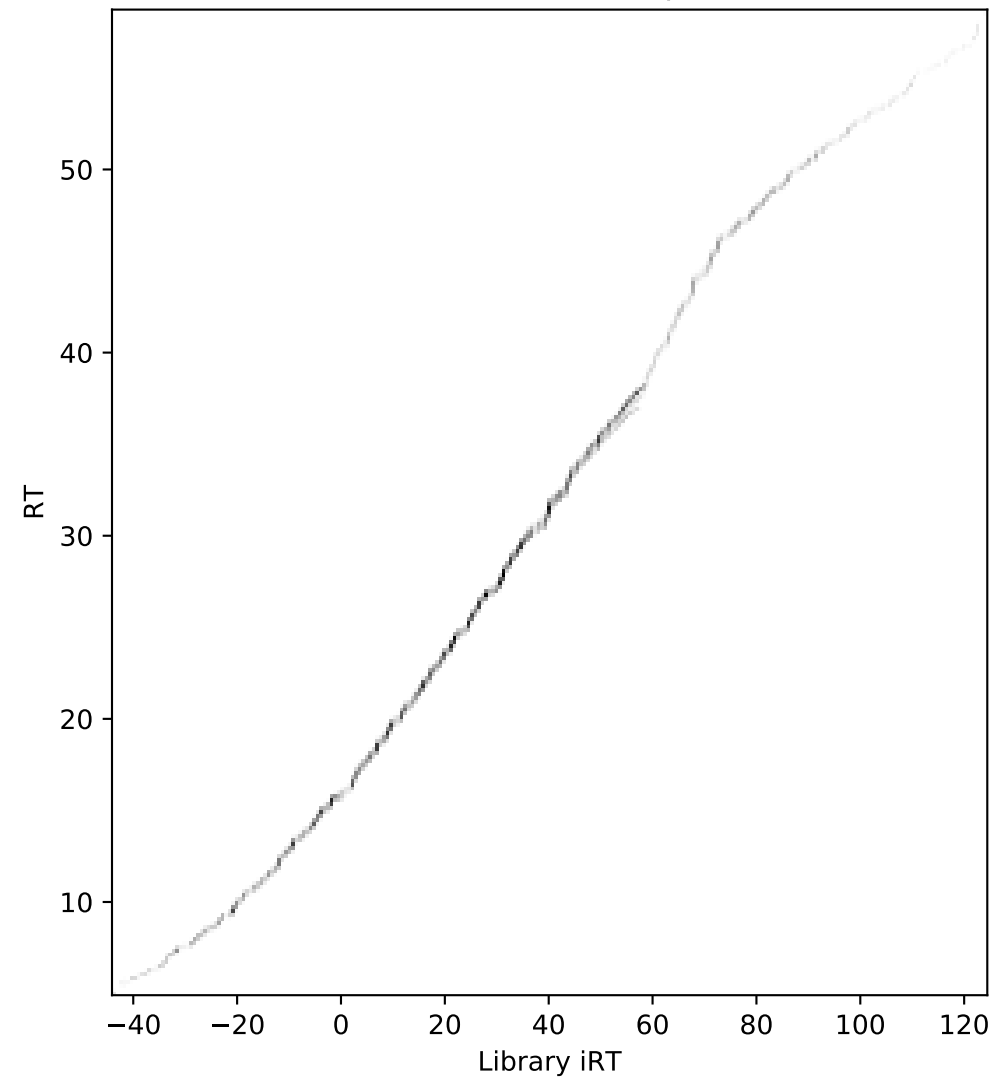
Identification consistency: protein groups, CDF



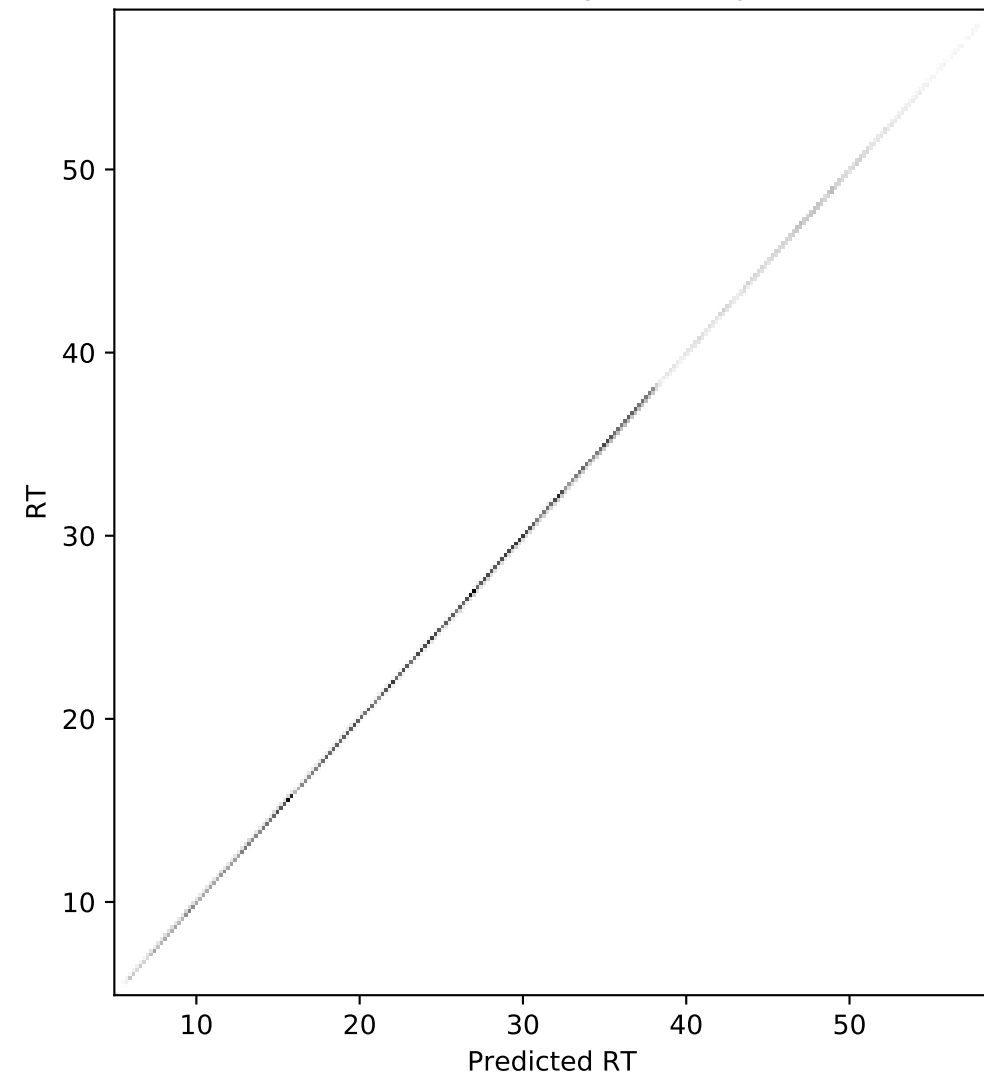
Identification consistency: genes groups, CDF



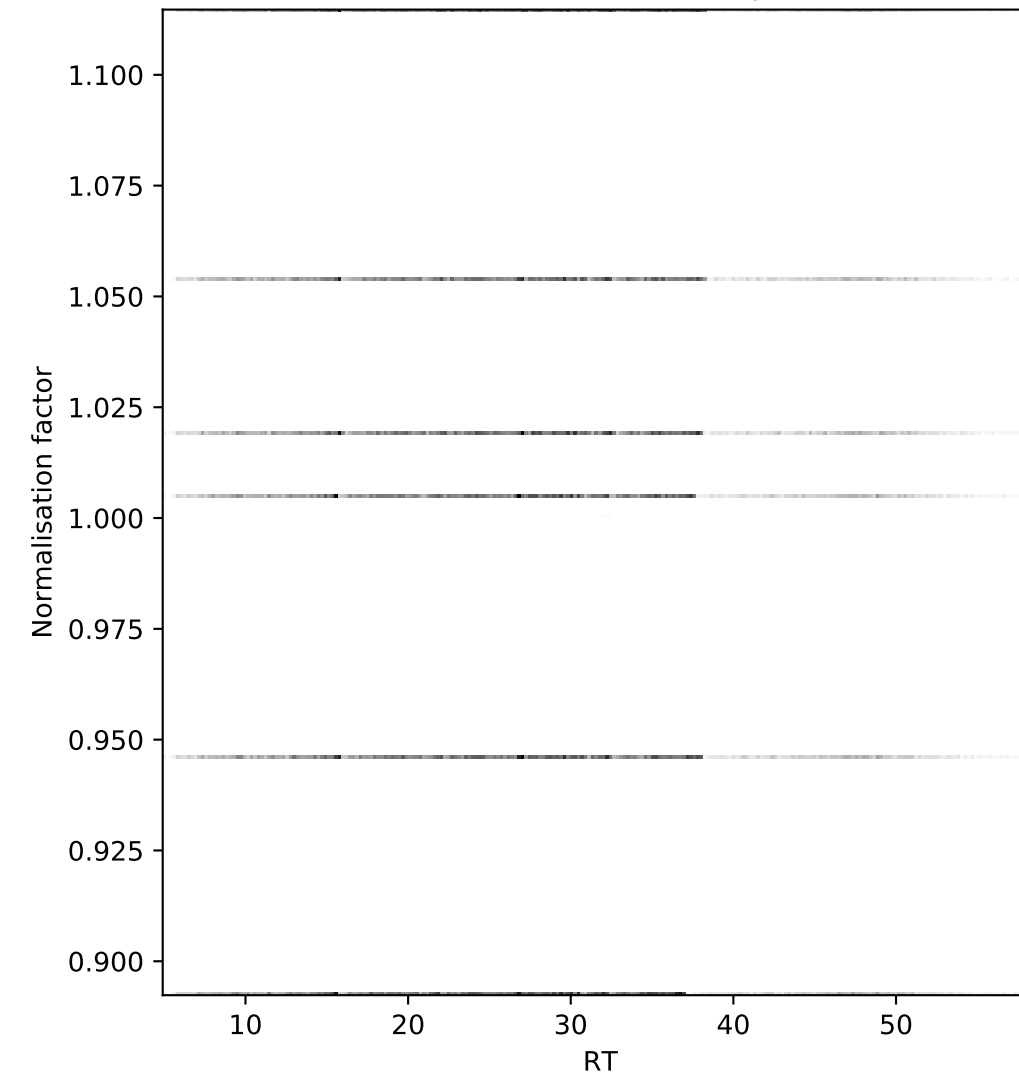
Retention times heatmap, all runs

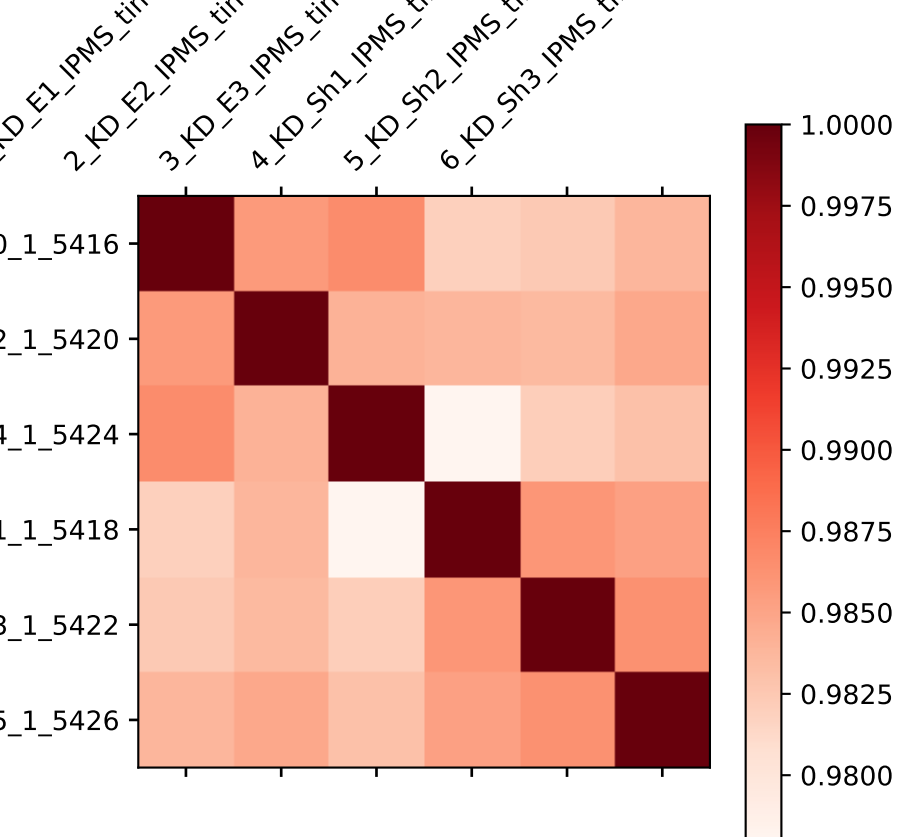


Retention time accuracy heatmap, all runs

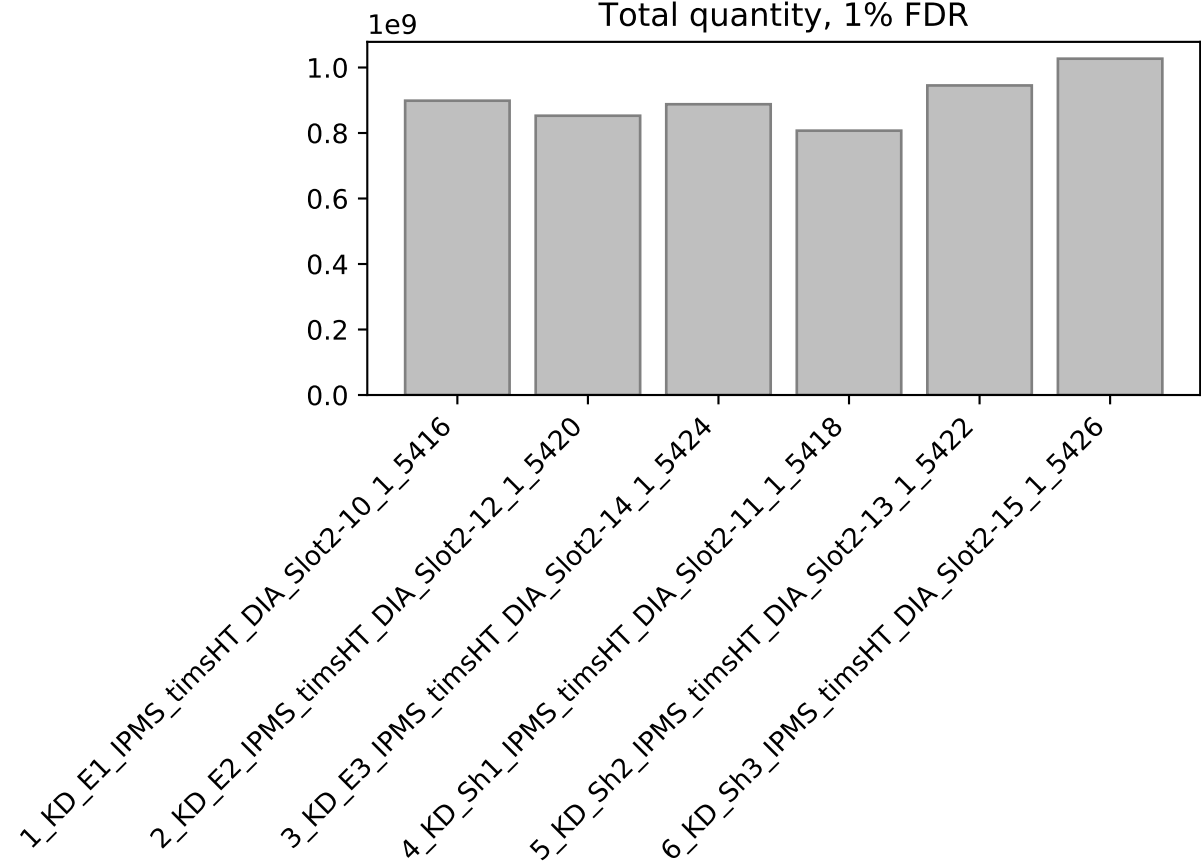


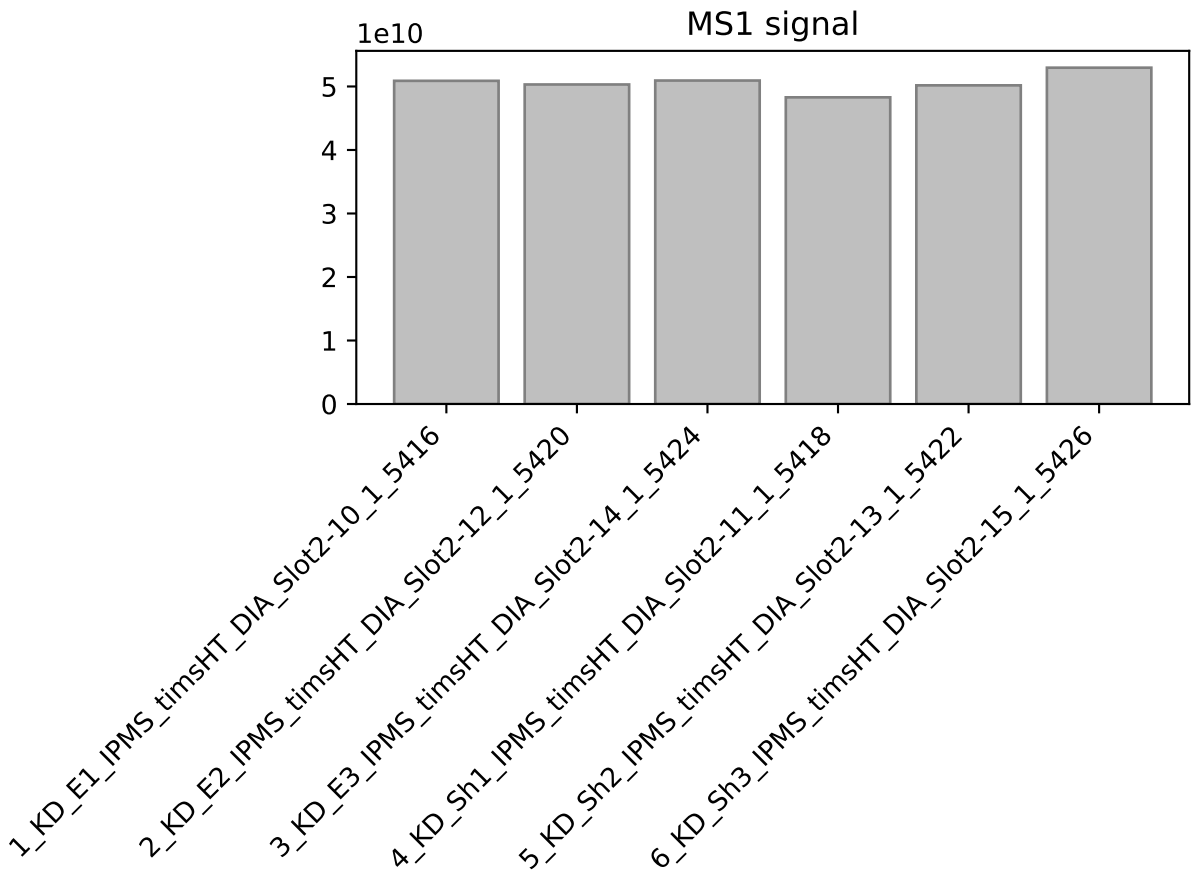
Normalisation factor heatmap, all runs





Total quantity, 1% FDR



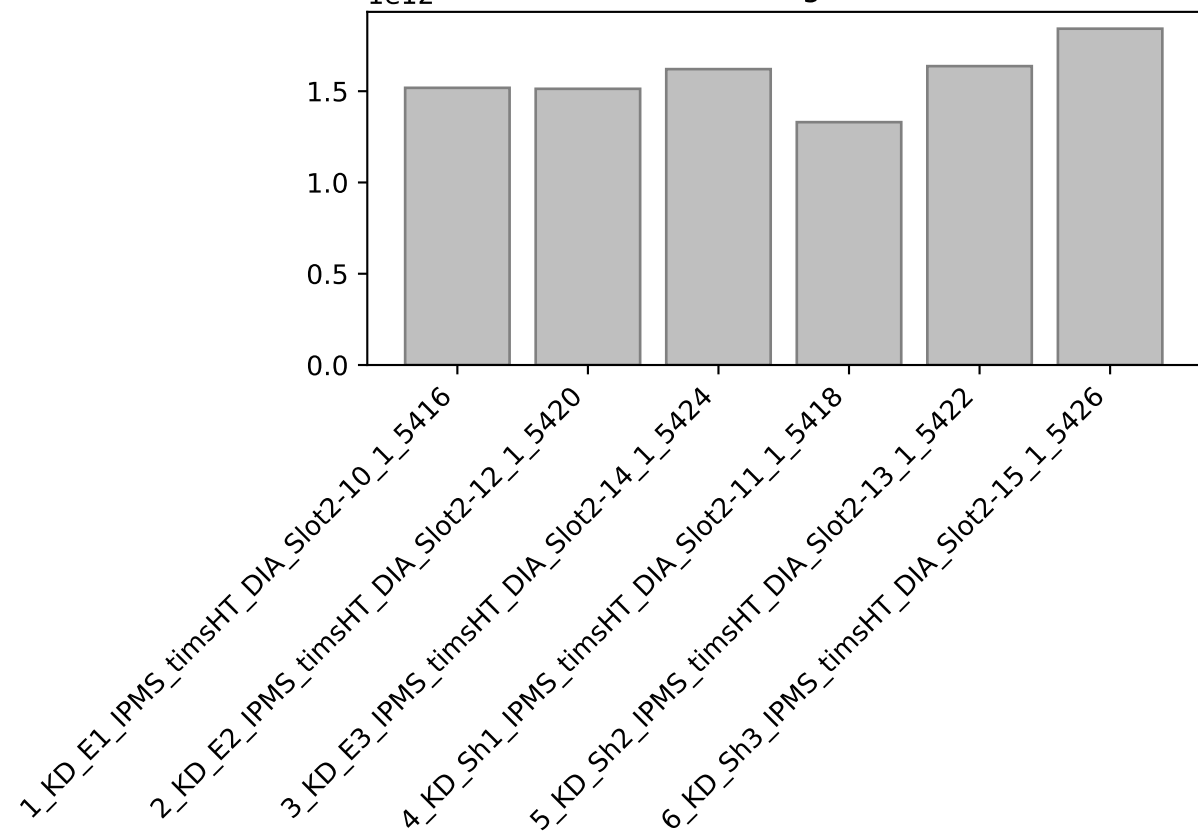


MS2 signal

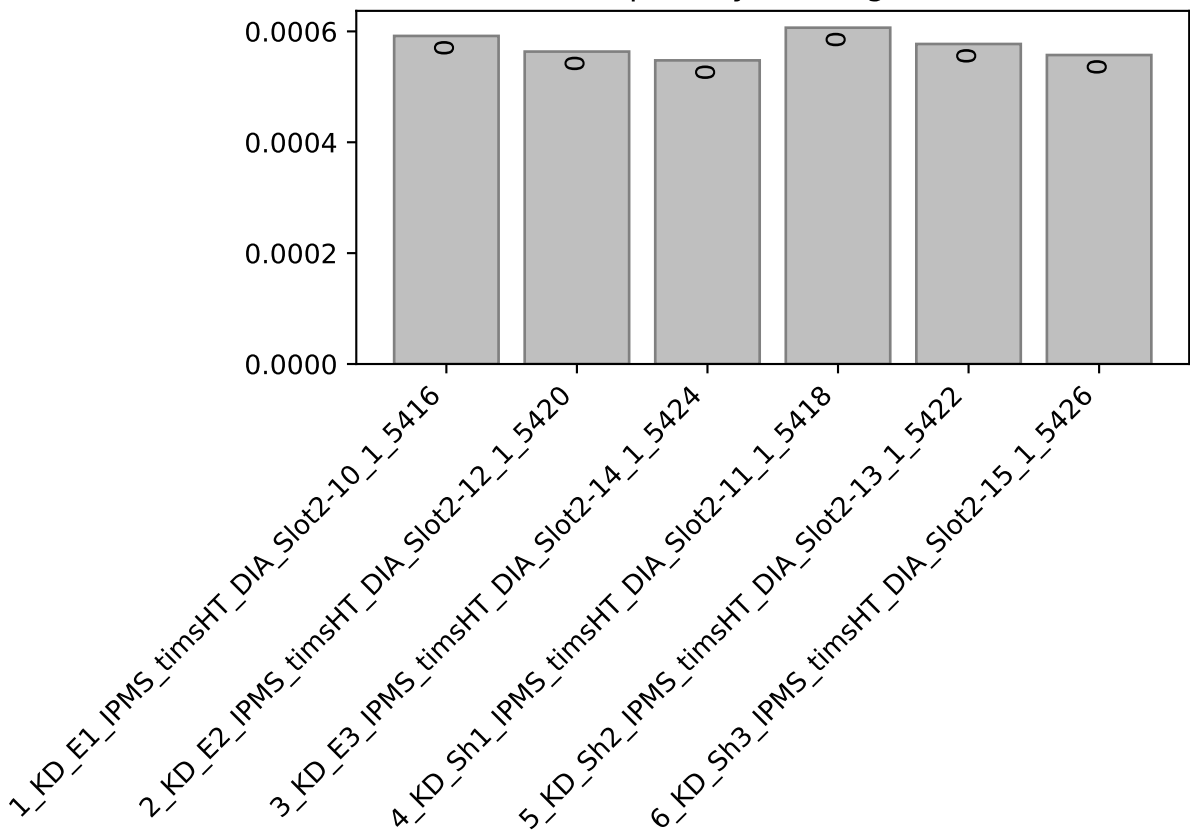
1e12

1.5  
1.0  
0.5  
0.0

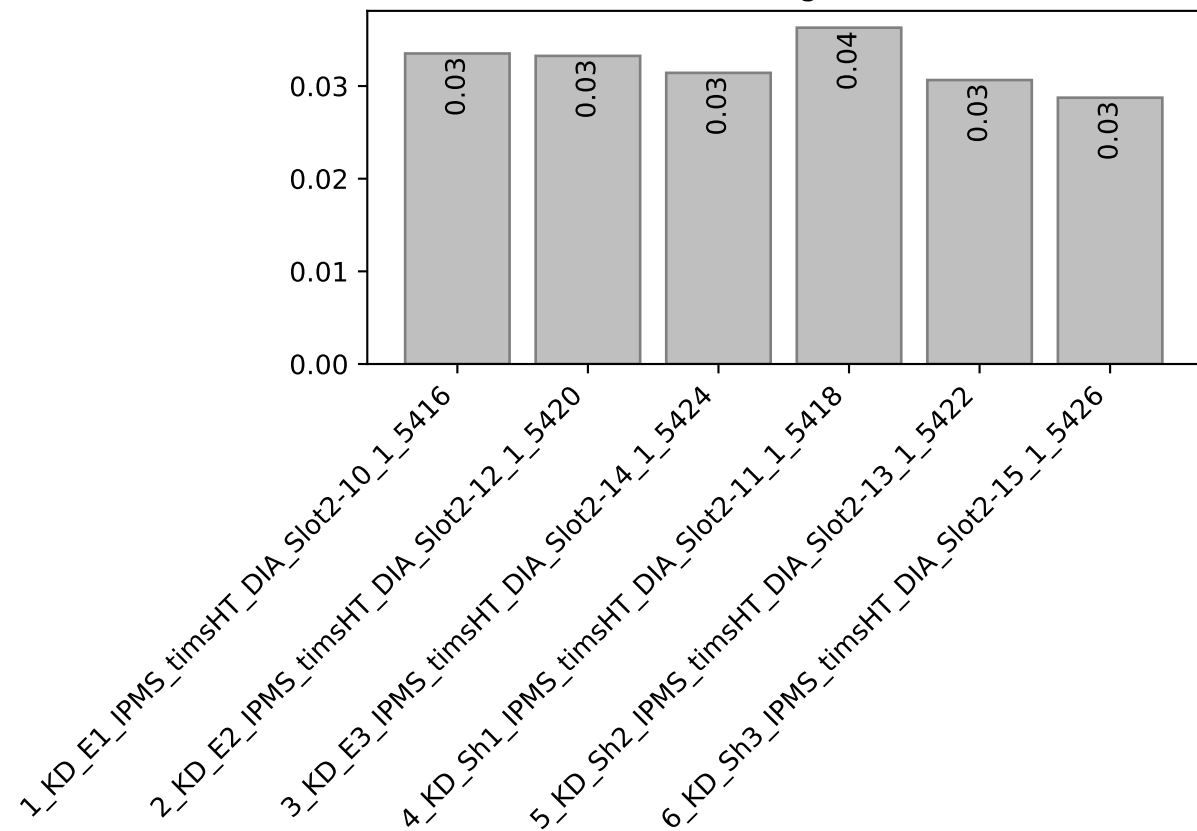
1\_KD\_E1\_IPMS\_timsHT\_DIA\_Slot2-10\_1\_5416  
2\_KD\_E2\_IPMS\_timsHT\_DIA\_Slot2-12\_1\_5420  
3\_KD\_E3\_IPMS\_timsHT\_DIA\_Slot2-14\_1\_5424  
4\_KD\_Sh1\_IPMS\_timsHT\_DIA\_Slot2-11\_1\_5418  
5\_KD\_Sh2\_IPMS\_timsHT\_DIA\_Slot2-13\_1\_5422  
6\_KD\_Sh3\_IPMS\_timsHT\_DIA\_Slot2-15\_1\_5426



Total quantity/MS2 signal ratio

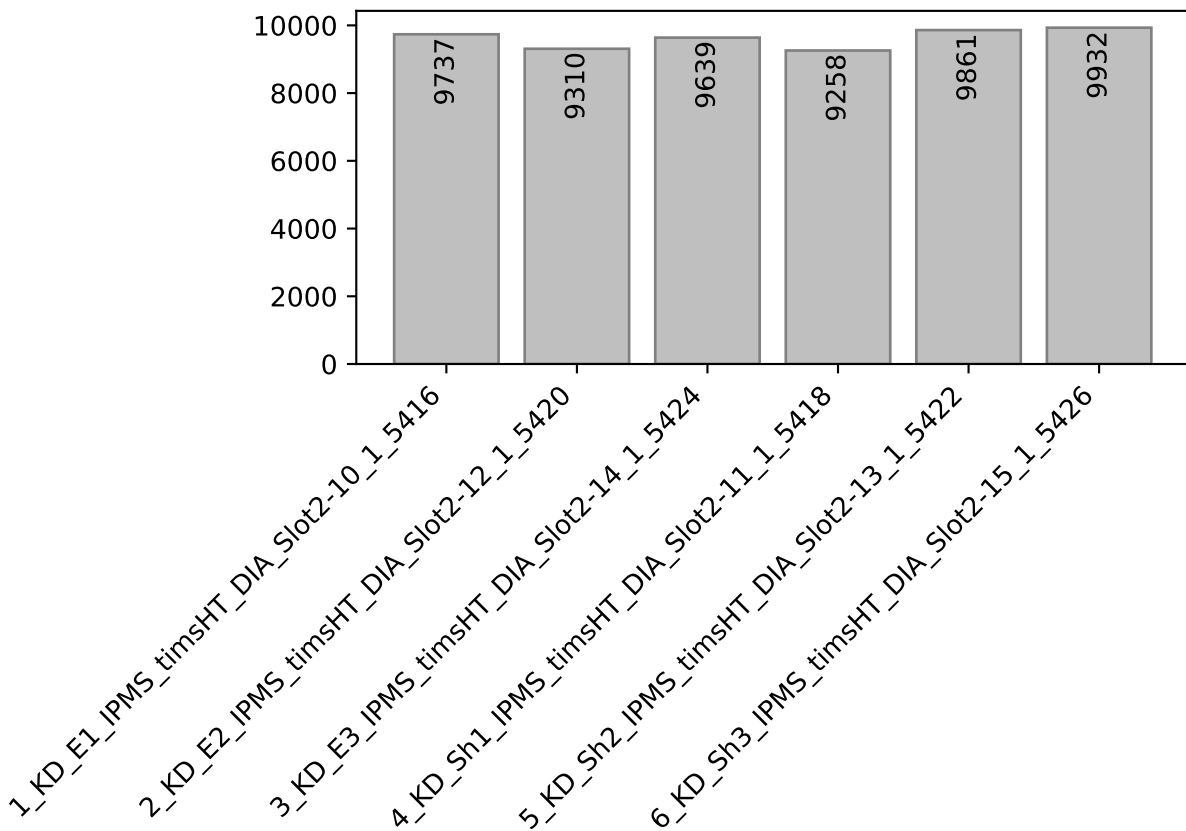


MS1/MS2 signal ratio

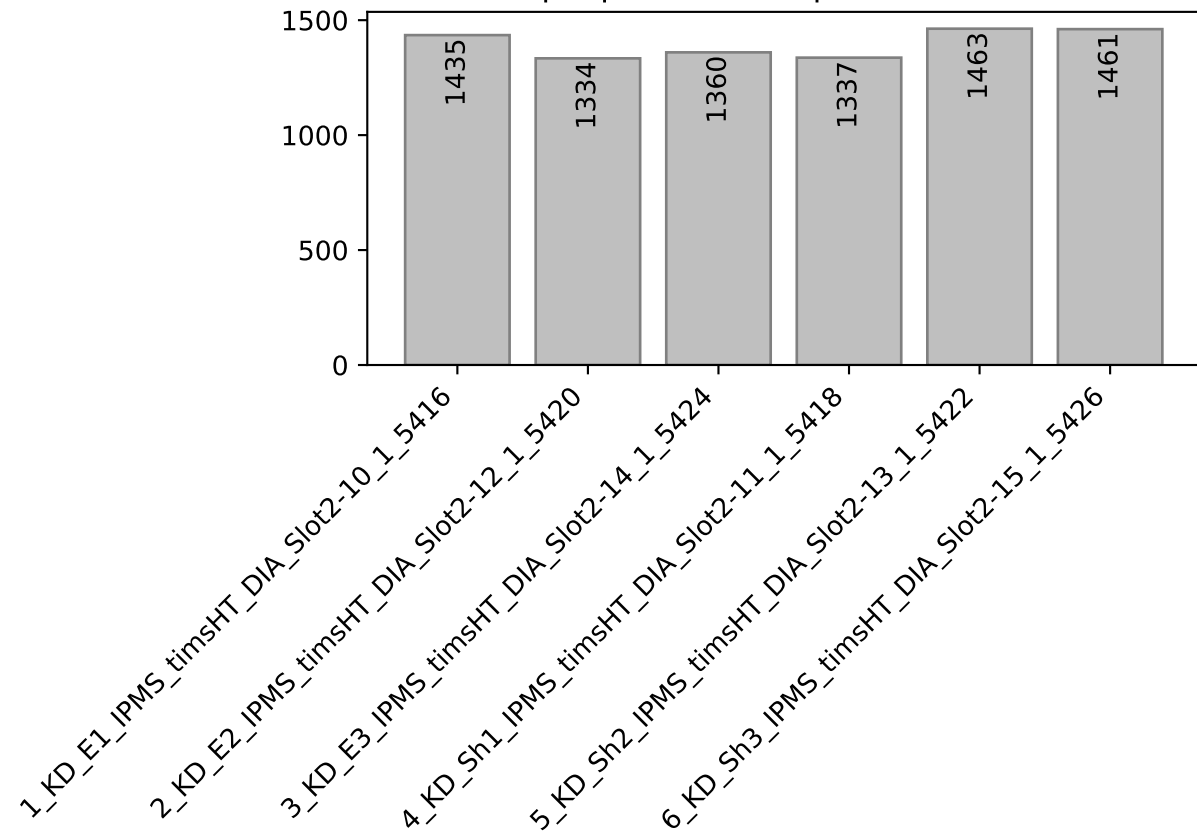




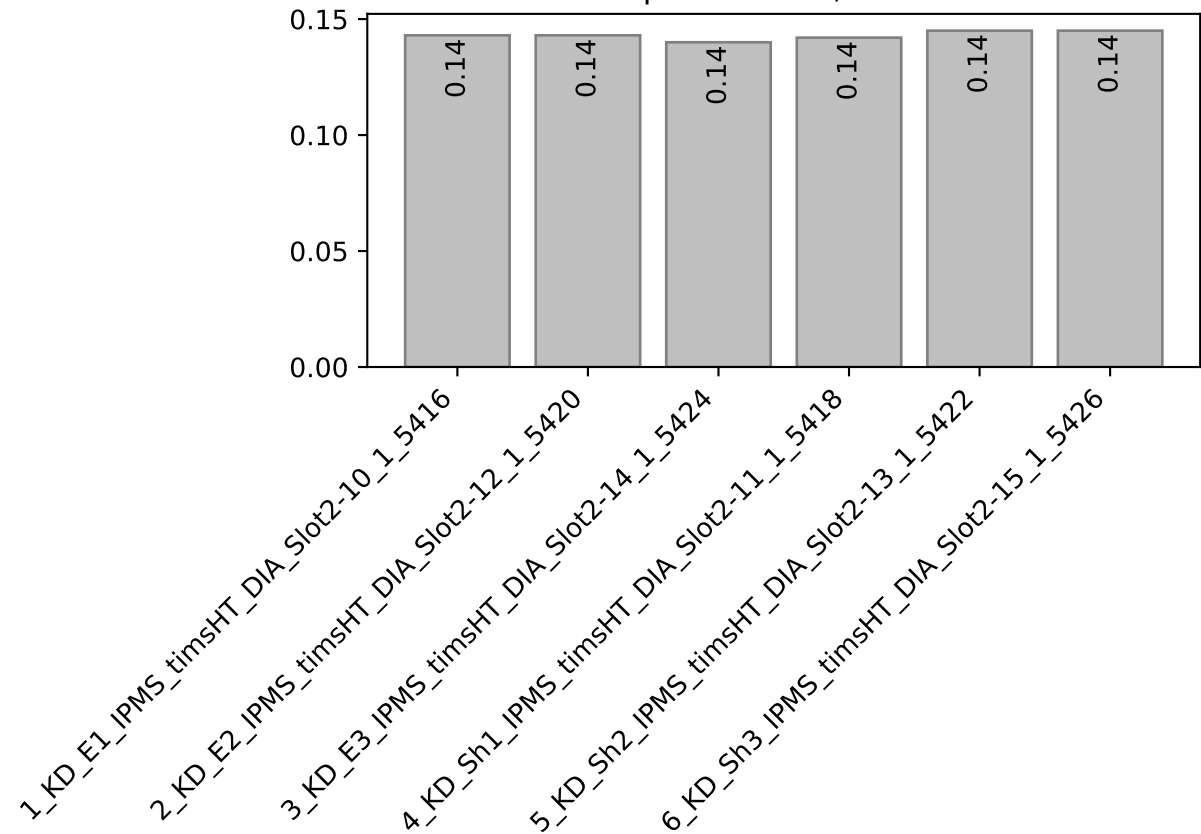
Precursors, 1% FDR



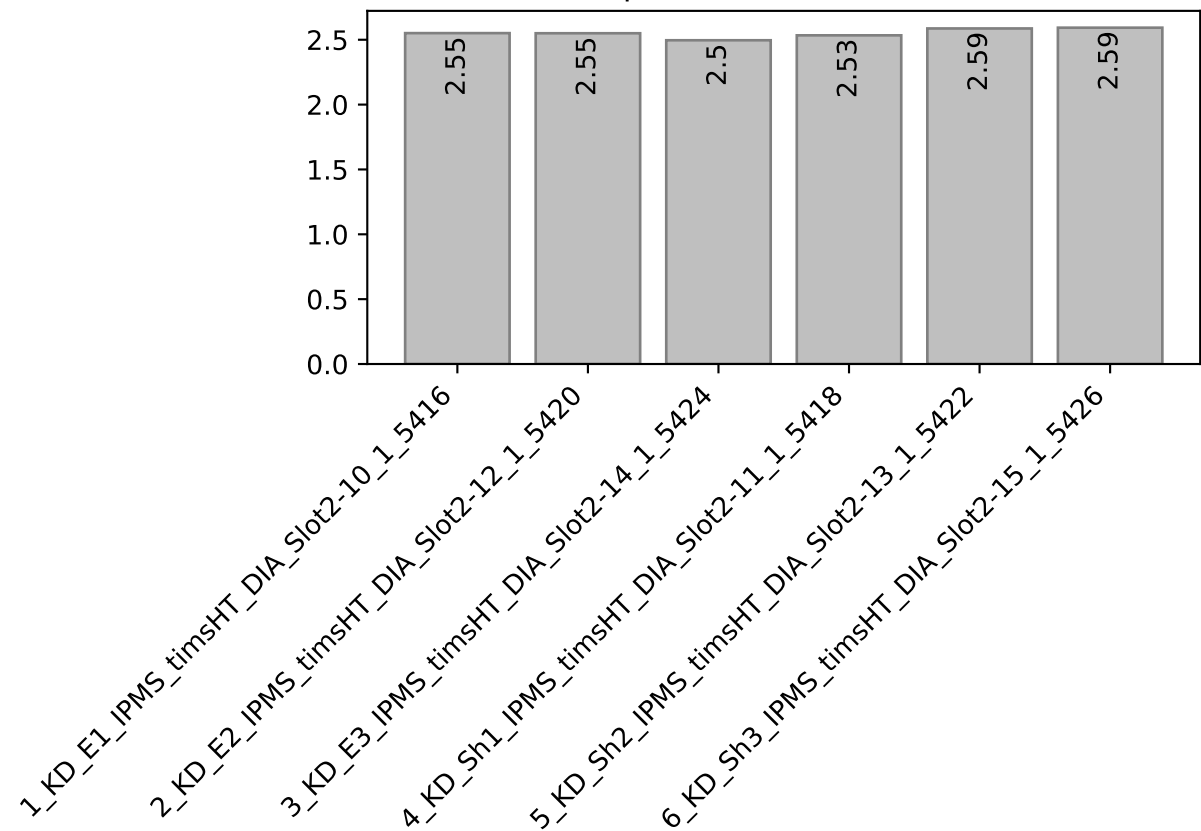
Unique proteins, 1% protein-level FDR



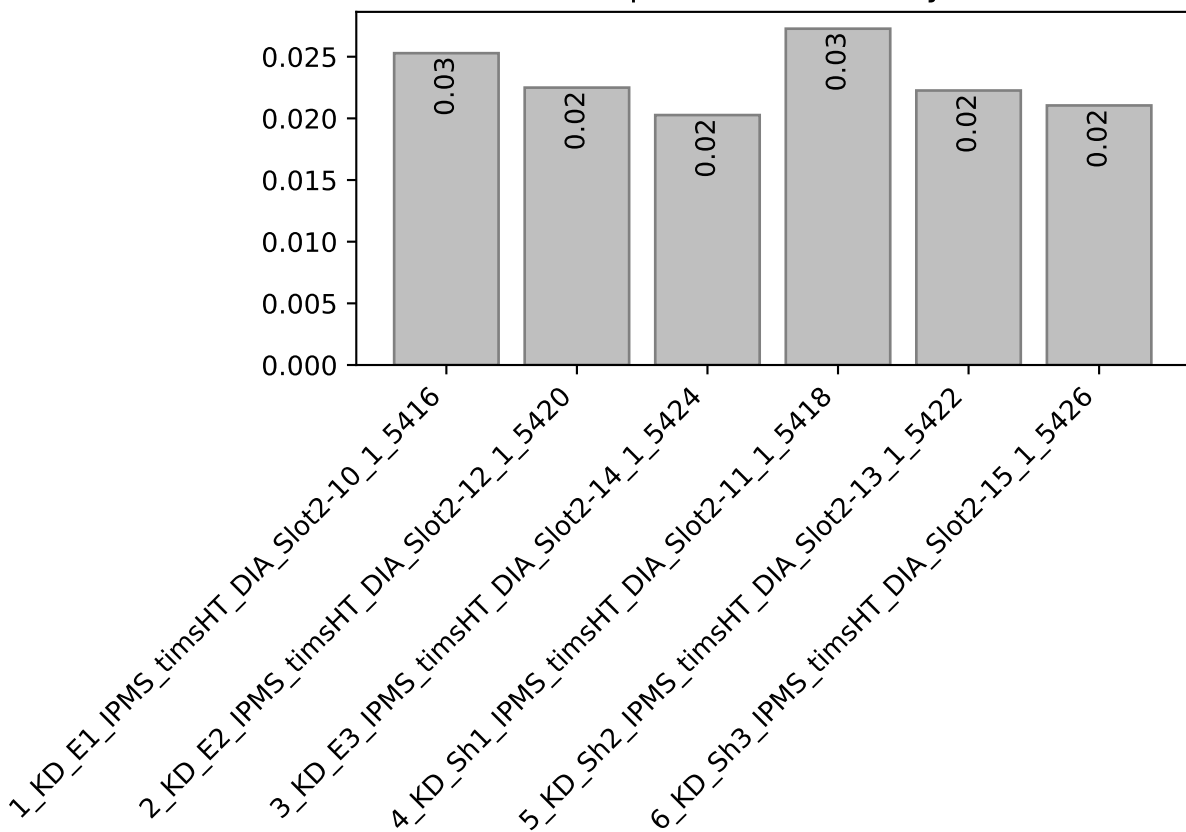
Mean peak FWHM, in minutes



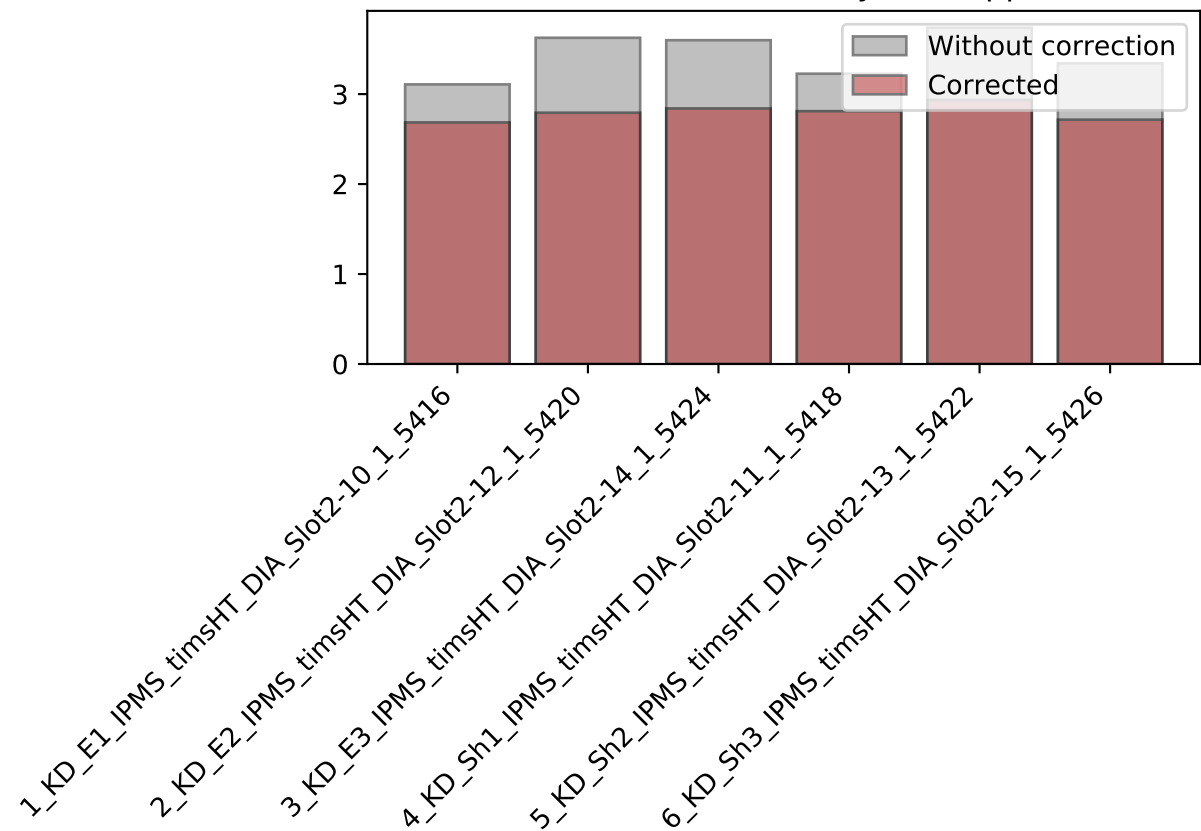
Mean peak FWHM, in MS2 scans



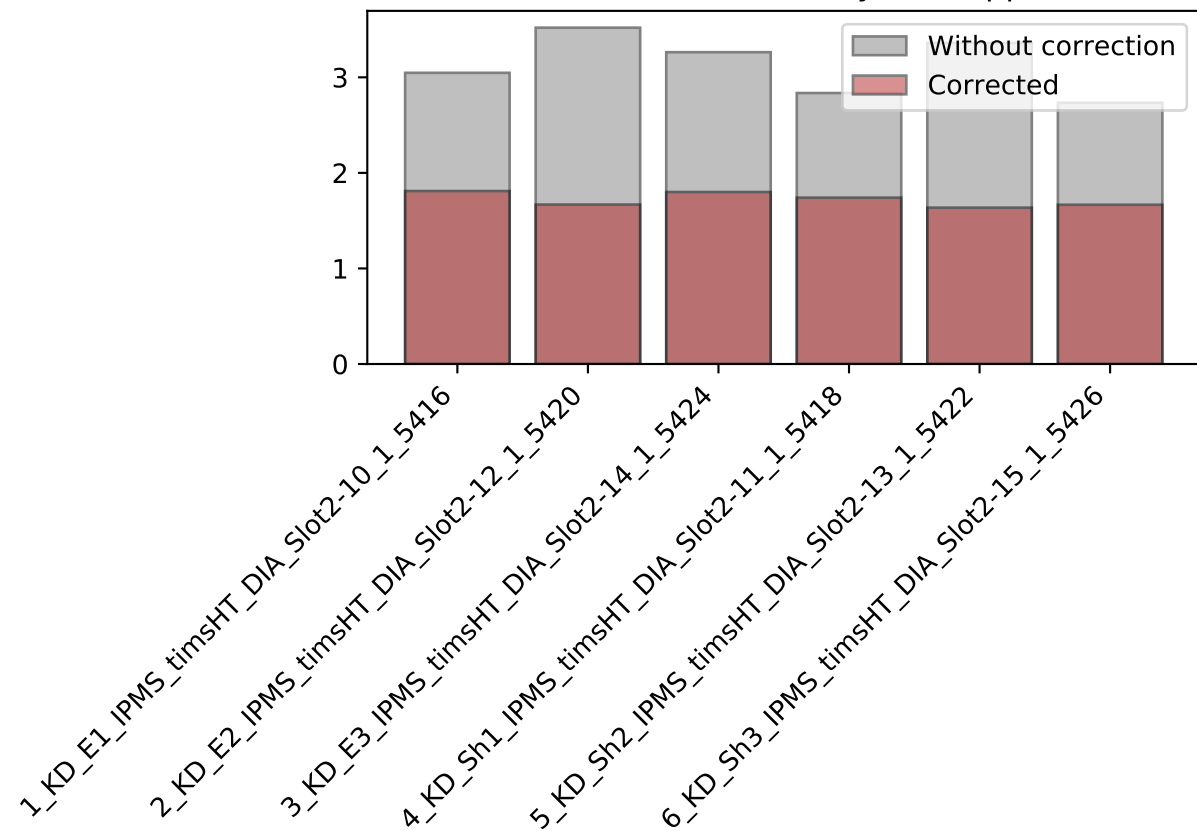
Median RT prediction accuracy, minutes



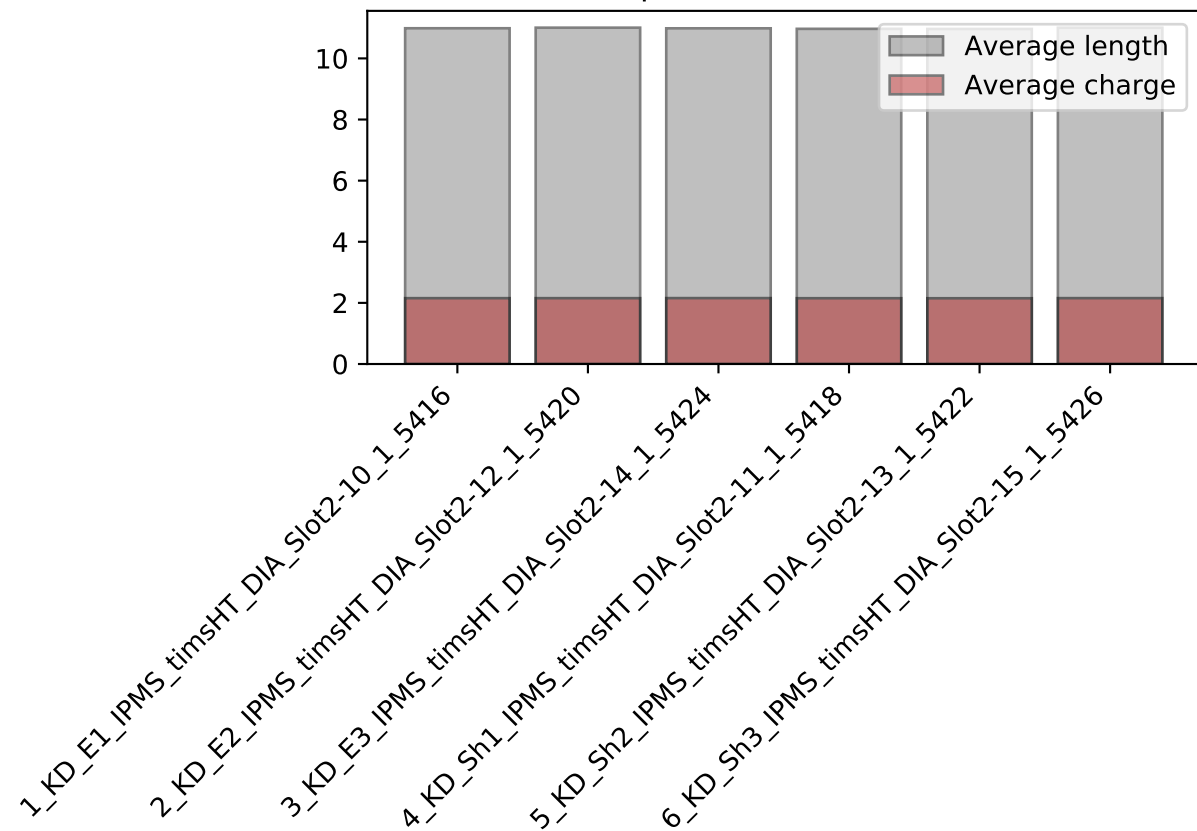
Median mass accuracy, MS2, ppm



Median mass accuracy, MS1, ppm



## Peptide characteristics





Average missed tryptic cleavages

