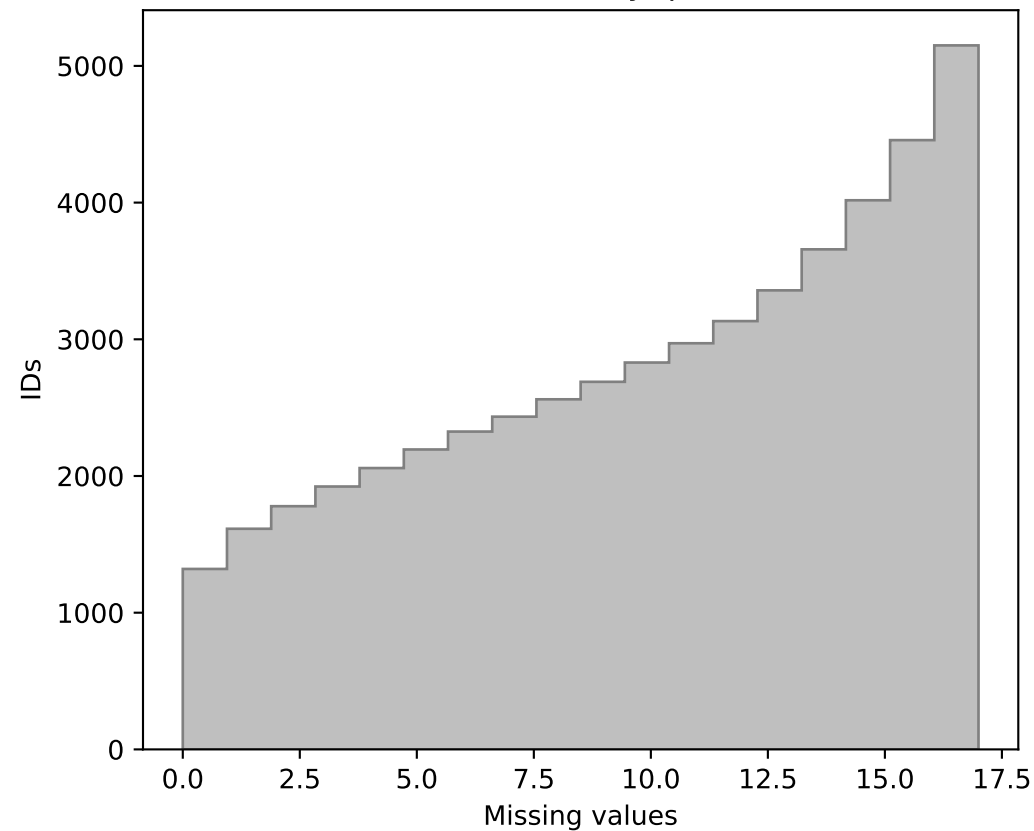
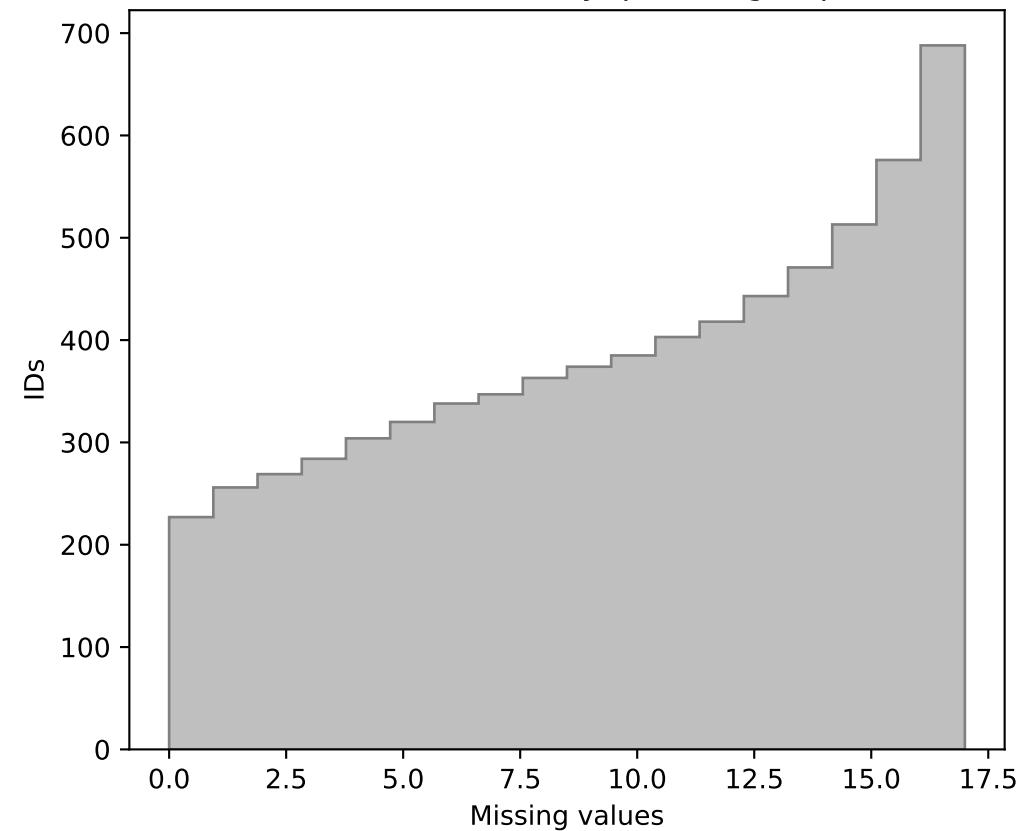


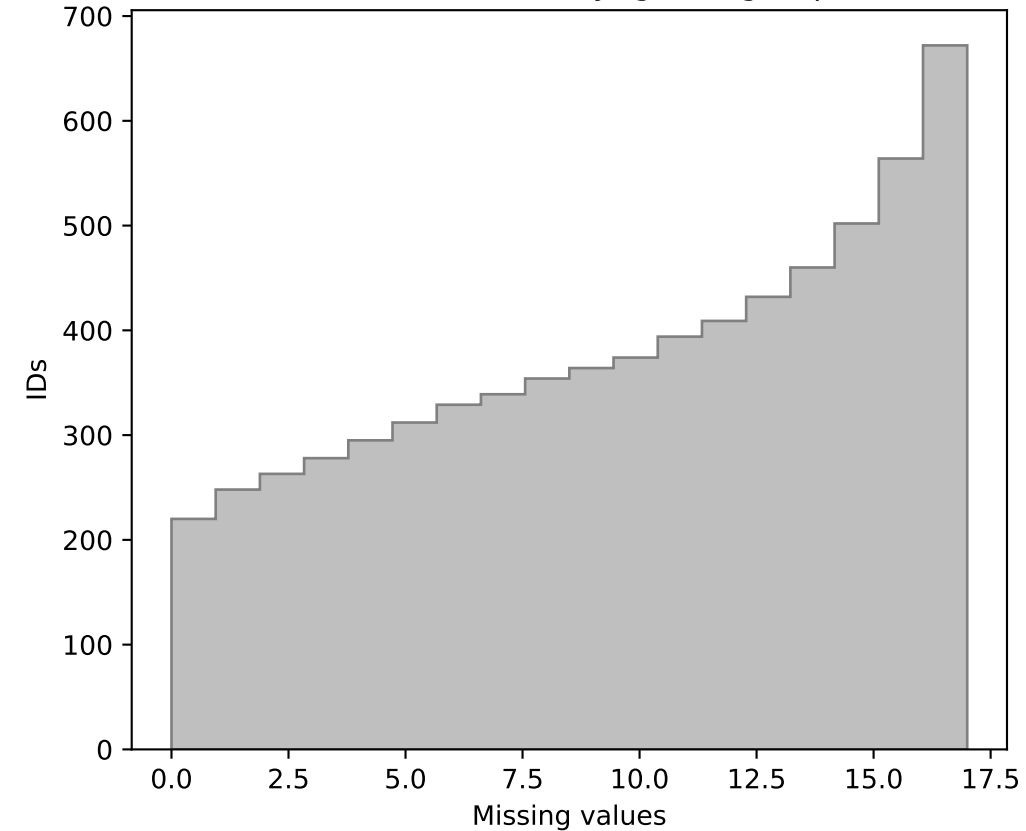
Identification consistency: precursors, CDF



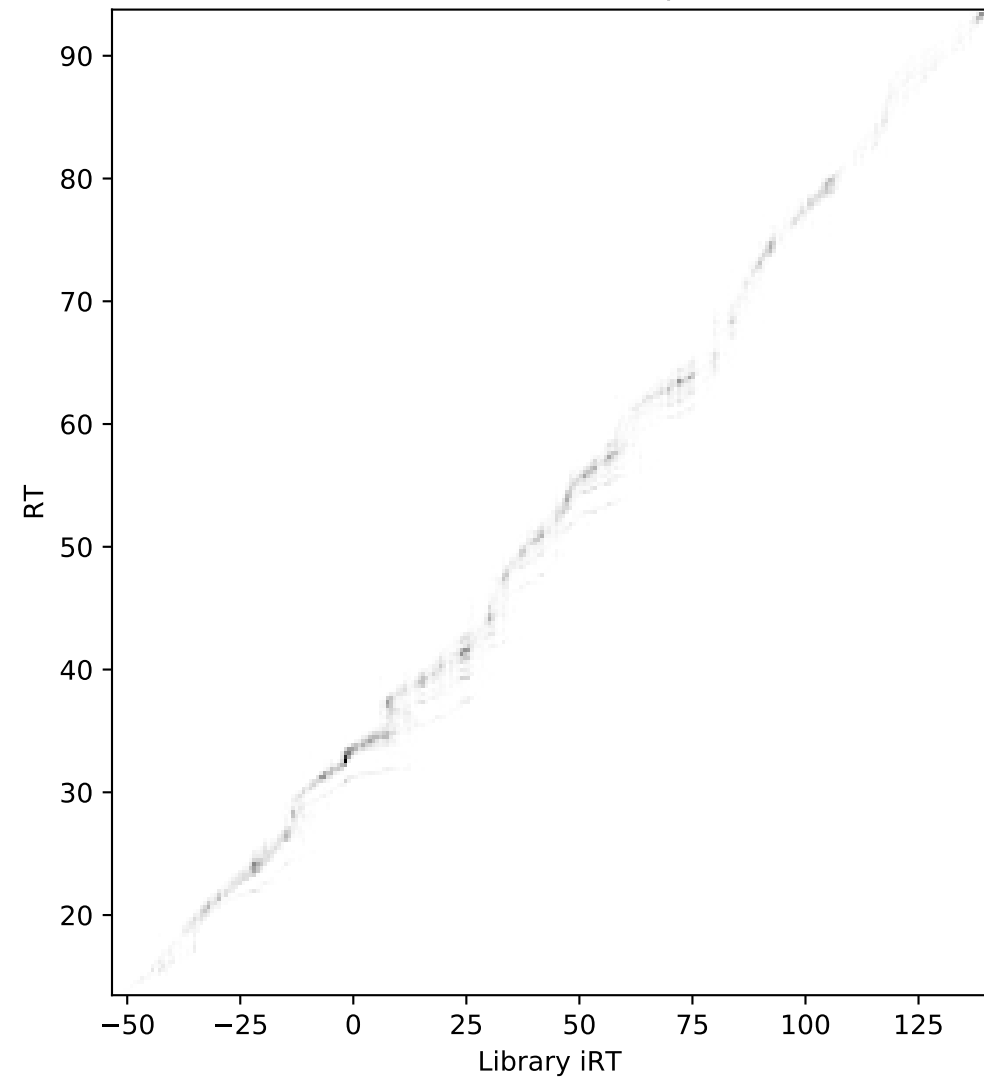
Identification consistency: protein groups, CDF



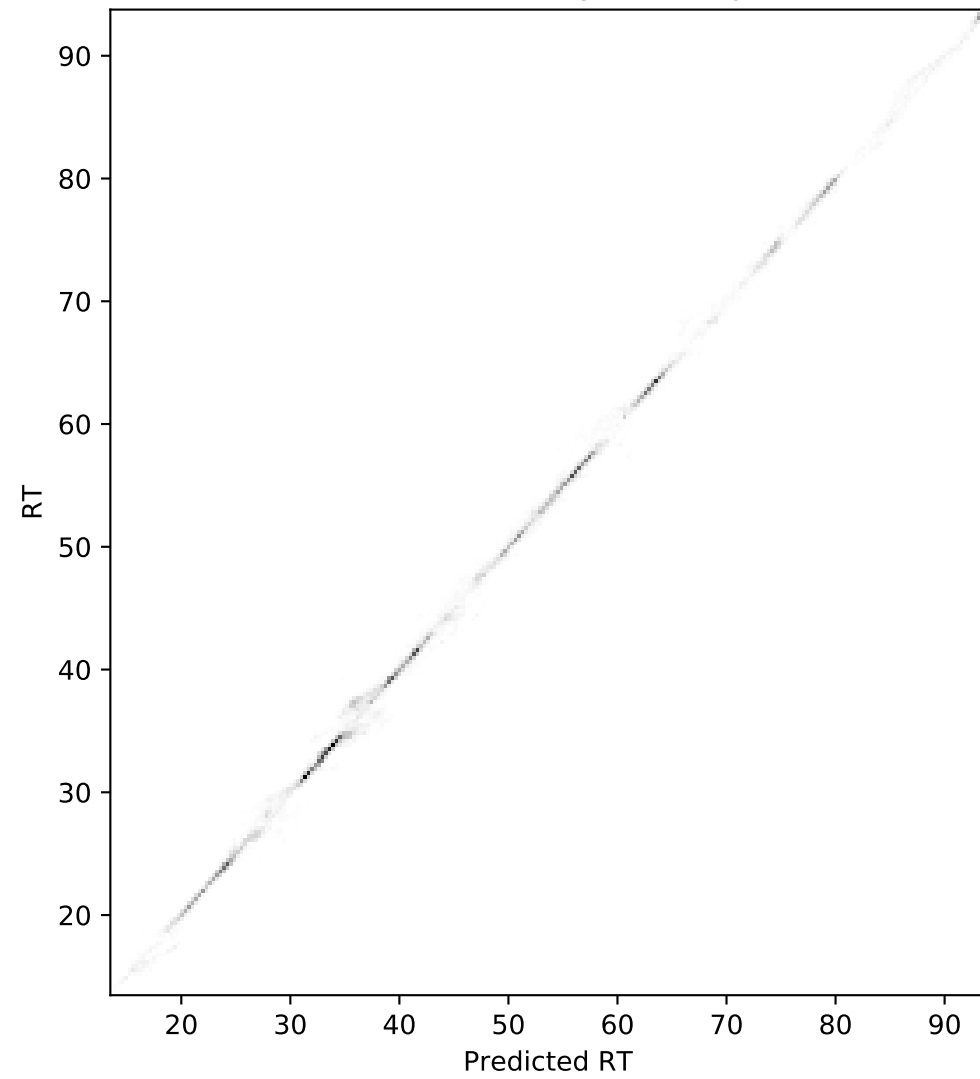
Identification consistency: genes groups, CDF



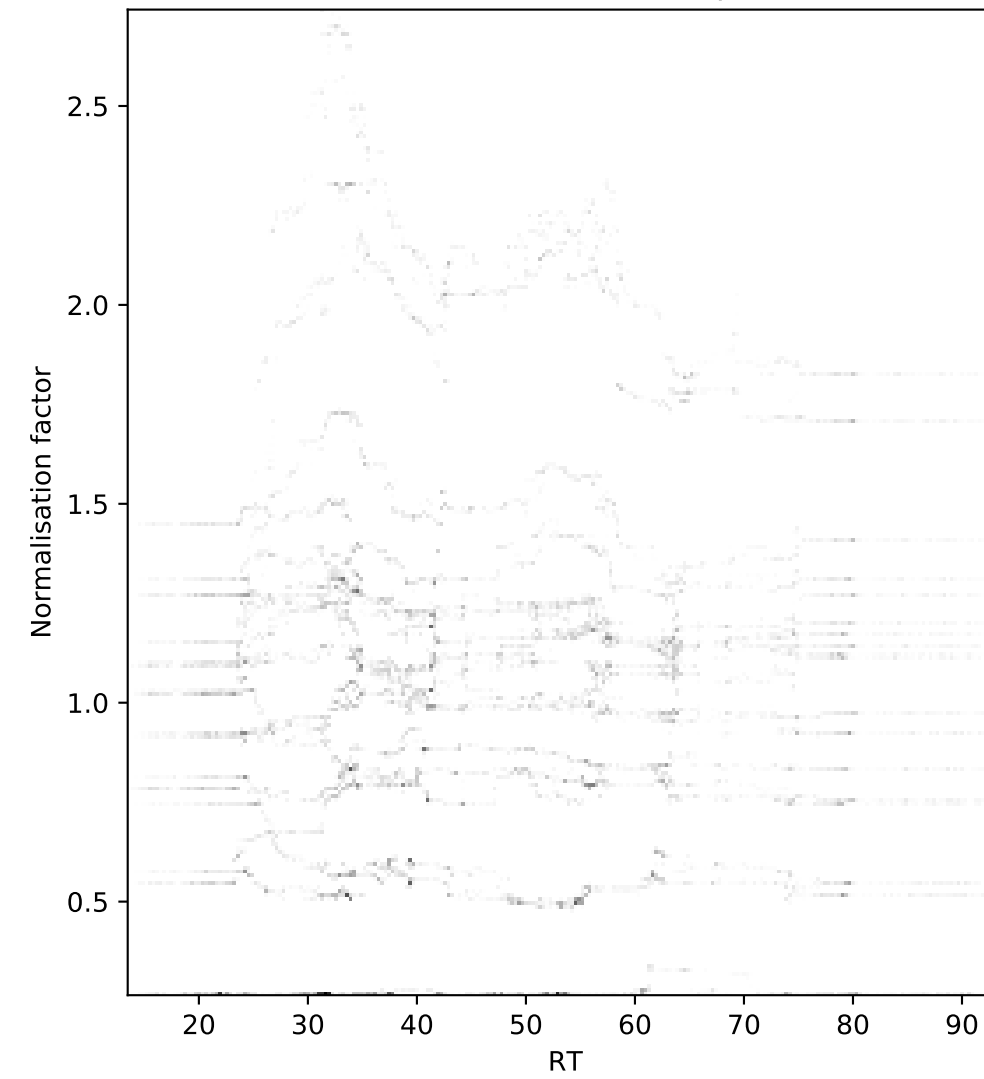
Retention times heatmap, all runs

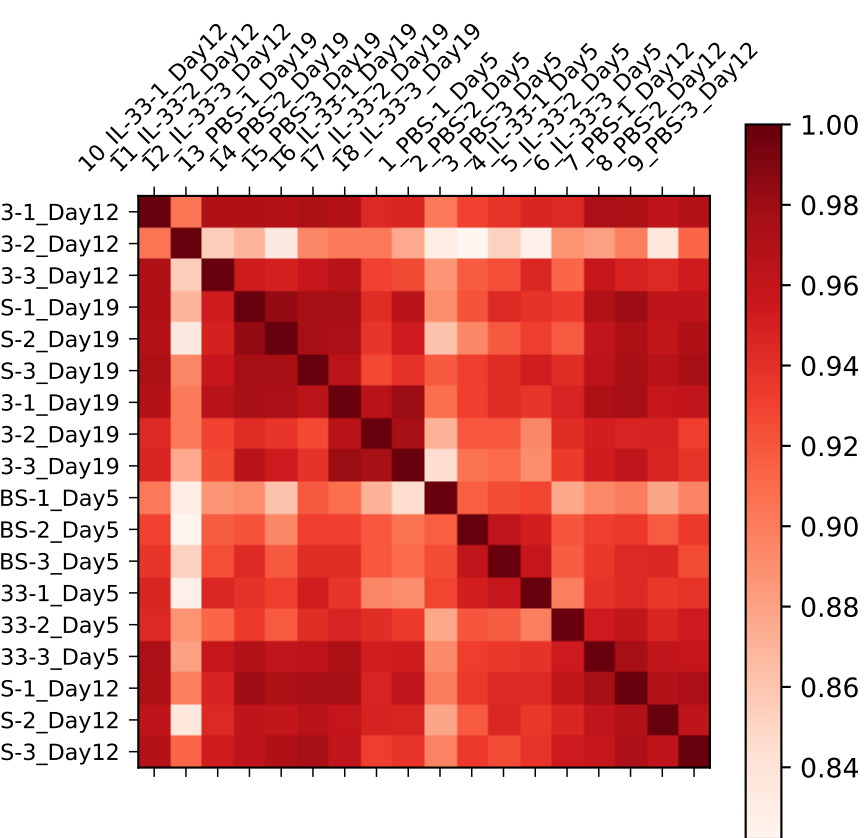


Retention time accuracy heatmap, all runs

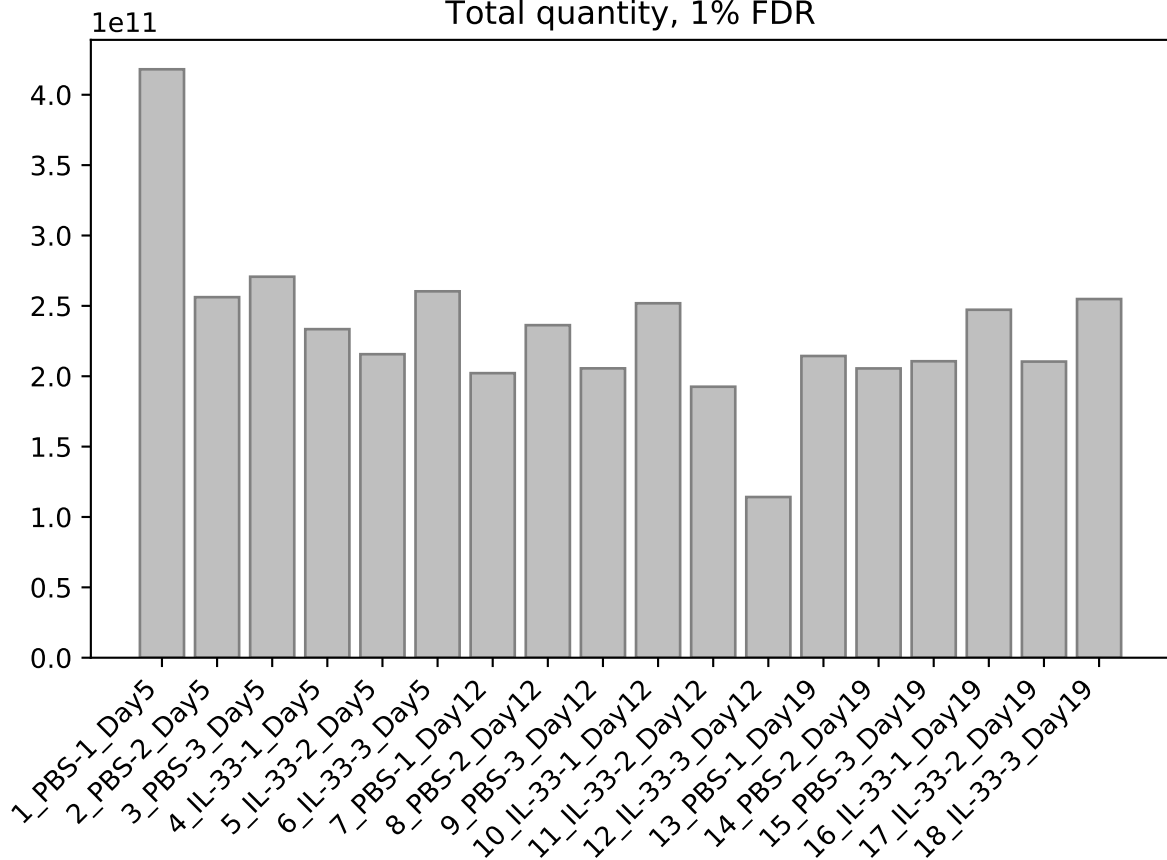


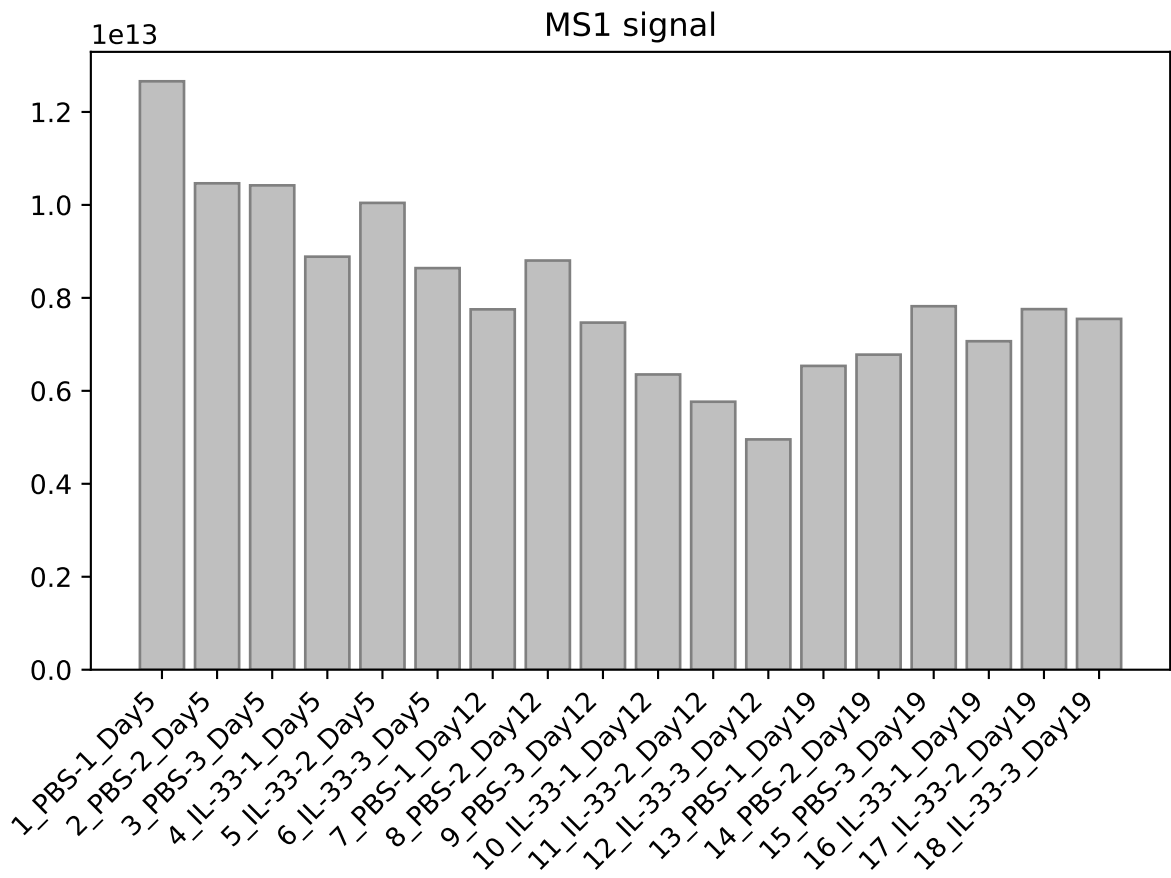
Normalisation factor heatmap, all runs



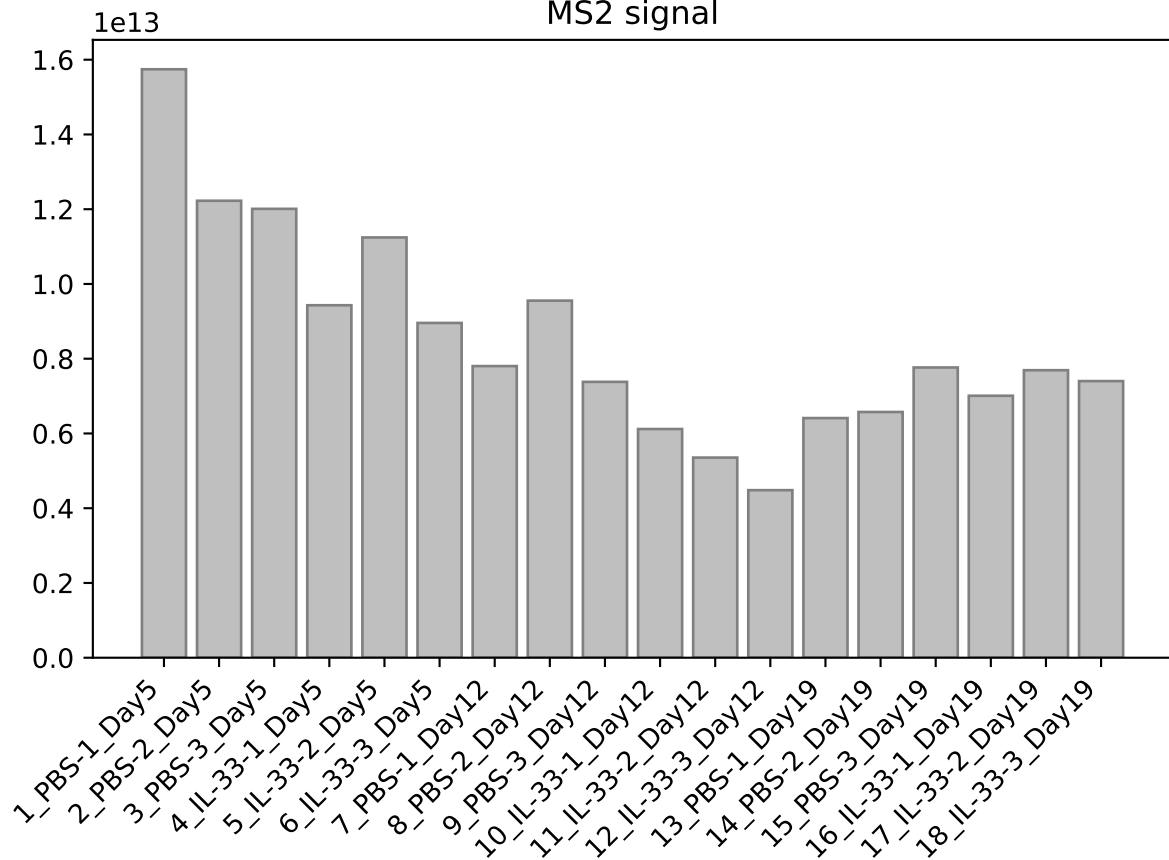


Total quantity, 1% FDR

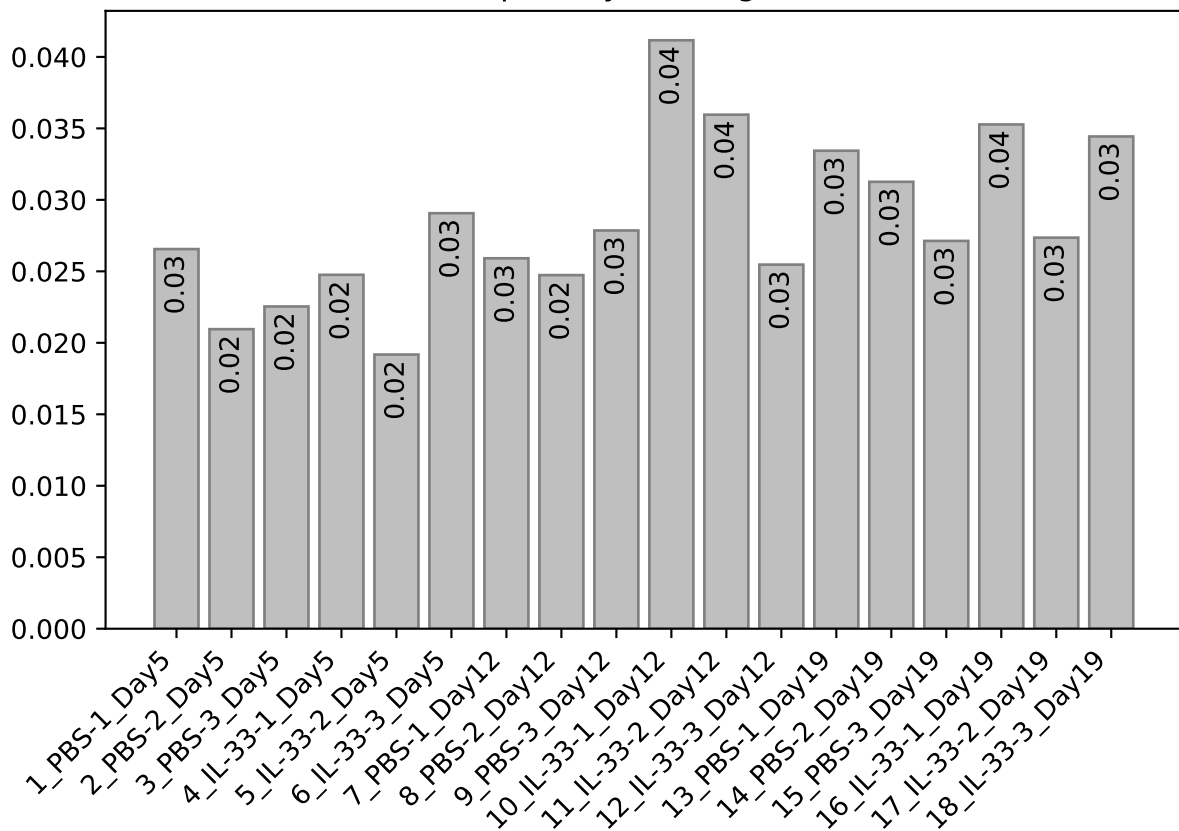




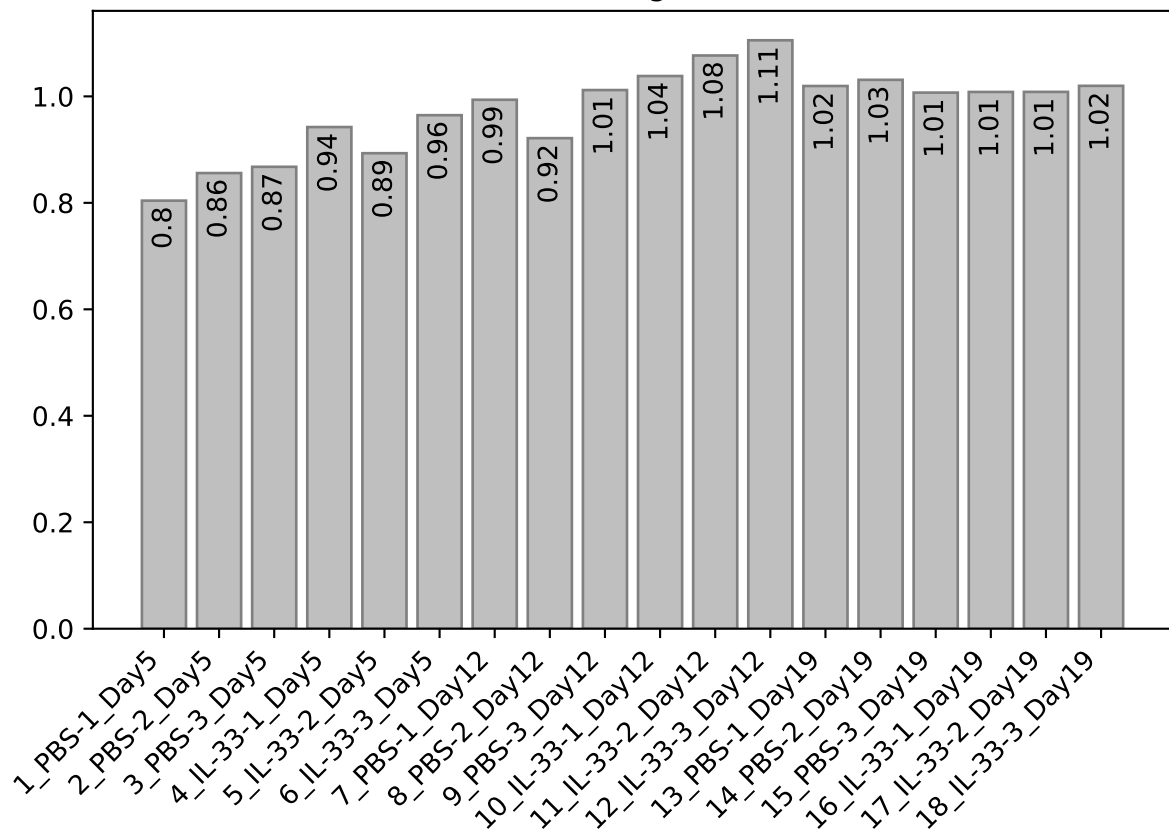
MS2 signal



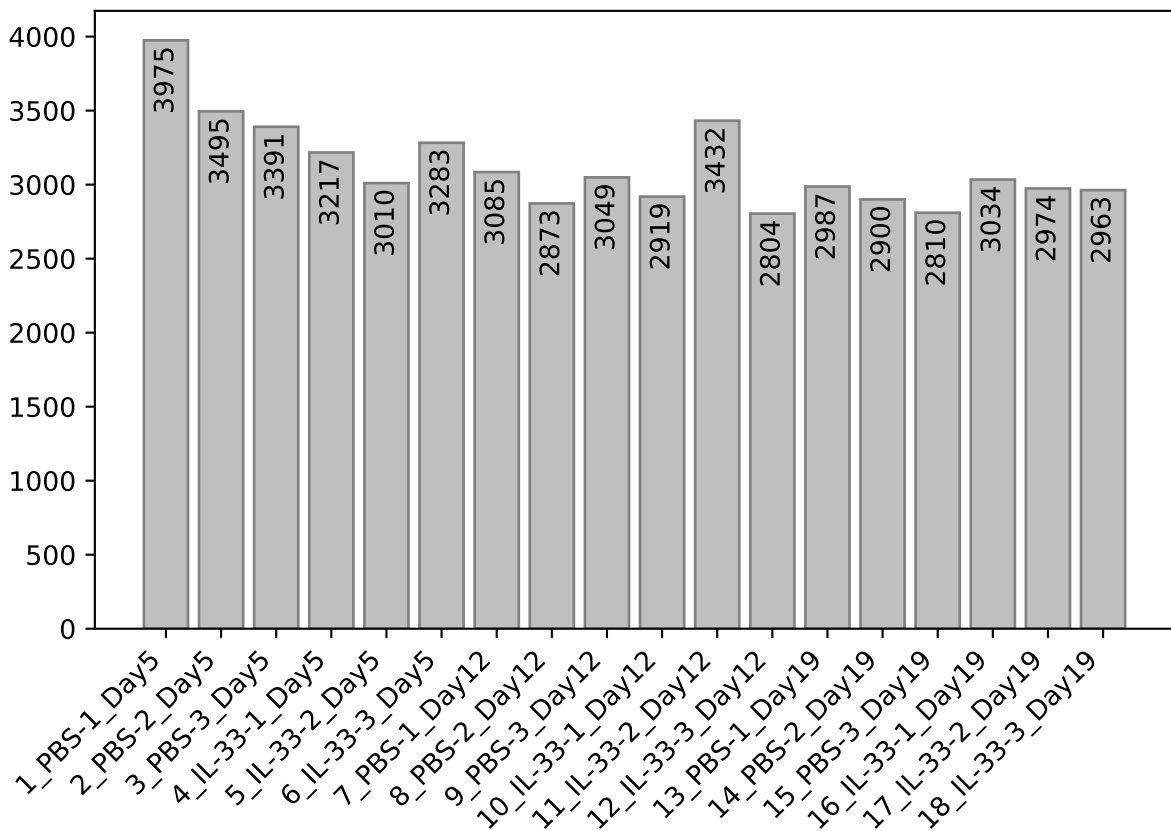
Total quantity/MS2 signal ratio



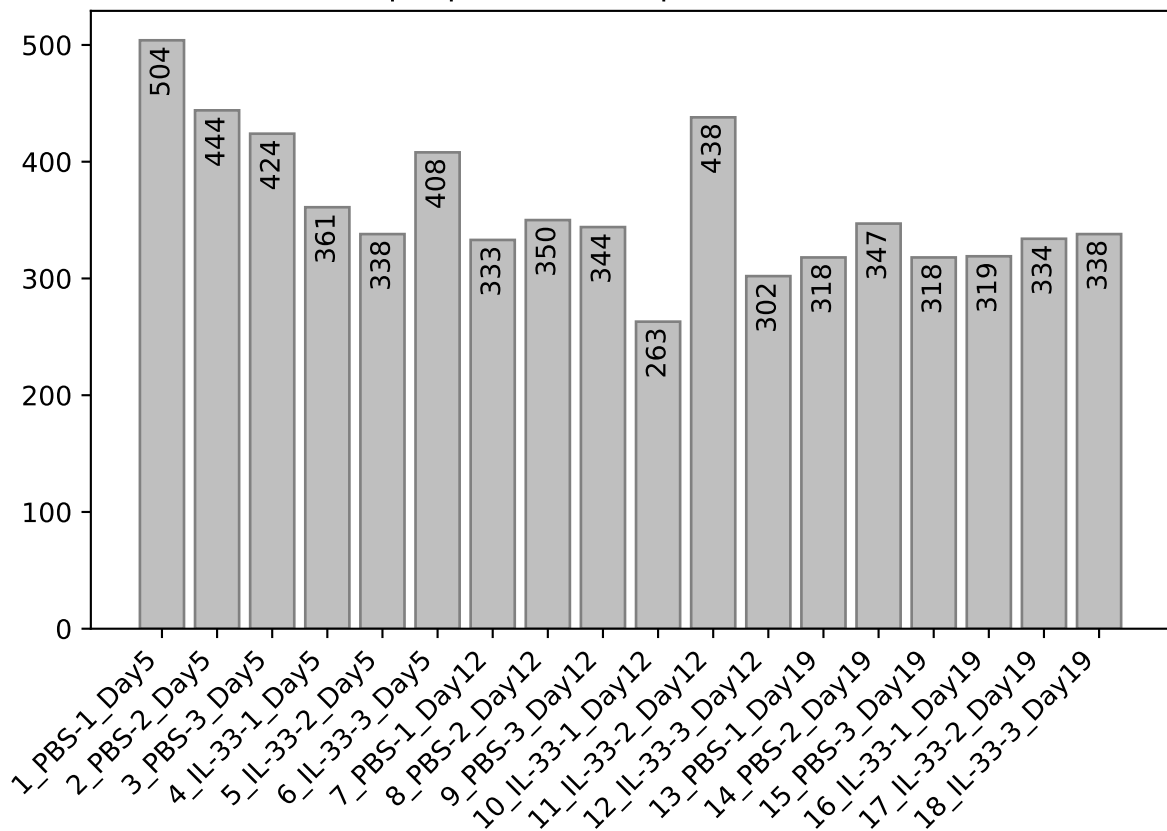
MS1/MS2 signal ratio



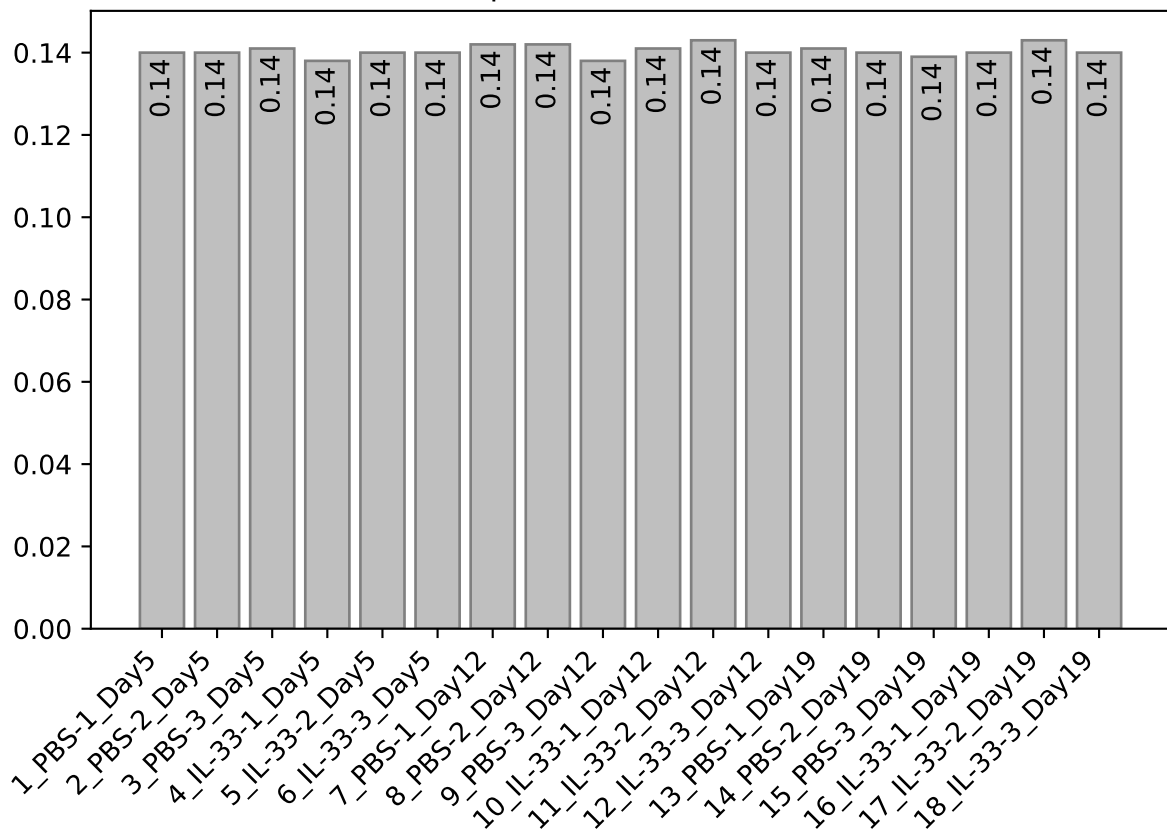
Precursors, 1% FDR



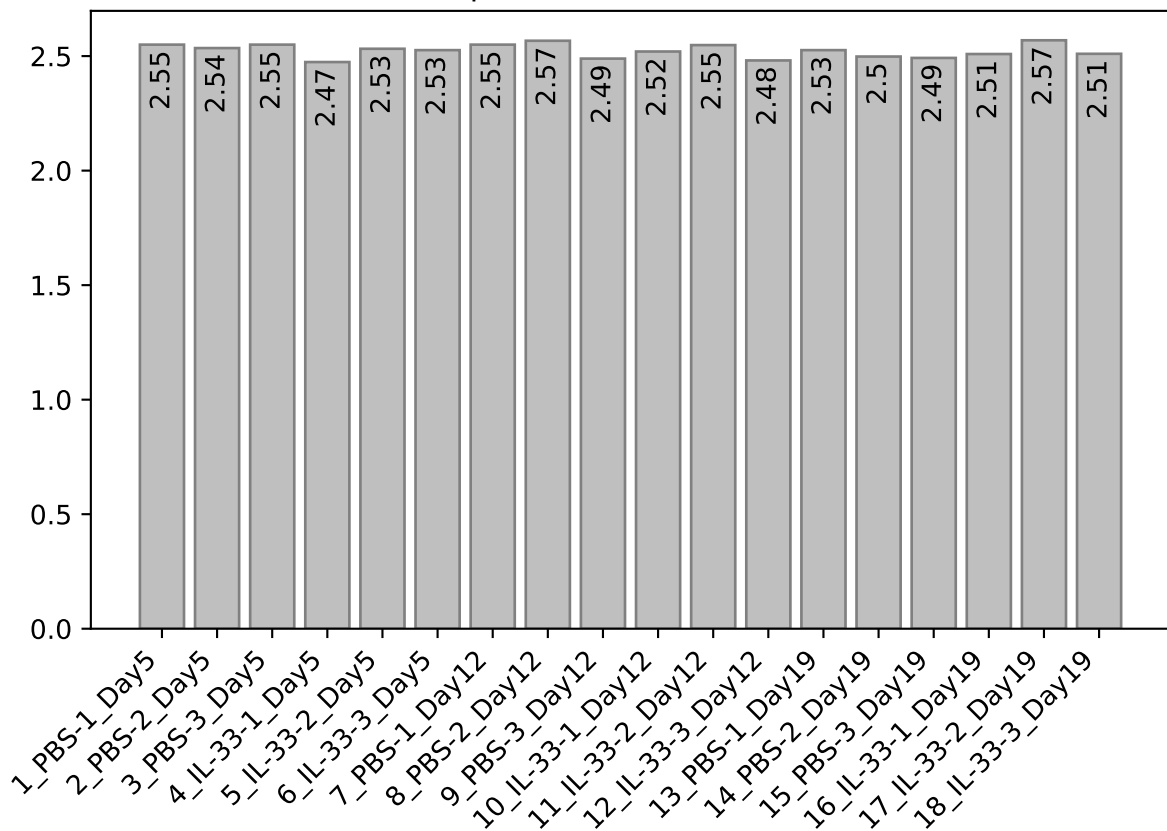
Unique proteins, 1% protein-level FDR



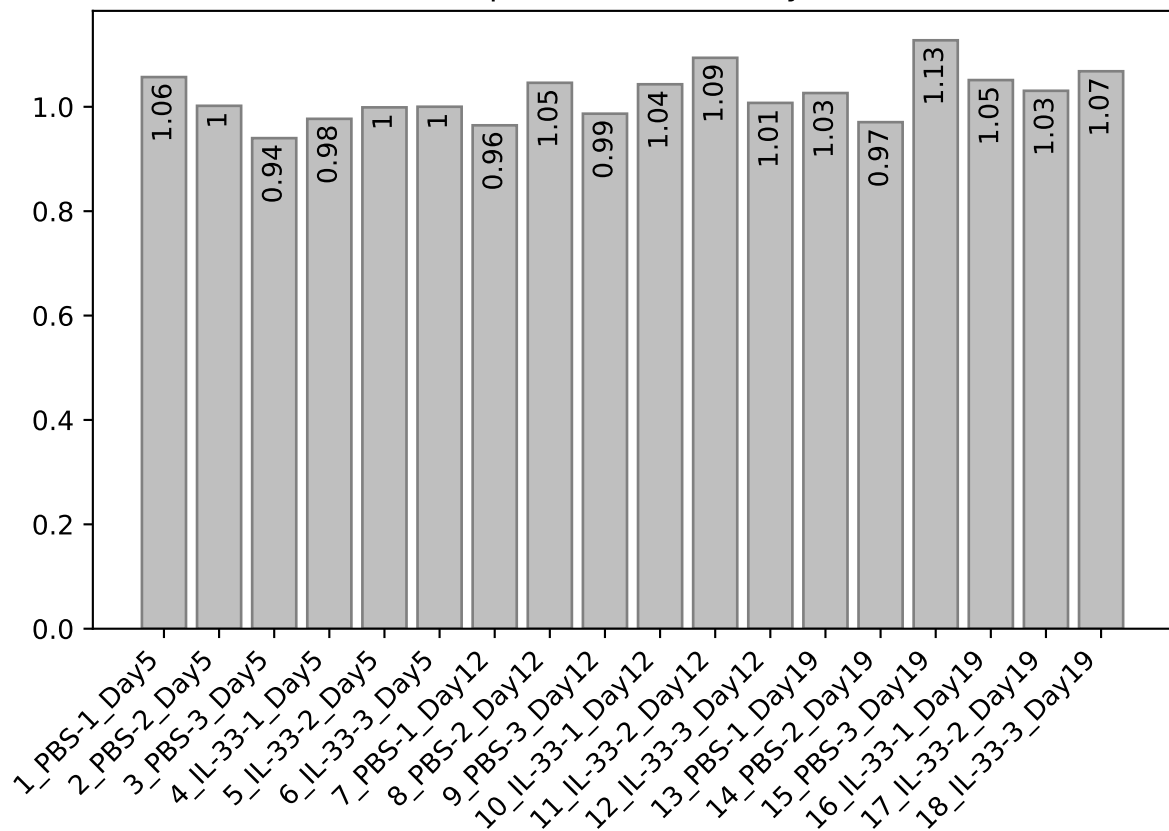
Mean peak FWHM, in minutes



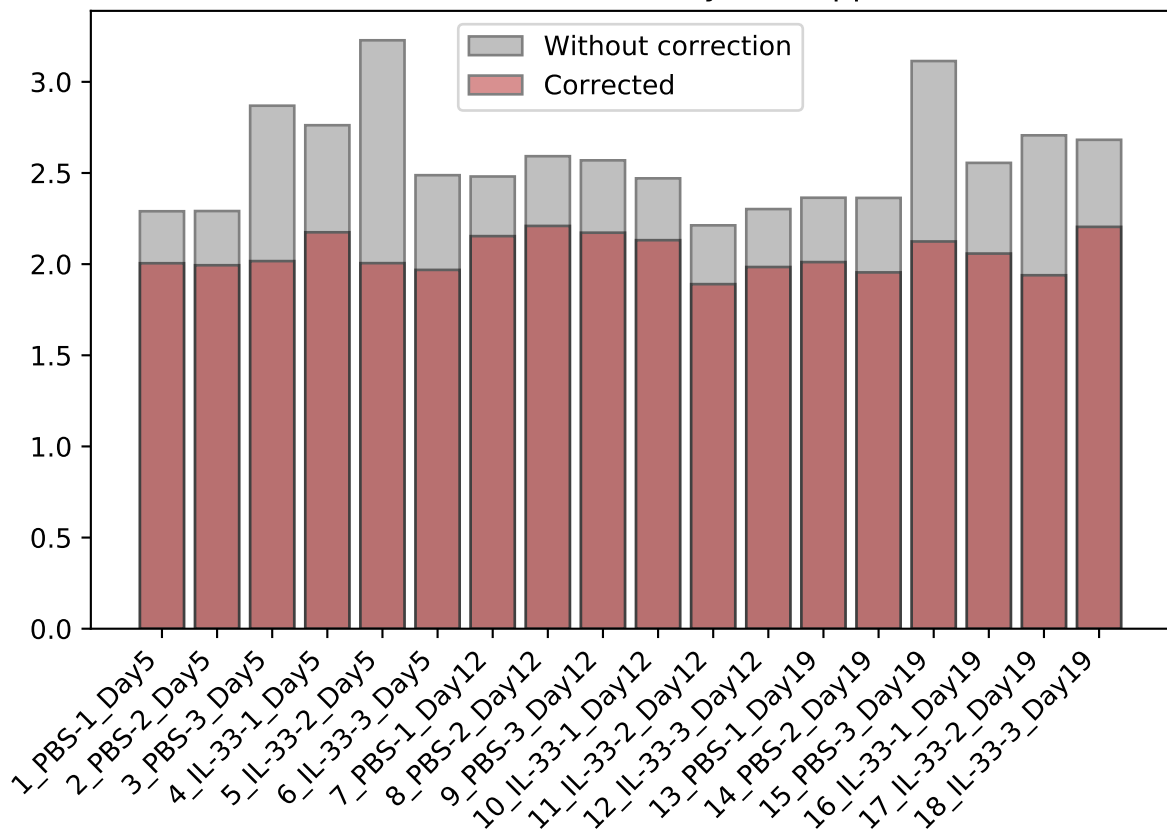
Mean peak FWHM, in MS2 scans



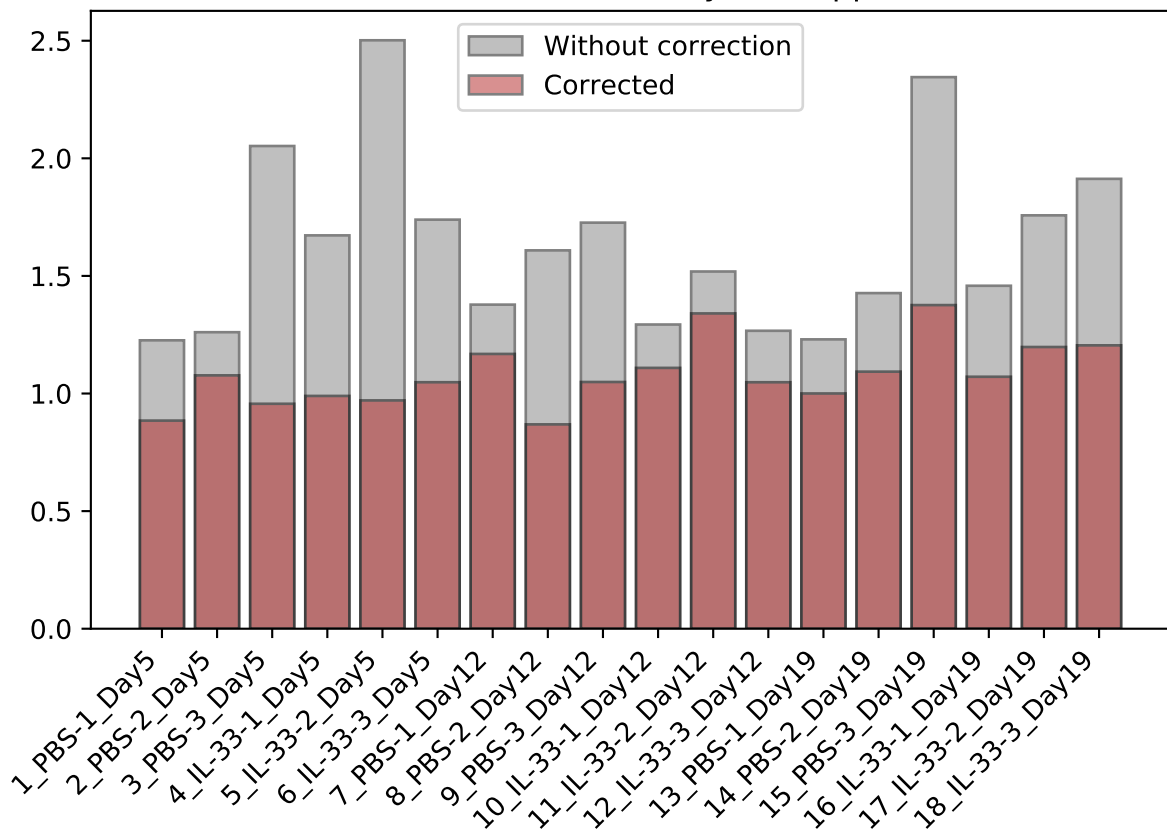
Median RT prediction accuracy, minutes



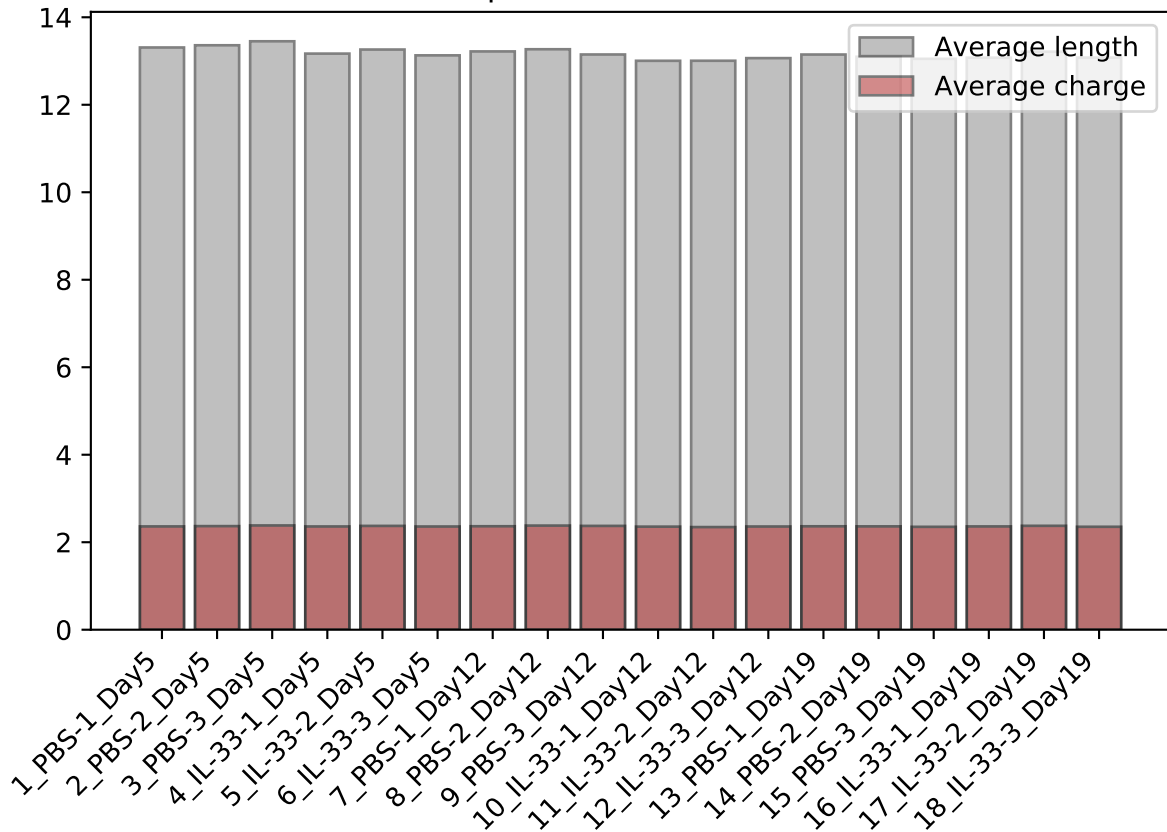
Median mass accuracy, MS2, ppm



Median mass accuracy, MS1, ppm



Peptide characteristics



Average missed tryptic cleavages

