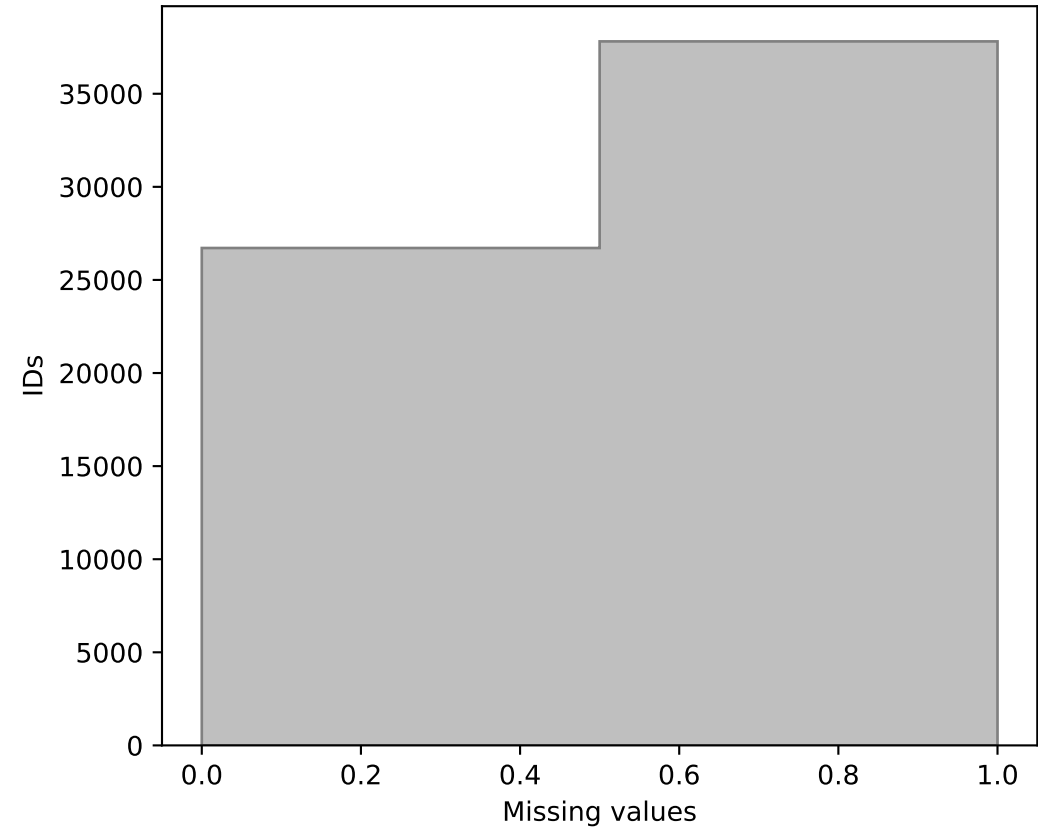
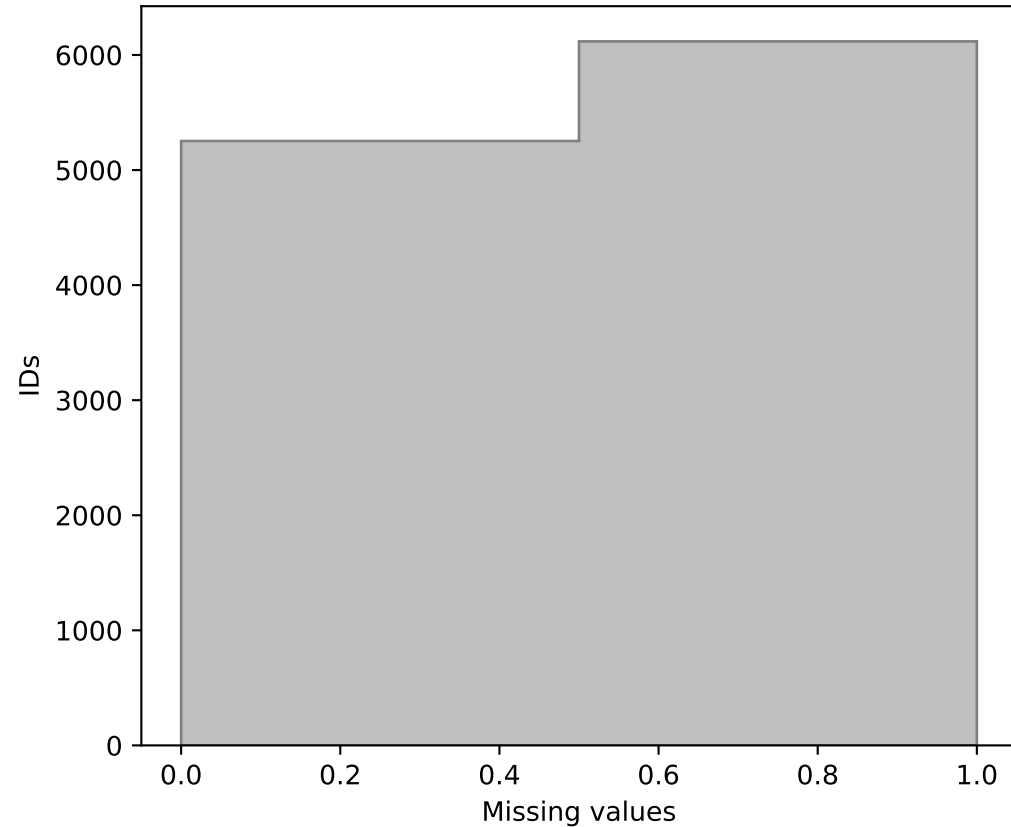


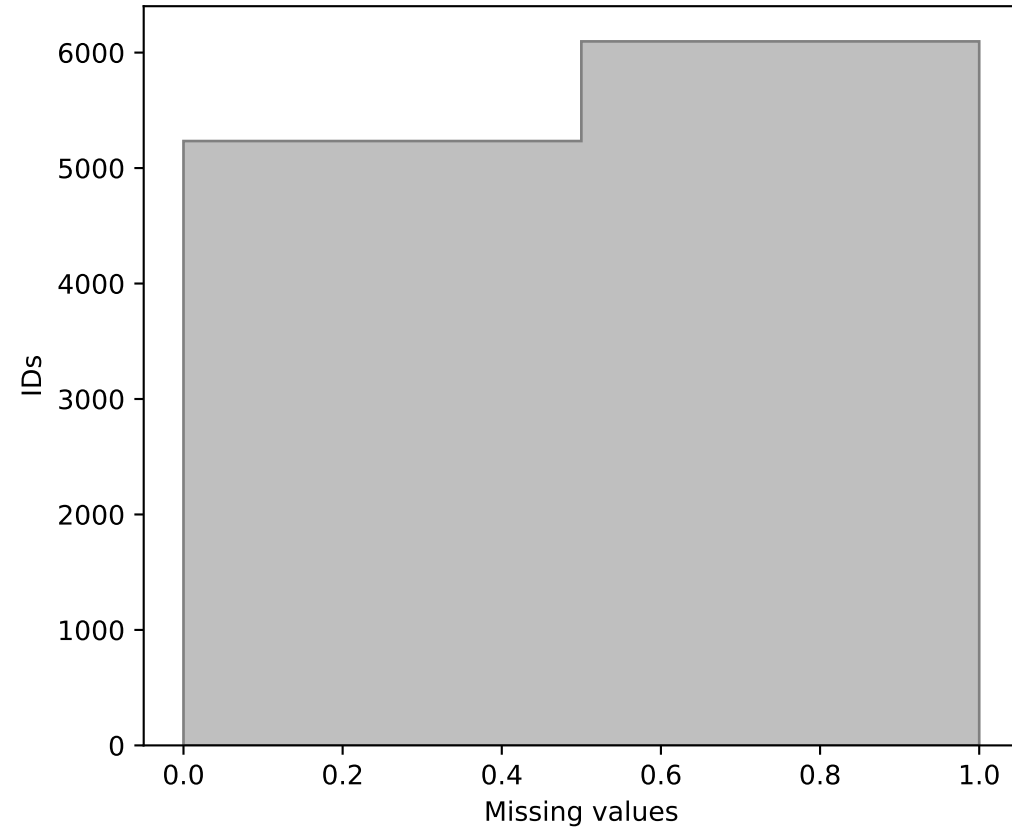
Identification consistency: precursors, CDF



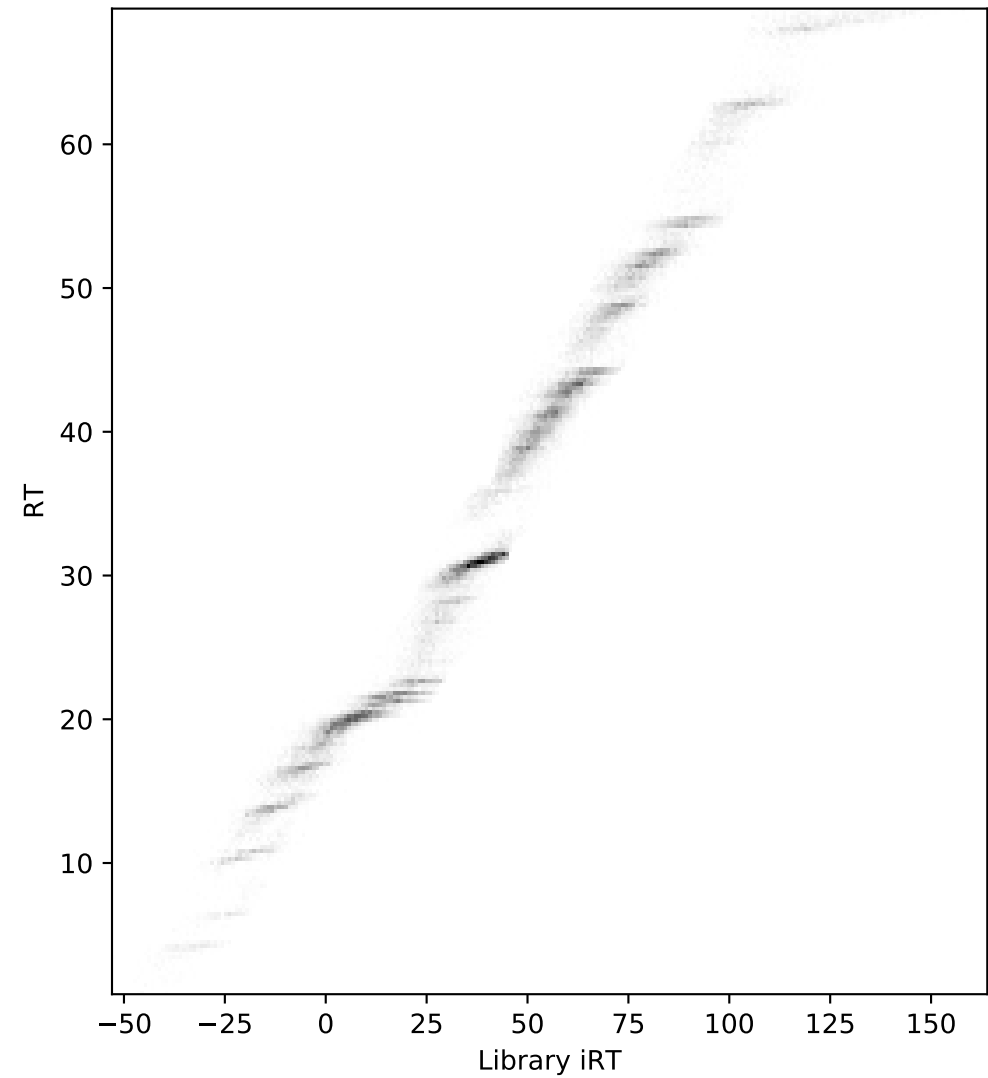
Identification consistency: protein groups, CDF



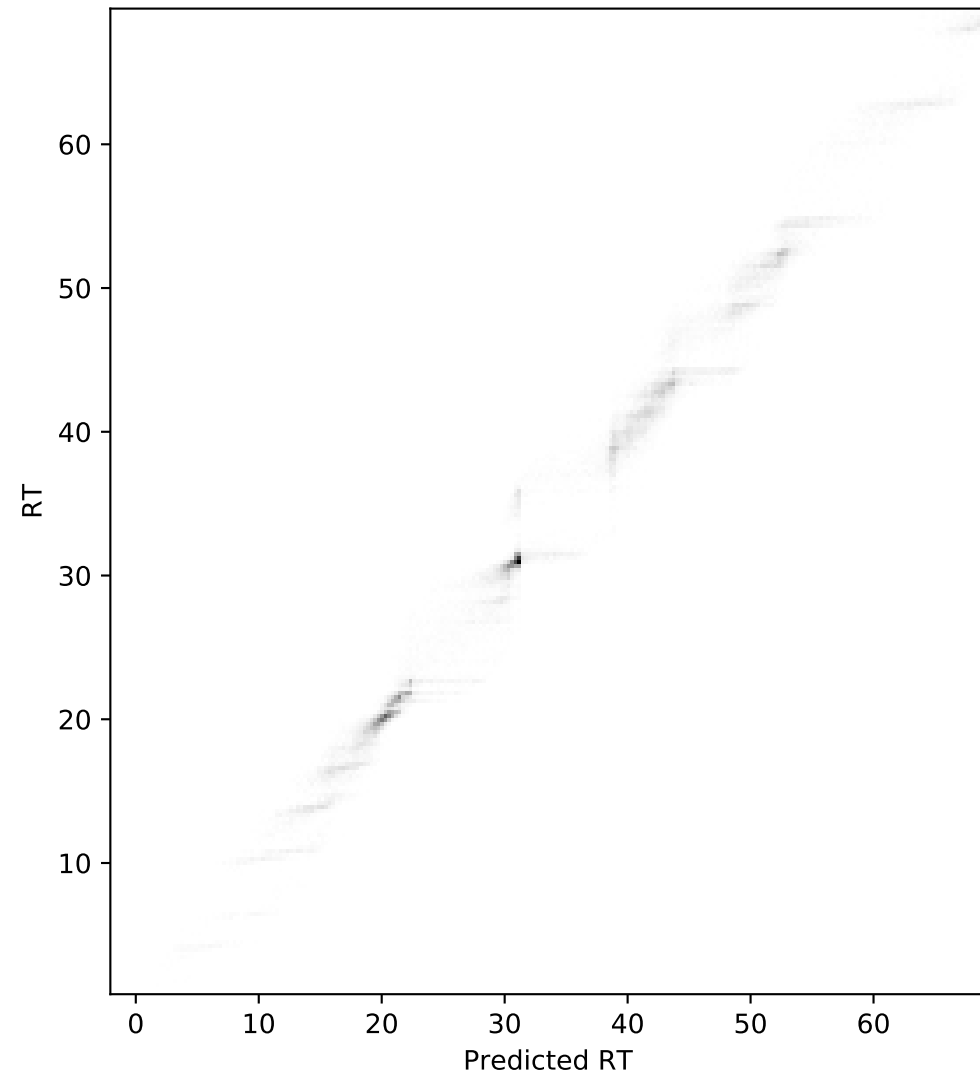
Identification consistency: genes groups, CDF



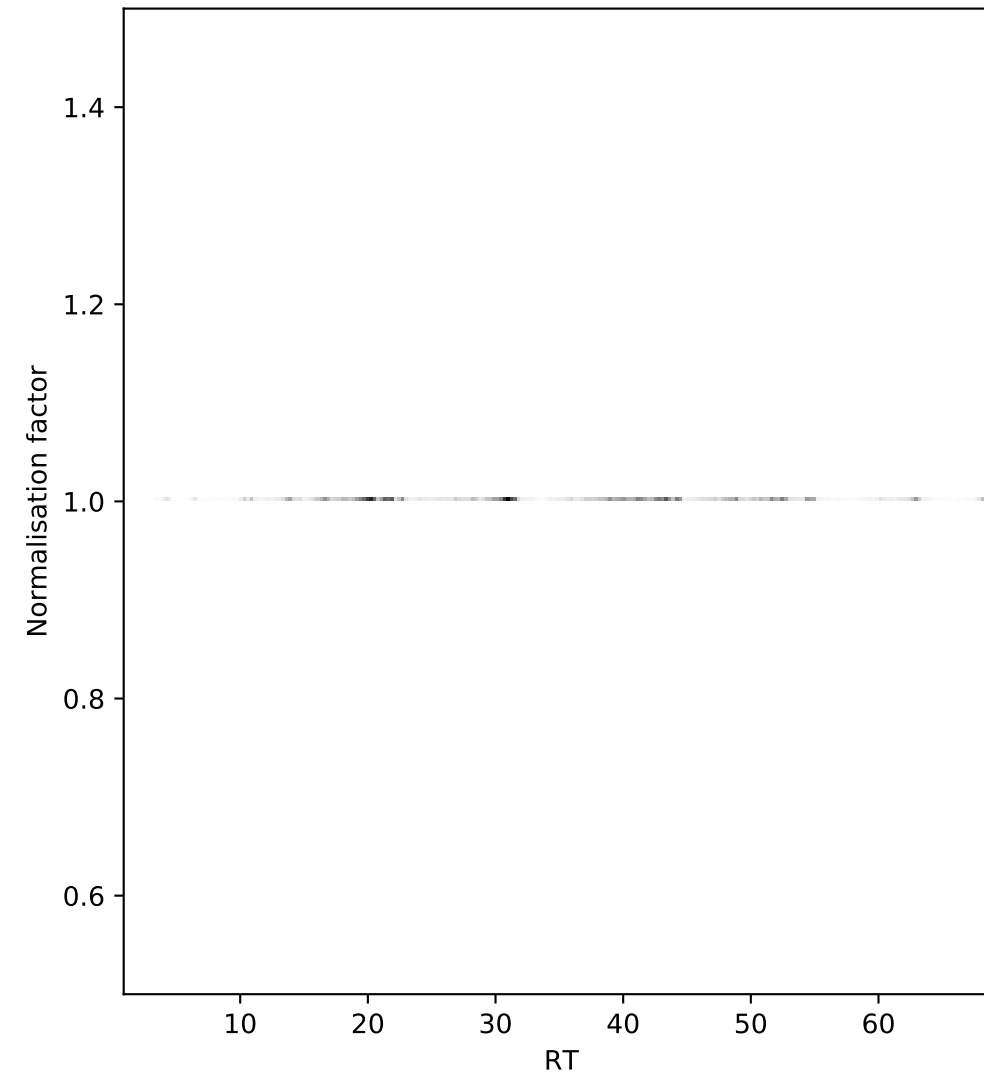
Retention times heatmap, all runs

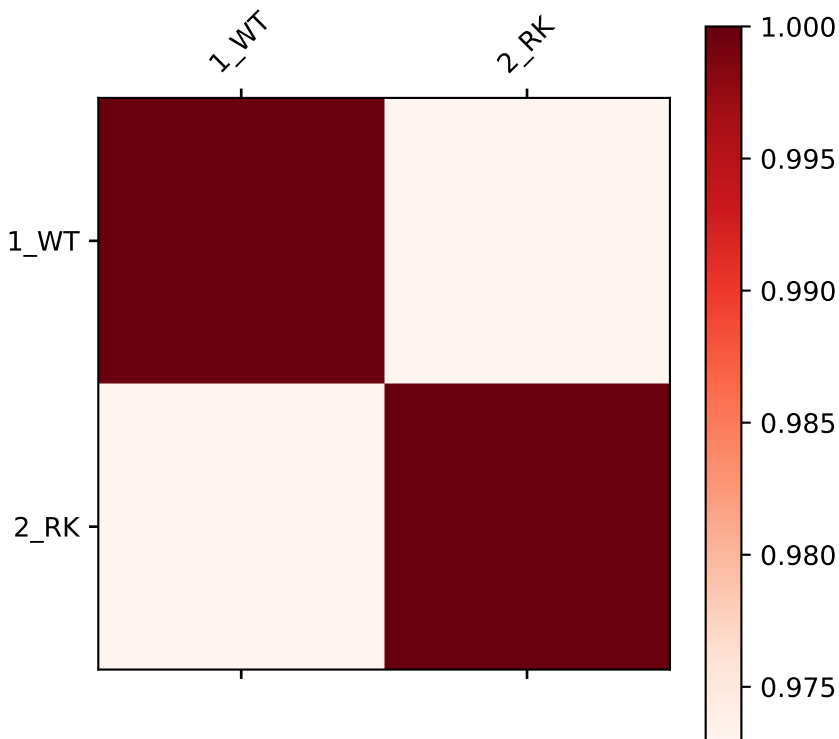


Retention time accuracy heatmap, all runs

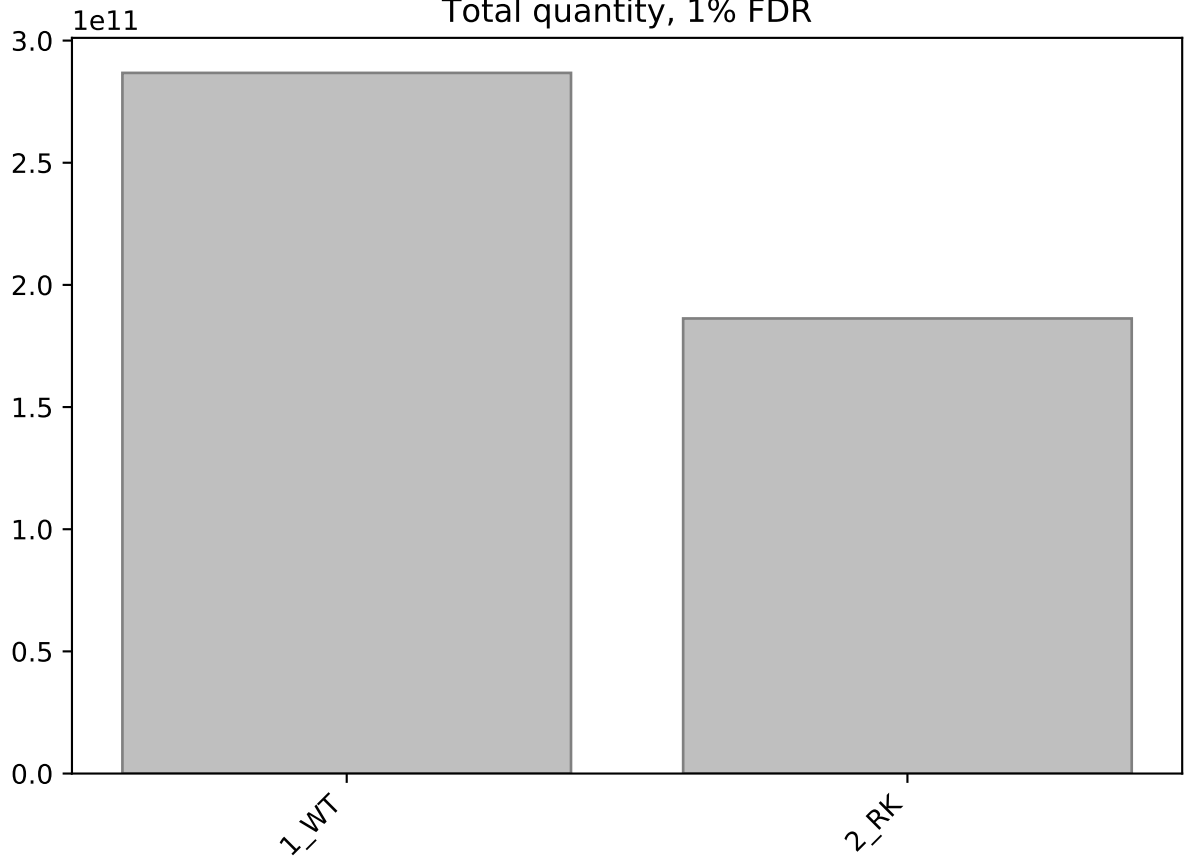


Normalisation factor heatmap, all runs



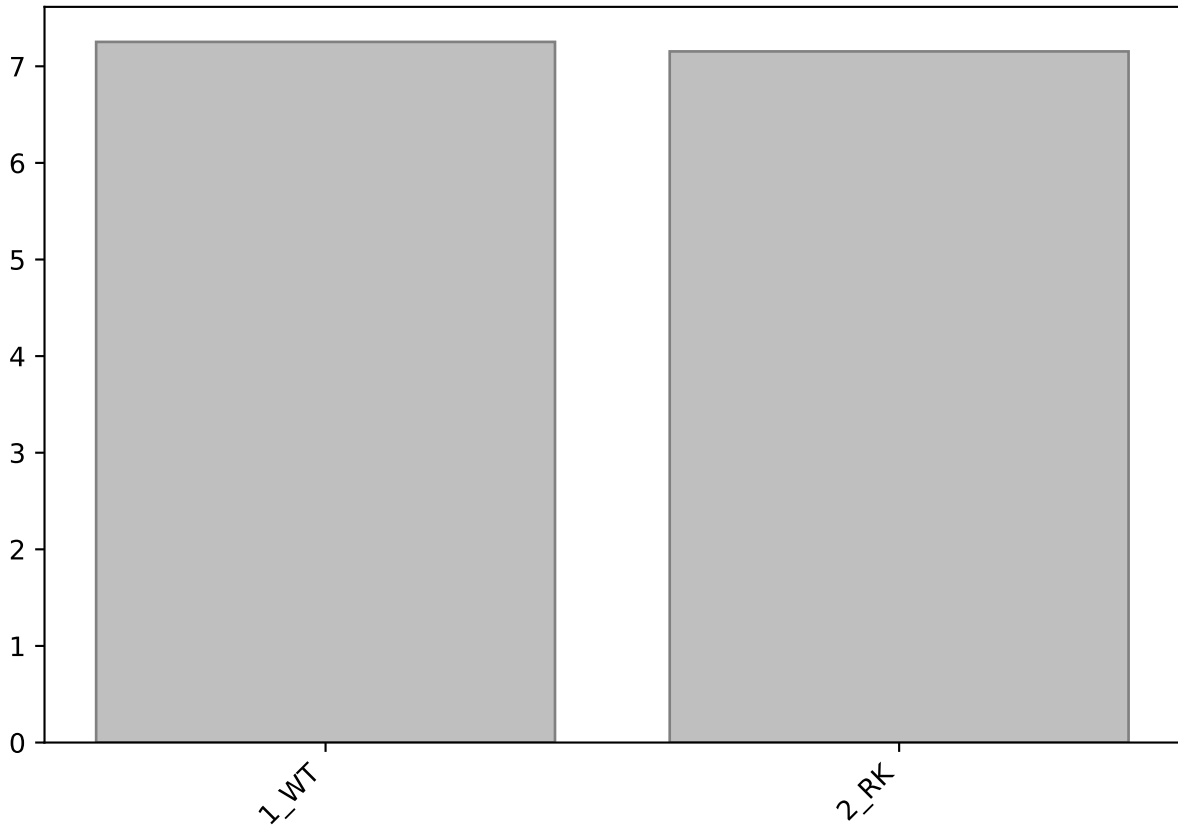


Total quantity, 1% FDR



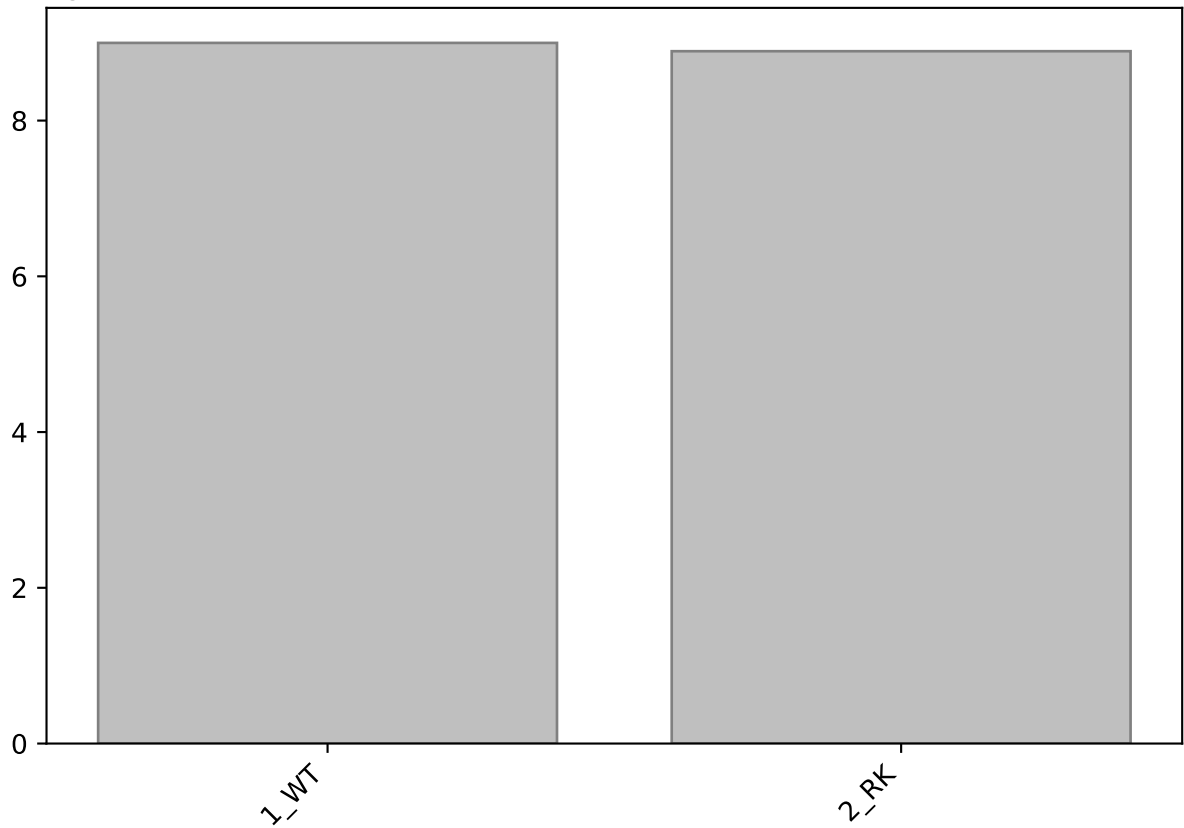
# MS1 signal

1e12

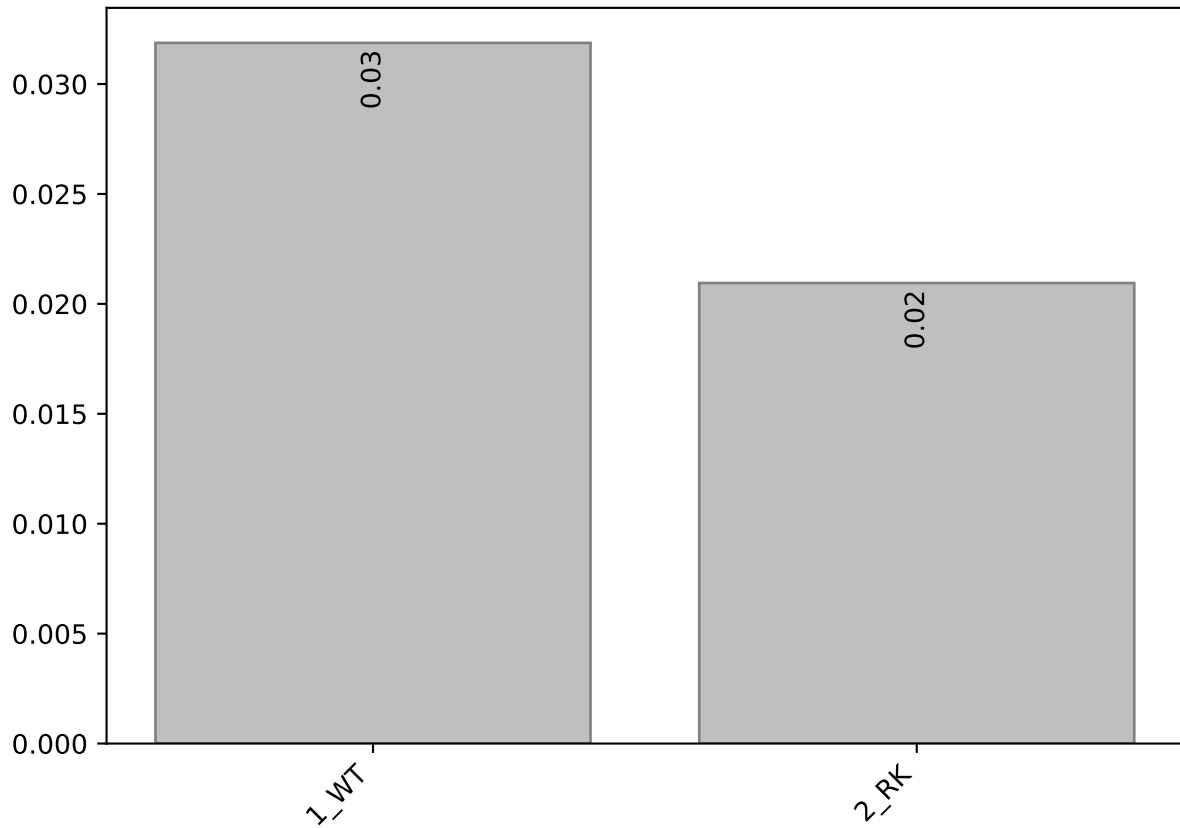


# MS2 signal

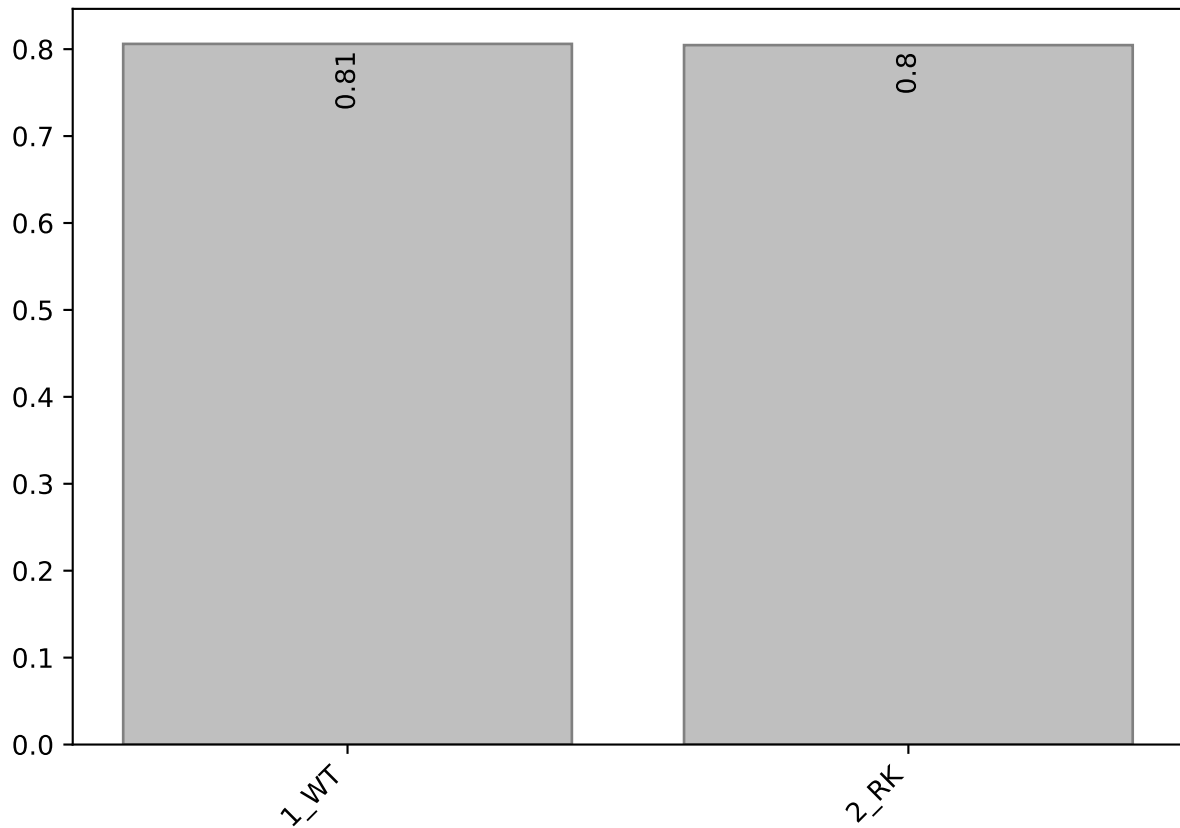
1e12



Total quantity/MS2 signal ratio

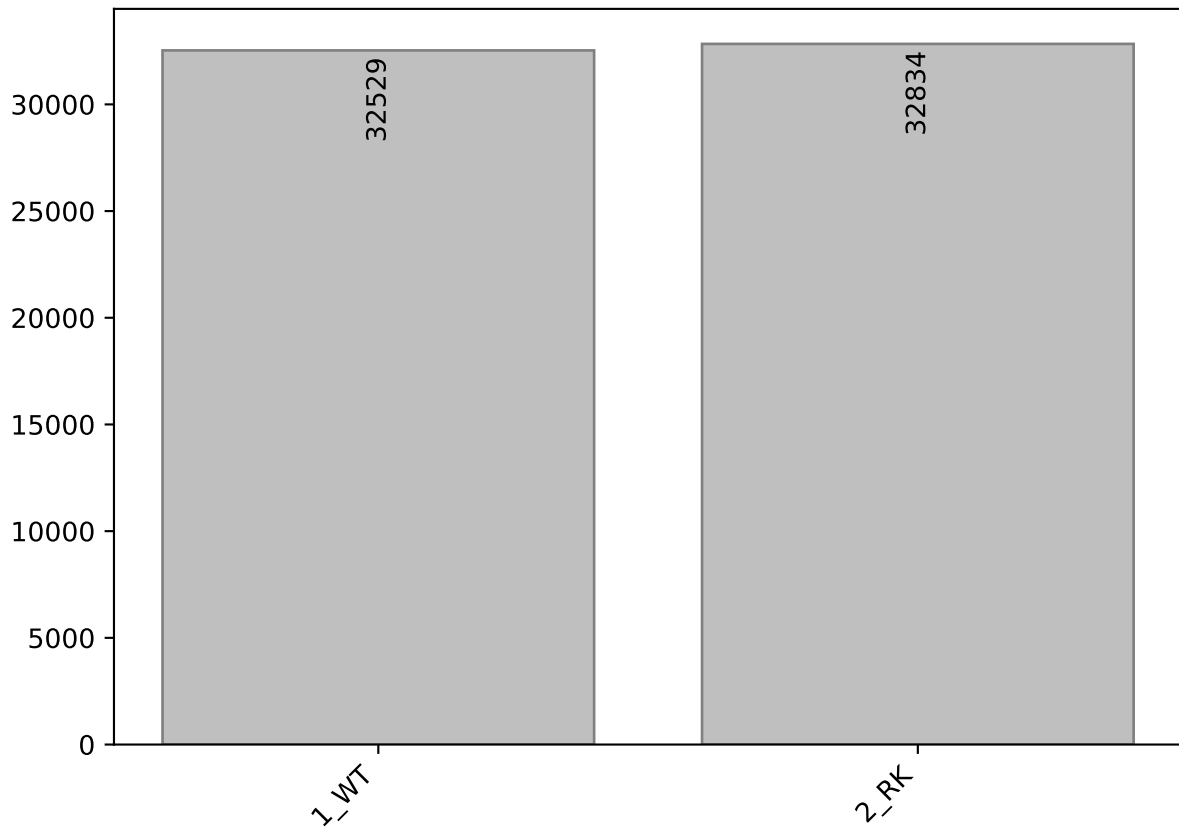


MS1/MS2 signal ratio

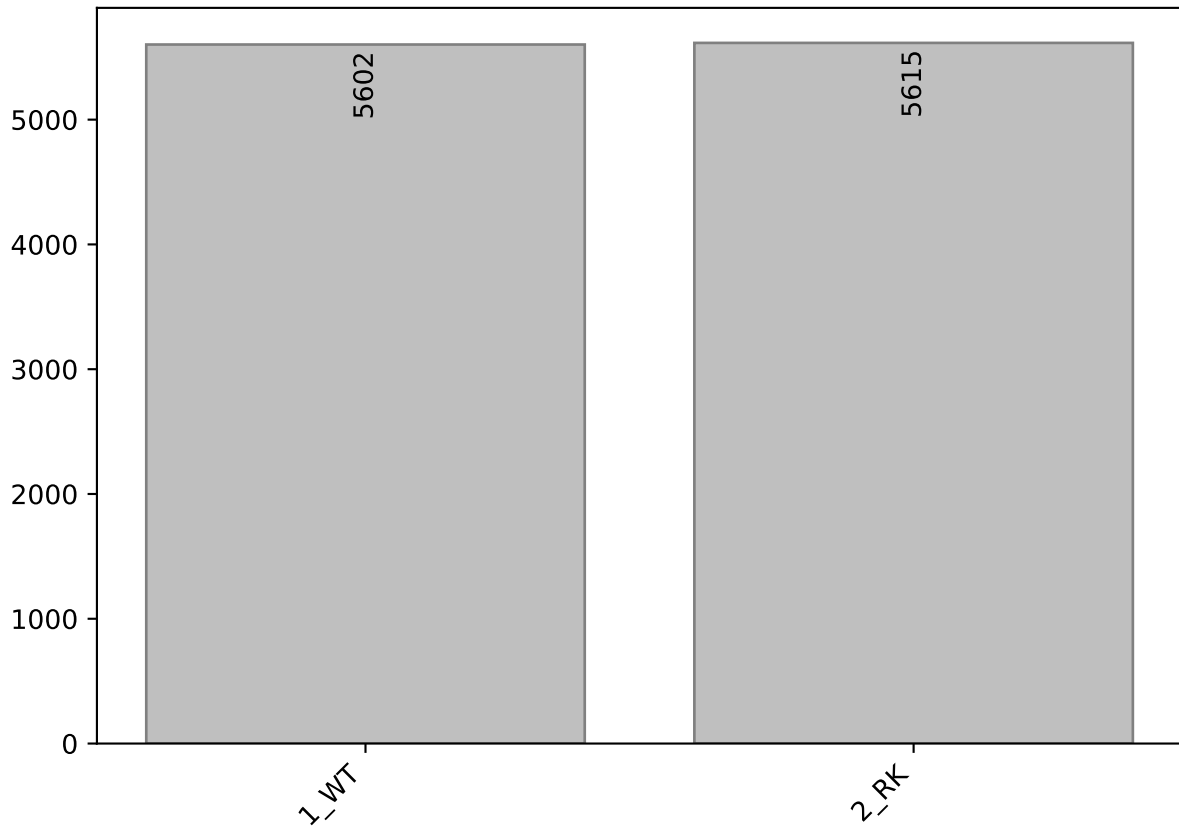




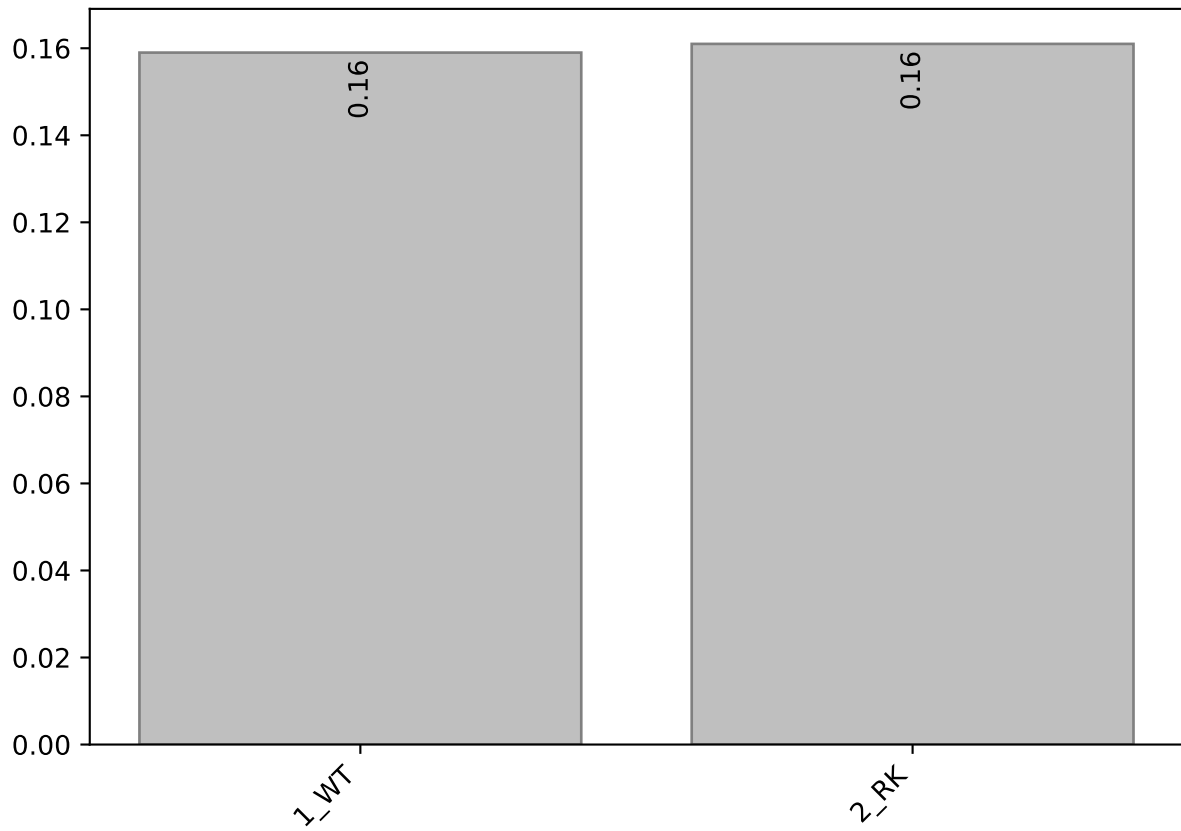
# Precursors, 1% FDR



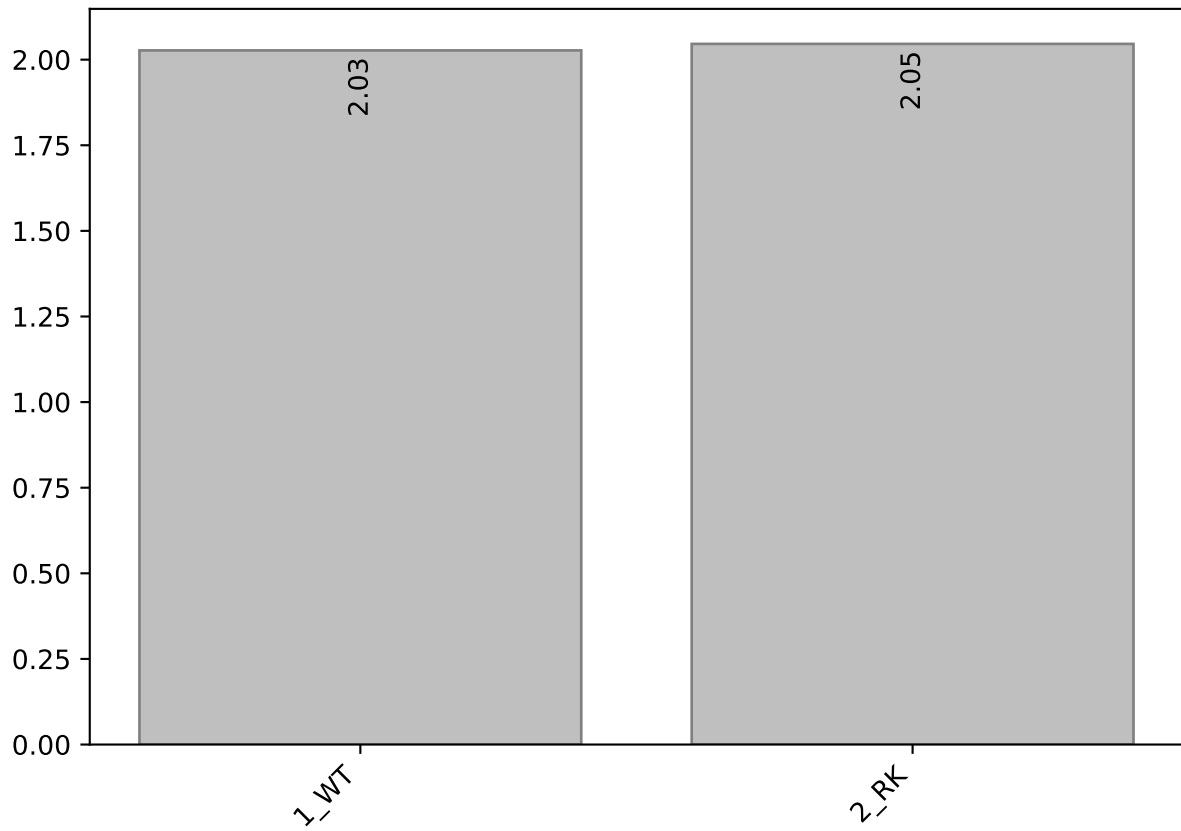
# Unique proteins, 1% protein-level FDR



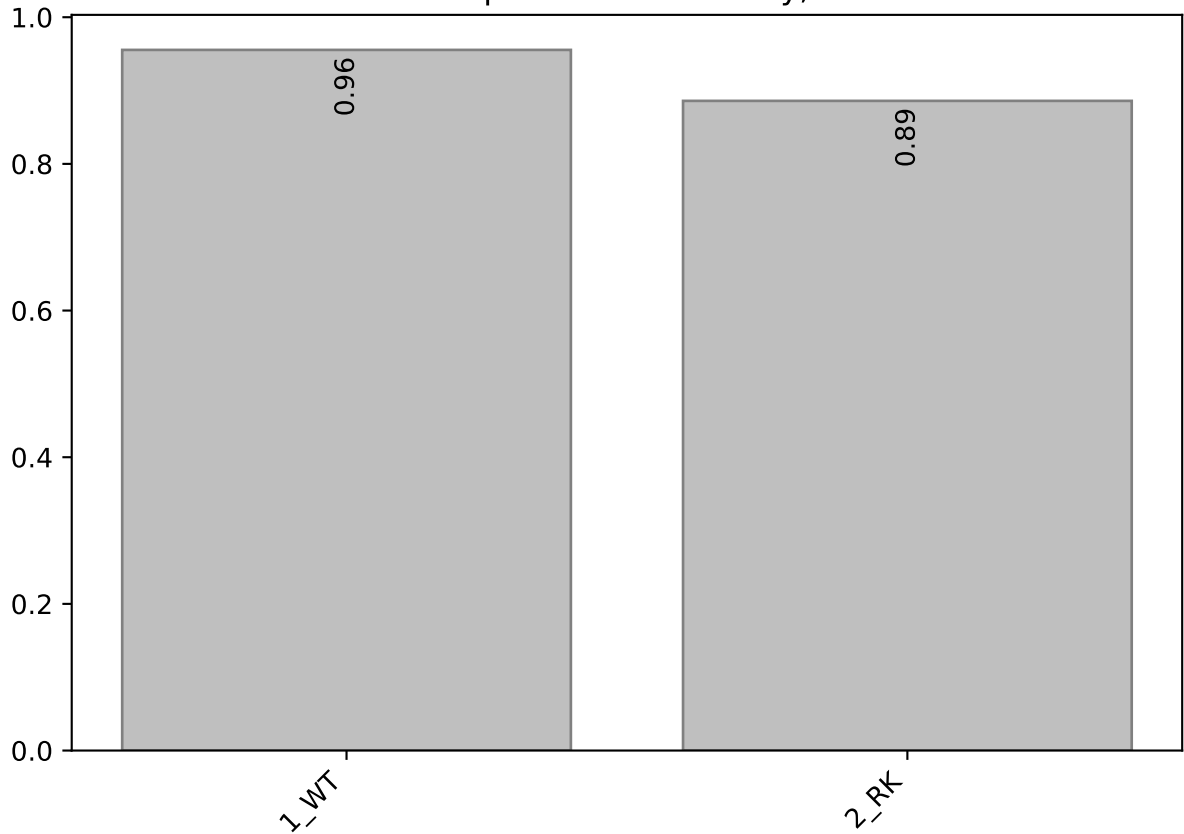
Mean peak FWHM, in minutes



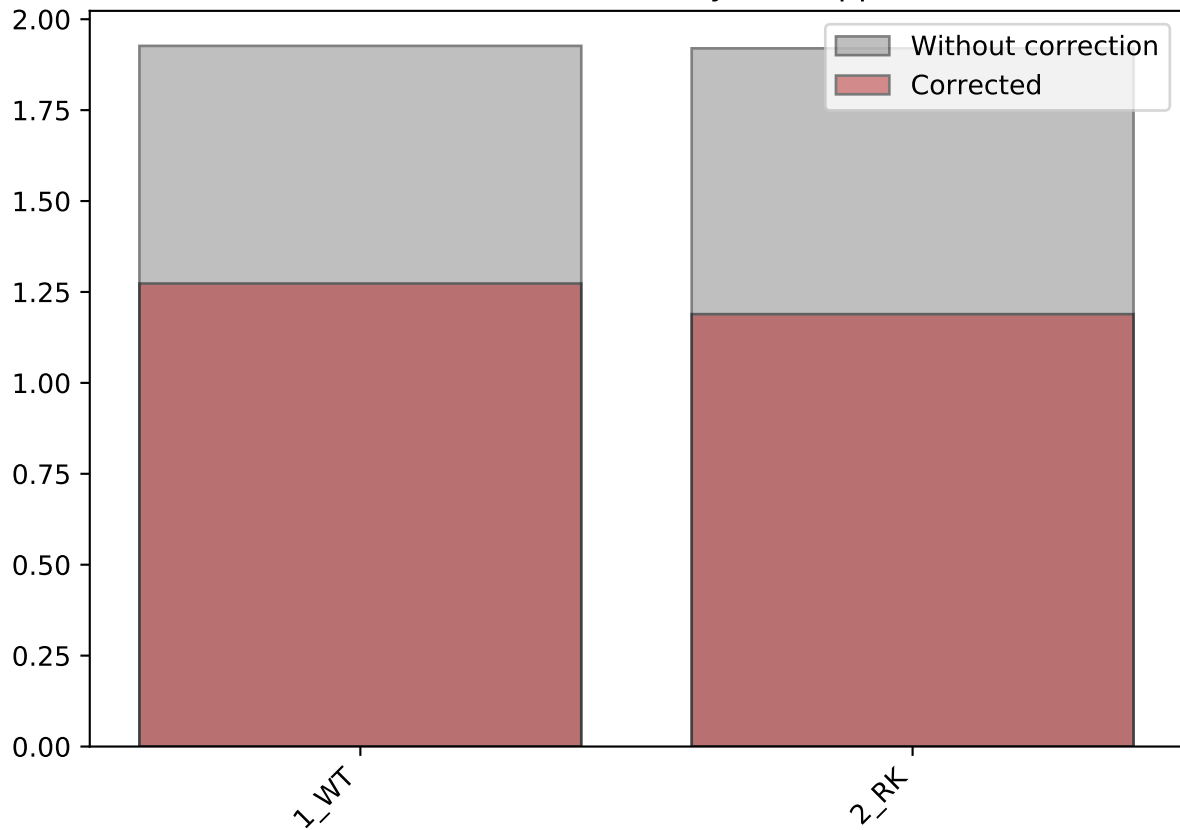
Mean peak FWHM, in MS2 scans



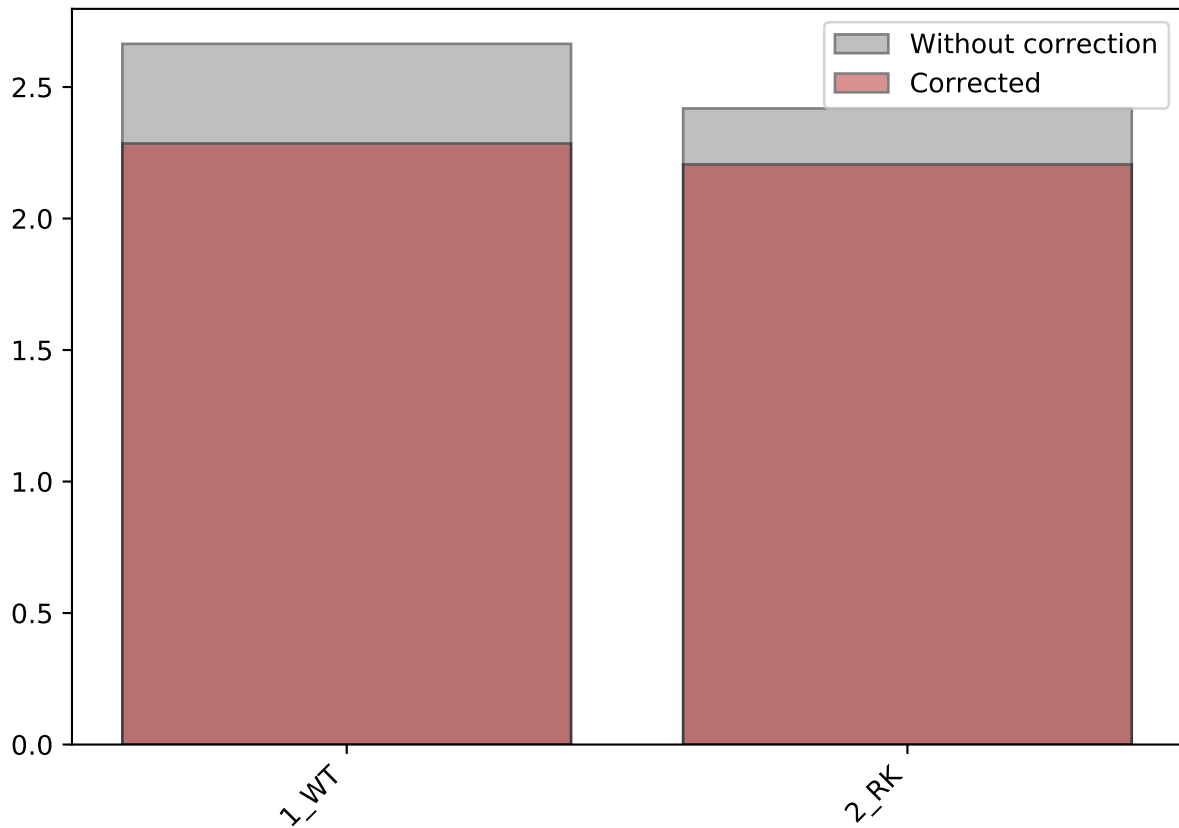
Median RT prediction accuracy, minutes



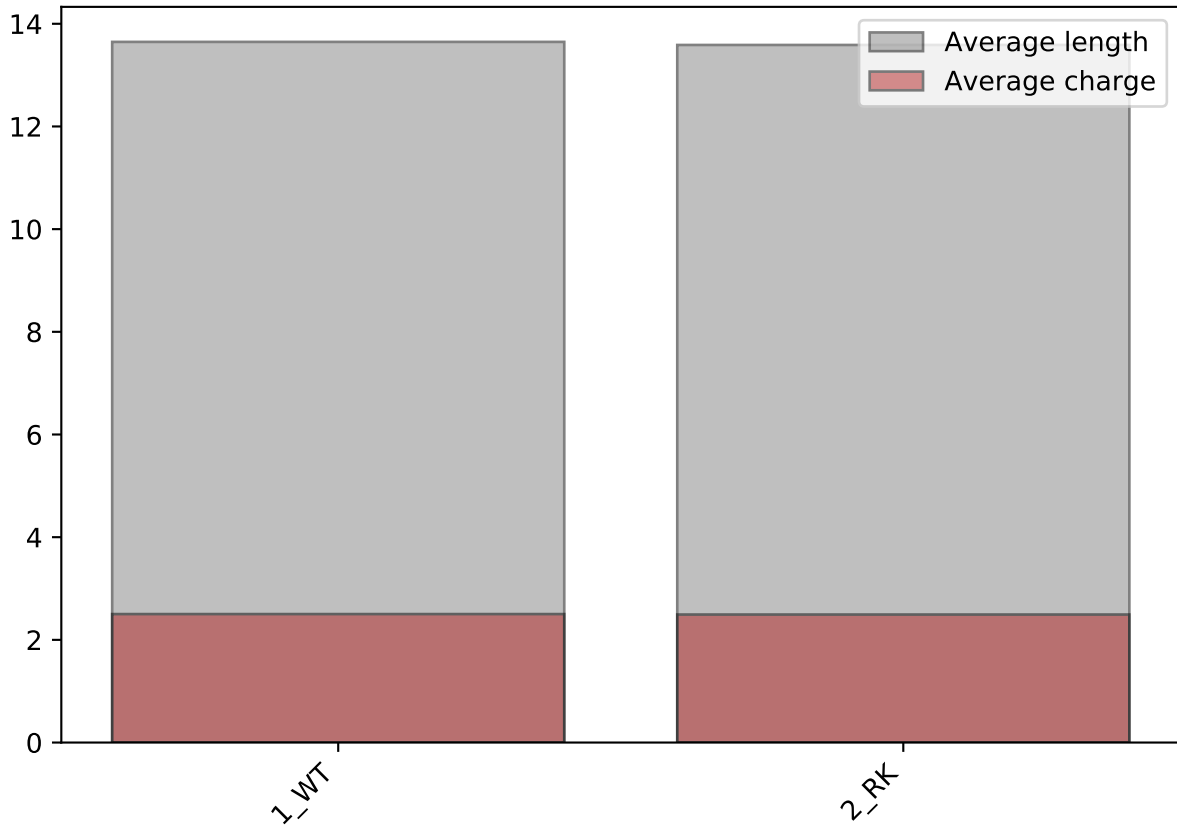
Median mass accuracy, MS2, ppm



Median mass accuracy, MS1, ppm



# Peptide characteristics





Average missed tryptic cleavages

