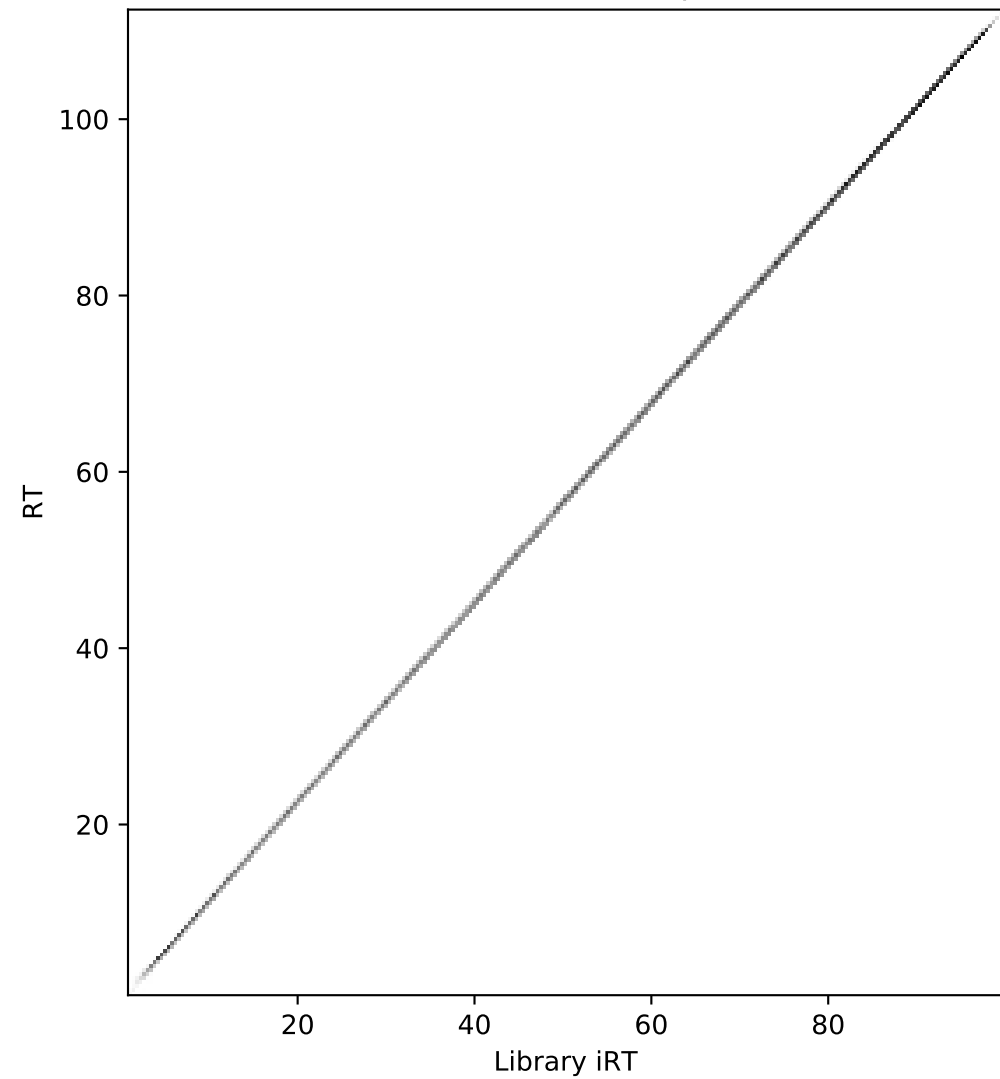
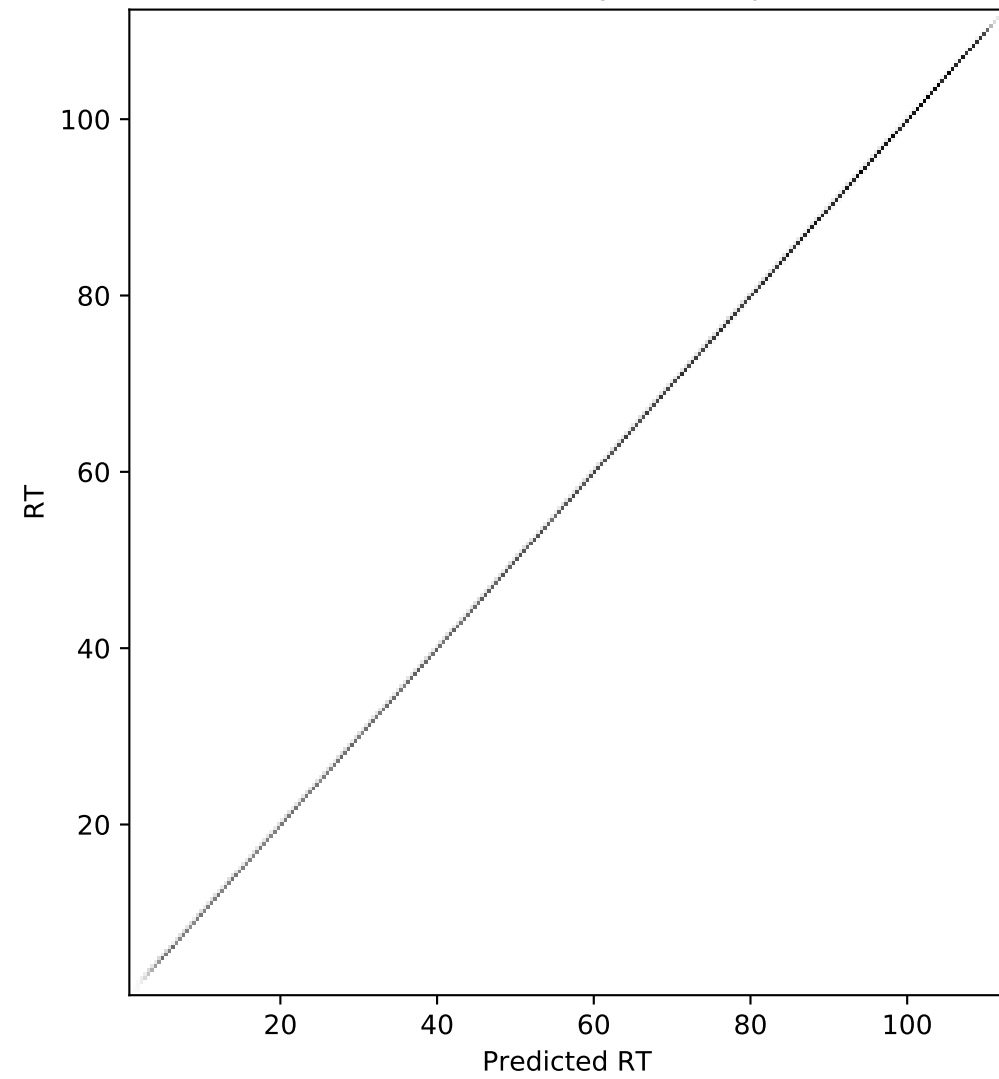


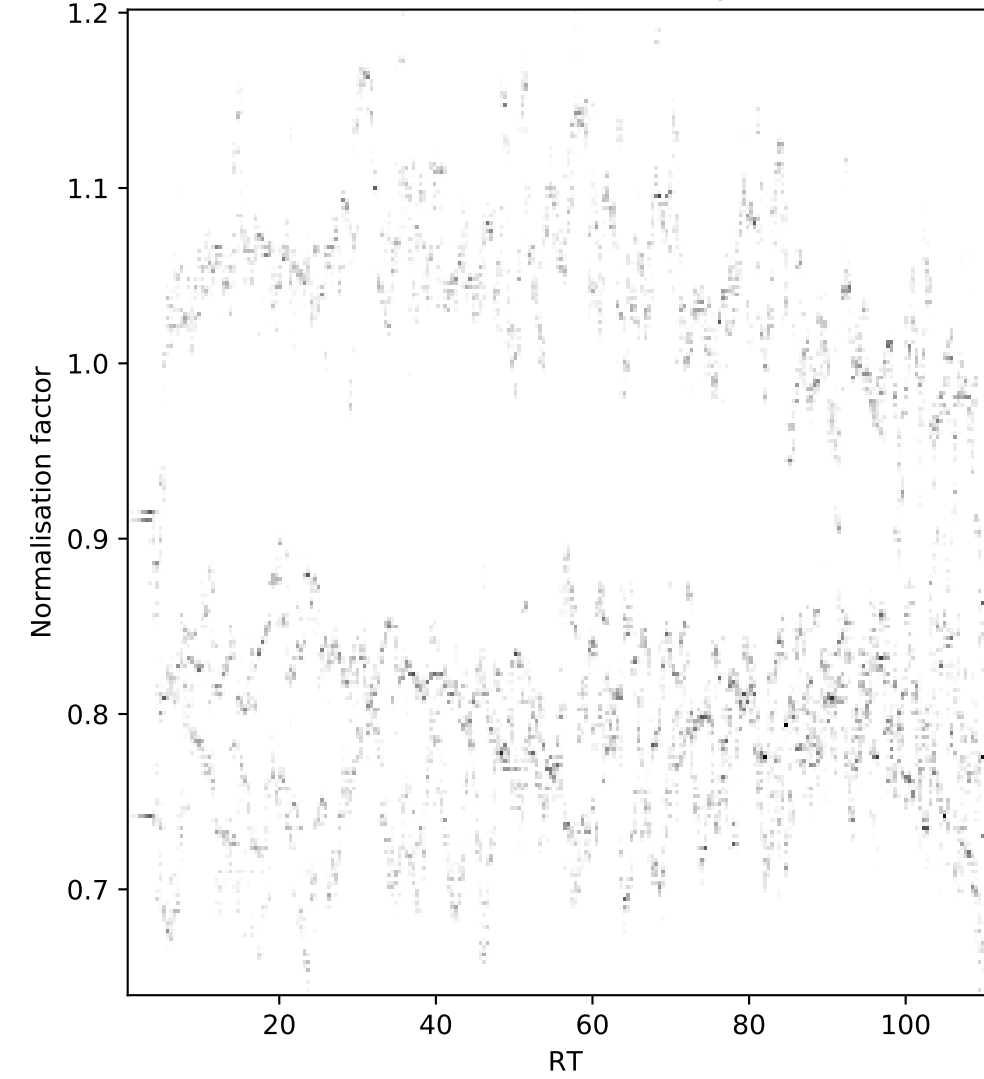
Retention times heatmap, all runs

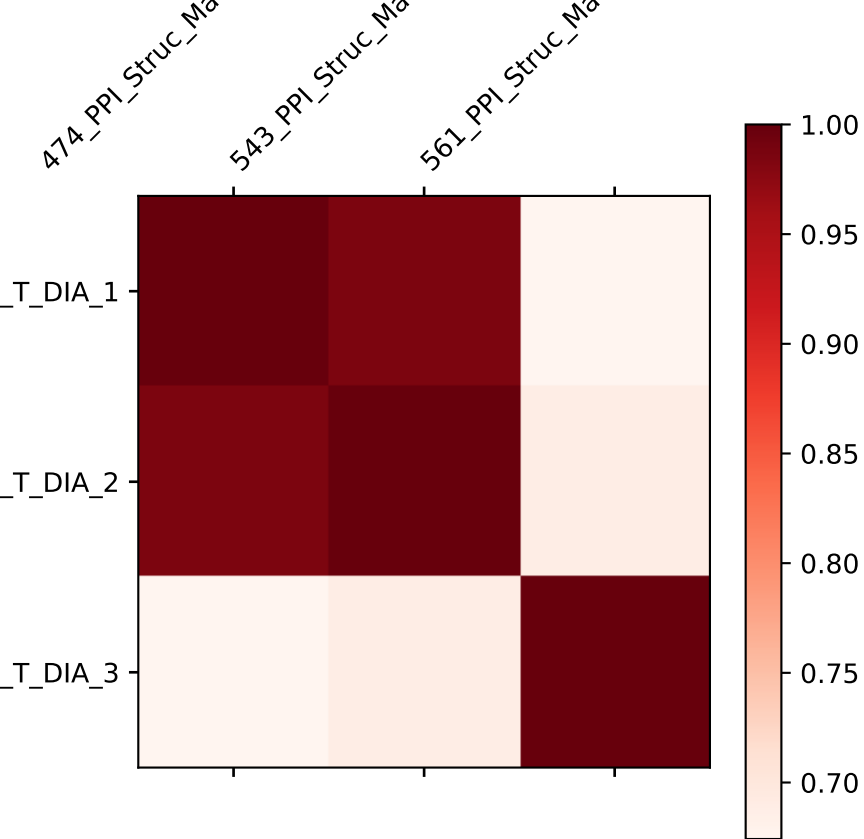


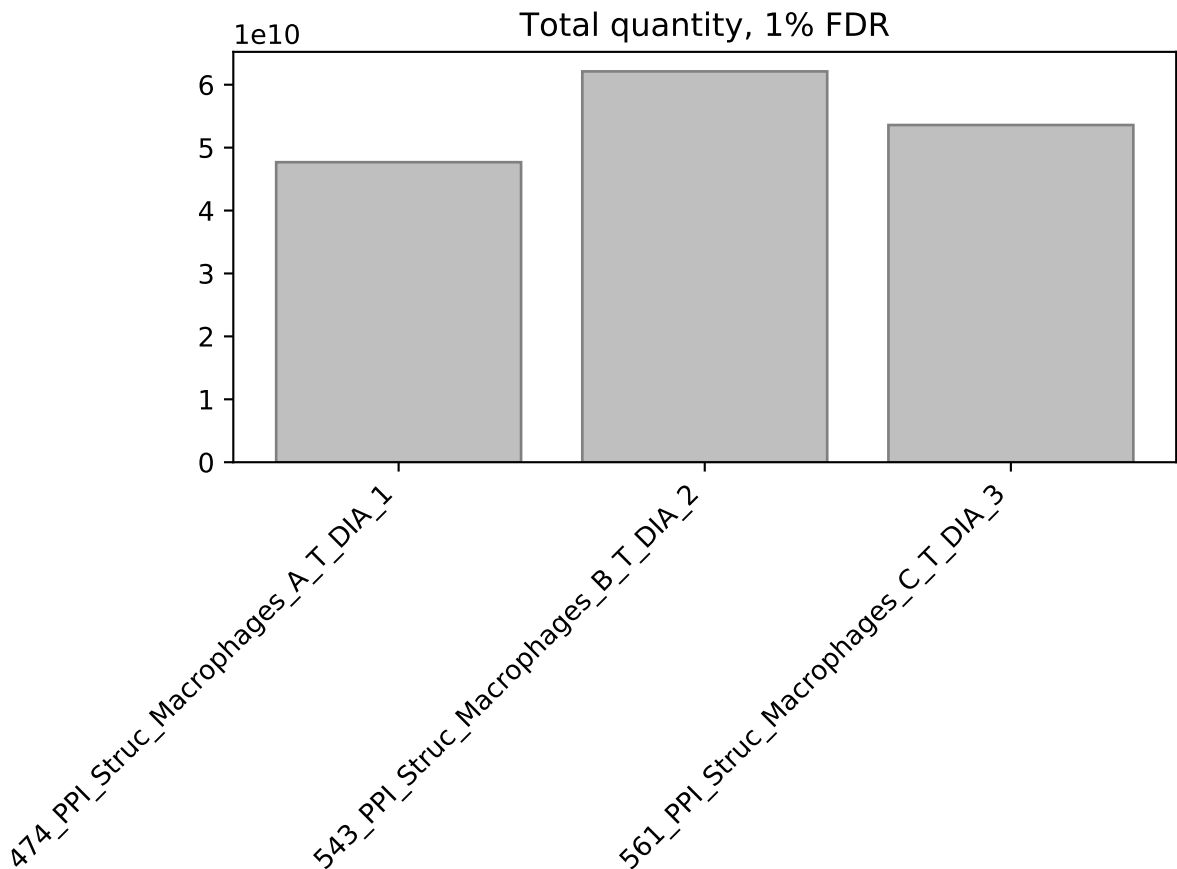
Retention time accuracy heatmap, all runs

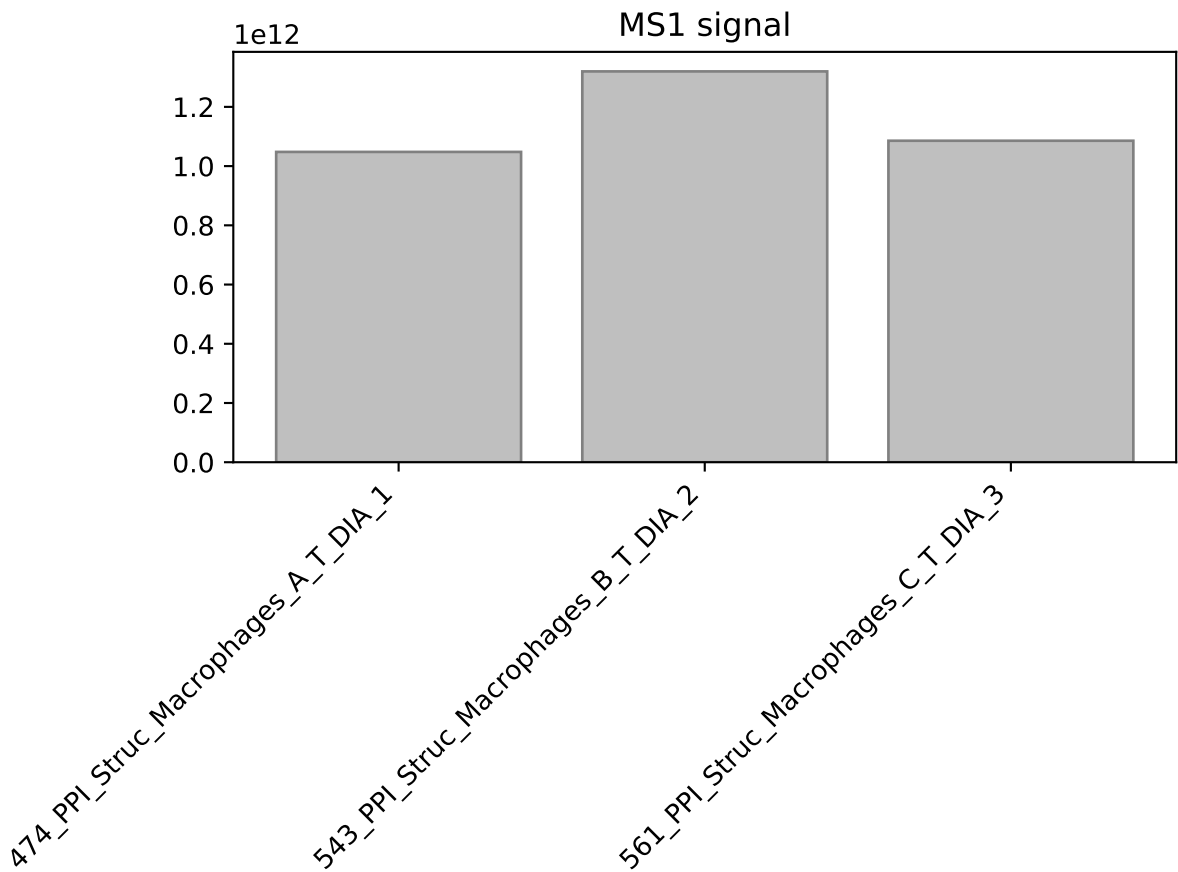


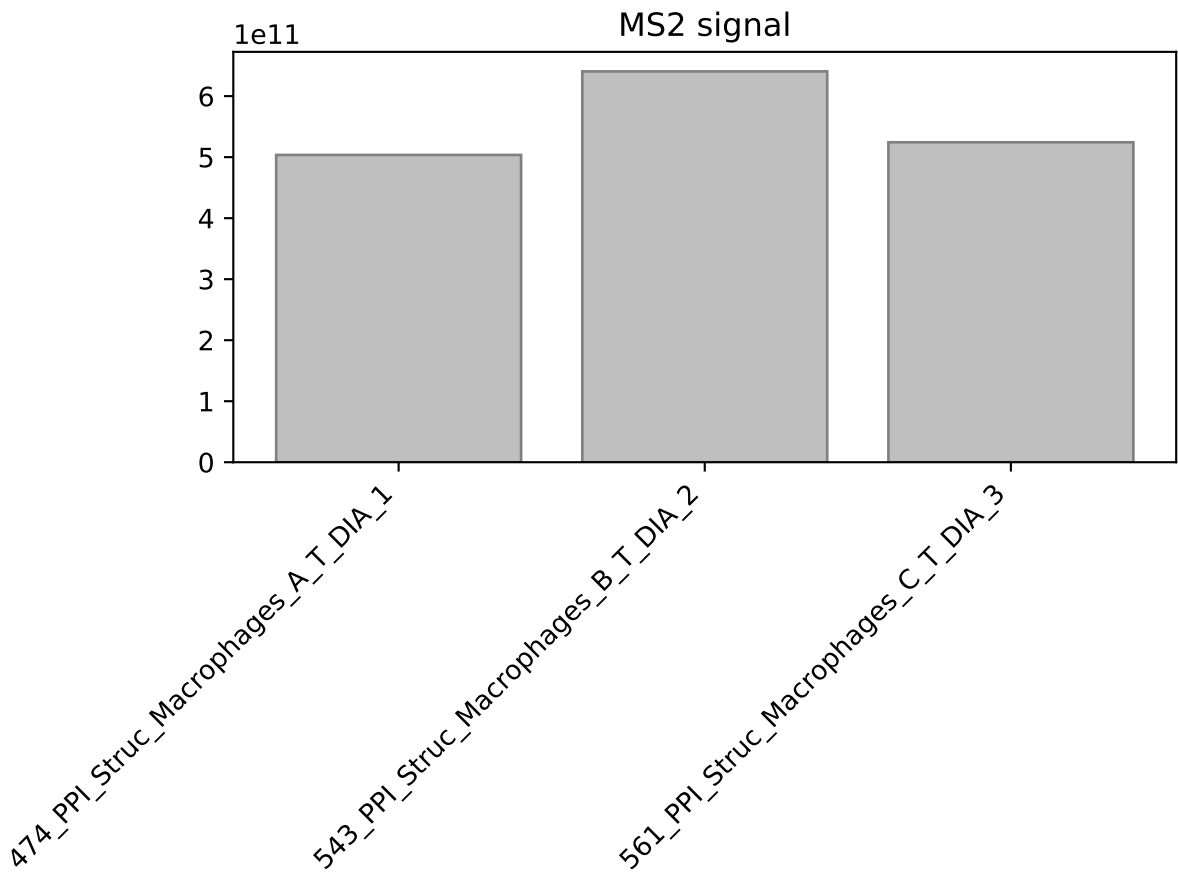
Normalisation factor heatmap, all runs



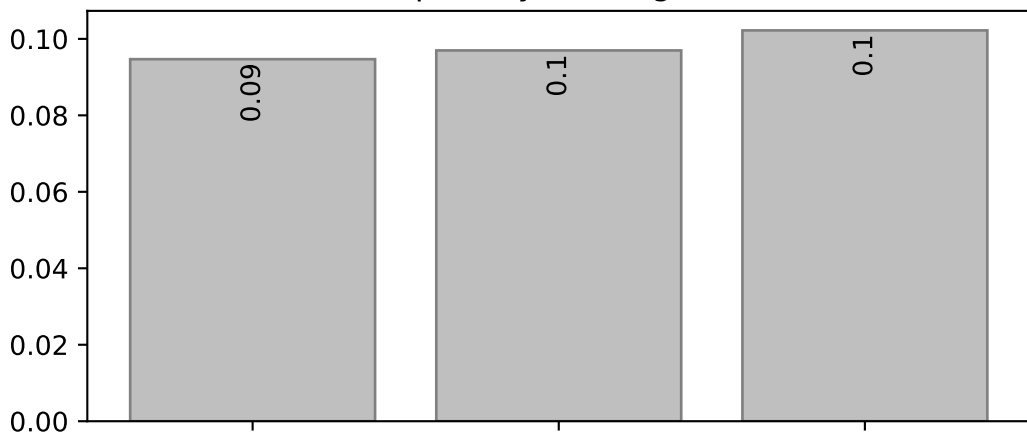








Total quantity/MS2 signal ratio

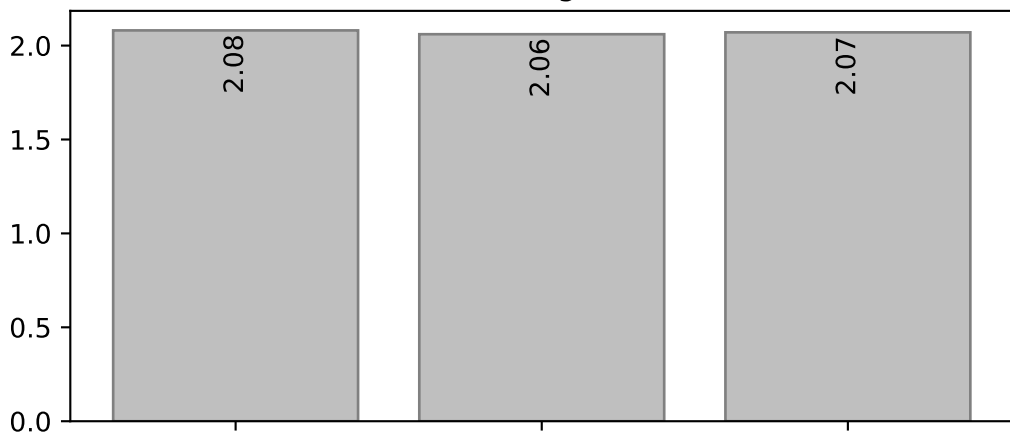


474_PPI_Struc_Macrophages_A_T_DIA_1

543_PPI_Struc_Macrophages_B_T_DIA_2

561_PPI_Struc_Macrophages_C_T_DIA_3

MS1/MS2 signal ratio

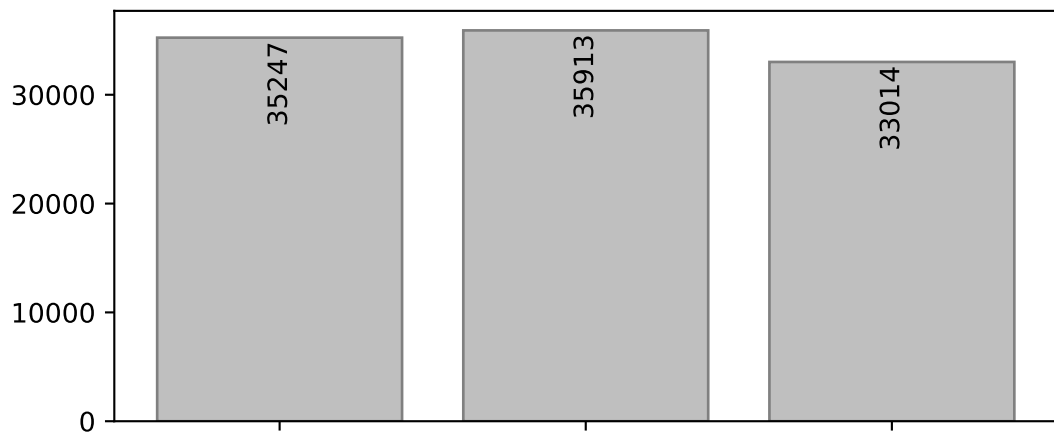


474_PPI_Struc_Macrophages_A_T_DIA_1

543_PPI_Struc_Macrophages_B_T_DIA_2

561_PPI_Struc_Macrophages_C_T_DIA_3

Precursors, 1% FDR

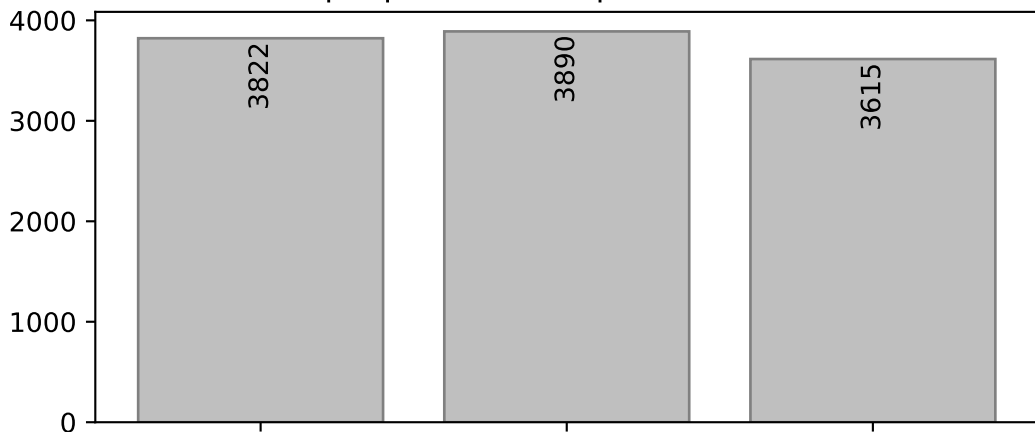


474_PPI_Struc_Macrophages_A_T_DIA_1

543_PPI_Struc_Macrophages_B_T_DIA_2

561_PPI_Struc_Macrophages_C_T_DIA_3

Unique proteins, 1% protein-level FDR

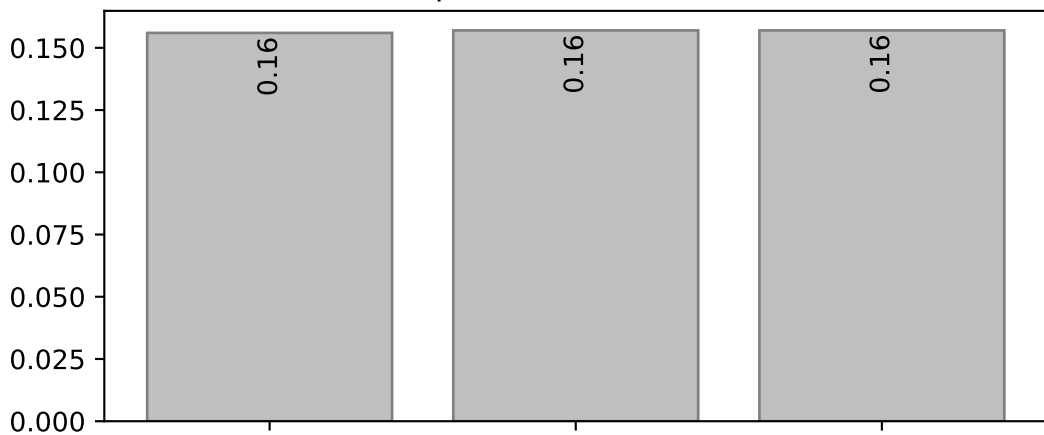


474_PPI_Struc_Macrophages_A_T_DIA_1

543_PPI_Struc_Macrophages_B_T_DIA_2

561_PPI_Struc_Macrophages_C_T_DIA_3

Mean peak FWHM, in minutes

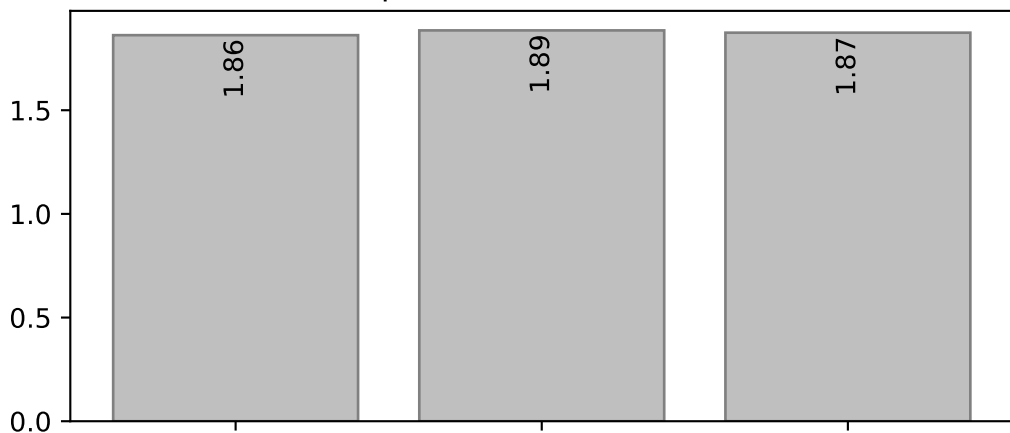


474_PPI_Struc_Macrophages_A_T_DIA_1

543_PPI_Struc_Macrophages_B_T_DIA_2

561_PPI_Struc_Macrophages_C_T_DIA_3

Mean peak FWHM, in MS2 scans

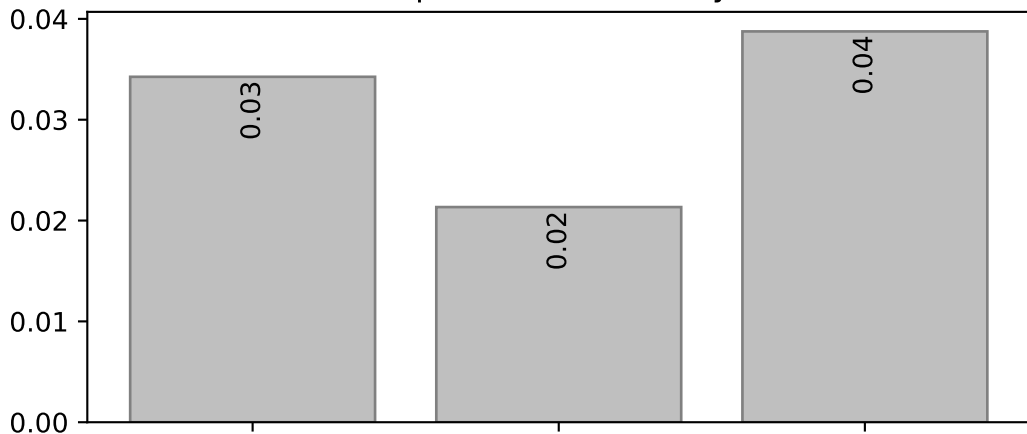


474_PPI_Struc_Macrophages_A_T_DIA_1

543_PPI_Struc_Macrophages_B_T_DIA_2

561_PPI_Struc_Macrophages_C_T_DIA_3

Median RT prediction accuracy, minutes

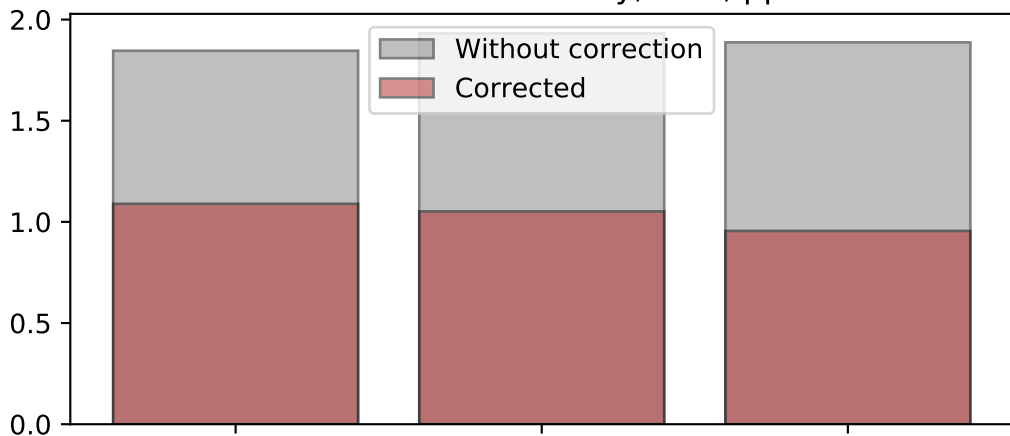


474_PPI_Struc_Macrophages_A.T_DIA_1

543_PPI_Struc_Macrophages_B.T_DIA_2

561_PPI_Struc_Macrophages_C.T_DIA_3

Median mass accuracy, MS2, ppm

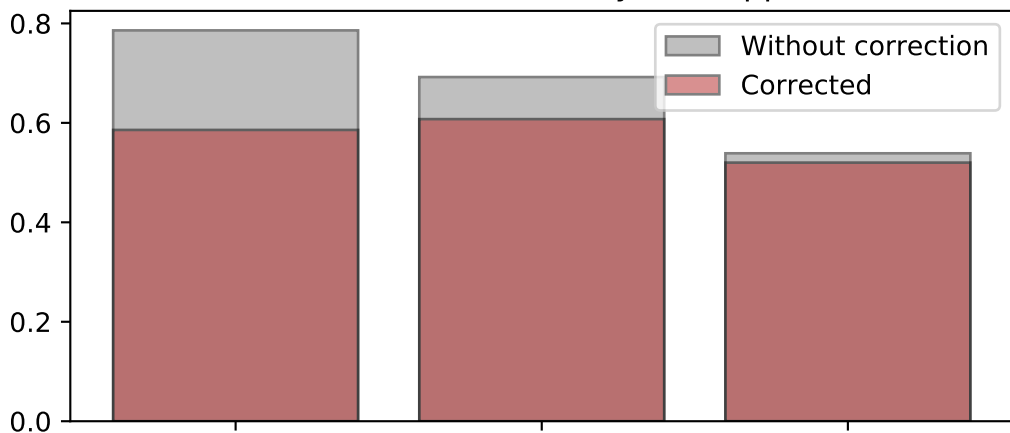


474_PPI_Struc_Macrophages_A.T_DIA_1

543_PPI_Struc_Macrophages_B.T_DIA_2

561_PPI_Struc_Macrophages_C.T_DIA_3

Median mass accuracy, MS1, ppm

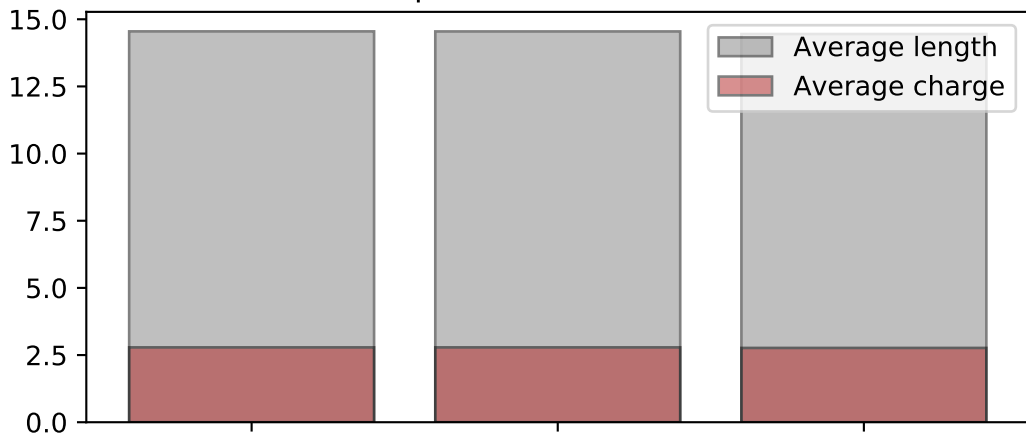


474_PPI_Struc_Macrophages_A_T_DIA_1

543_PPI_Struc_Macrophages_B_T_DIA_2

561_PPI_Struc_Macrophages_C_T_DIA_3

Peptide characteristics

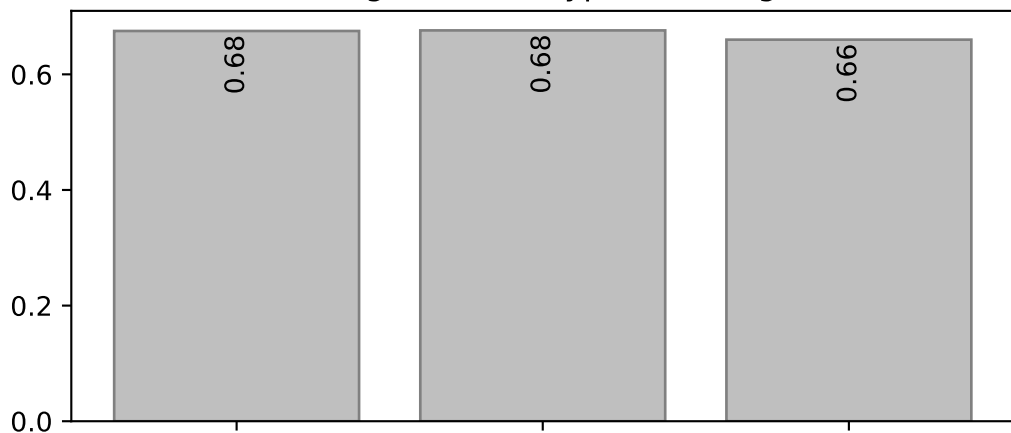


474_PPI_Struc_Macrophages_A_T_DIA_1

543_PPI_Struc_Macrophages_B_T_DIA_2

561_PPI_Struc_Macrophages_C_T_DIA_3

Average missed tryptic cleavages



474_PPI_Struc_Macrophages_A_T_DIA_1

543_PPI_Struc_Macrophages_B_T_DIA_2

561_PPI_Struc_Macrophages_C_T_DIA_3