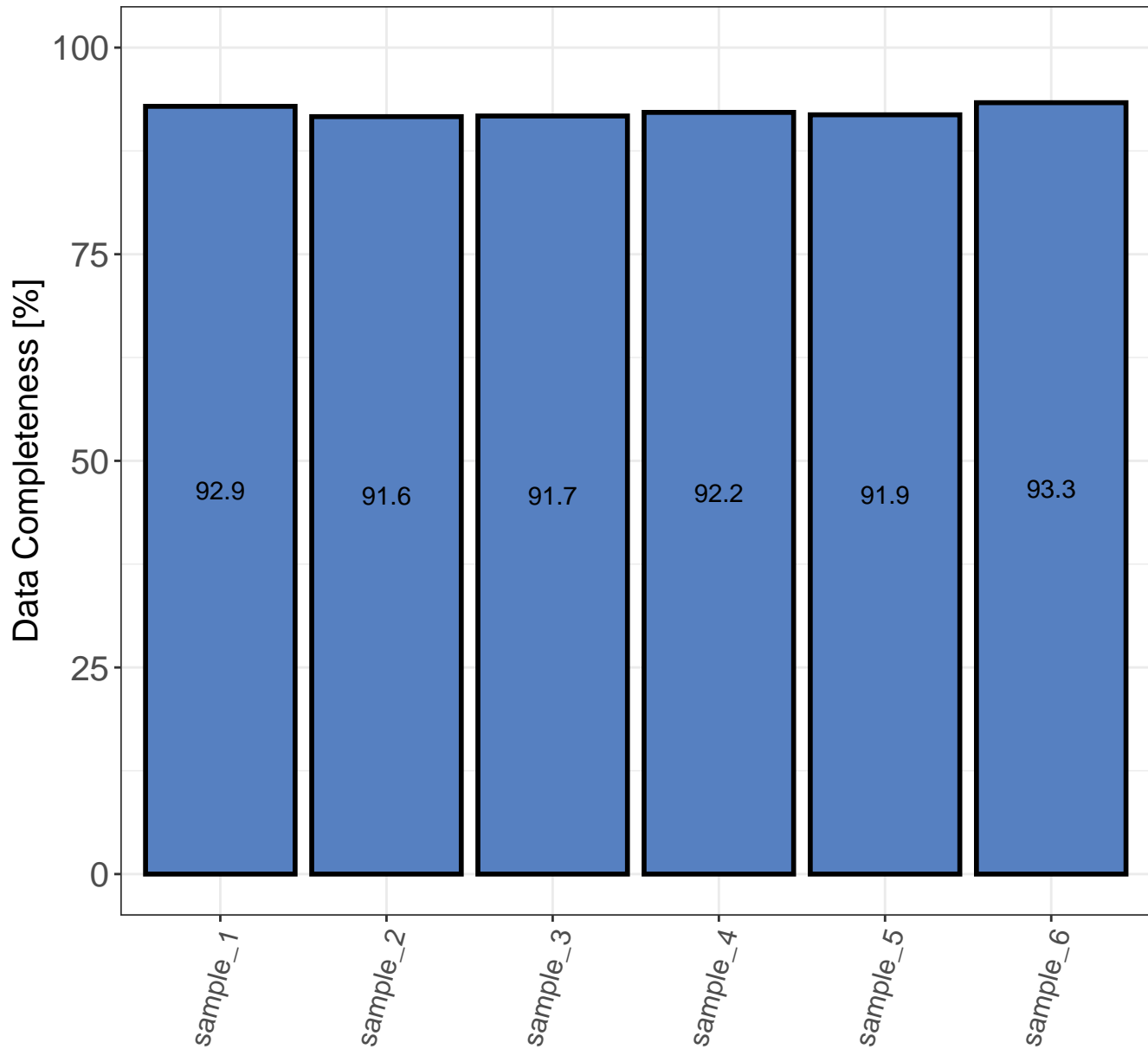
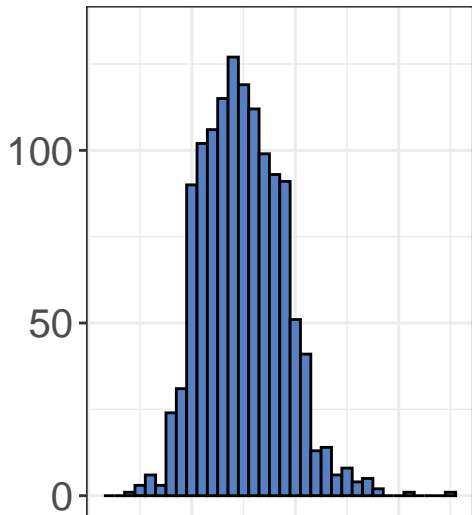


Data completeness per .raw file

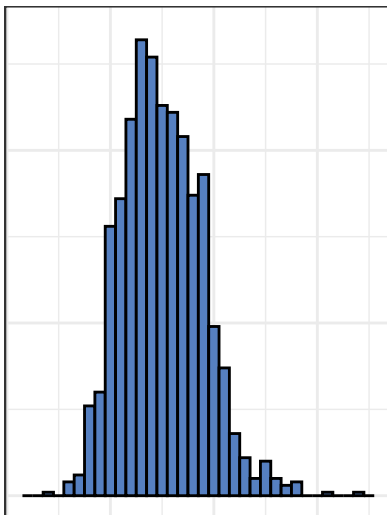


Overall log2 Intensity Distribution

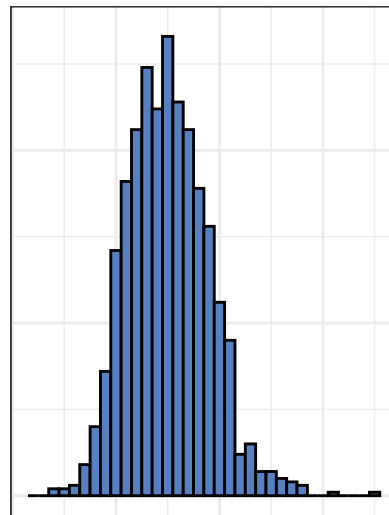
sample_1



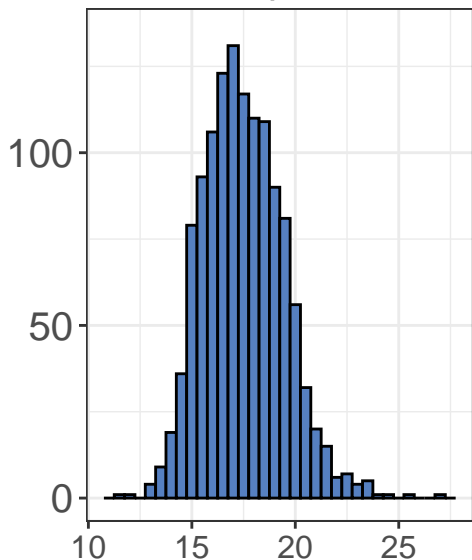
sample_2



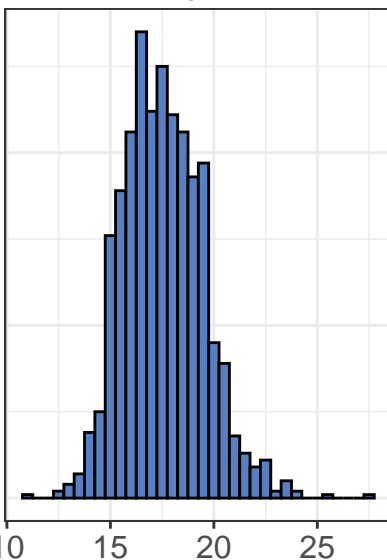
sample_3



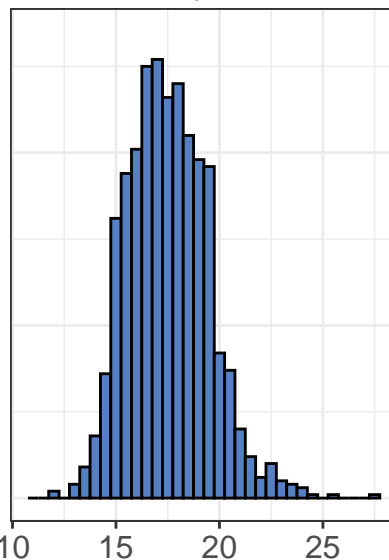
sample_4



sample_5

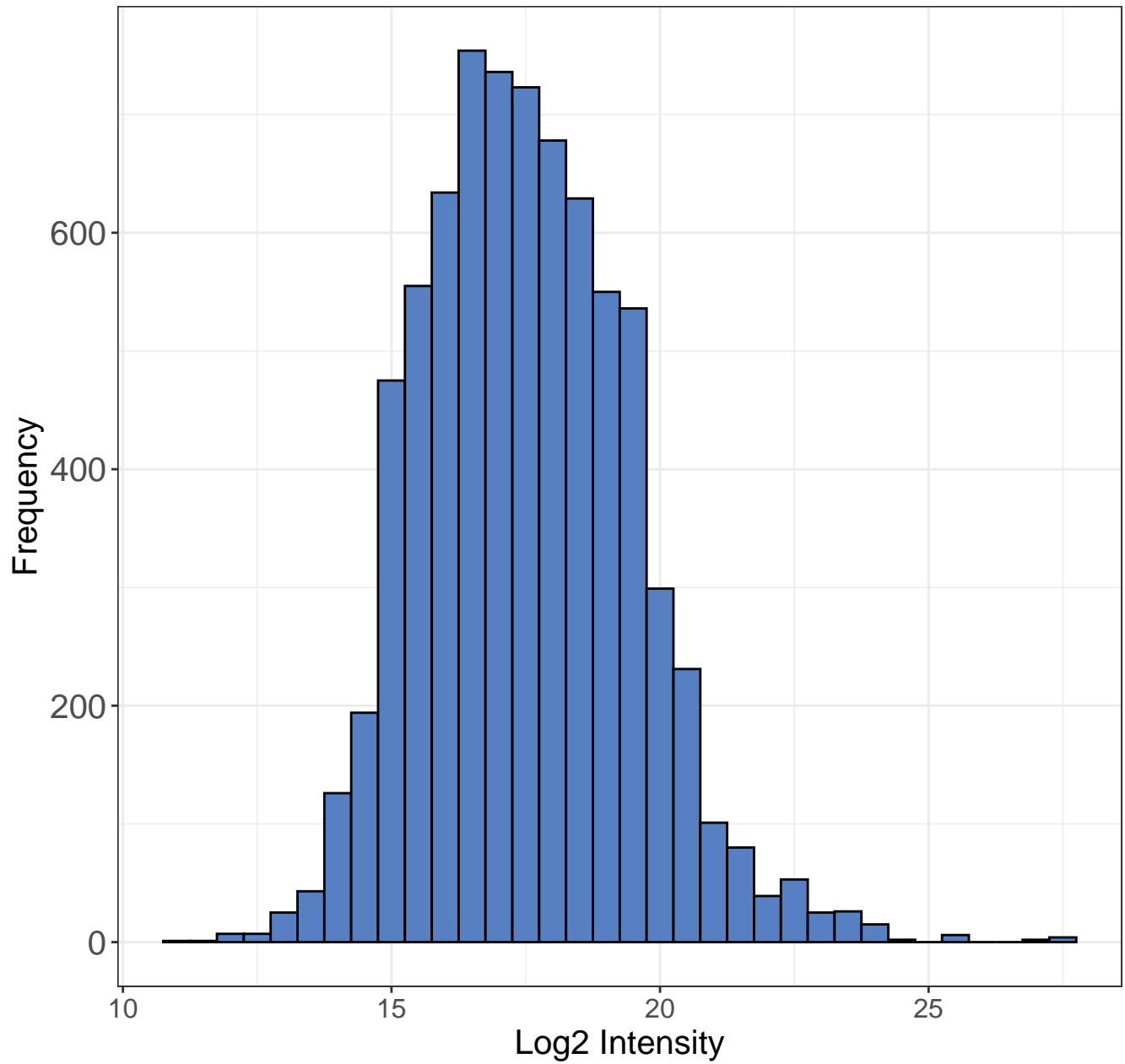


sample_6

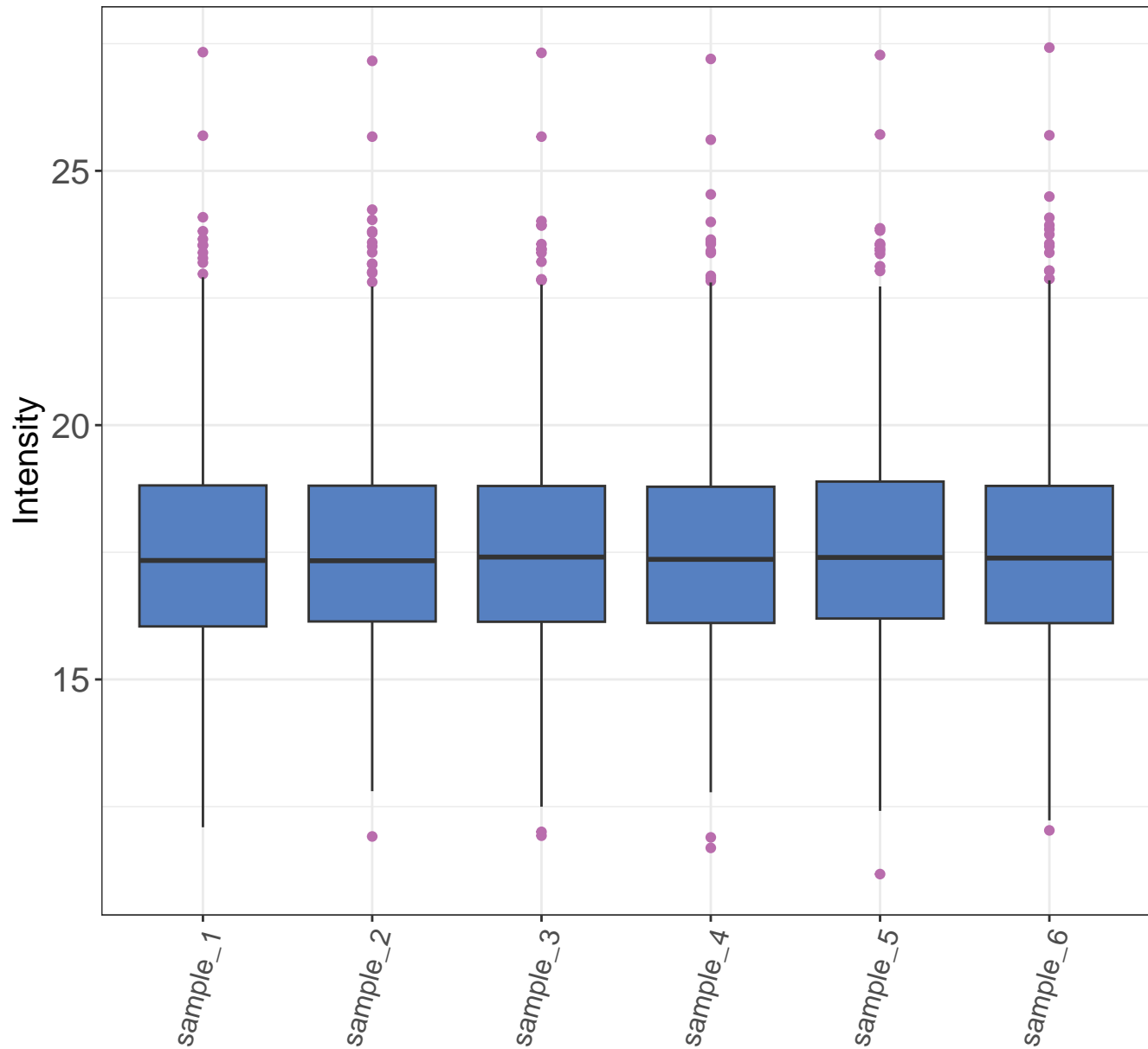


Log2 Intensity

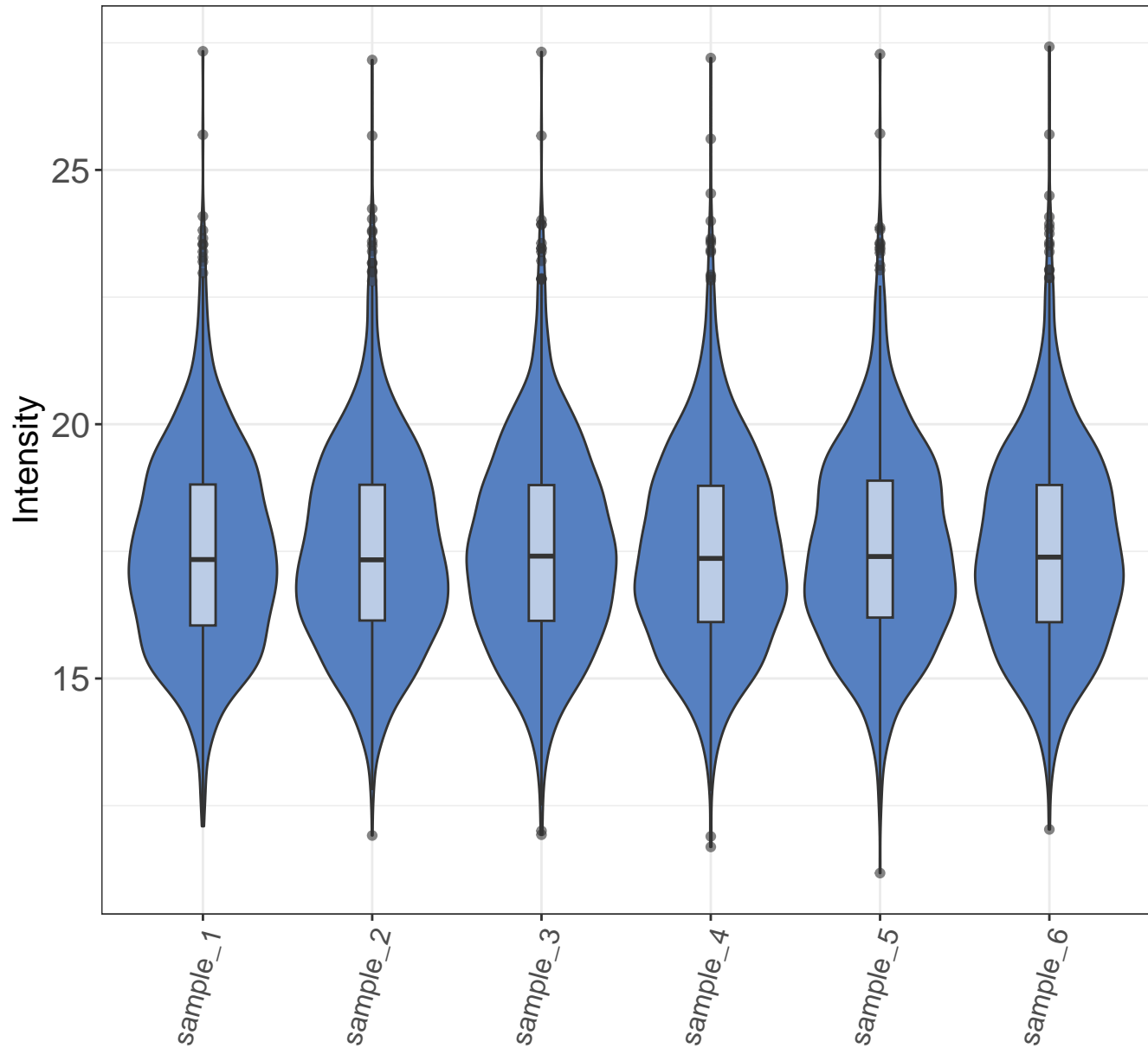
Overall log2 Intensity Distribution



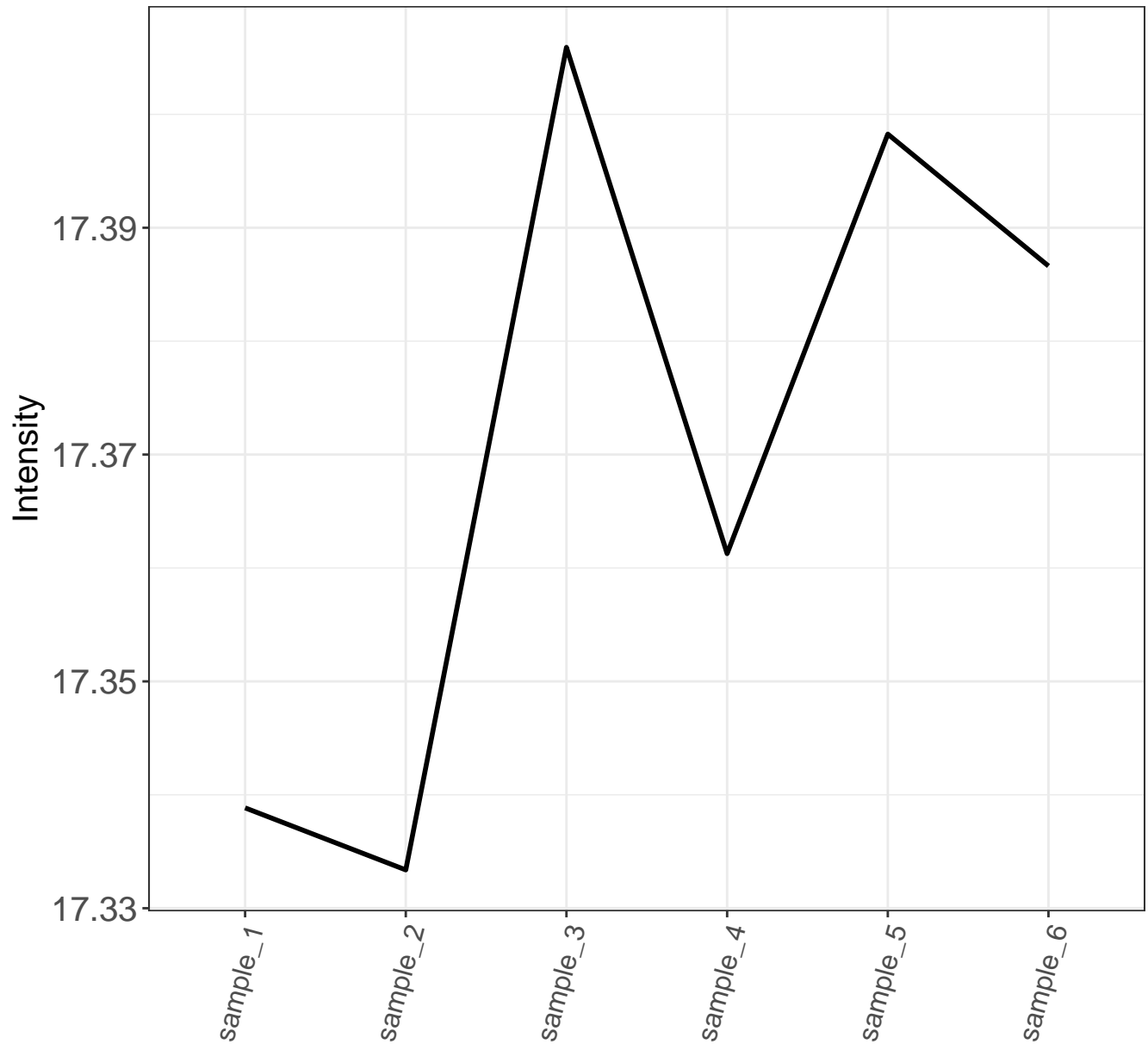
Run intensities



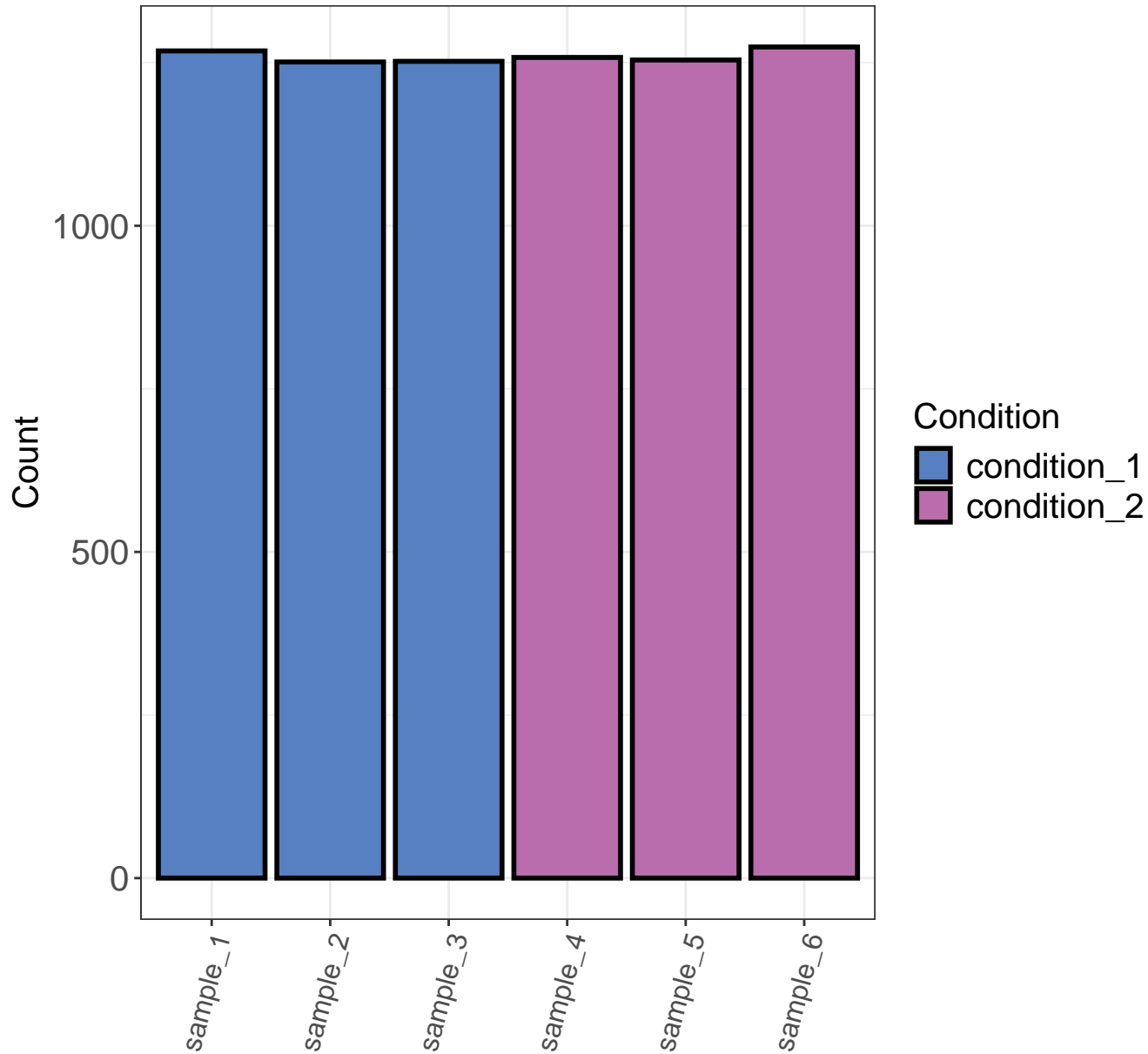
Run intensities



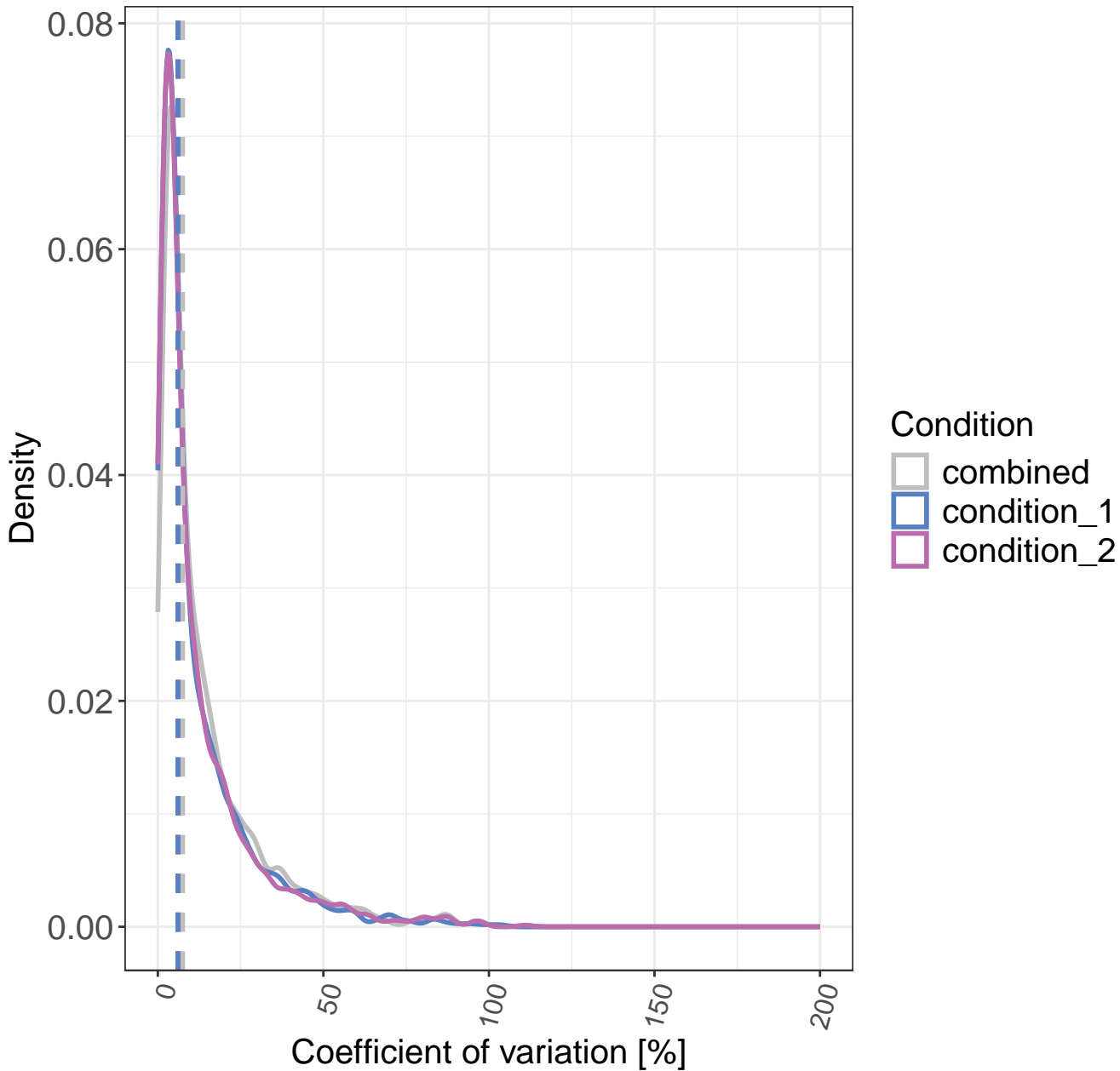
Medians of run intensities



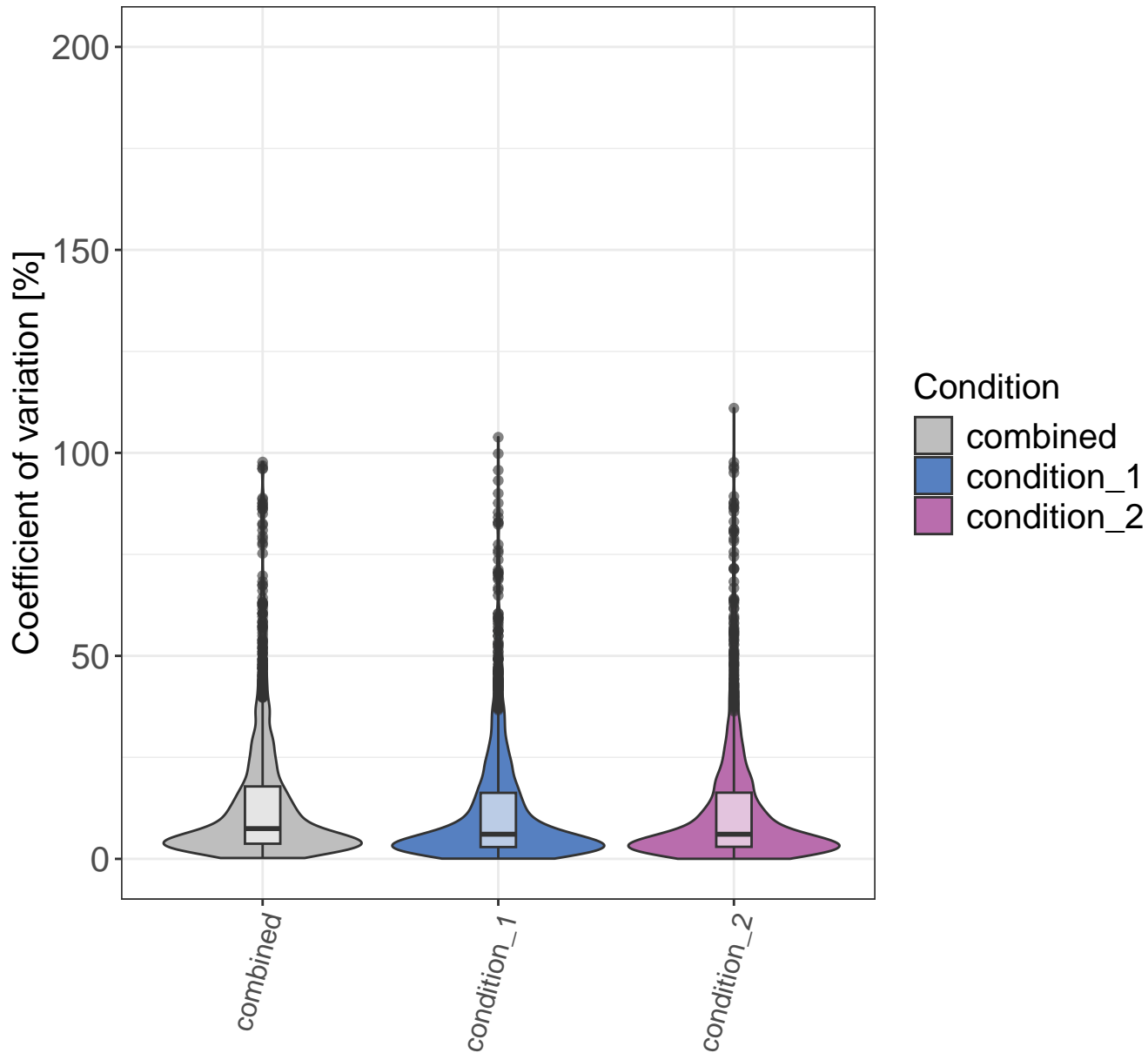
Test Title



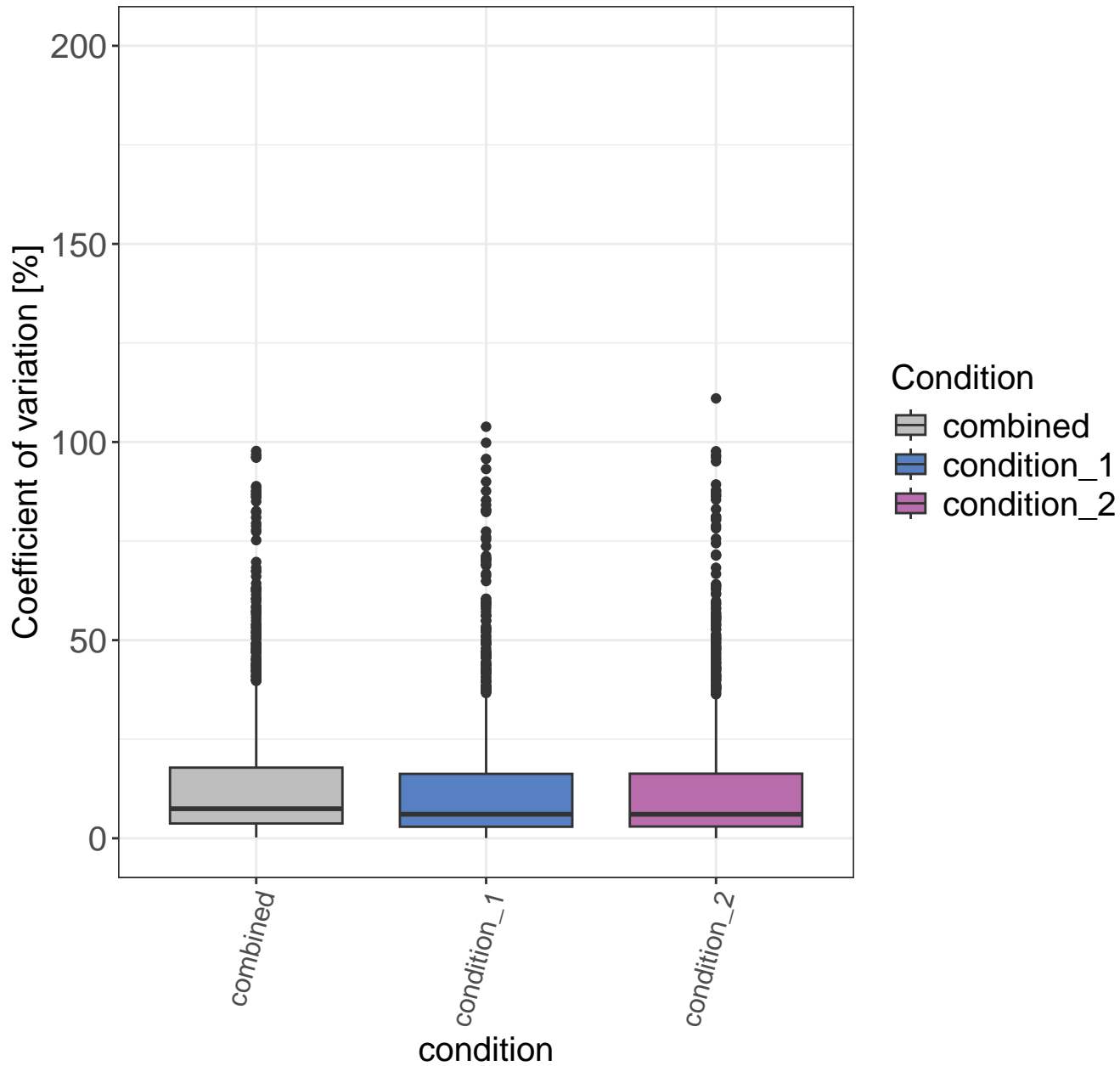
Coefficients of variation



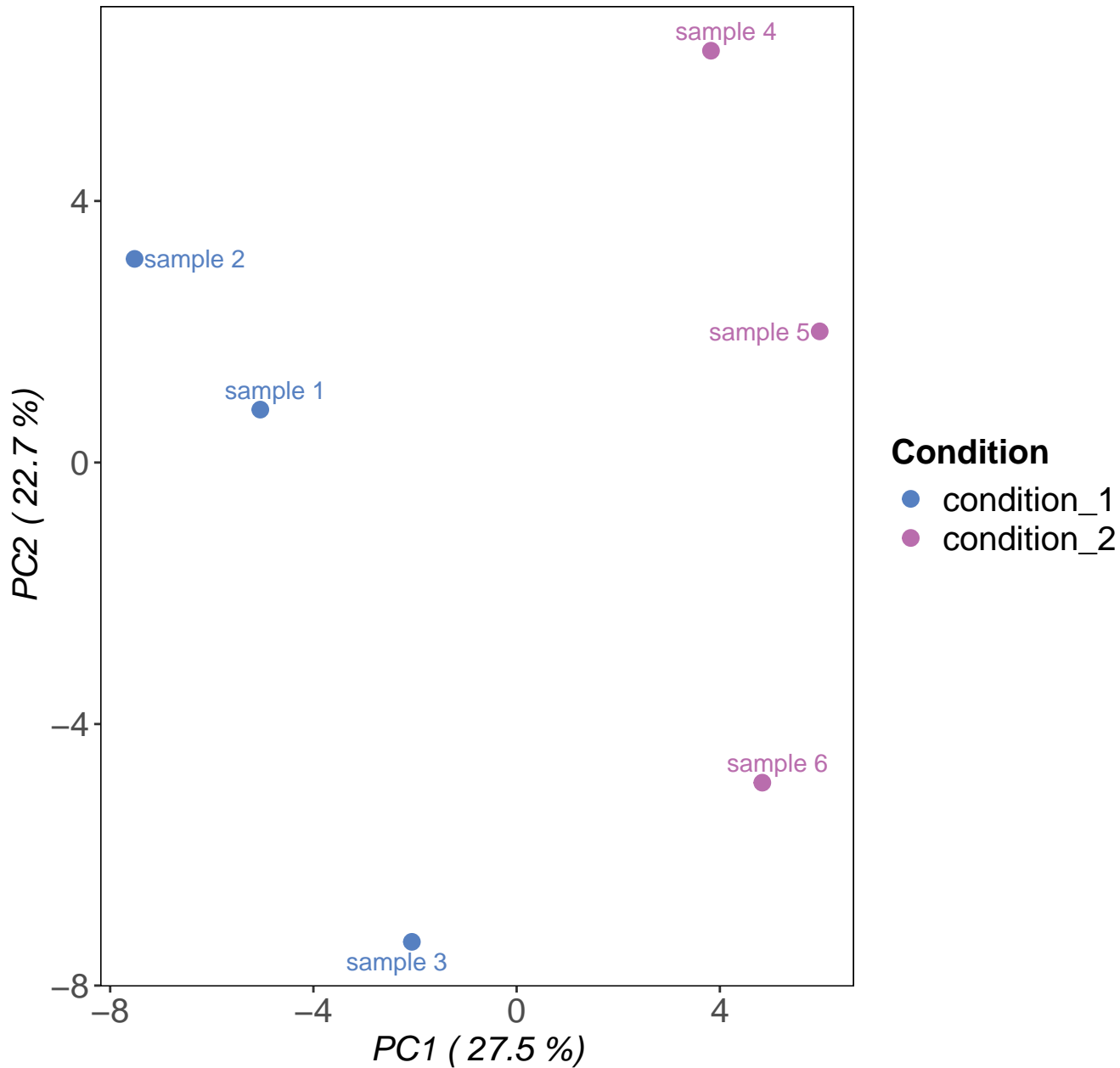
Coefficients of variation



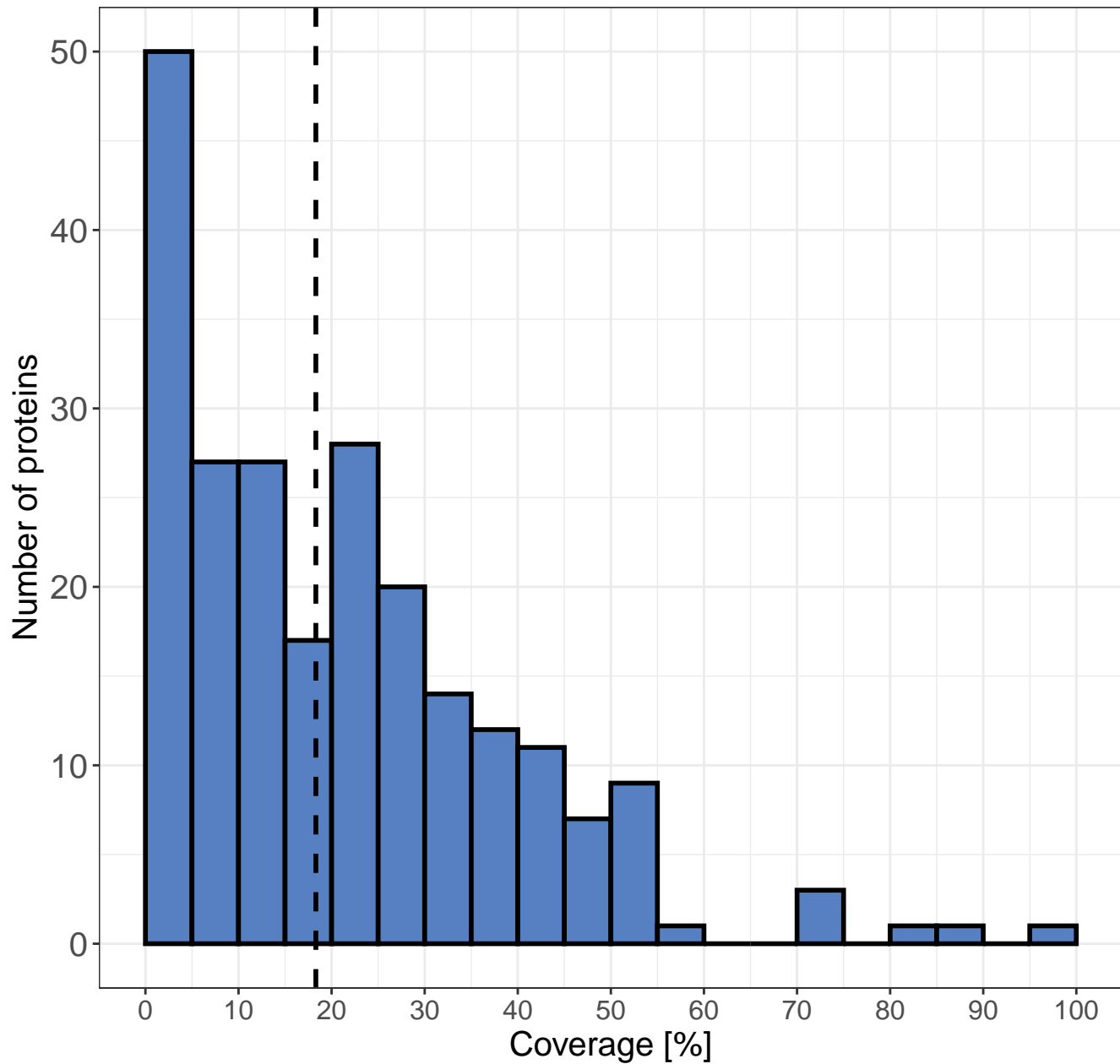
Coefficients of variation



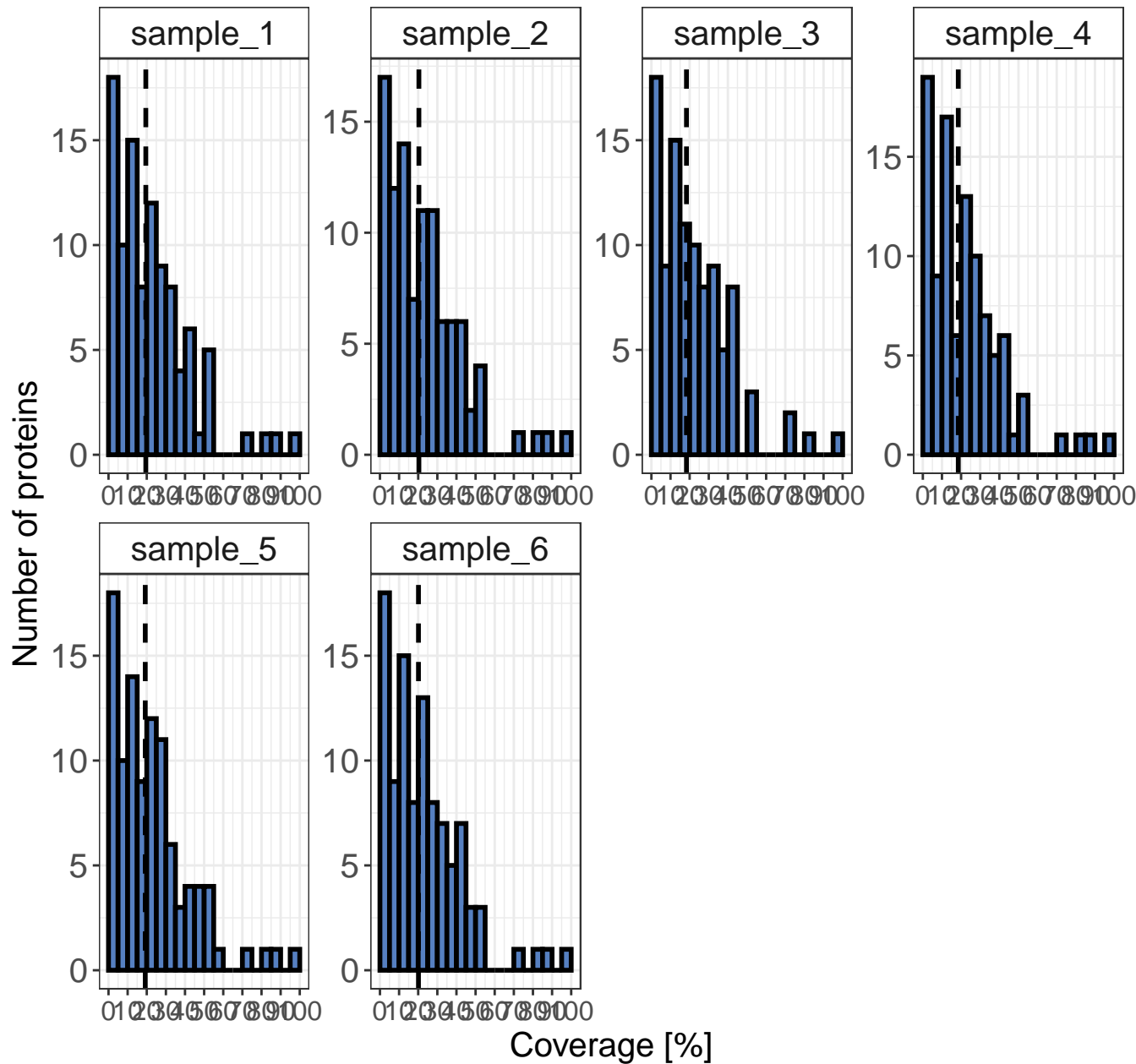
Principal component analysis



Protein coverage distribution

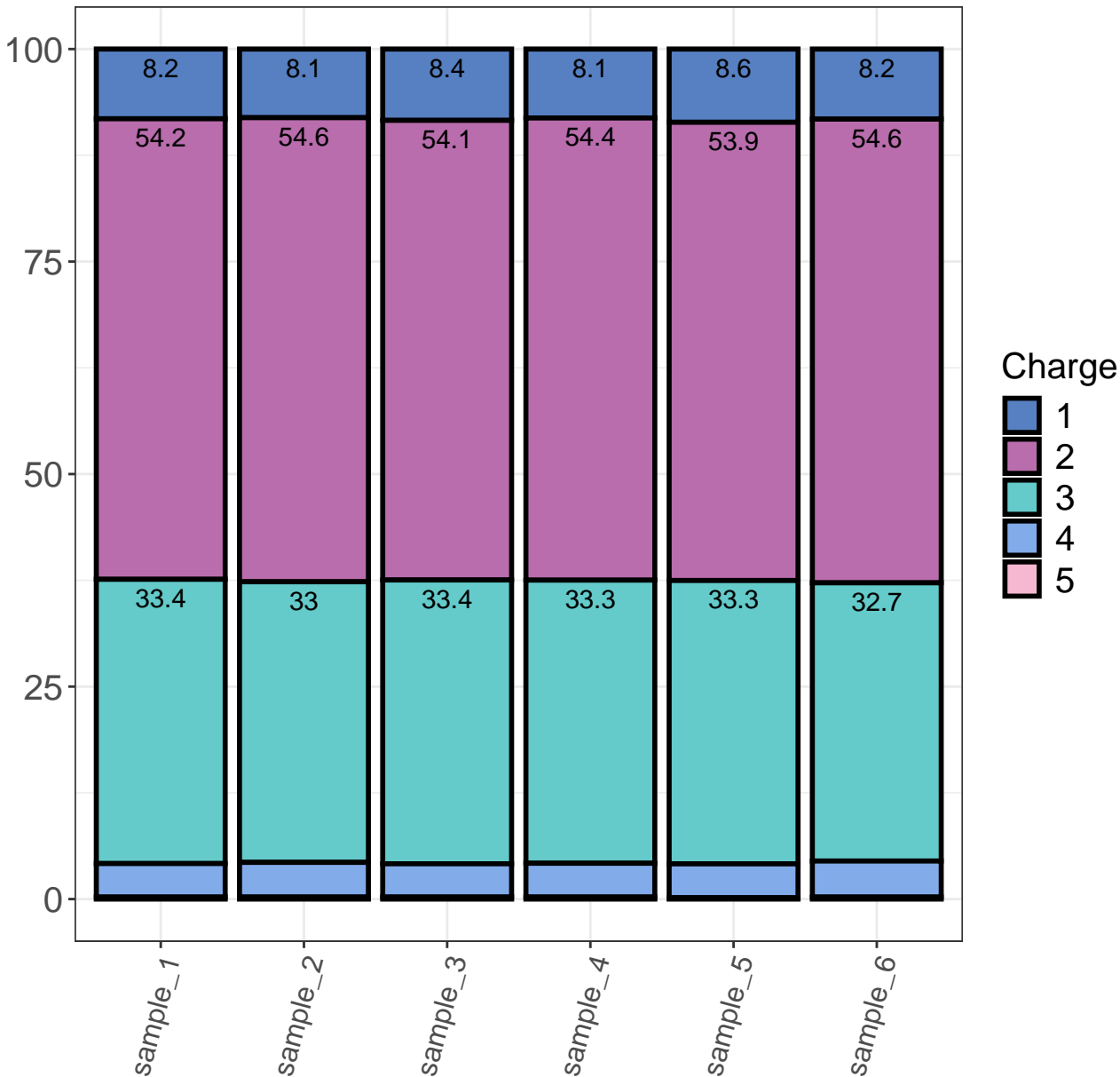


Protein coverage distribution



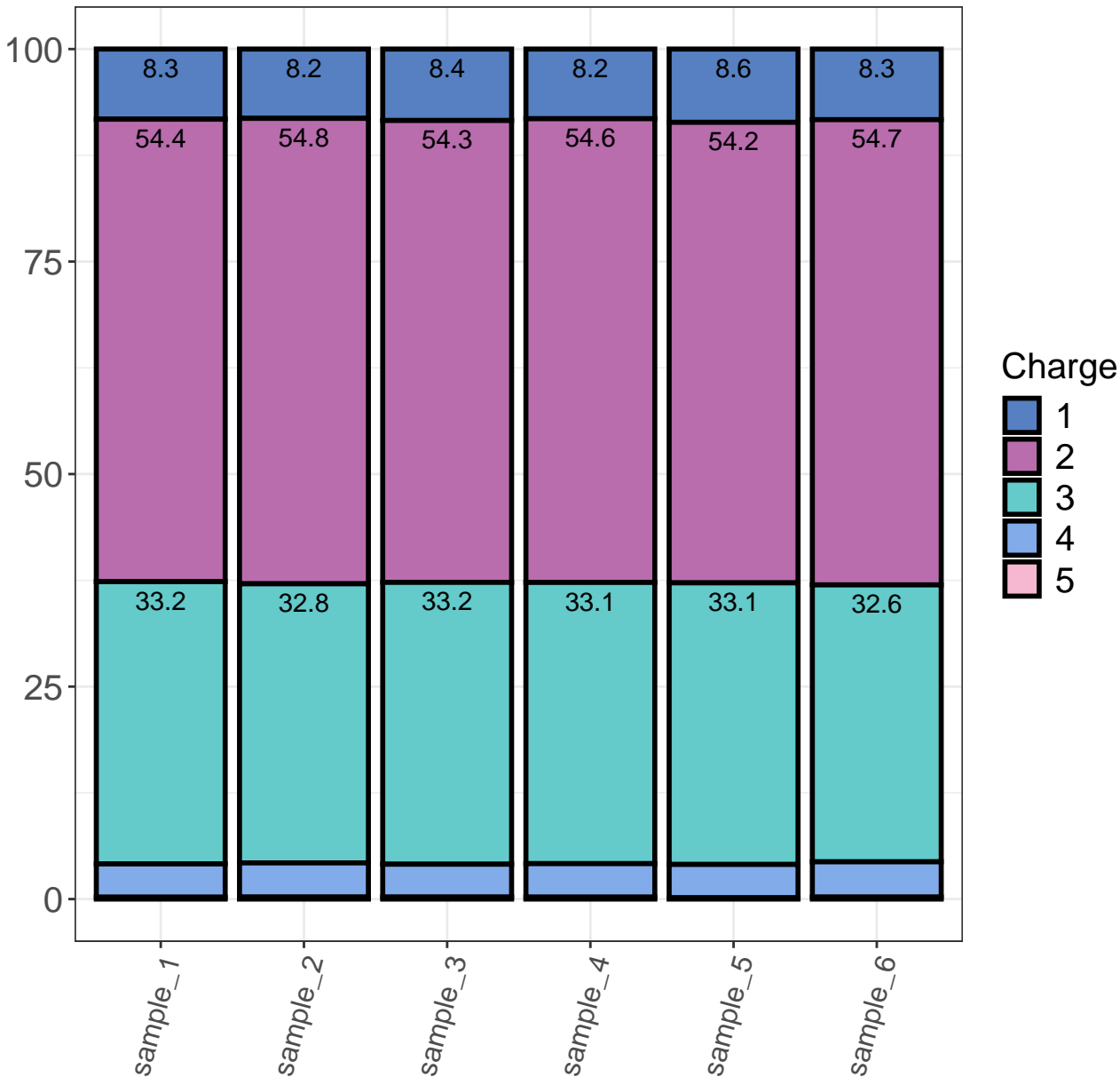
Charge distribution per .raw file

By percent of total peptide count



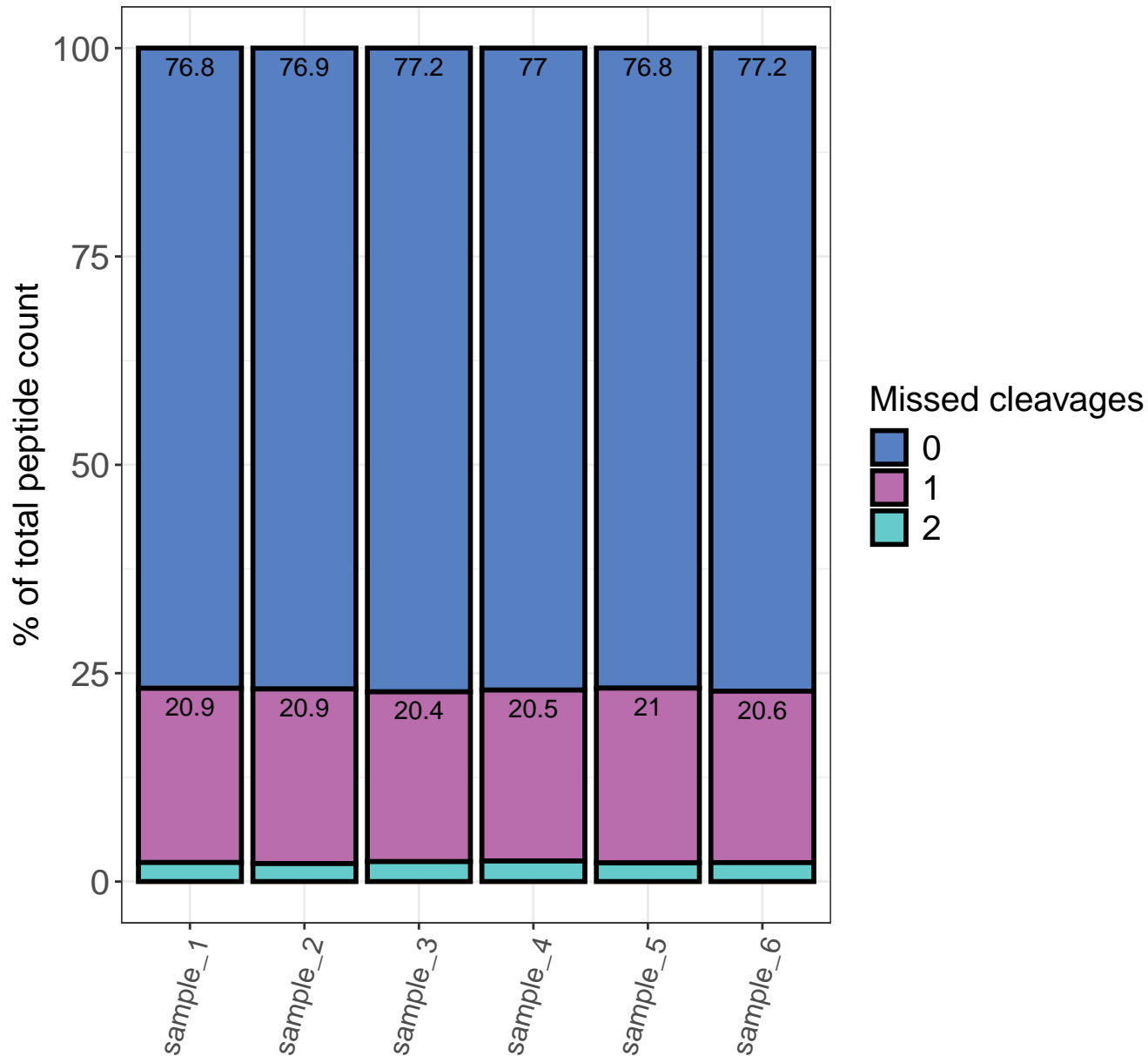
Charge distribution per .raw file

By percent of total intensity



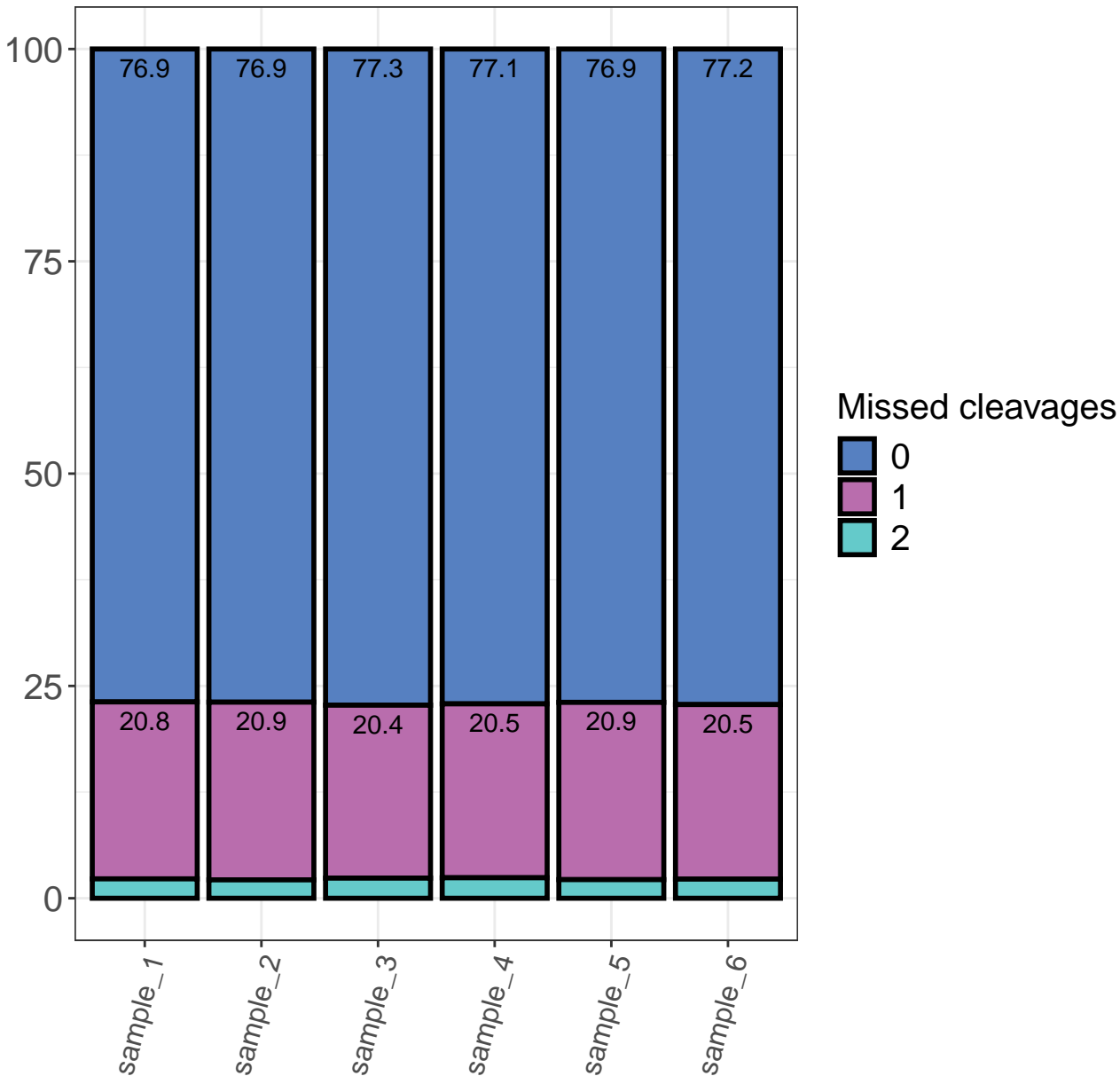
Missed cleavages per .raw file

By percent of total peptide count

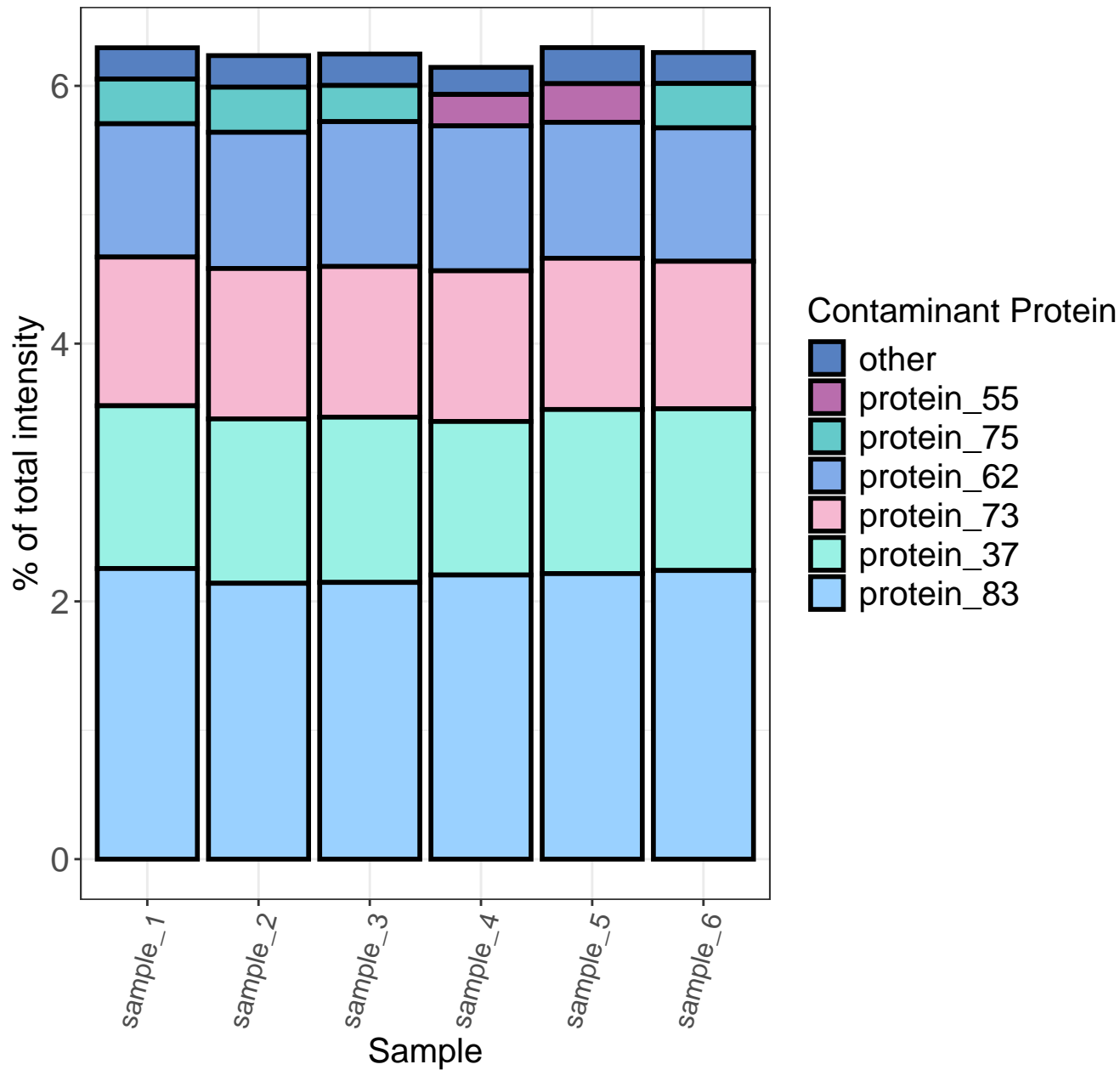


Missed cleavages per .raw file

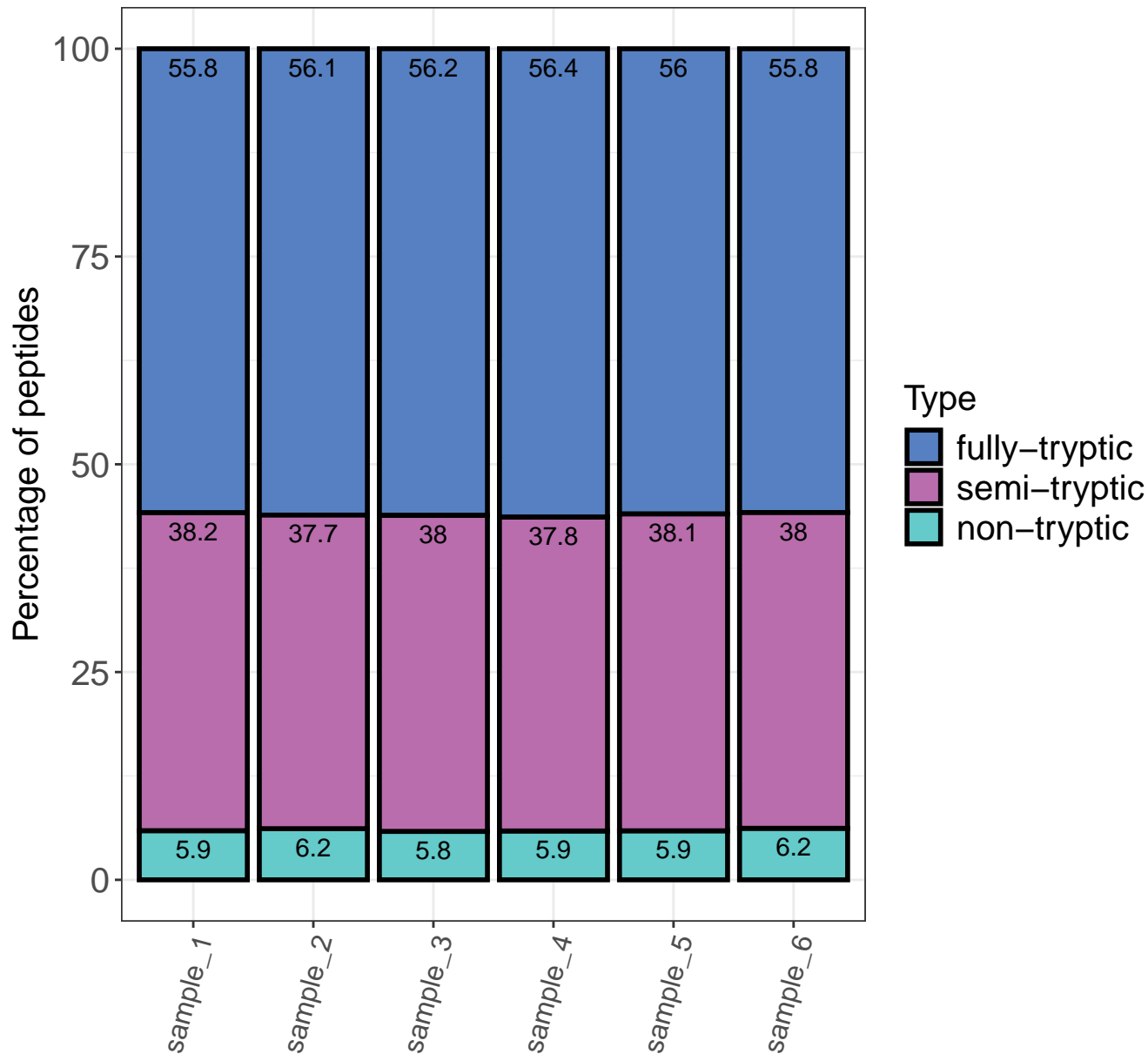
By percent of total intensity



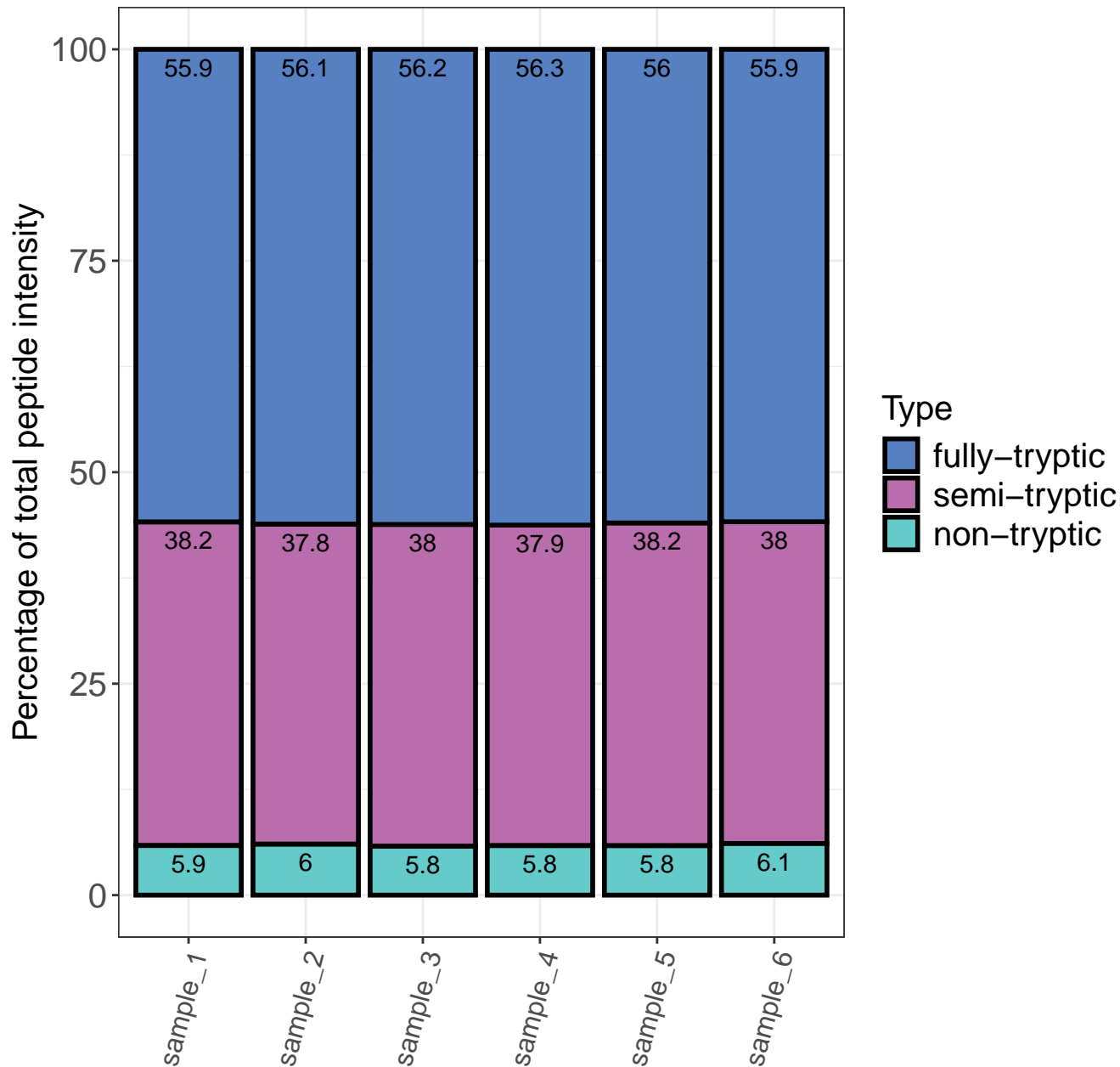
Contaminants per .raw file



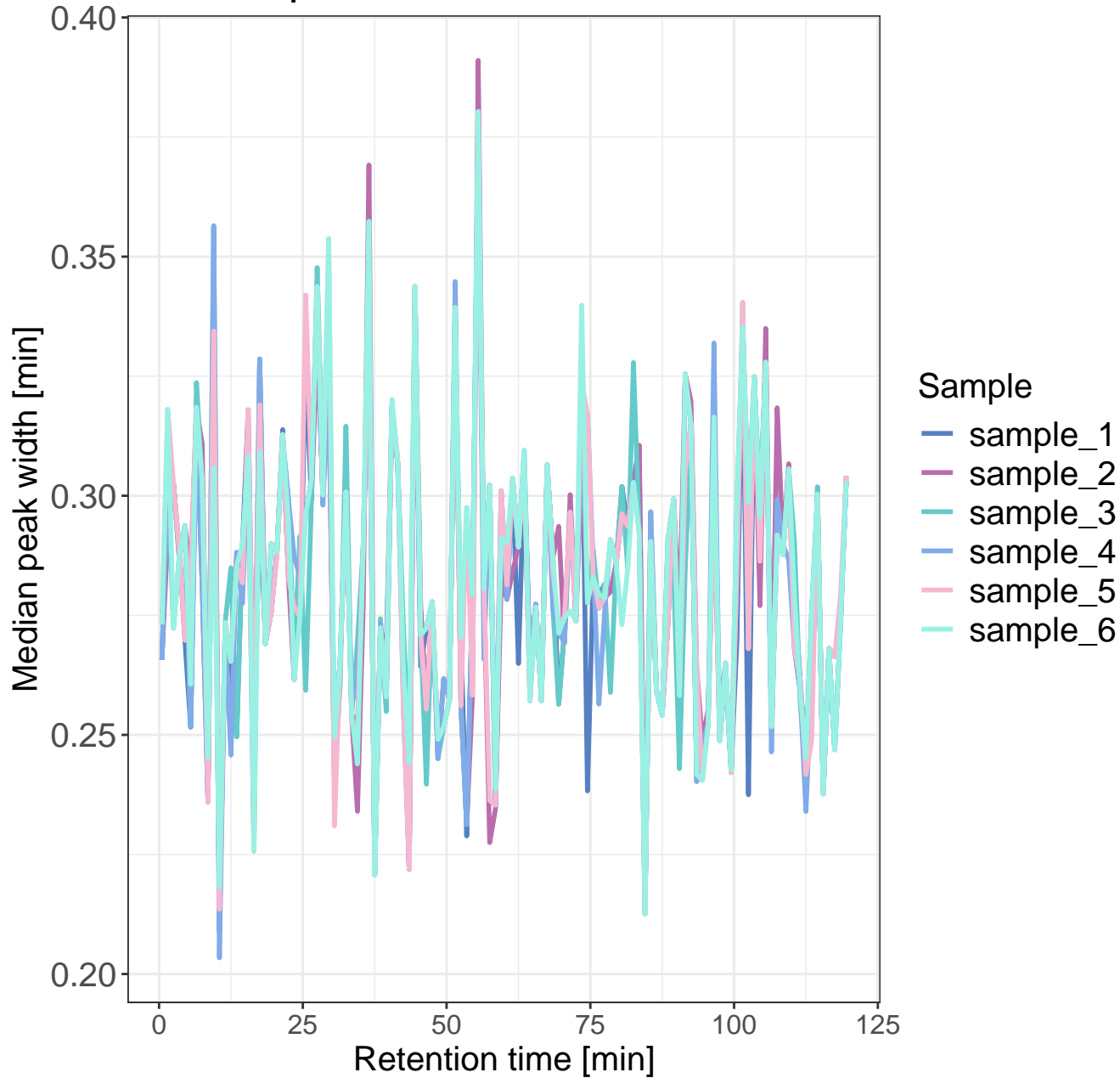
Peptide types per .raw file



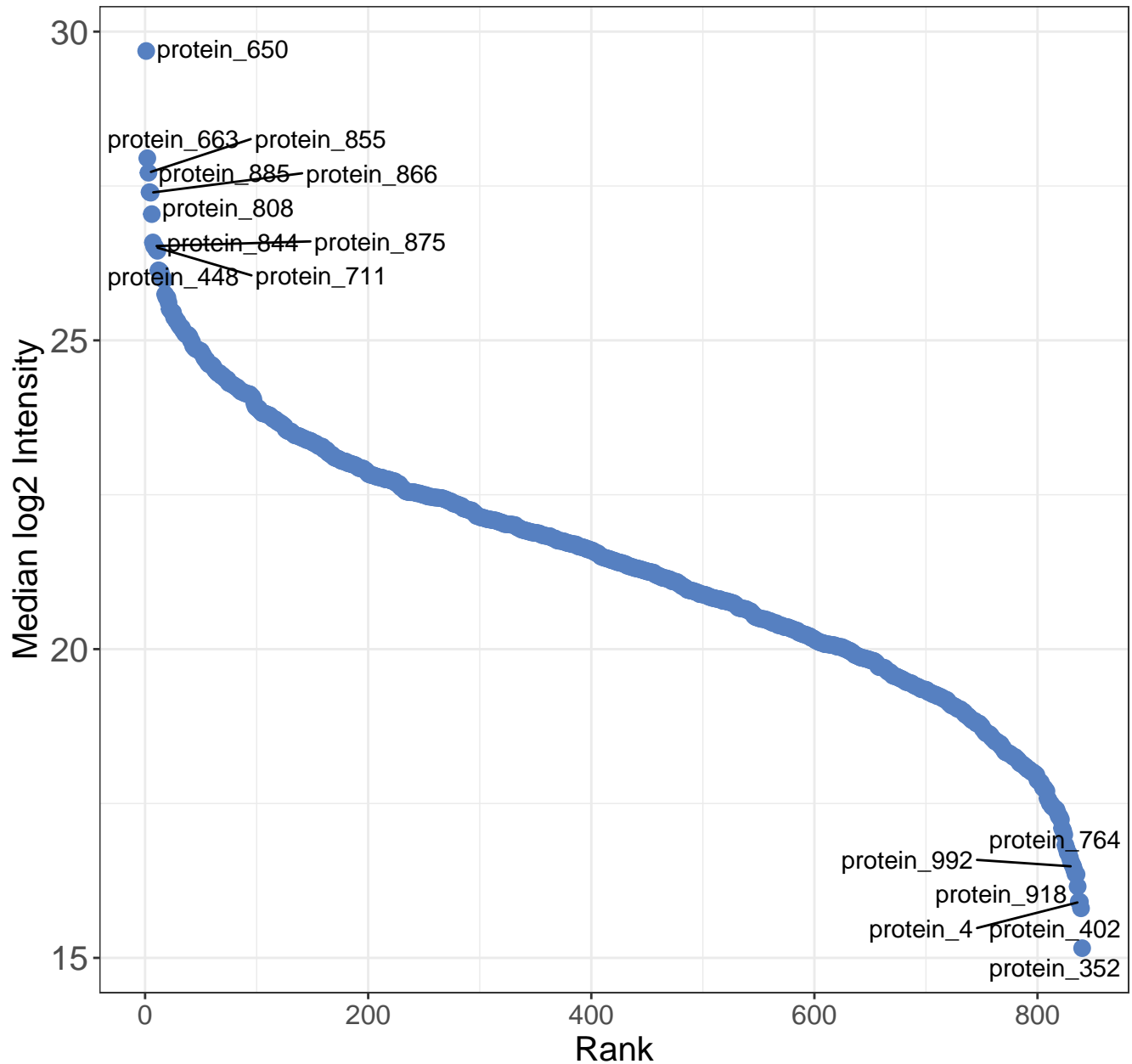
Peptide type intensity per .raw file



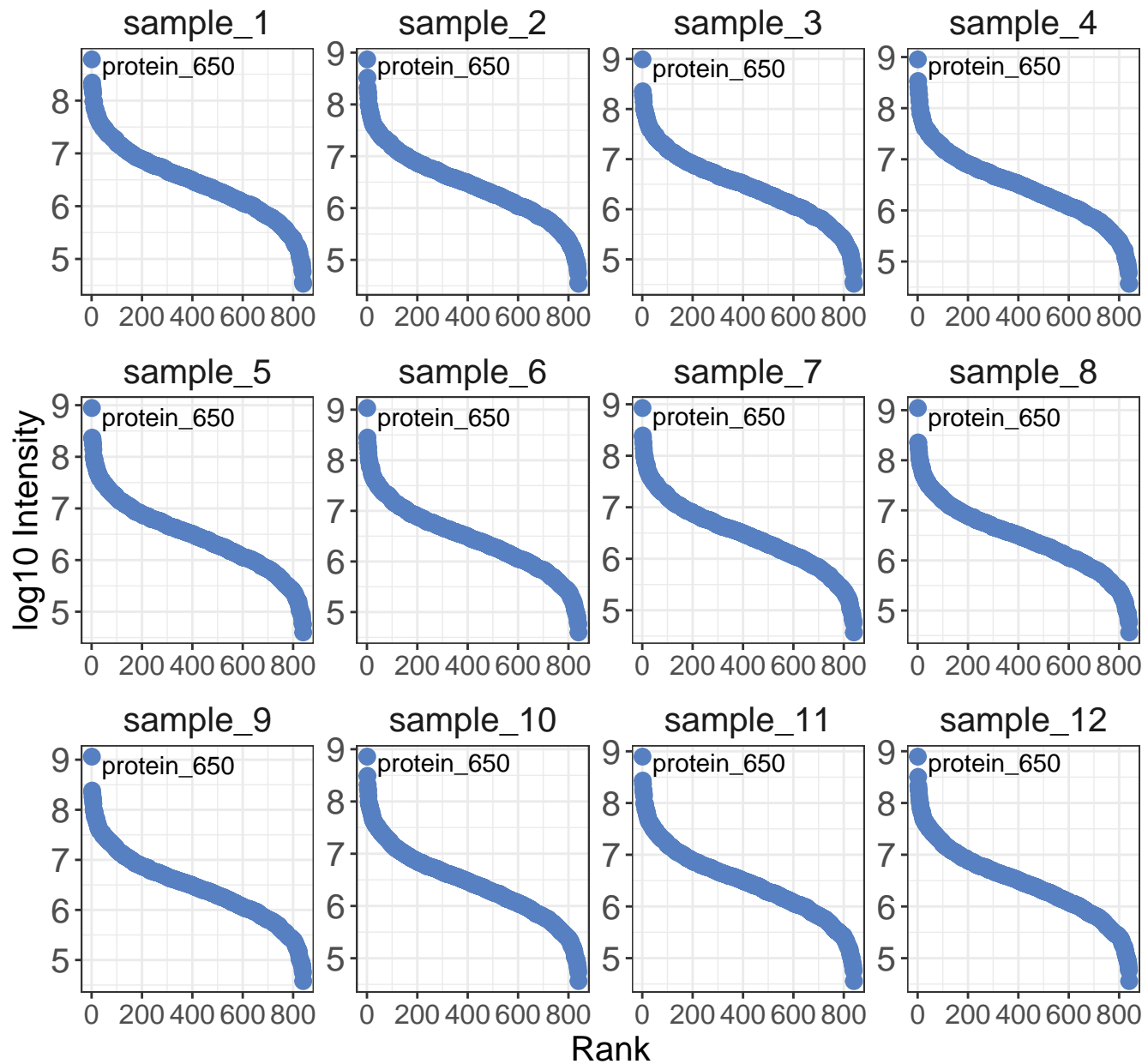
Median peak width over retention time



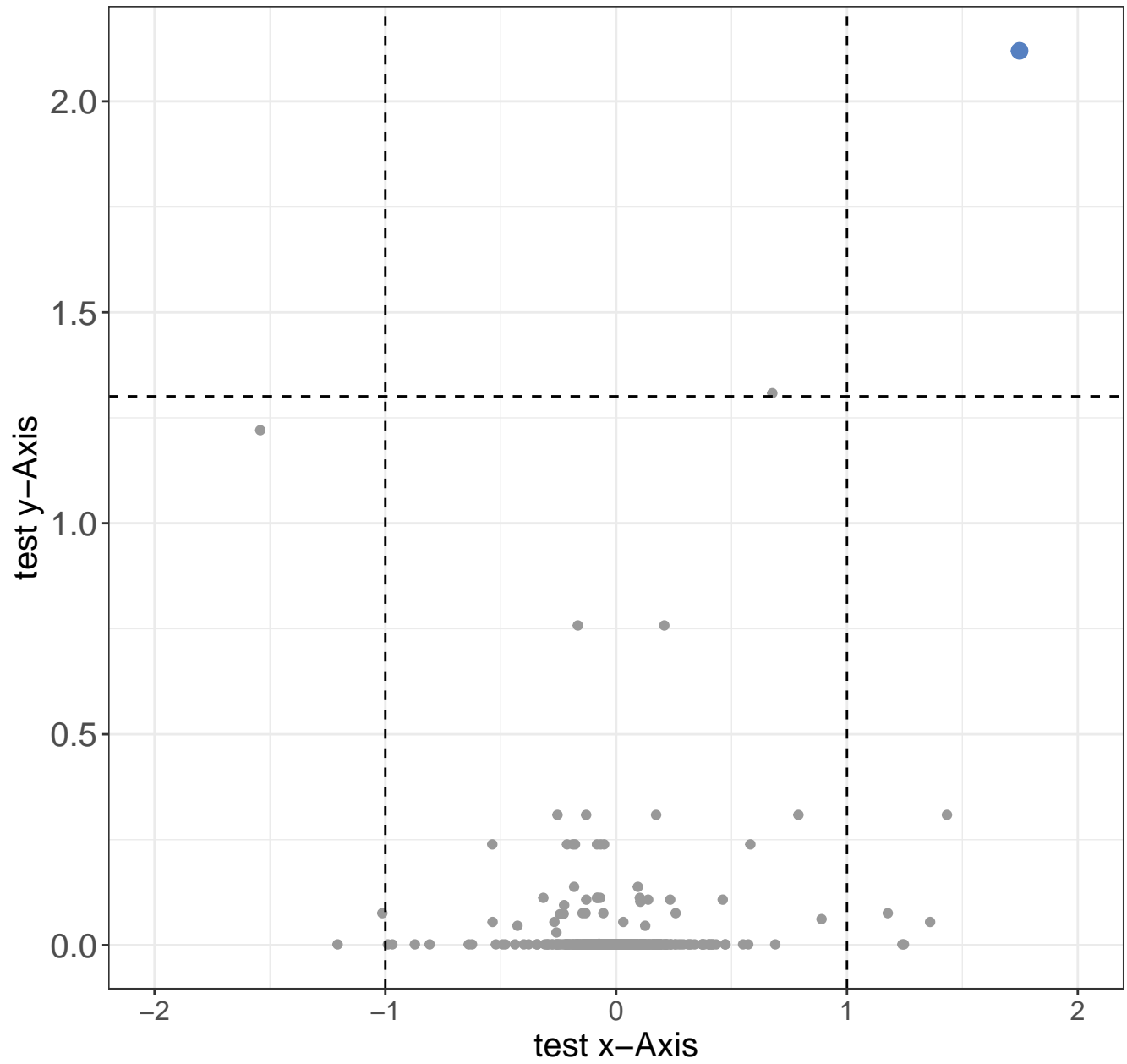
Ranked Intensities



Ranked Intensities



Test tile



Test tile

