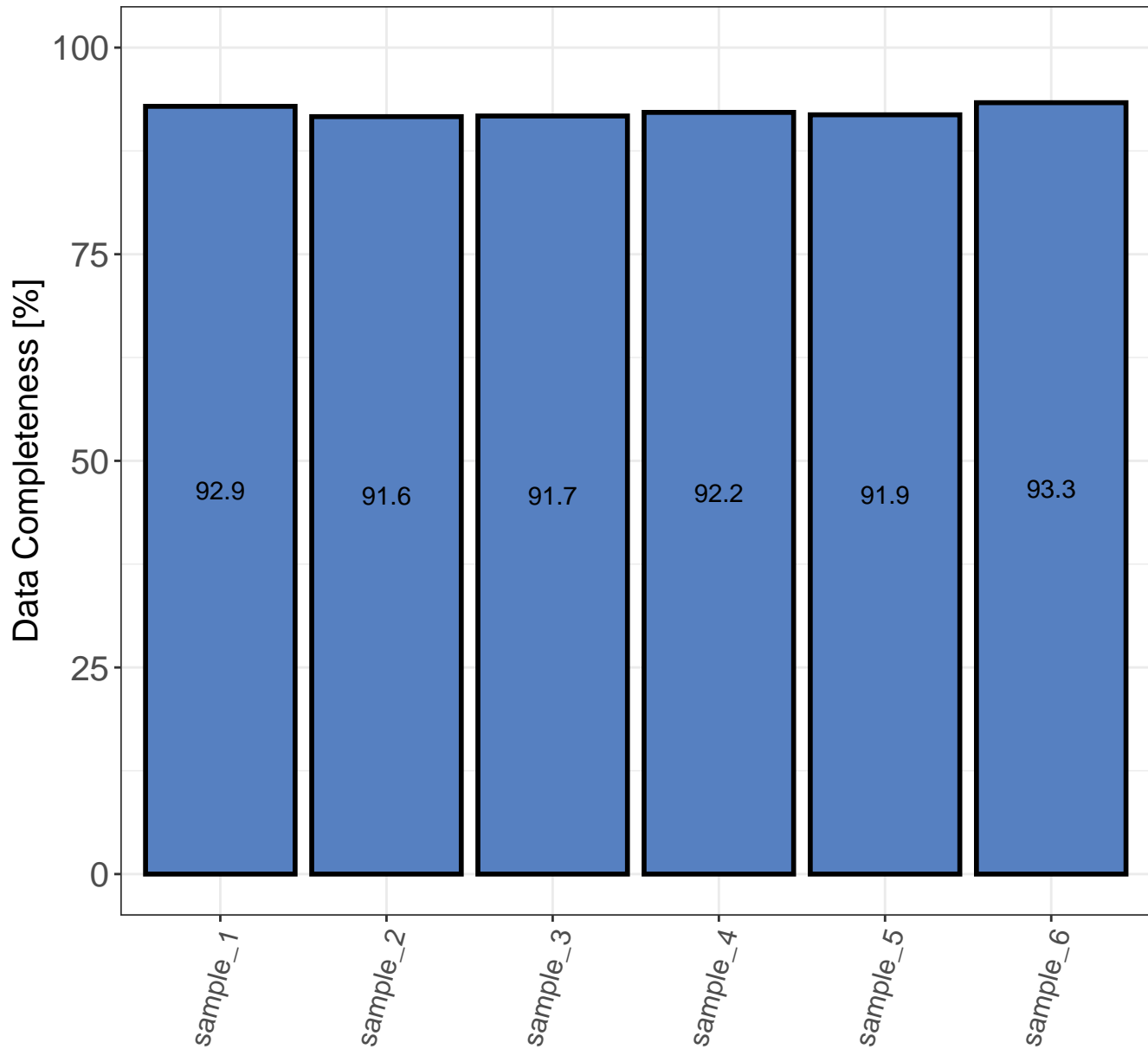
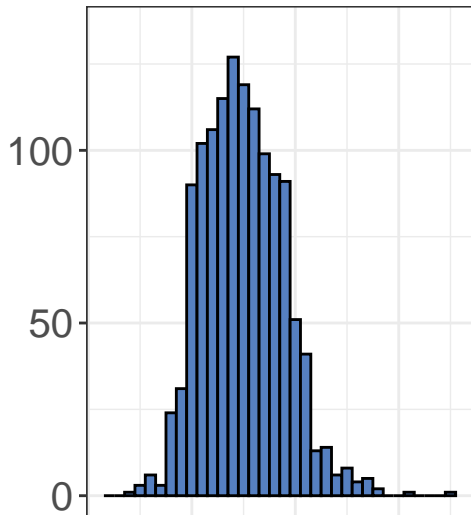


# Data completeness per .raw file

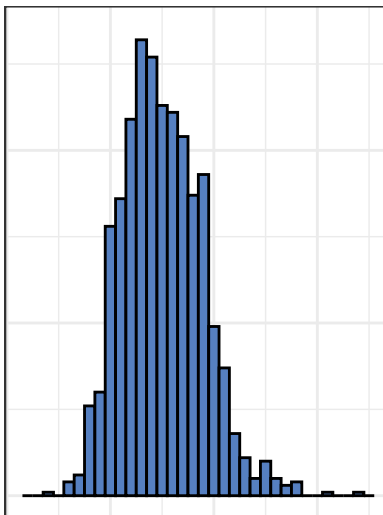


# Overall log2 Intensity Distribution

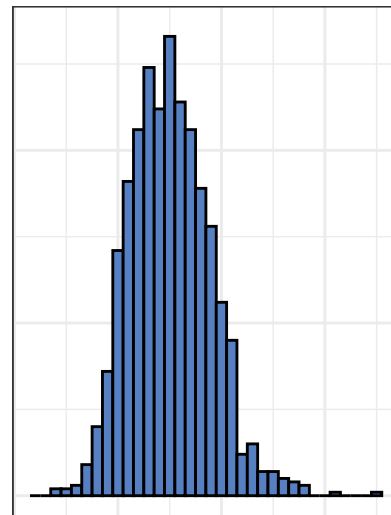
sample\_1



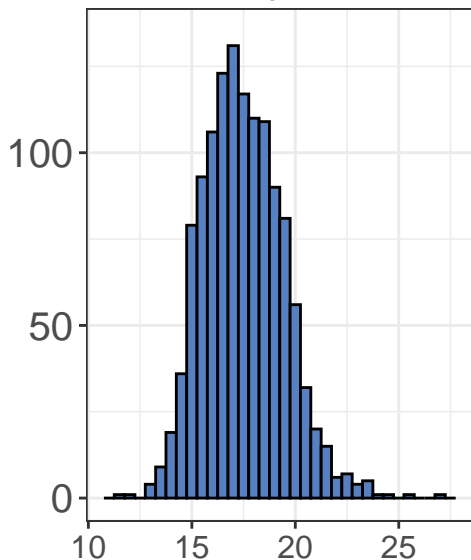
sample\_2



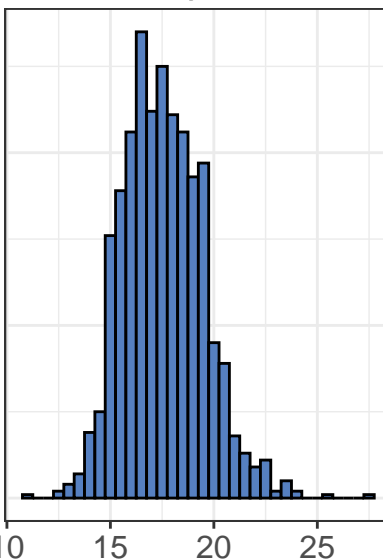
sample\_3



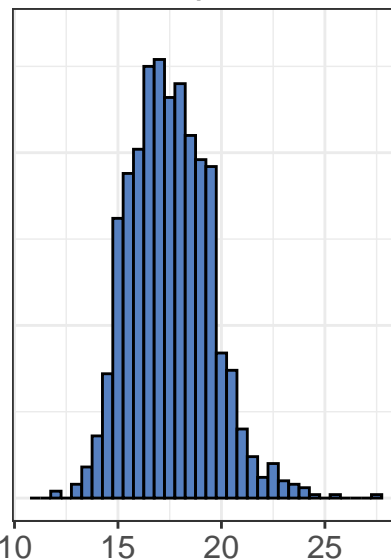
sample\_4



sample\_5

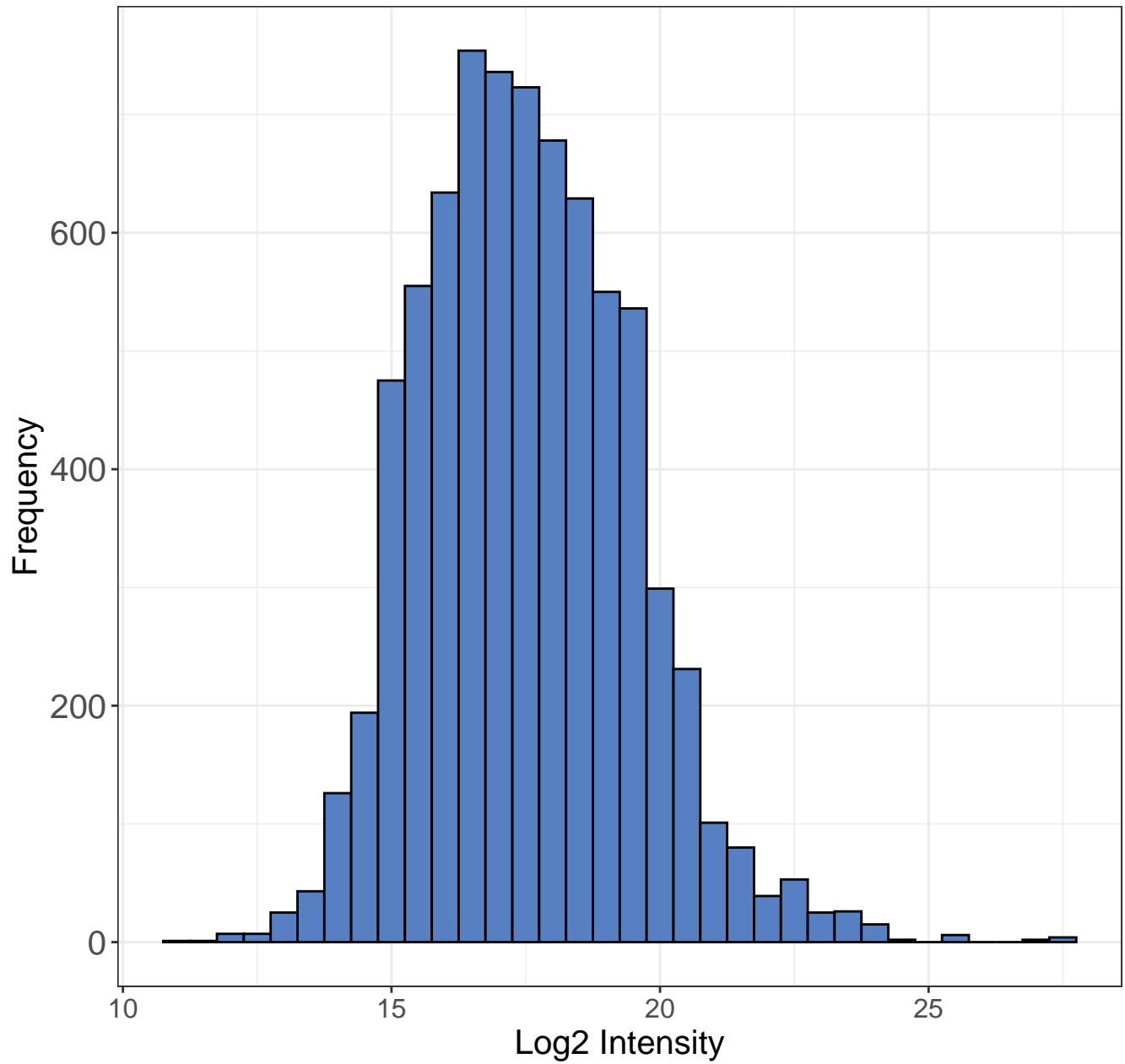


sample\_6

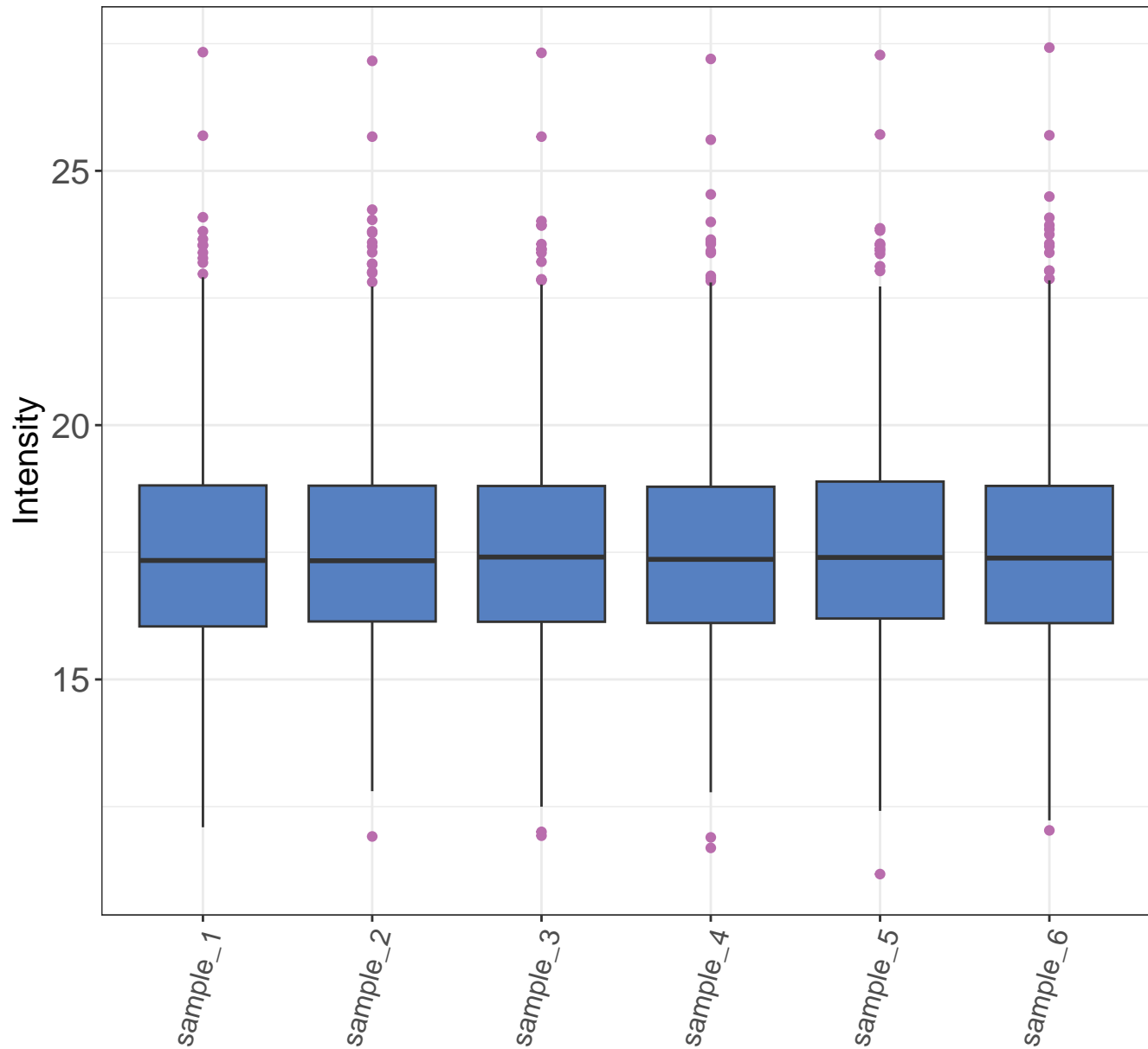


Log2 Intensity

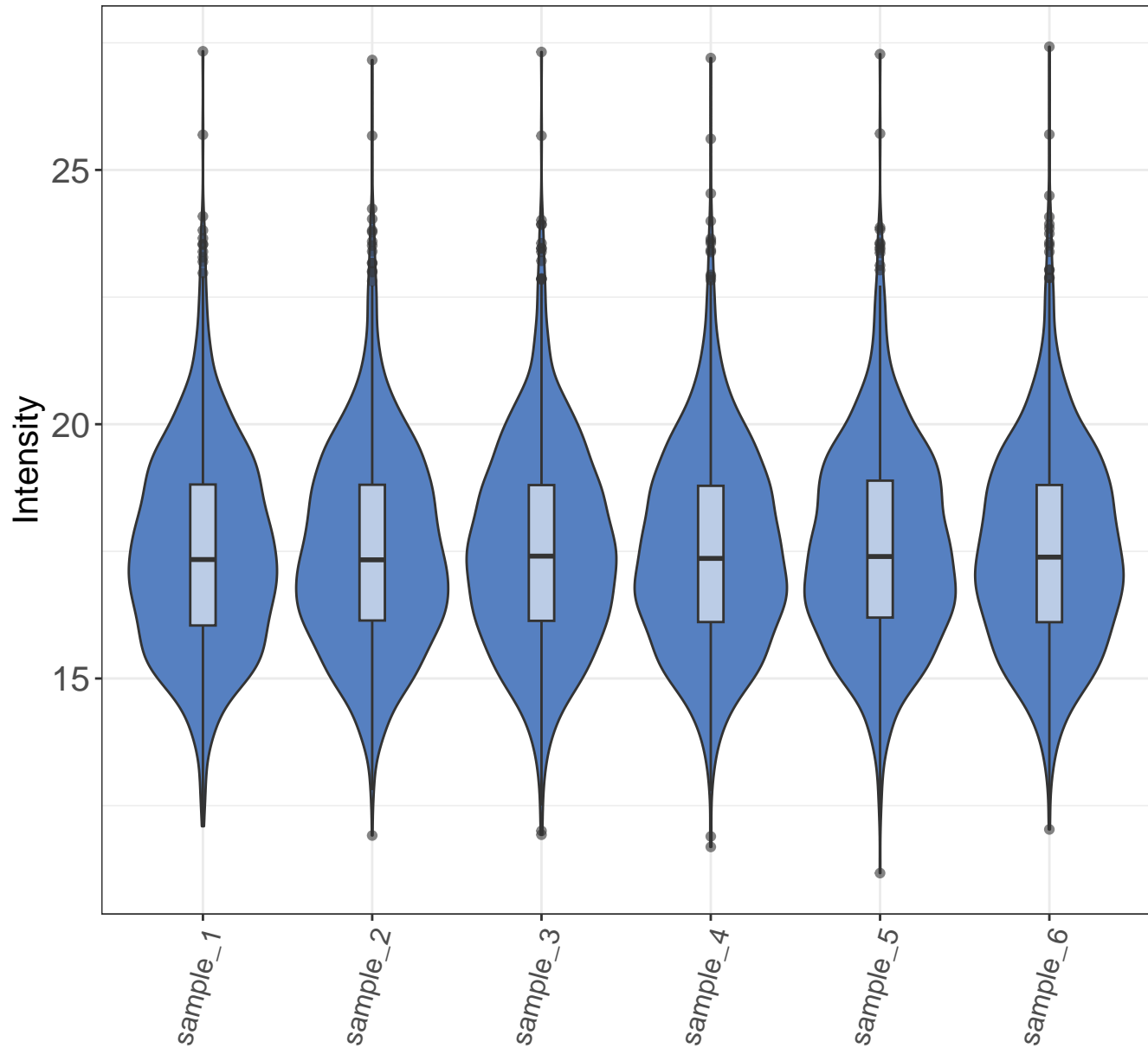
# Overall log2 Intensity Distribution



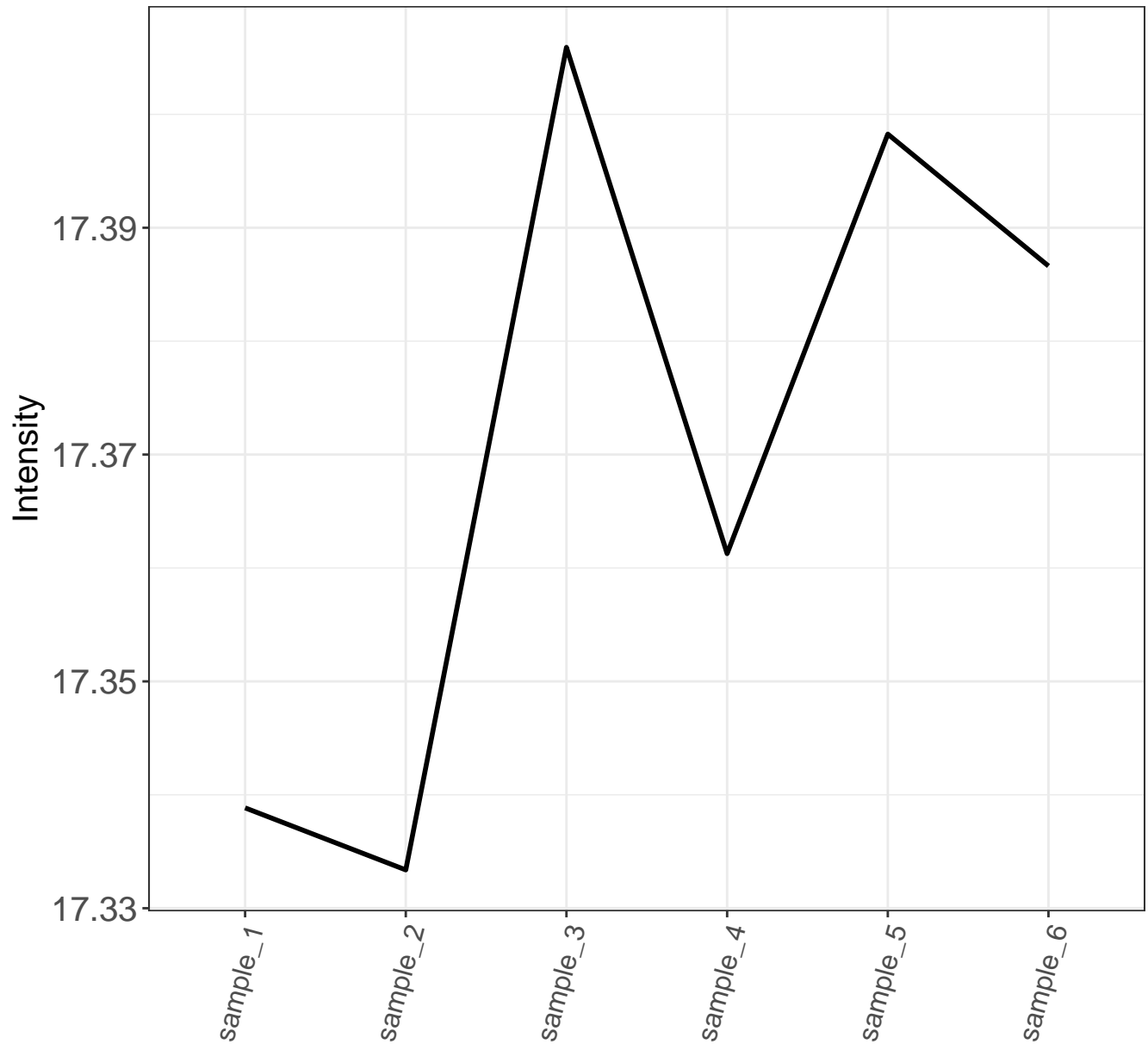
# Run intensities



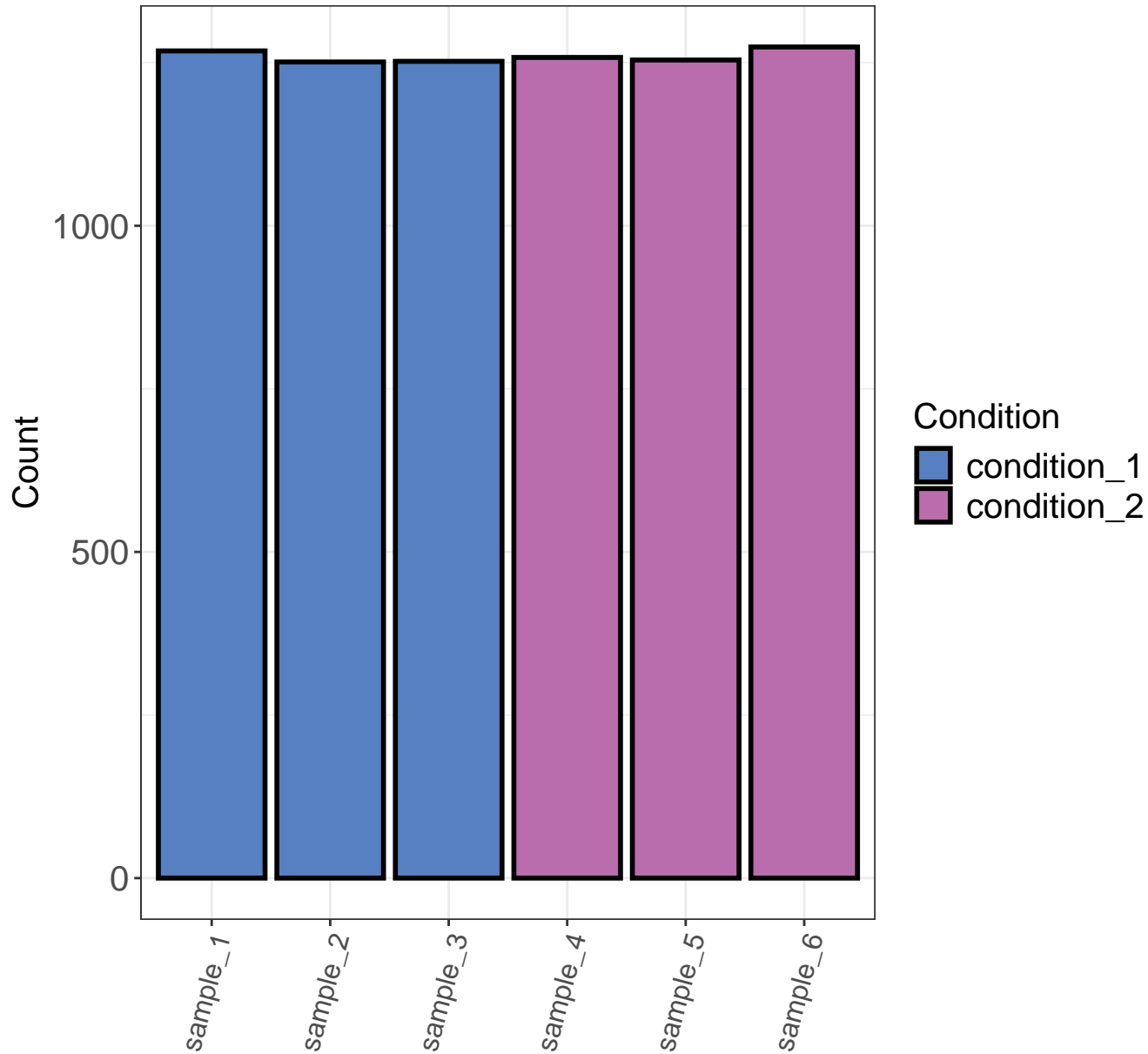
# Run intensities



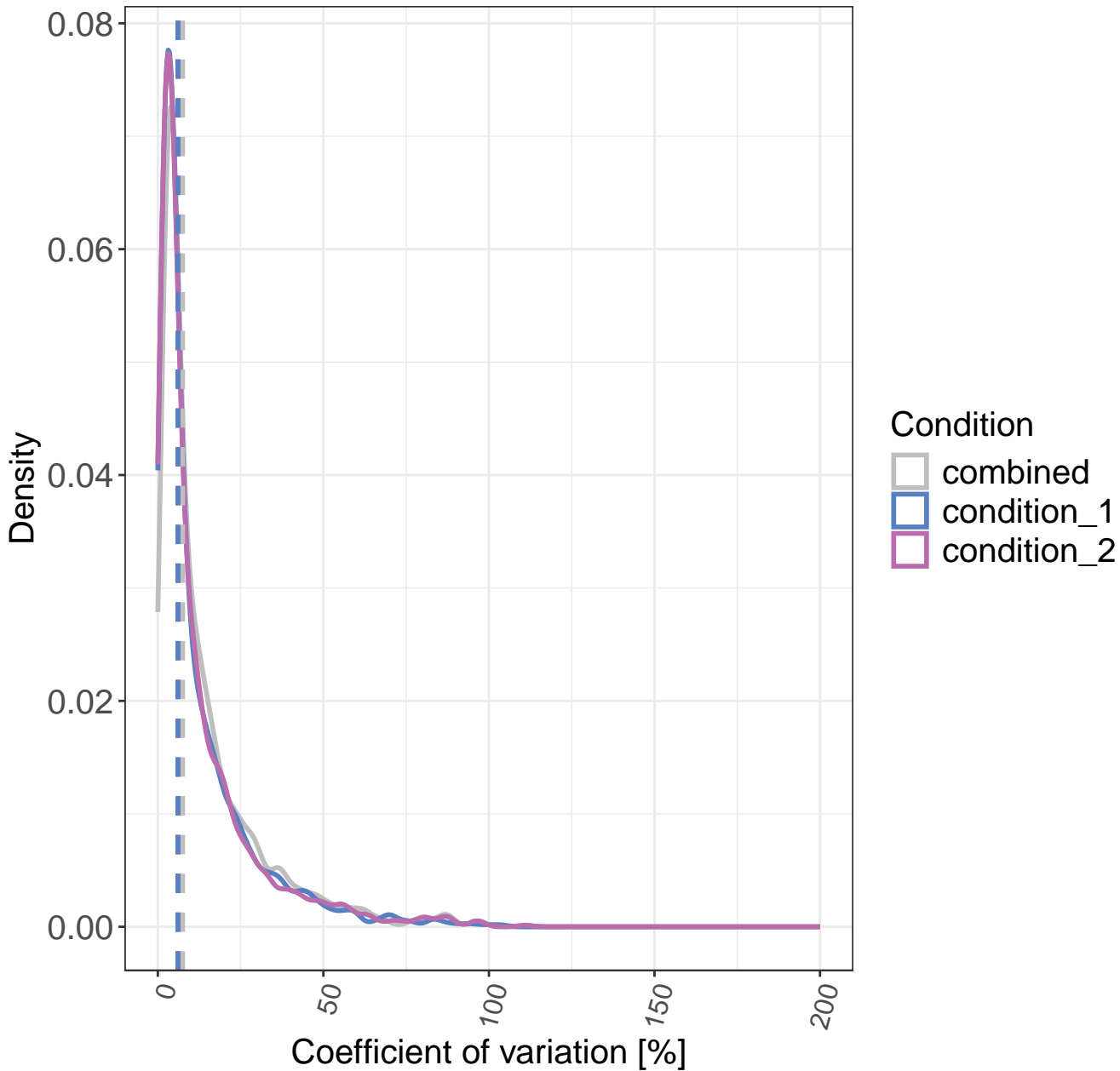
# Medians of run intensities



# Test Title

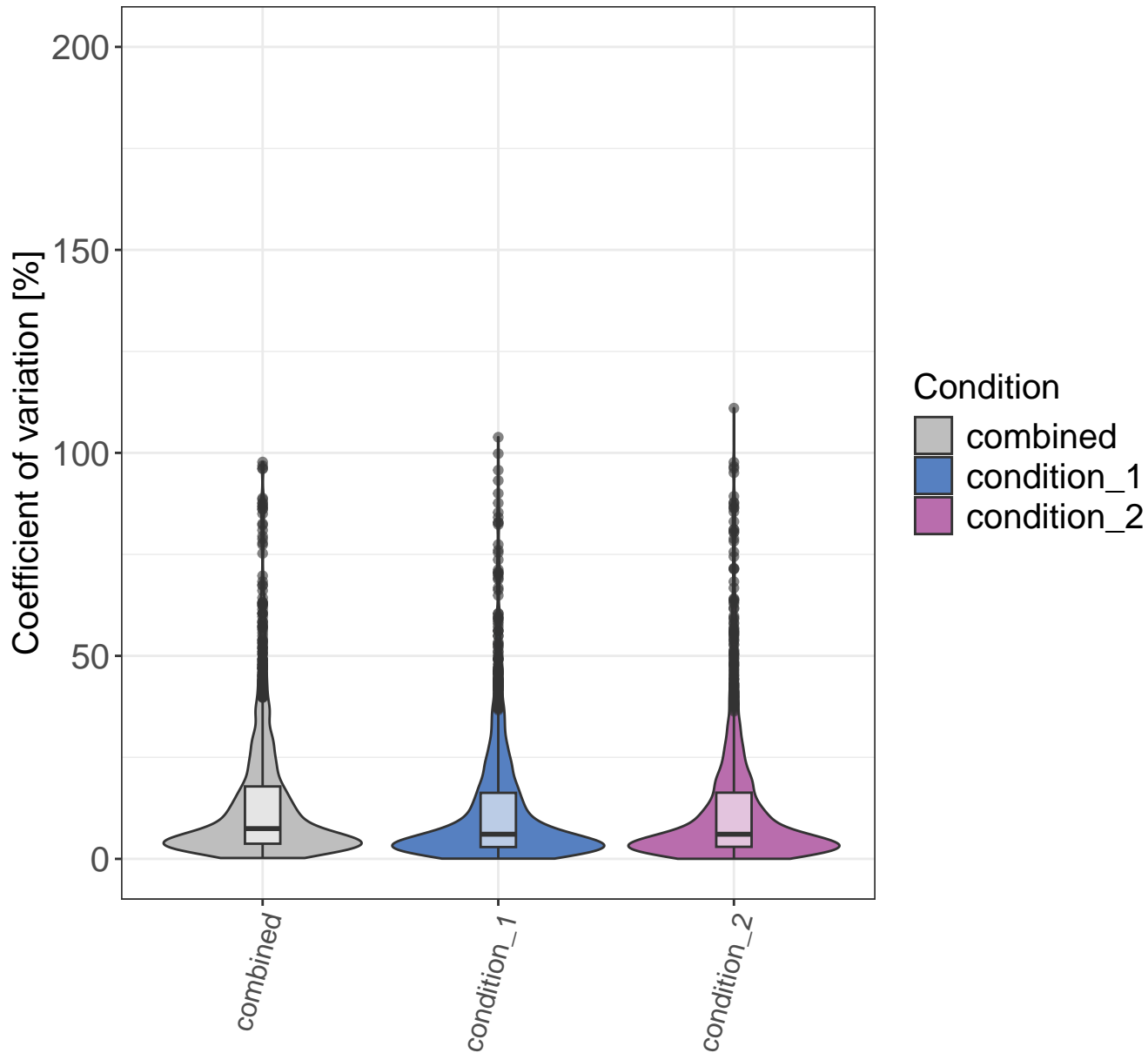


# Coefficients of variation

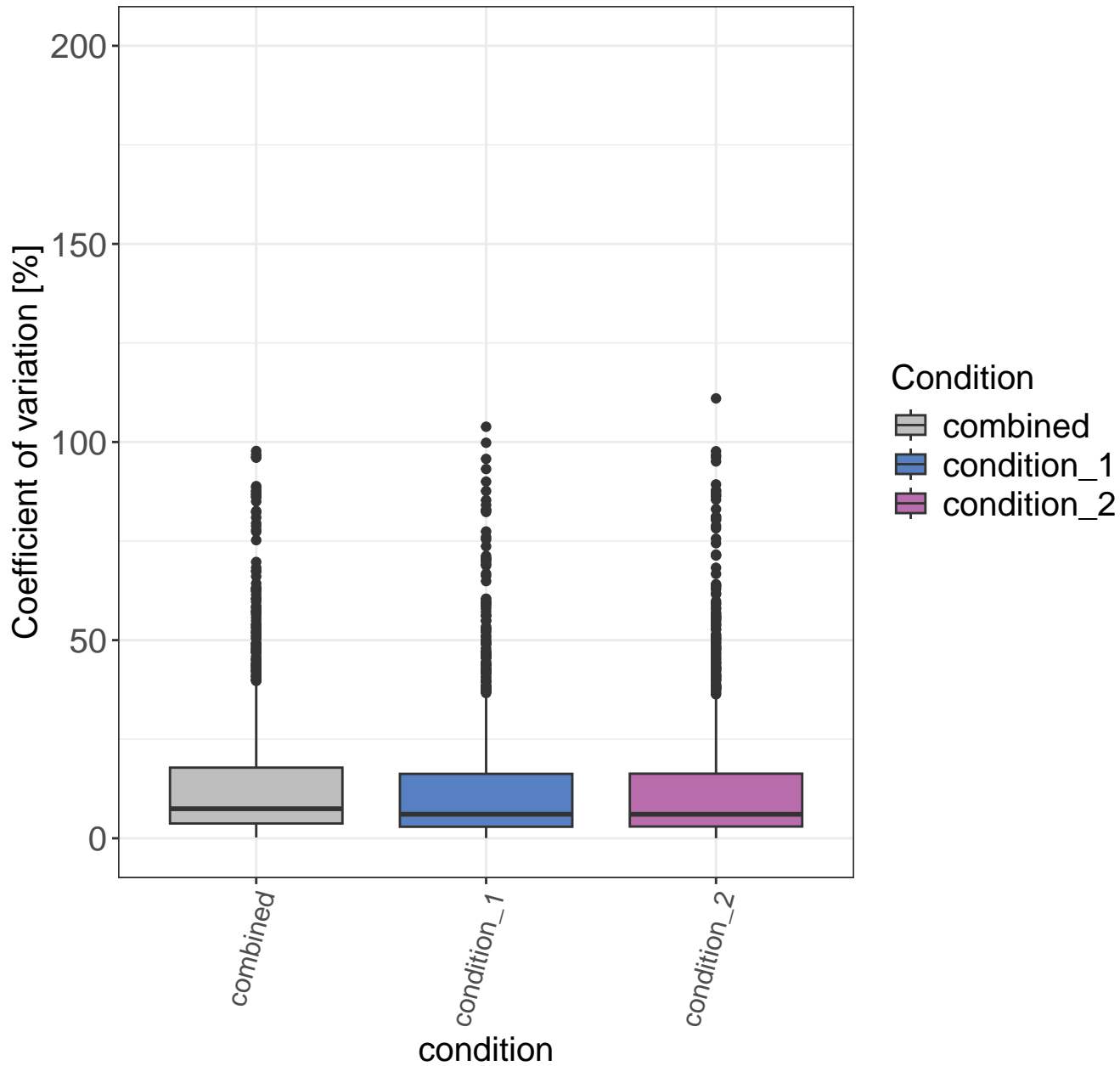




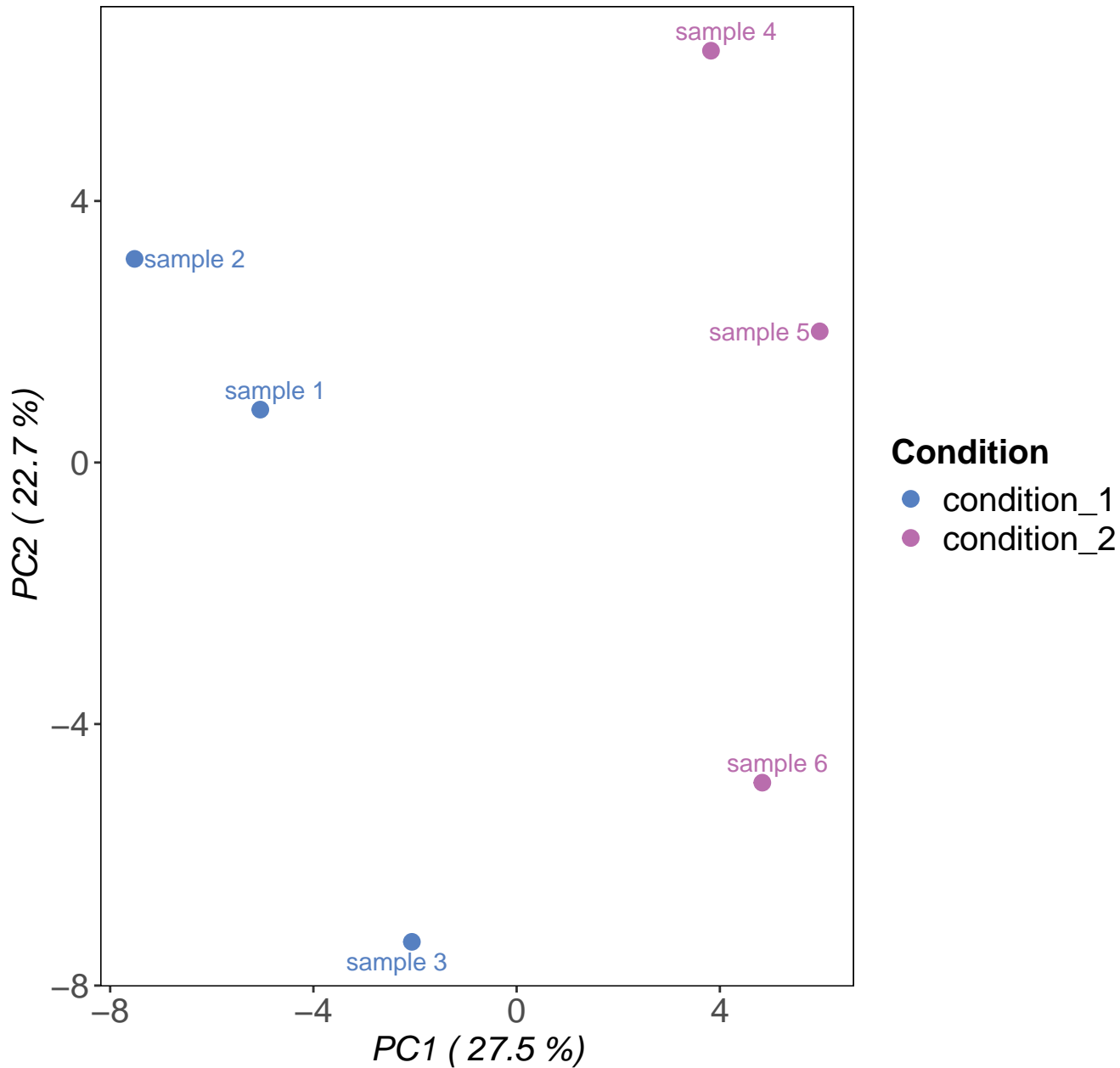
# Coefficients of variation



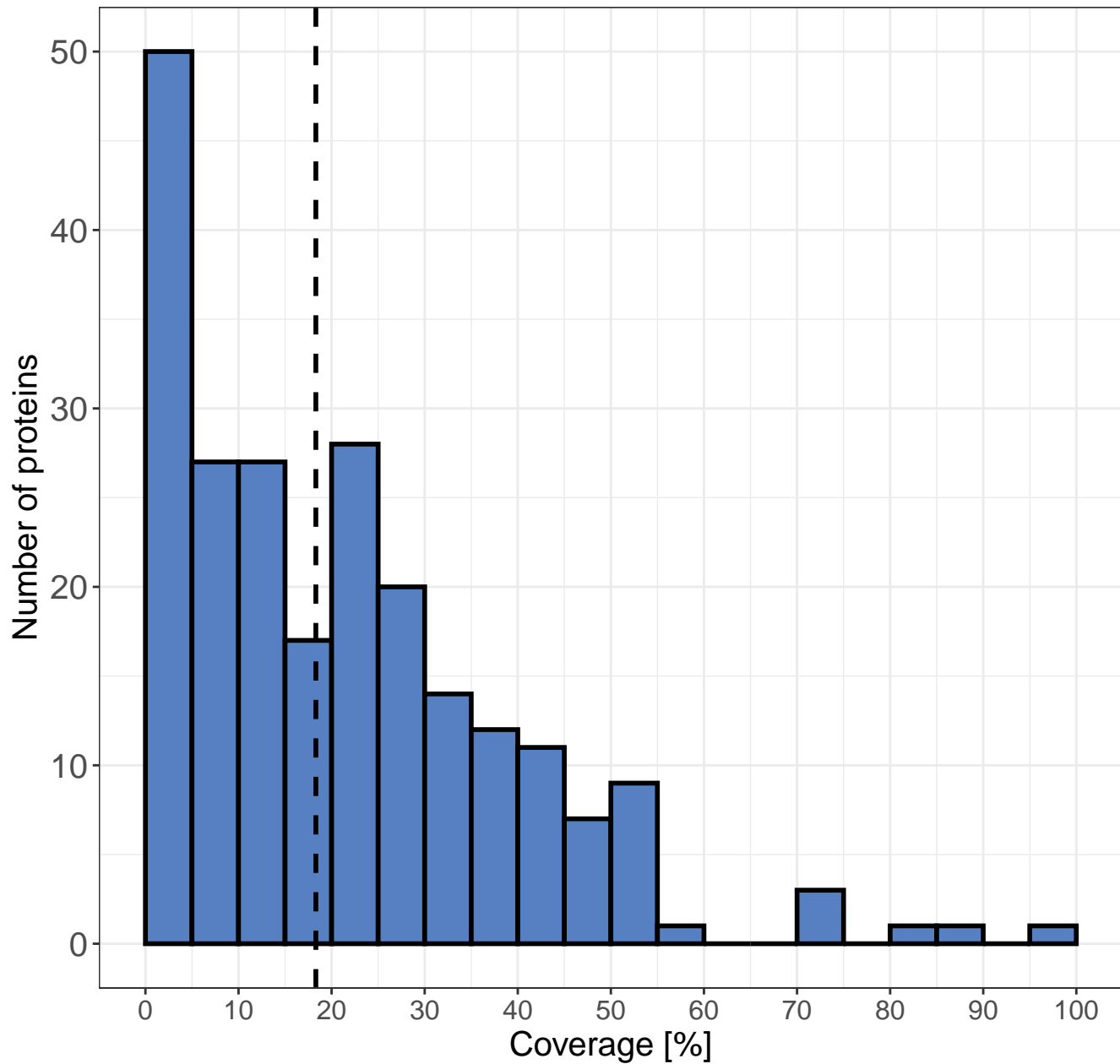
# Coefficients of variation



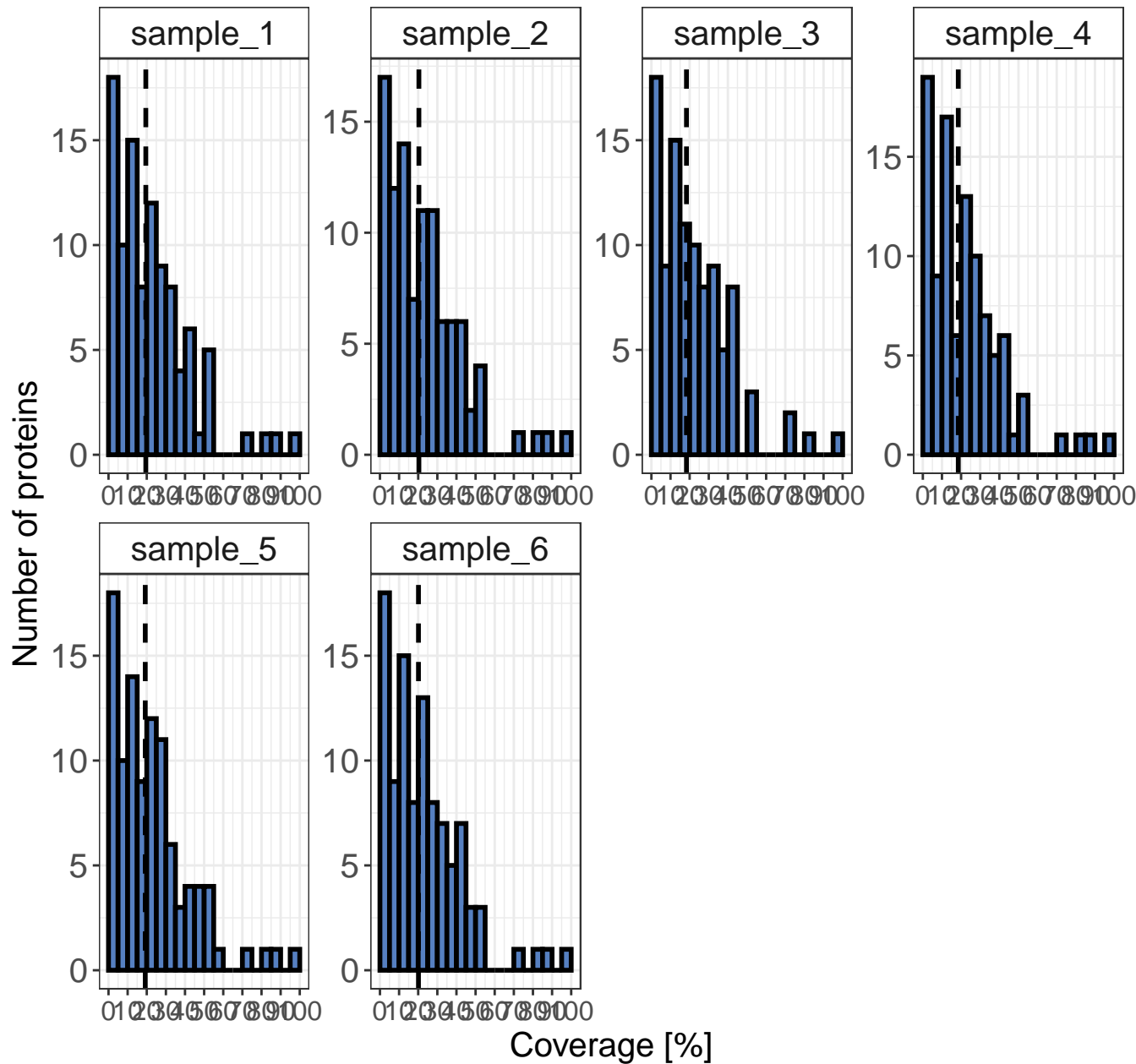
# Principal component analysis



# Protein coverage distribution

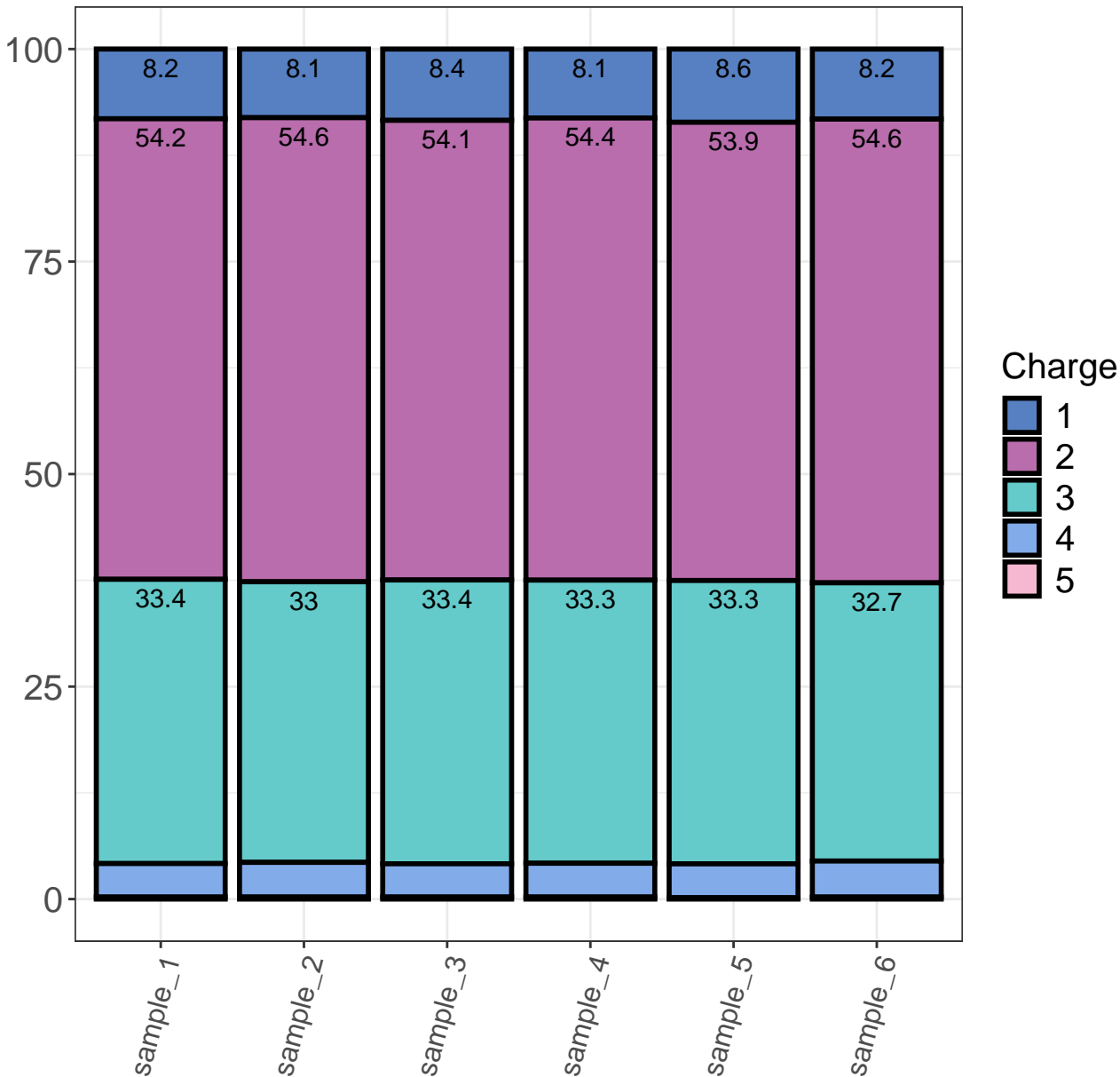


# Protein coverage distribution



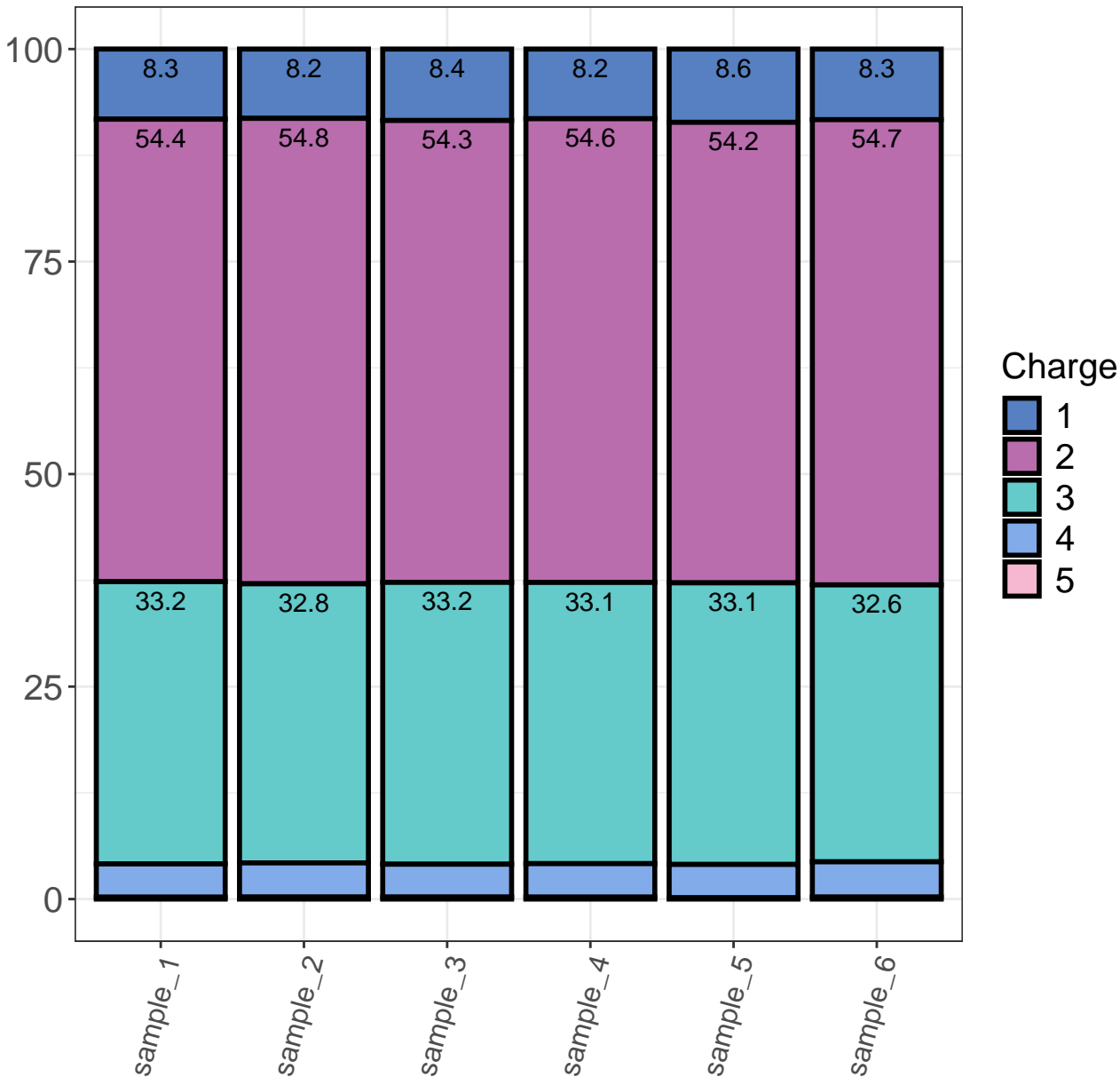
# Charge distribution per .raw file

By percent of total peptide count



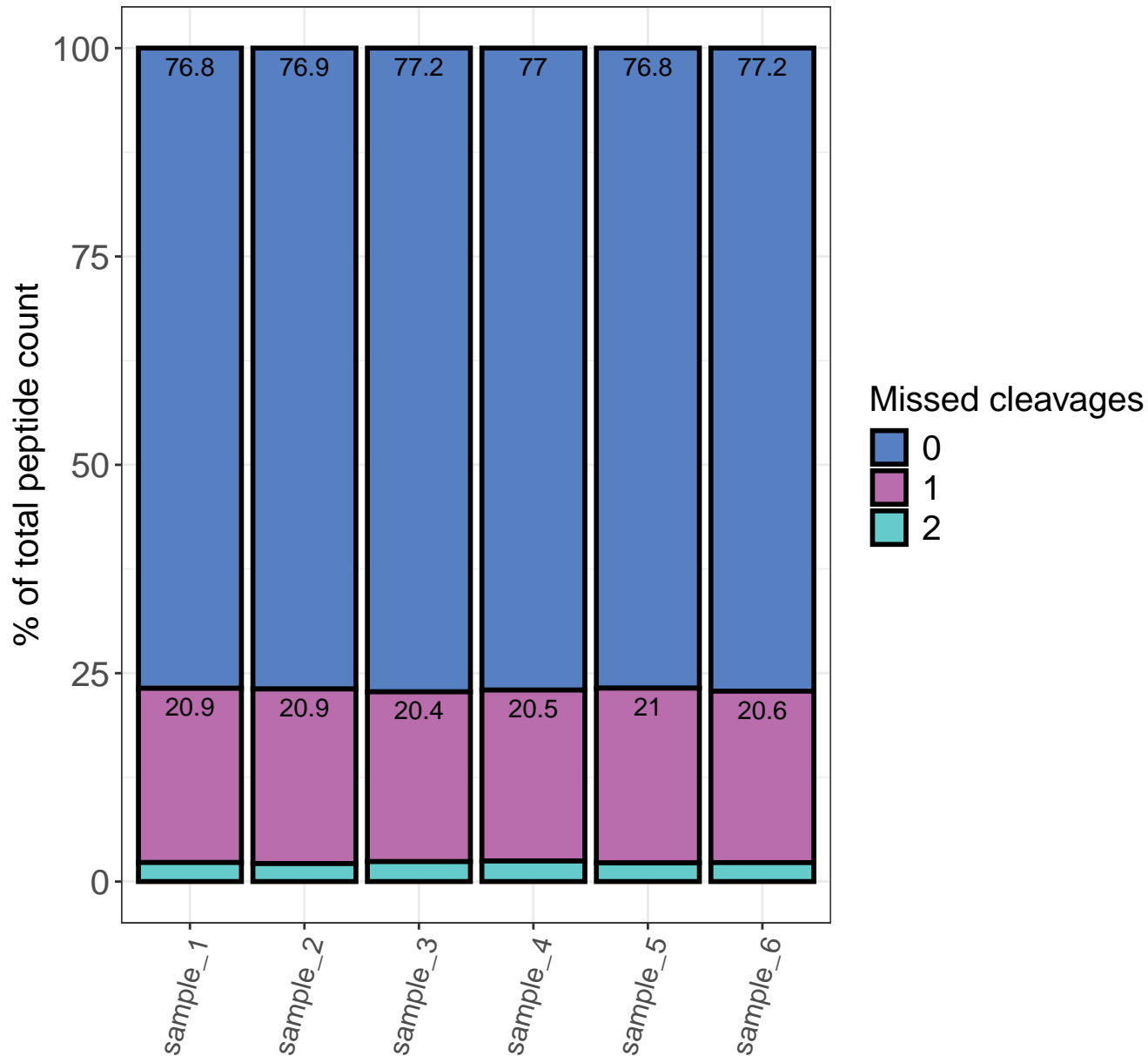
# Charge distribution per .raw file

By percent of total intensity



# Missed cleavages per .raw file

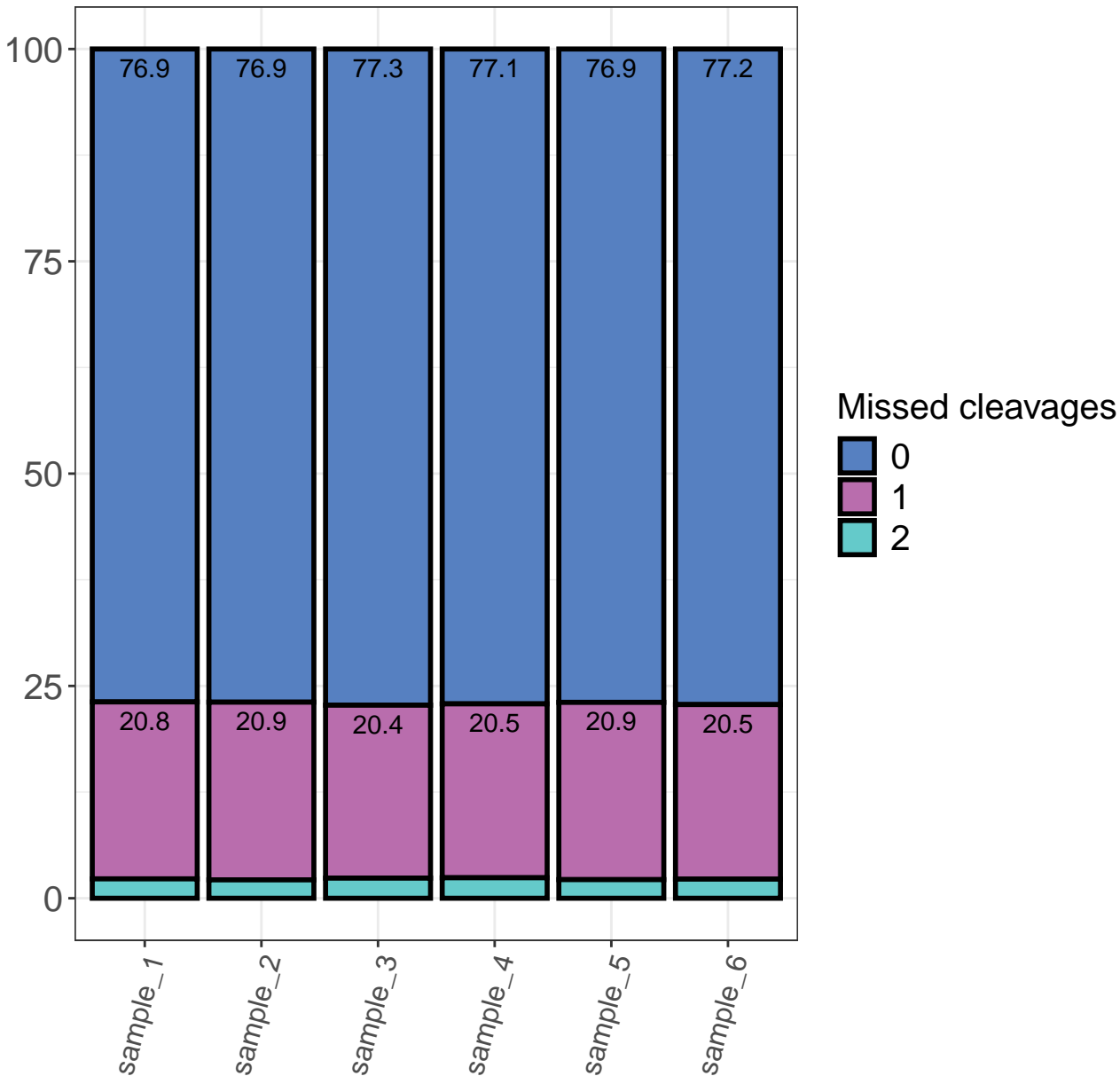
By percent of total peptide count



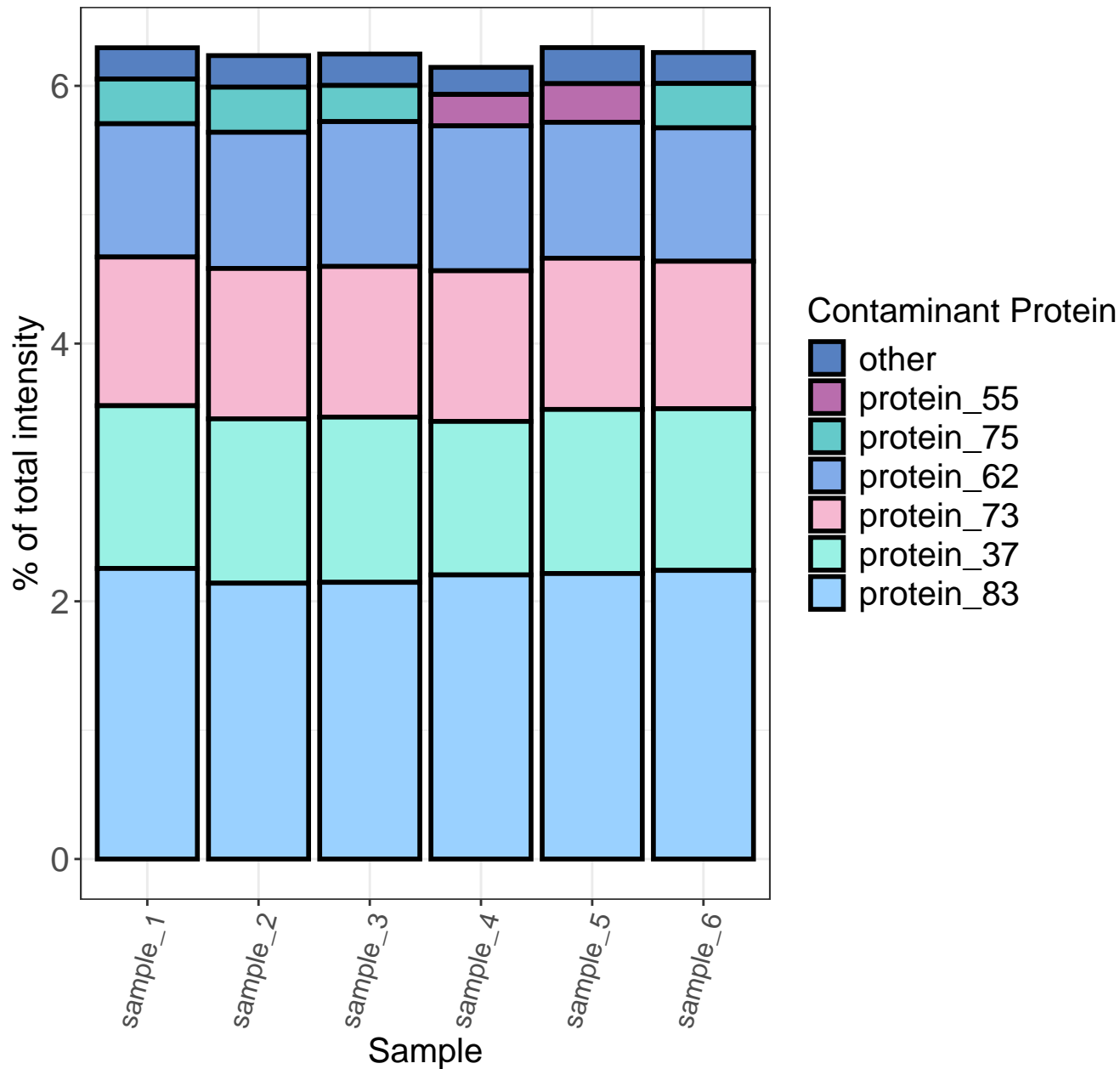


# Missed cleavages per .raw file

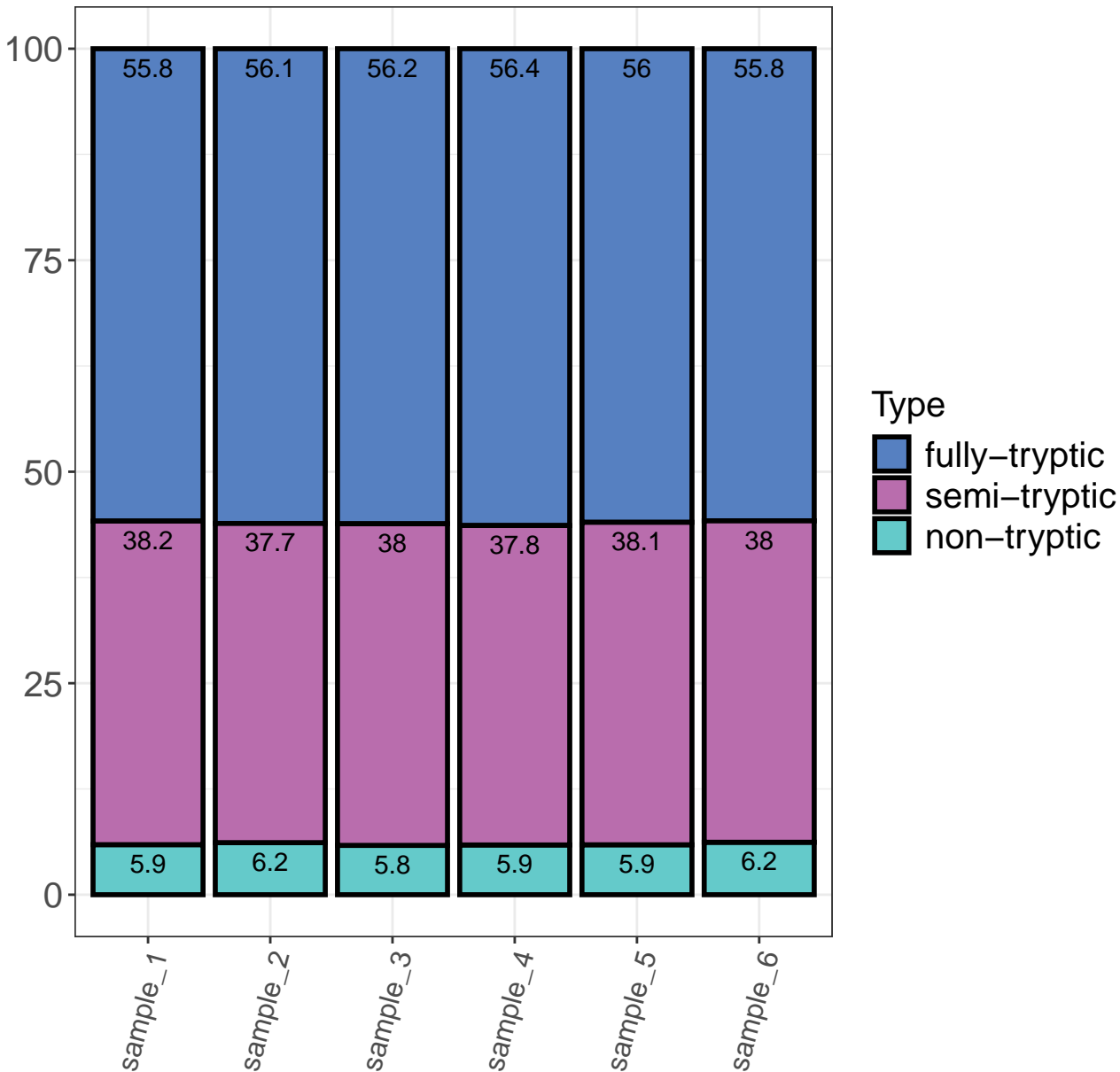
By percent of total intensity



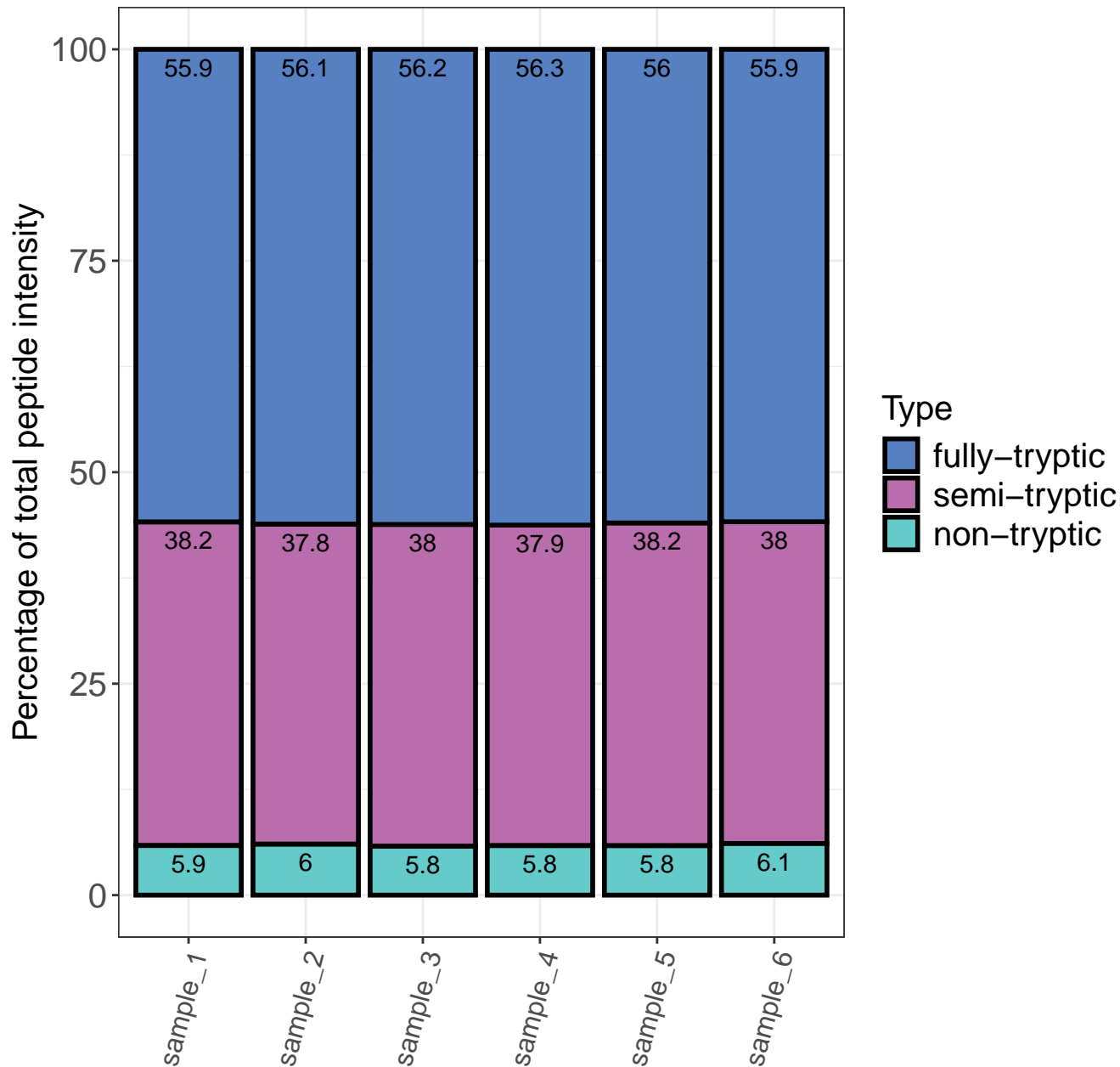
# Contaminants per .raw file



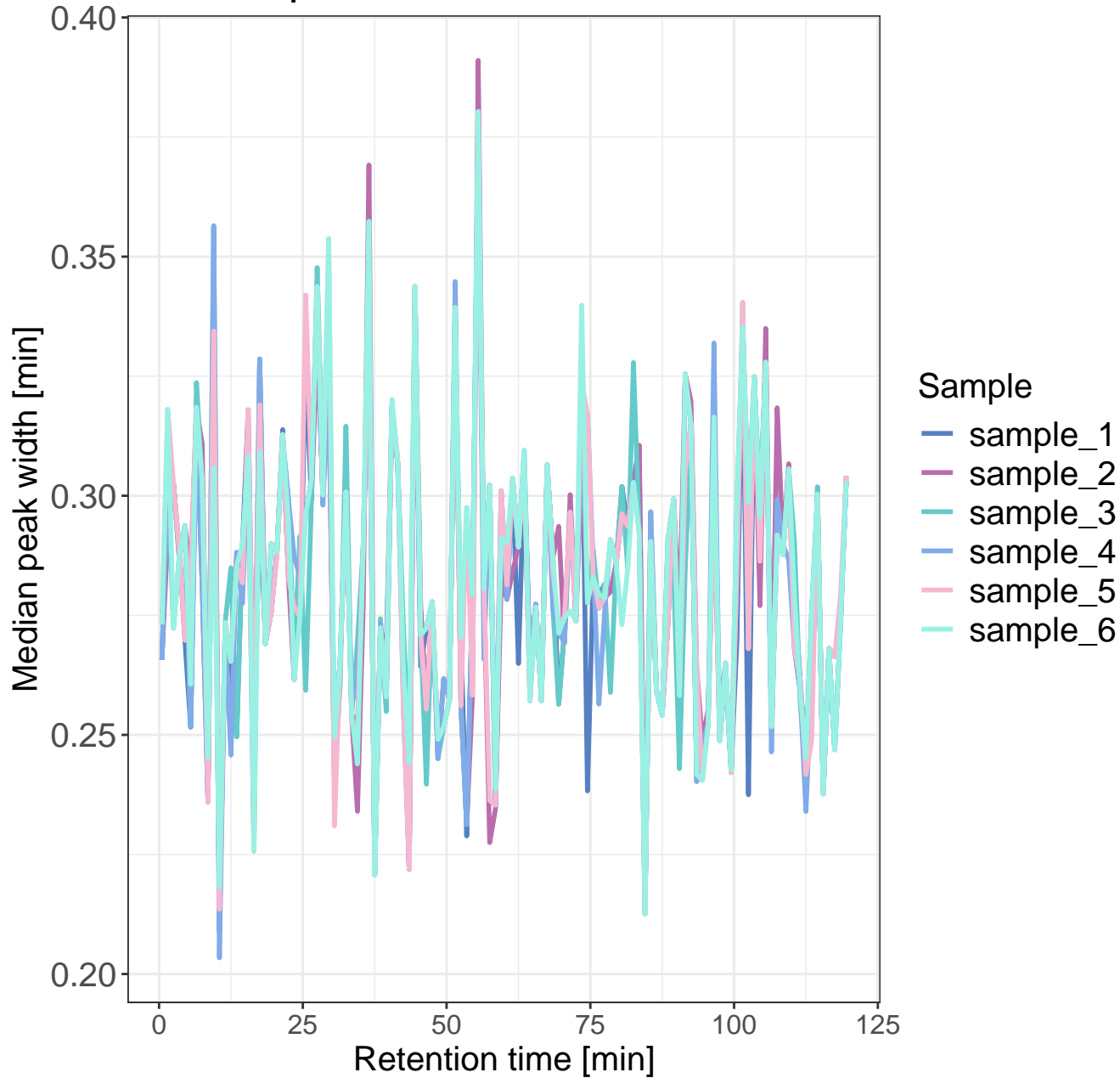
# Peptide types per .raw file



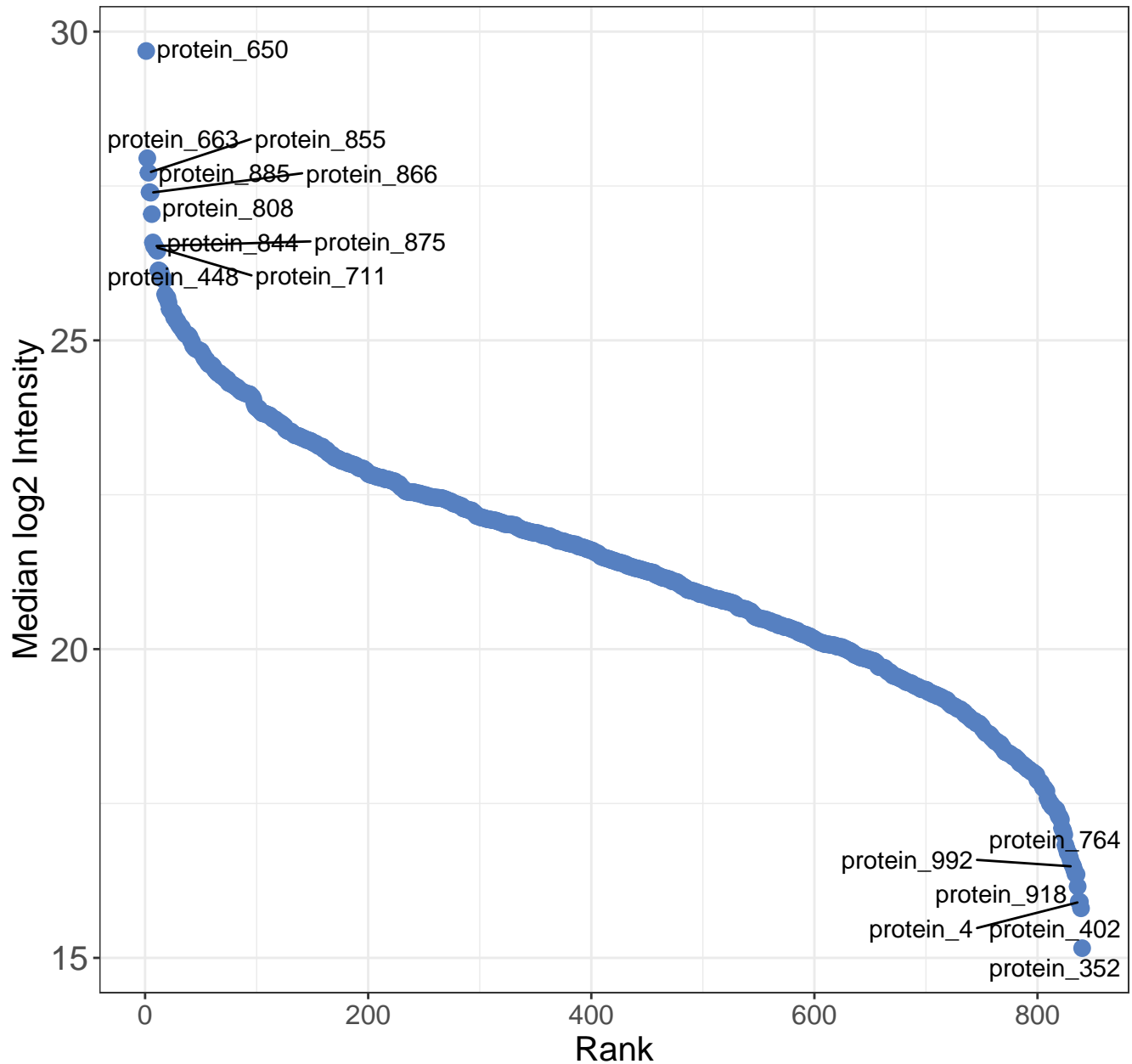
# Peptide type intensity per .raw file



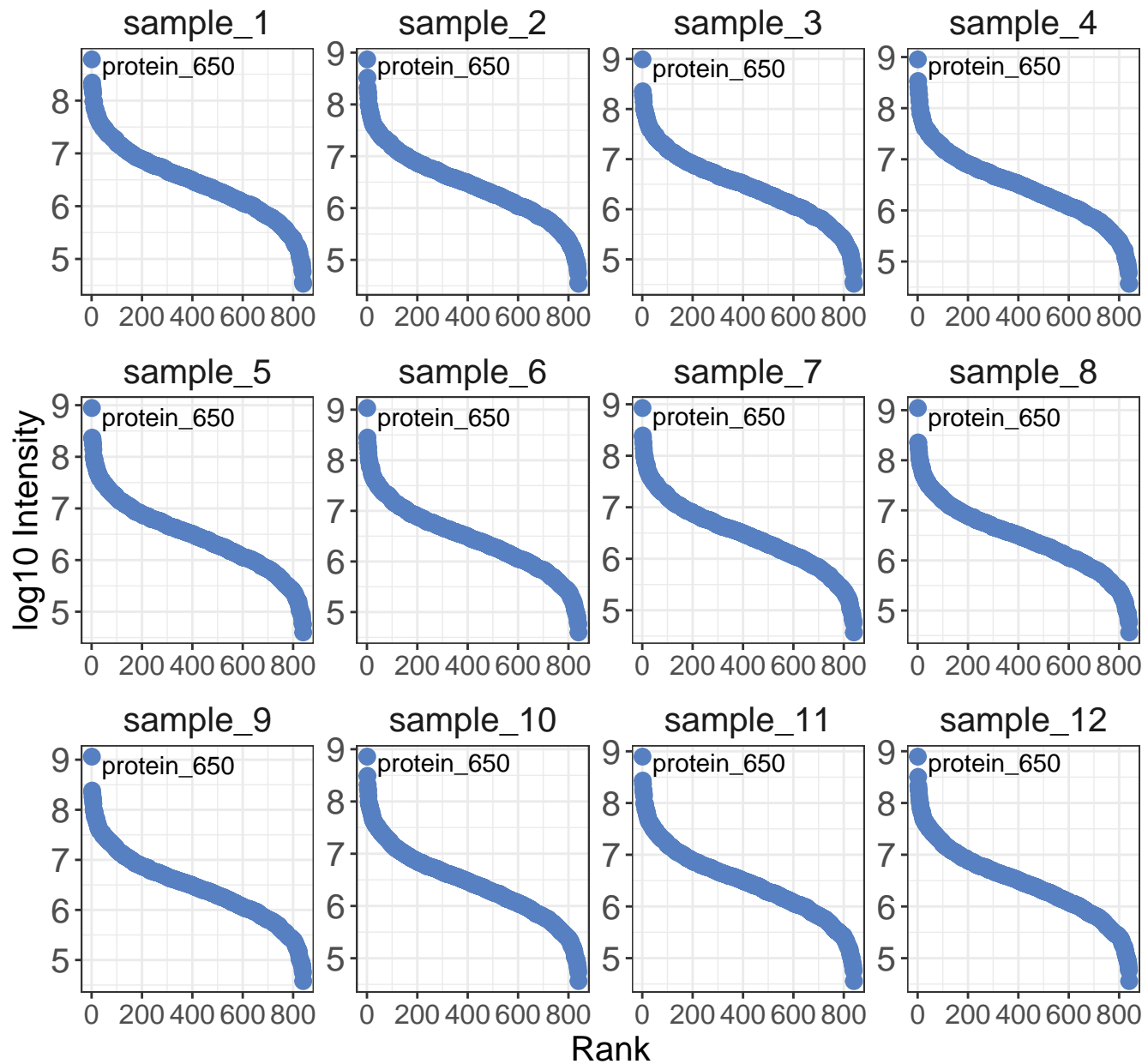
# Median peak width over retention time



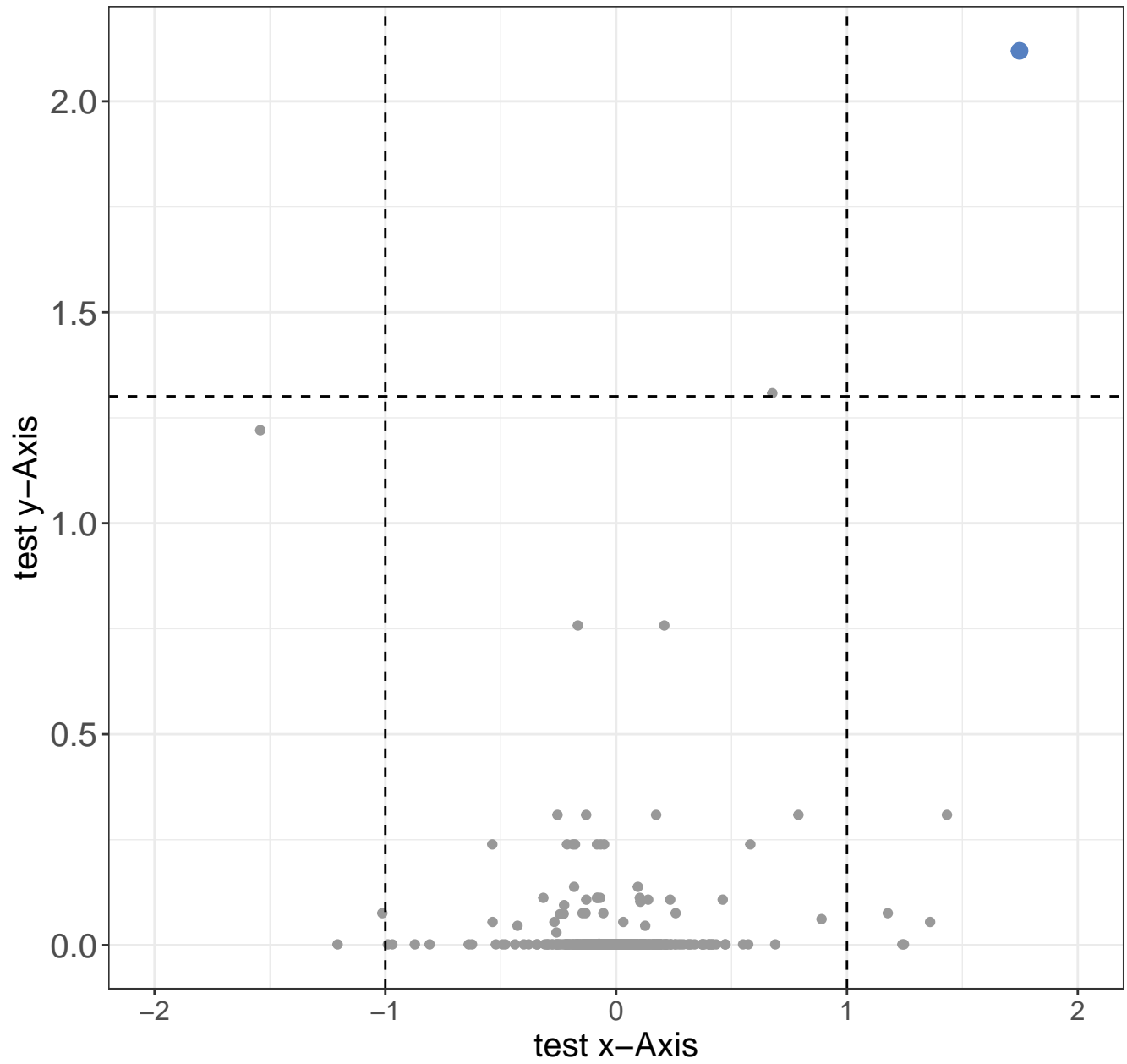
# Ranked Intensities



# Ranked Intensities



# Test tile





# Test tile

