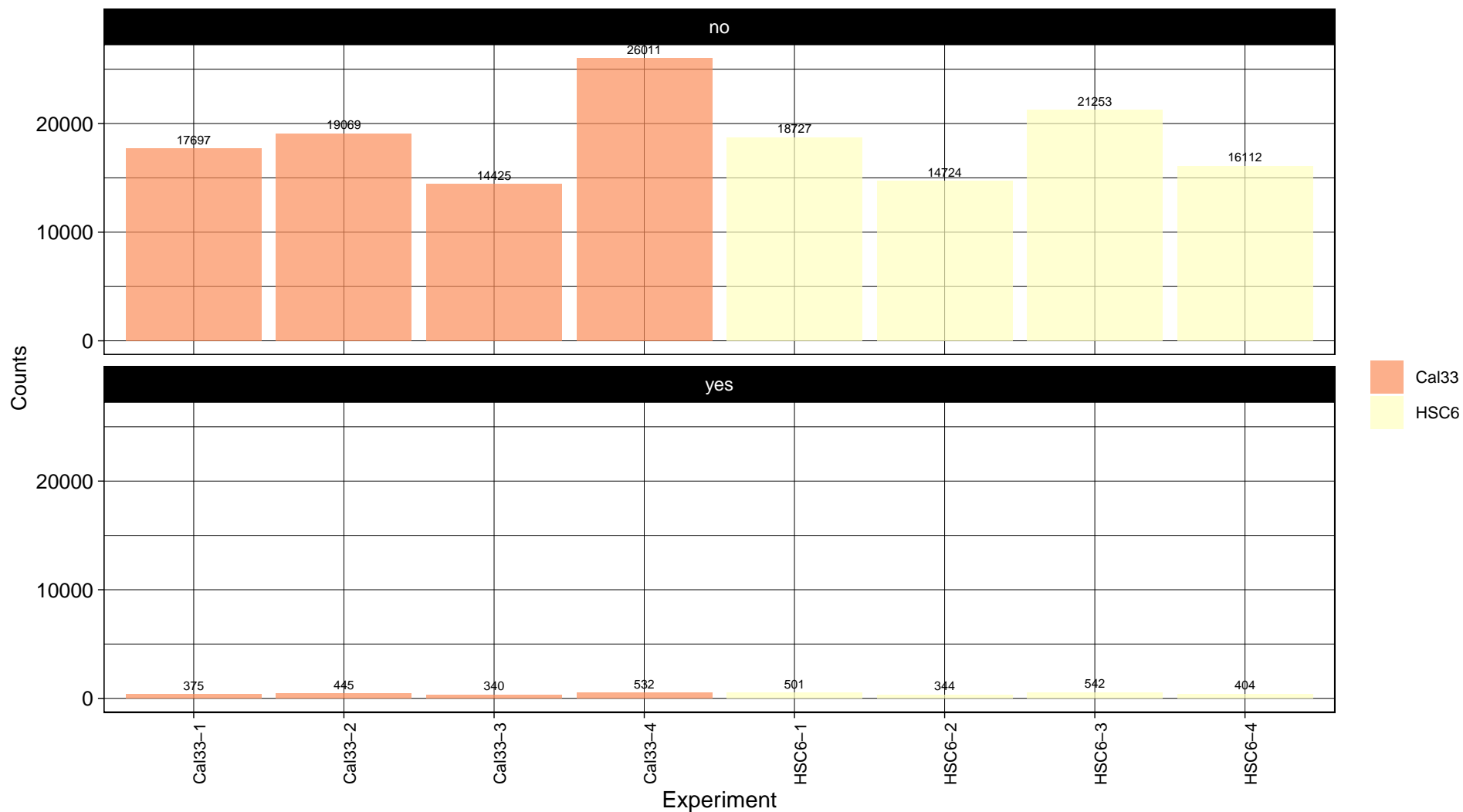


Number of unique Peptide Ions



bottom = Potential contaminants; top = non-contaminants

Mean number of unique Peptide Ions

Error bar = std error of the mean

