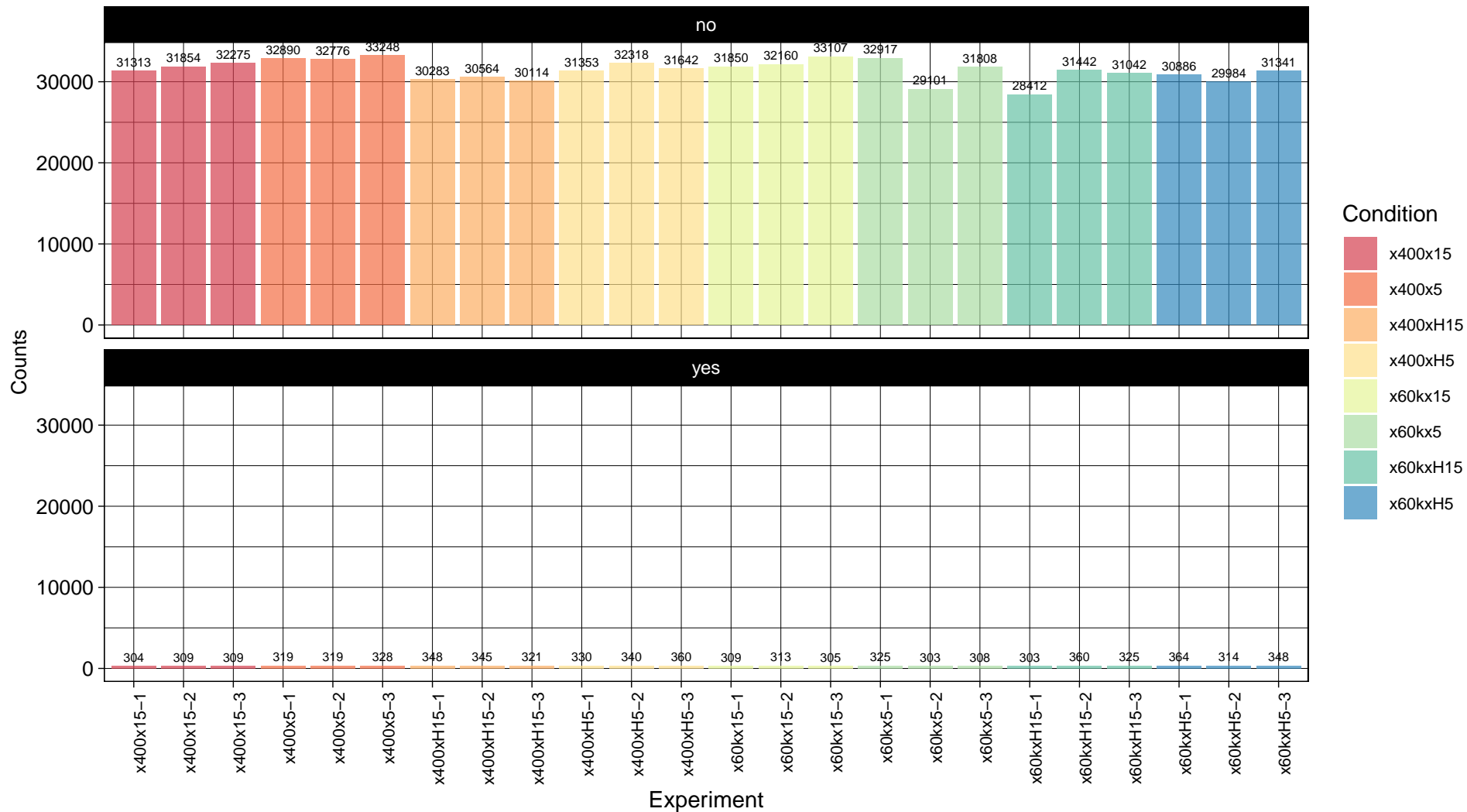


# Number of unique Peptides



bottom = Potential contaminants; top = non-contaminants

Number of unique Peptides

