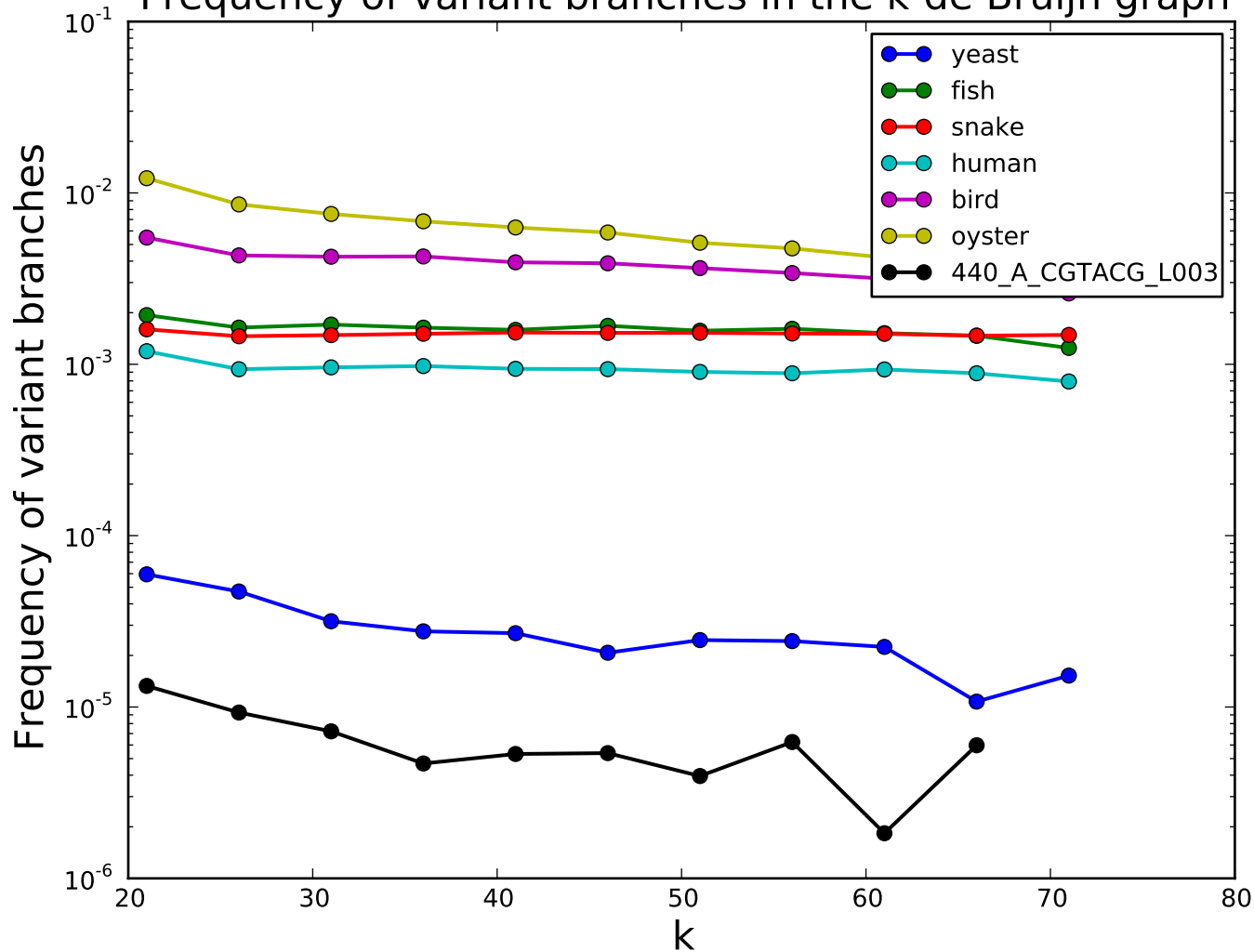
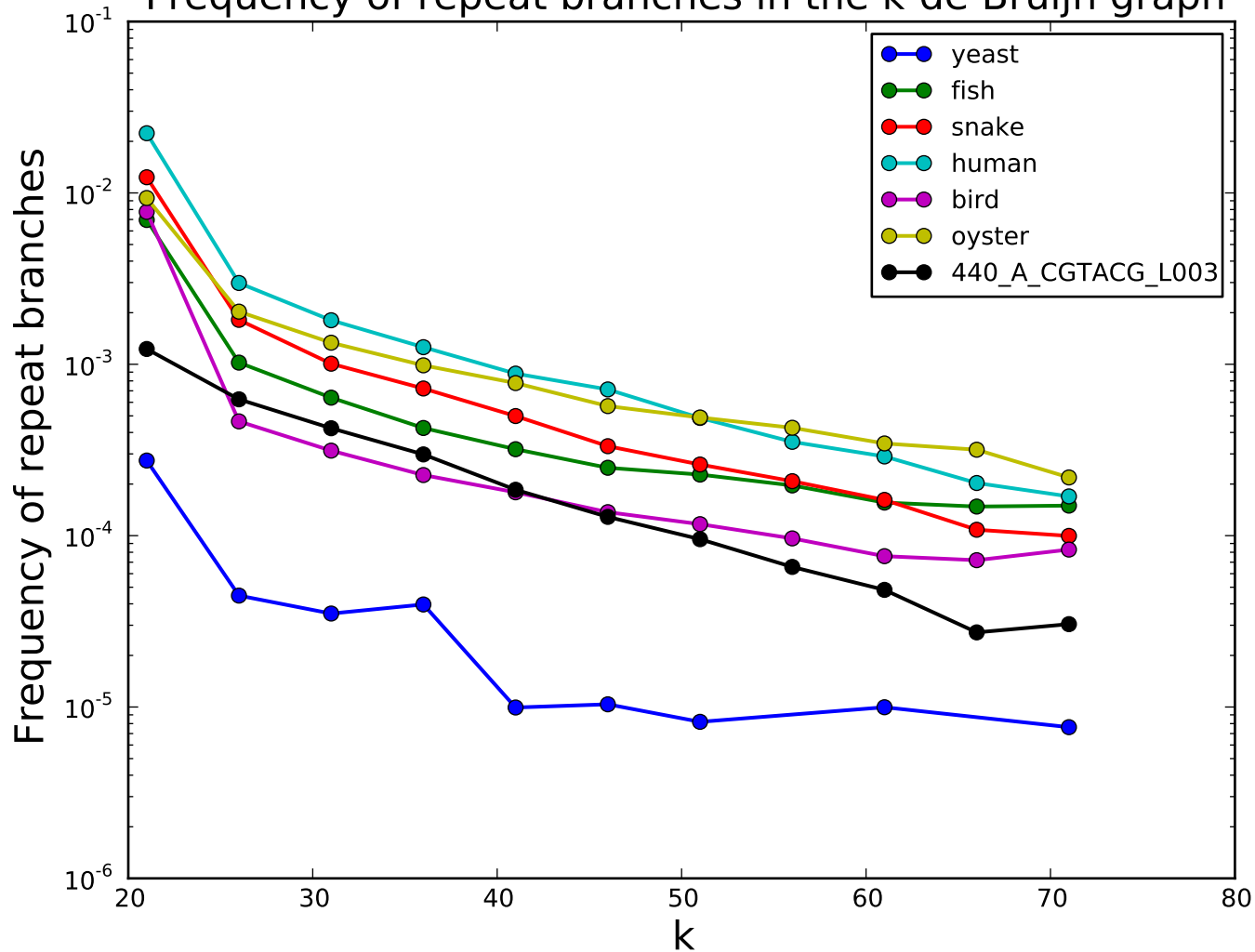


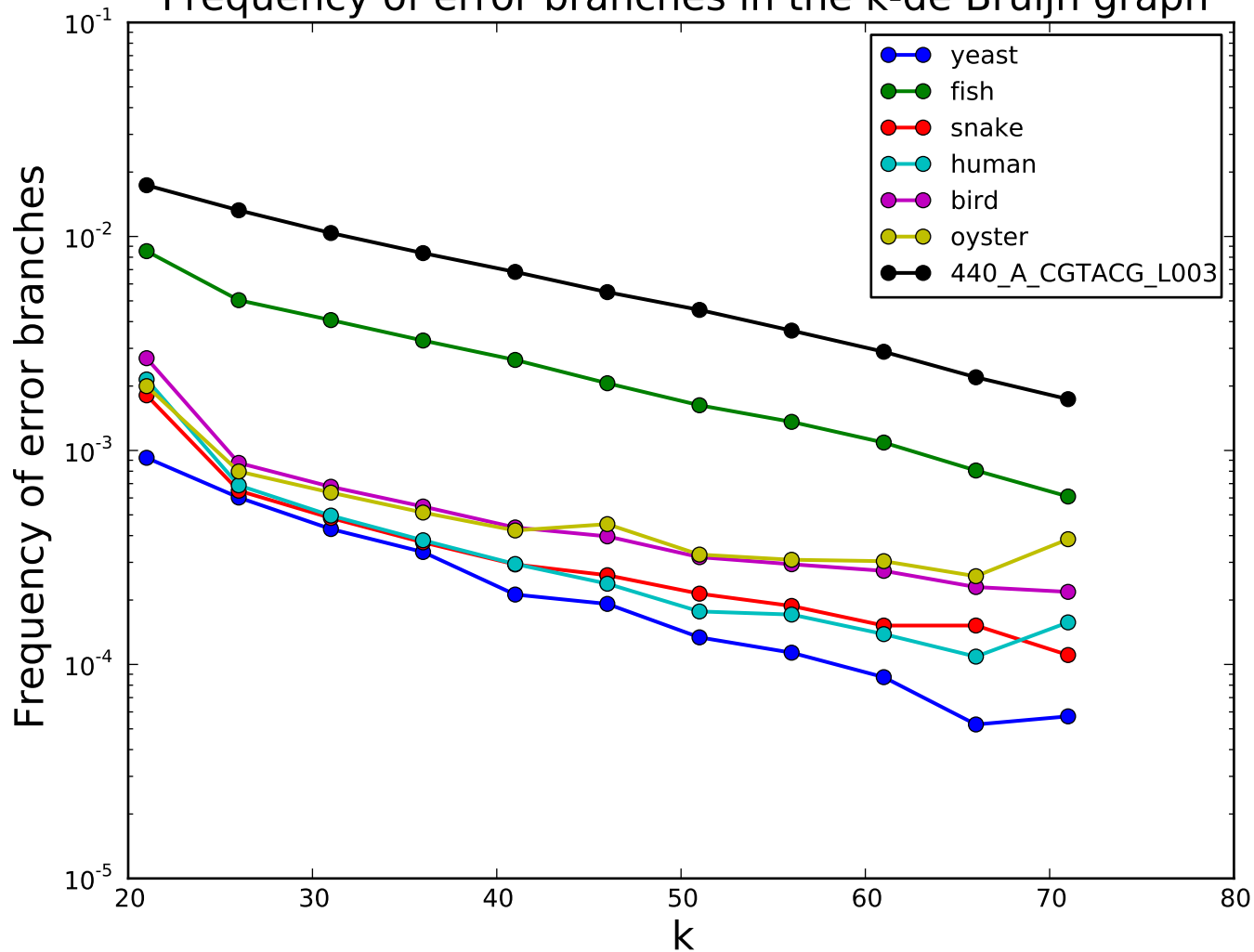
# Frequency of variant branches in the k-de Bruijn graph



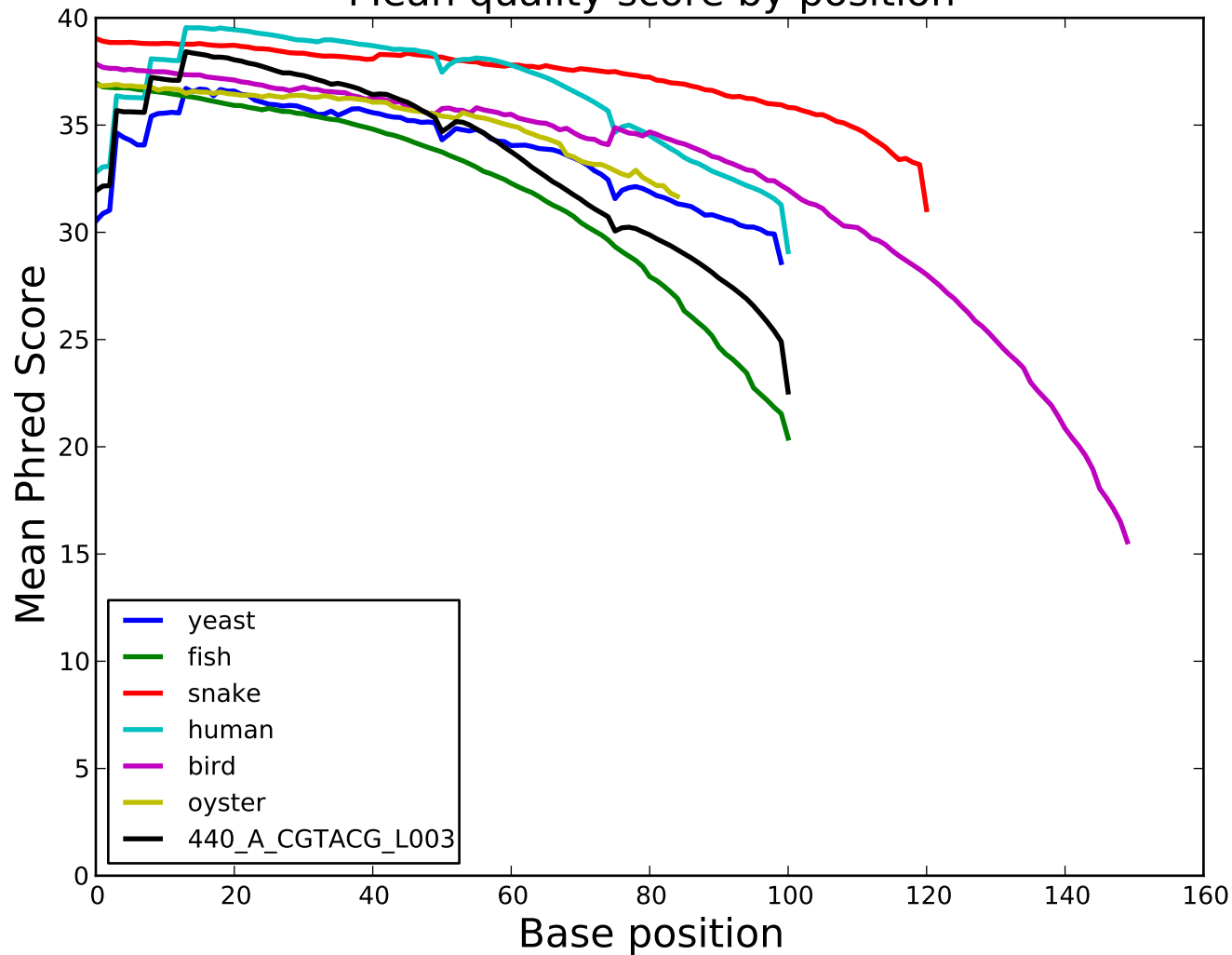
Frequency of repeat branches in the k-de Bruijn graph



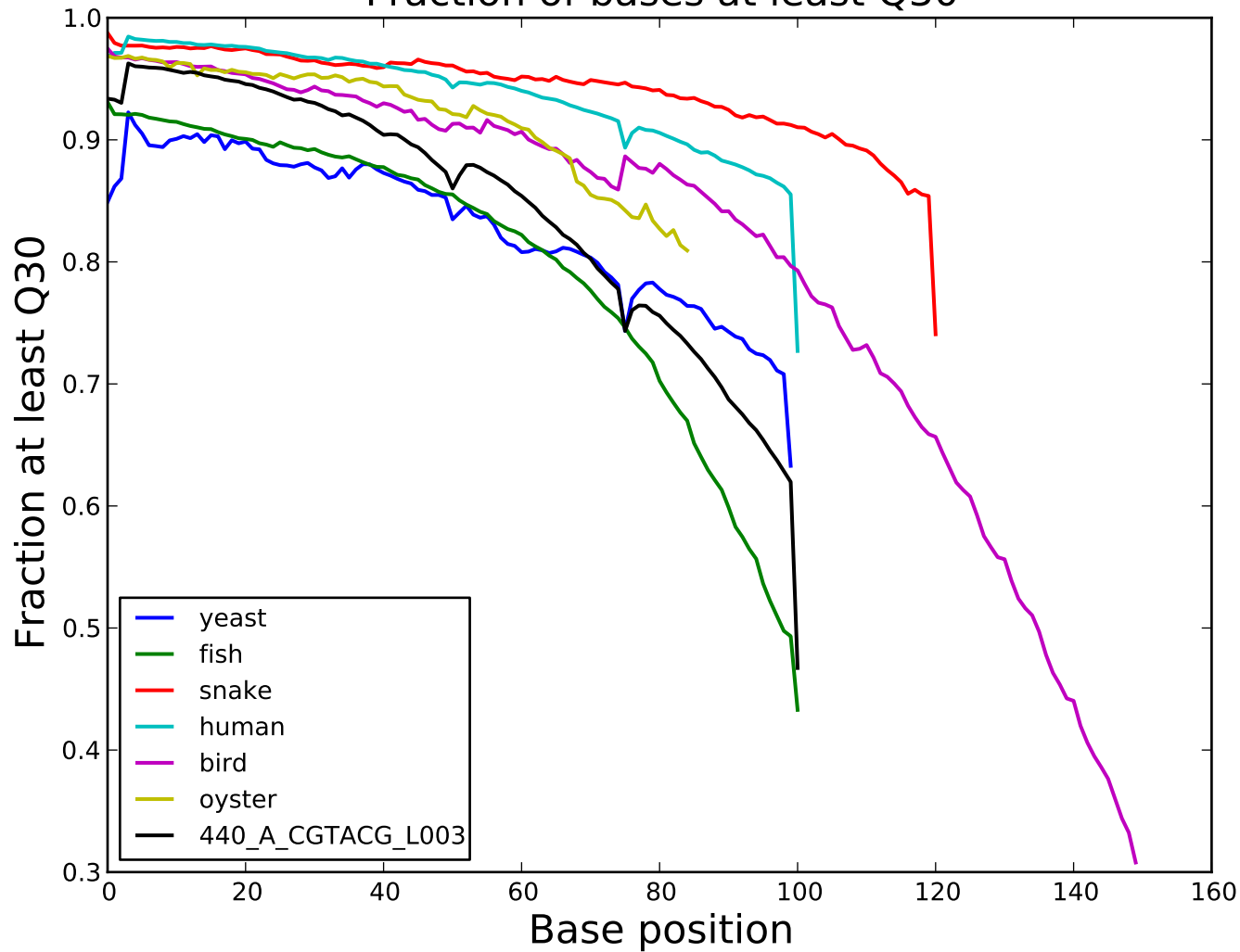
Frequency of error branches in the k-de Bruijn graph



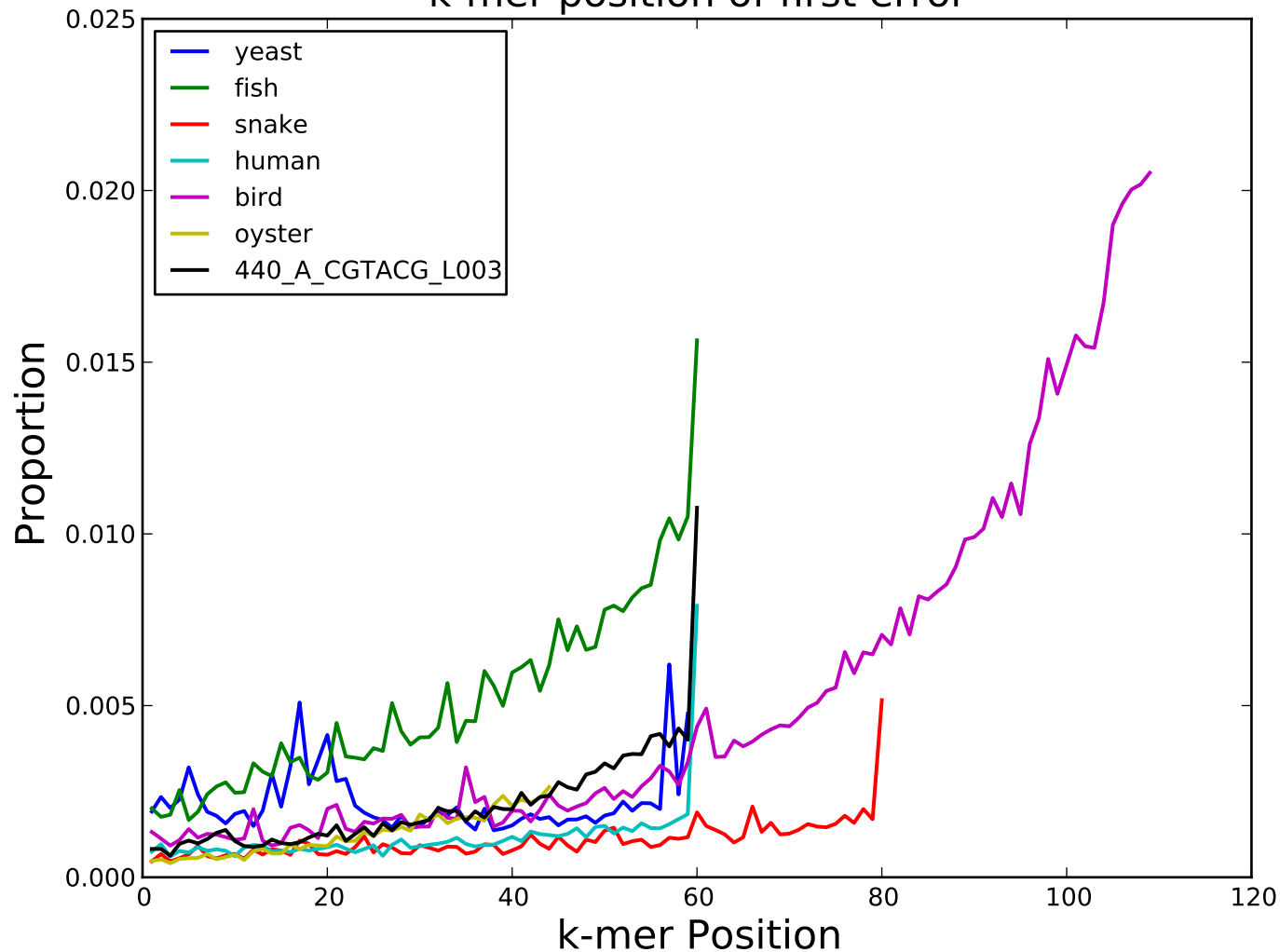
Mean quality score by position



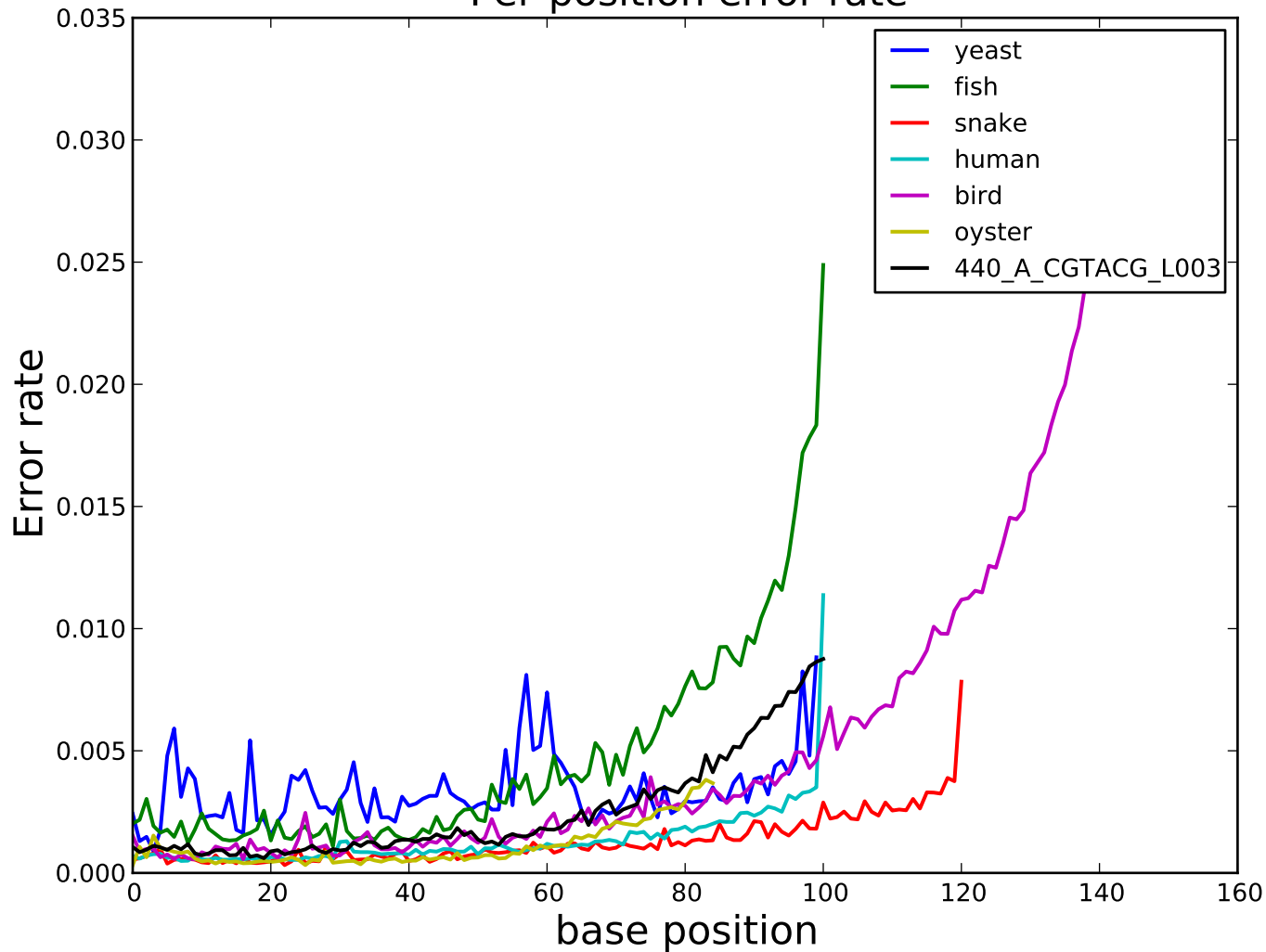
Fraction of bases at least Q30



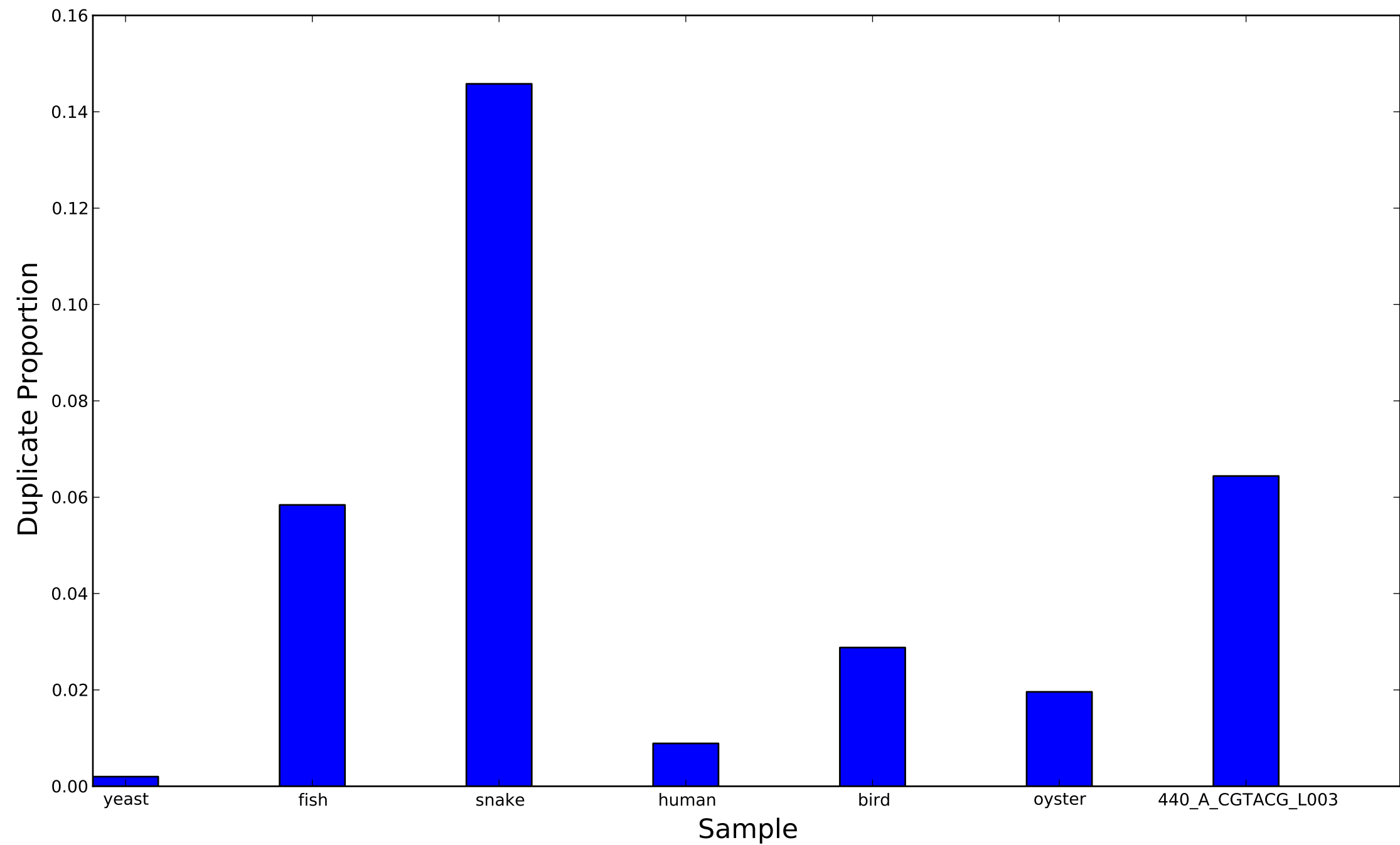
k-mer position of first error



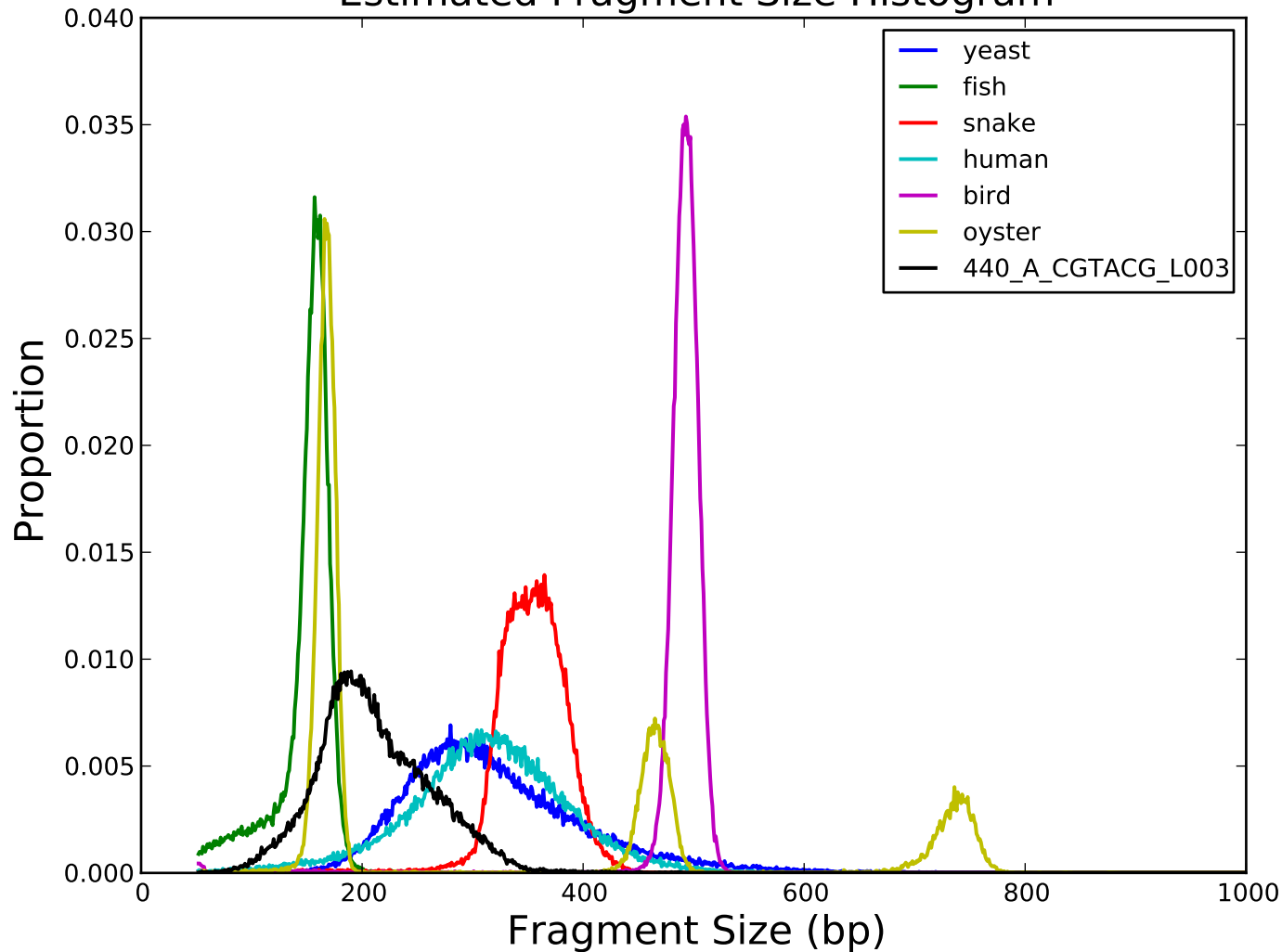
Per-position error rate



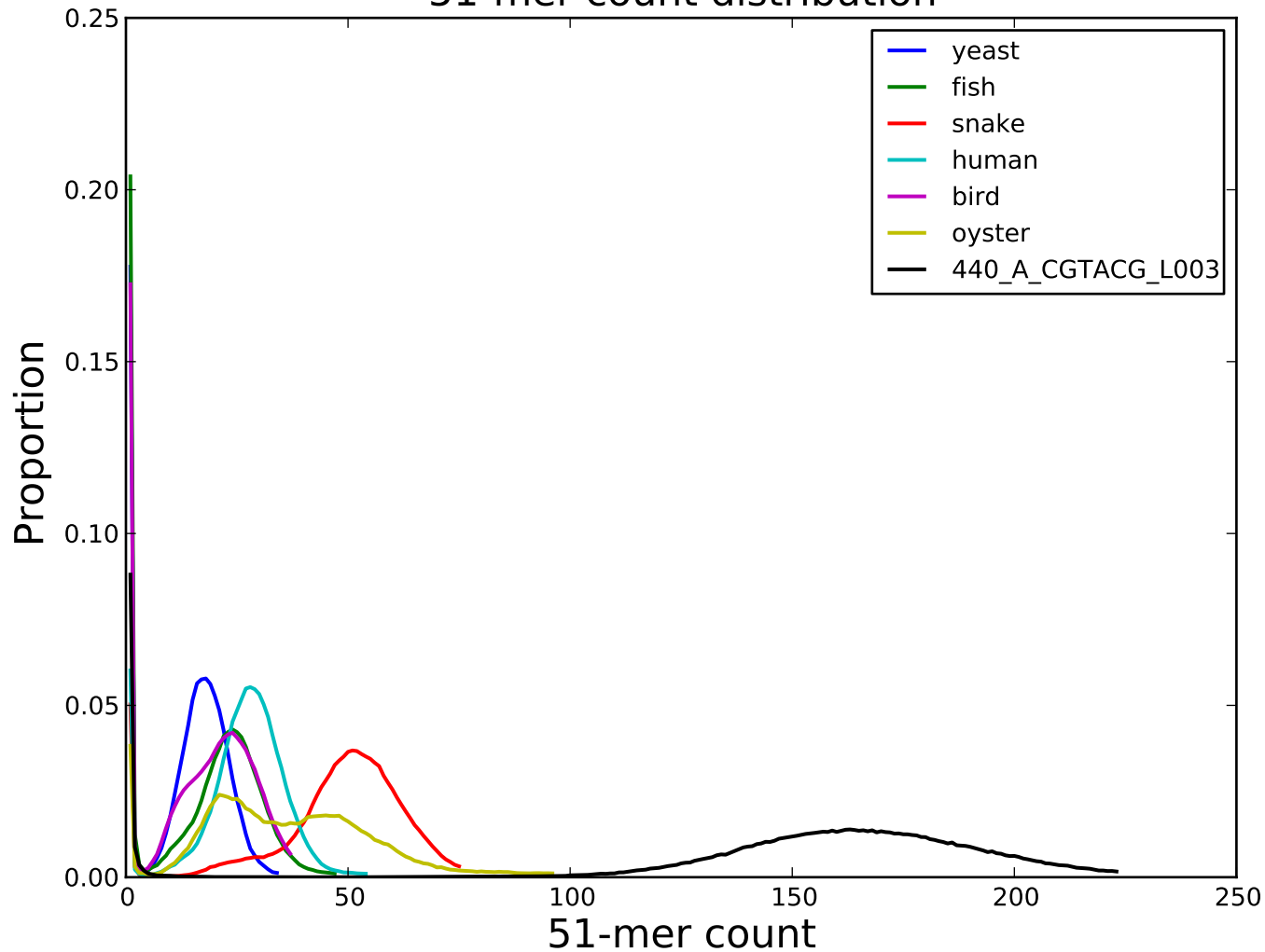




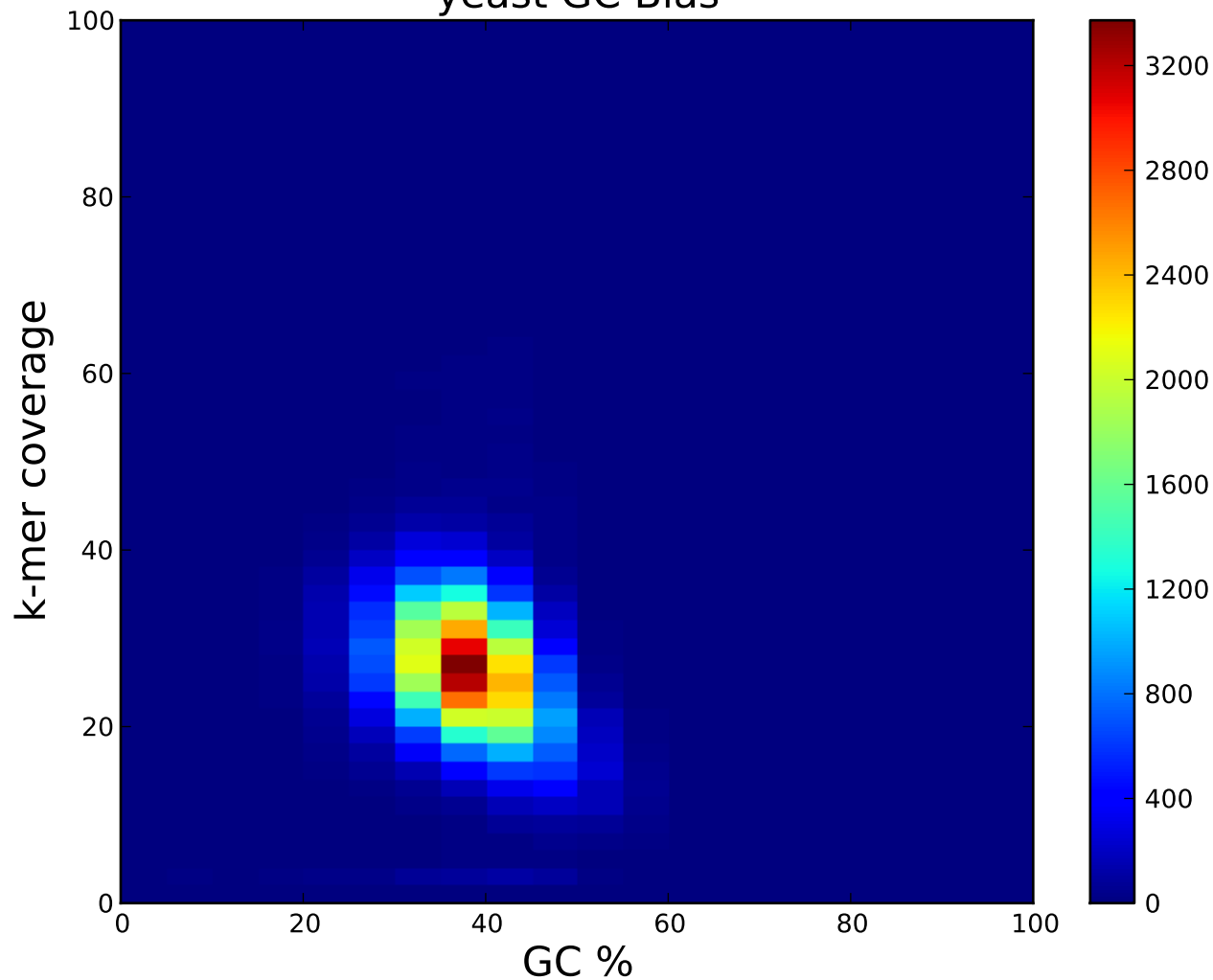
# Estimated Fragment Size Histogram



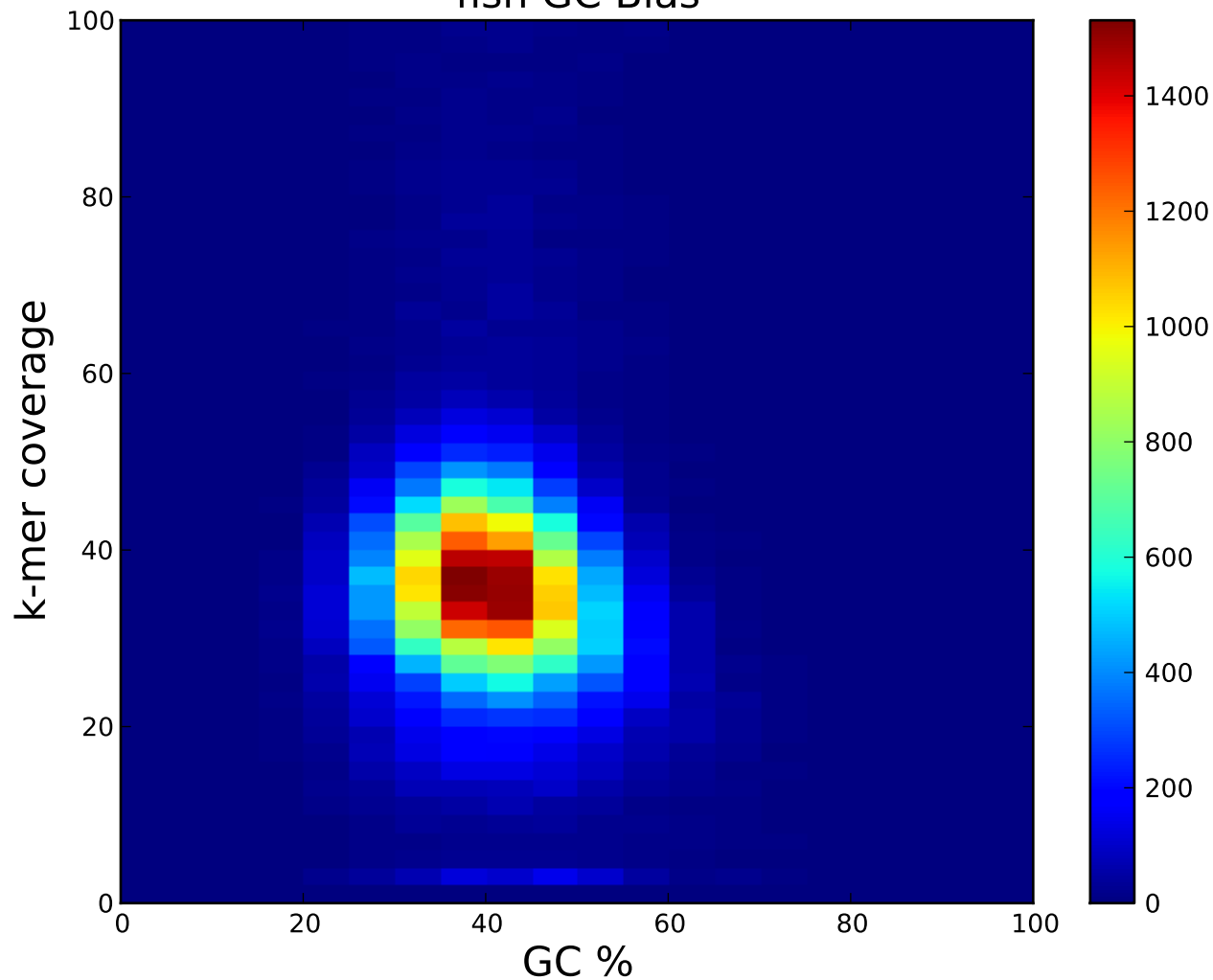
51-mer count distribution



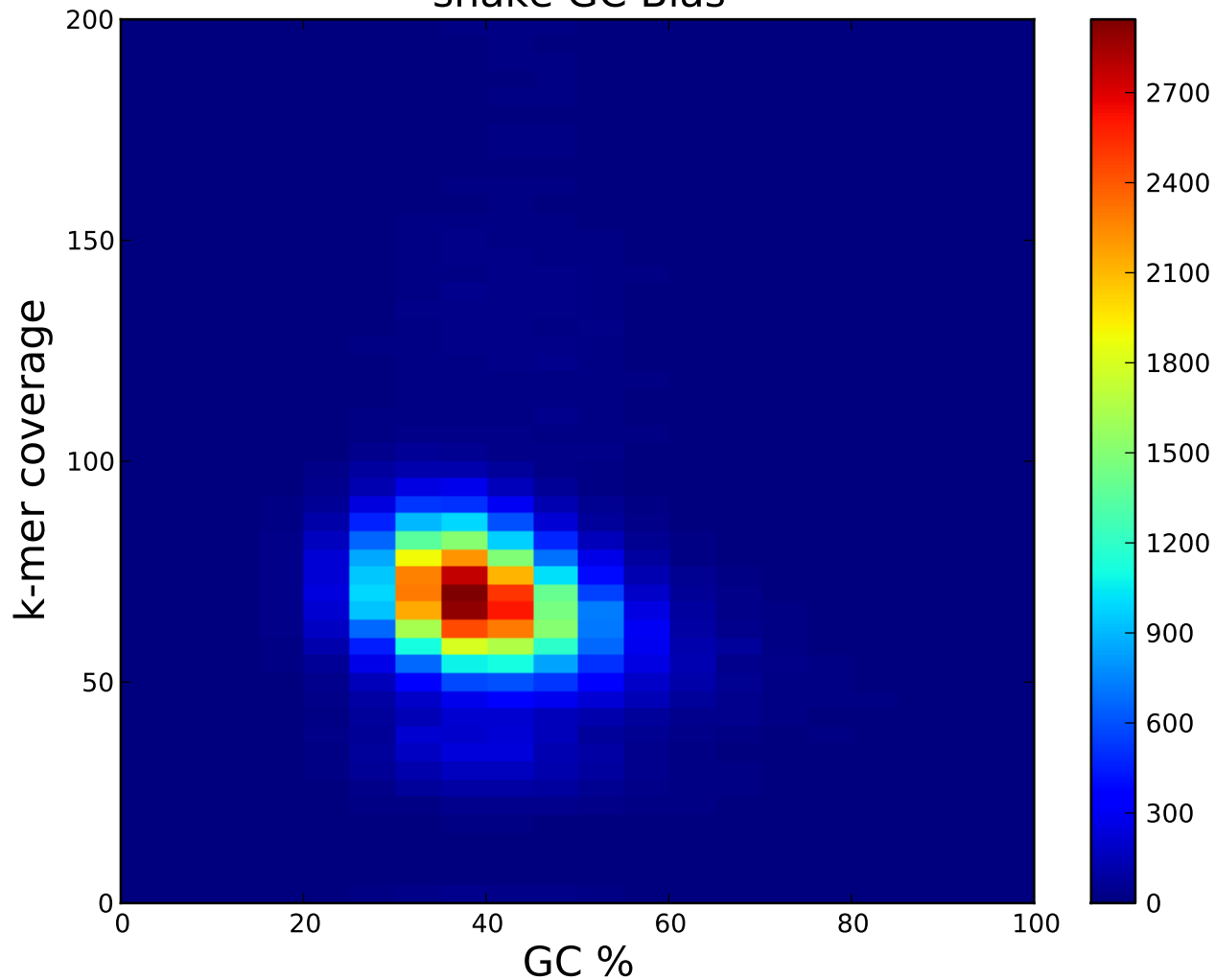
# yeast GC Bias



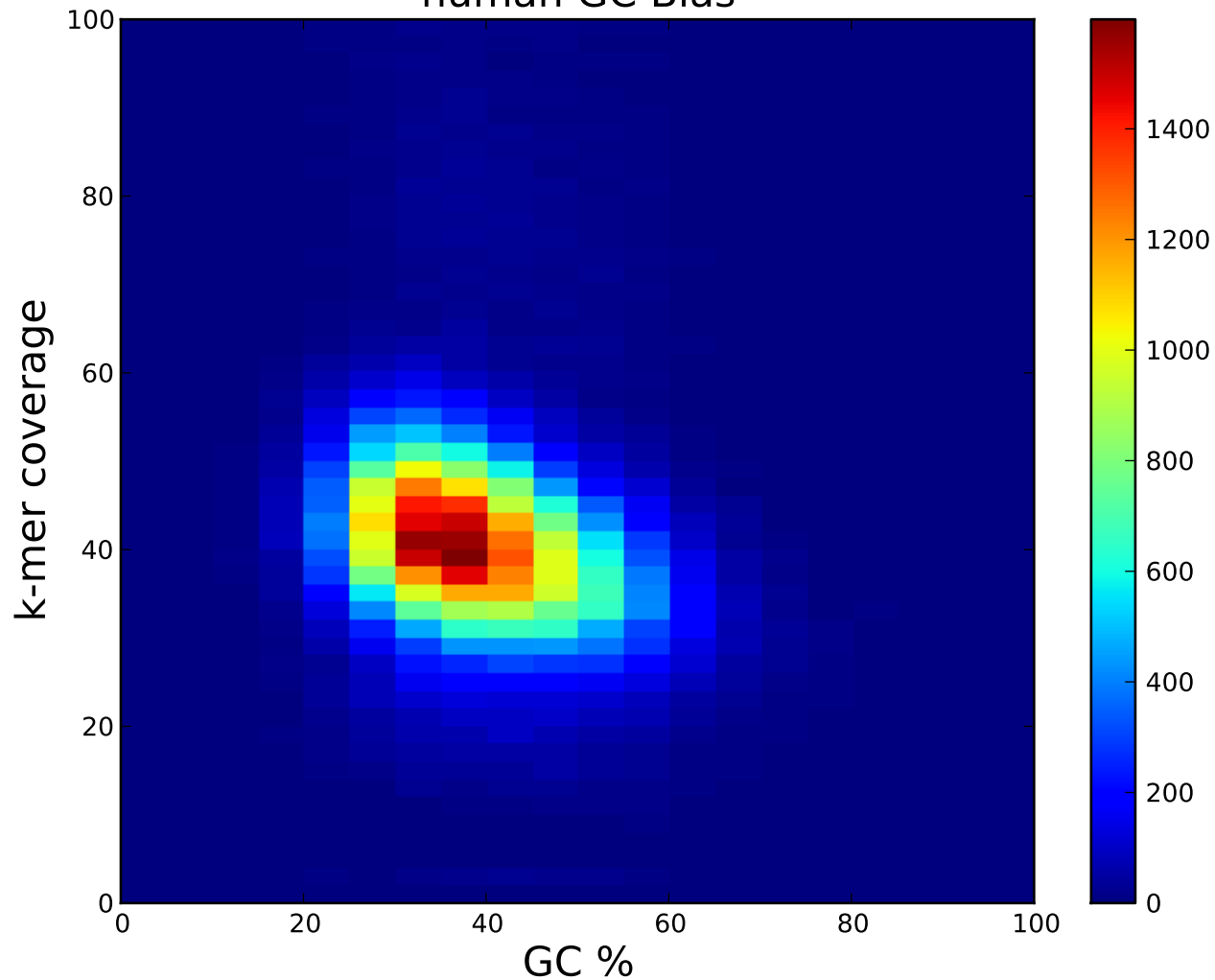
# fish GC Bias



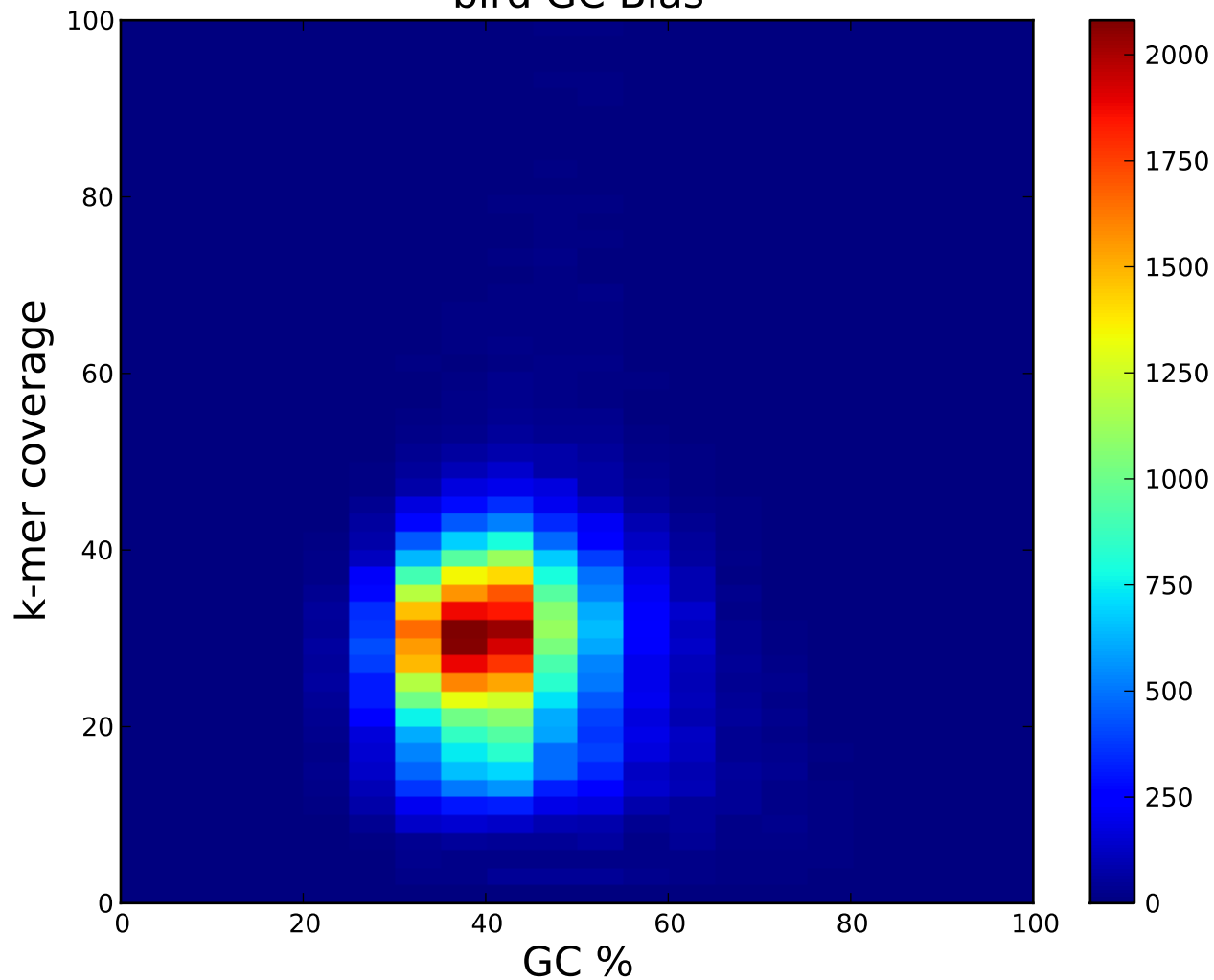
snake GC Bias



human GC Bias

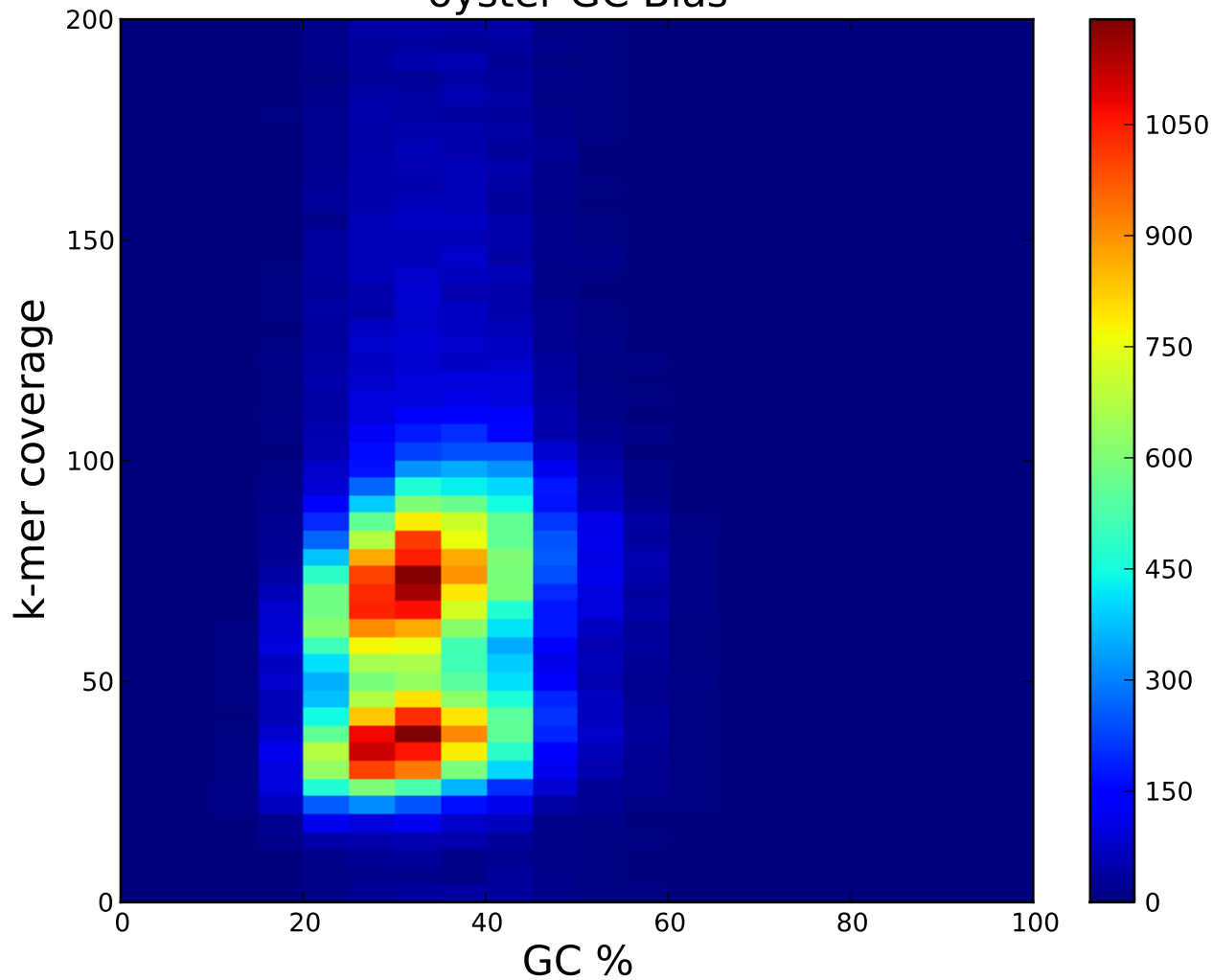


bird GC Bias

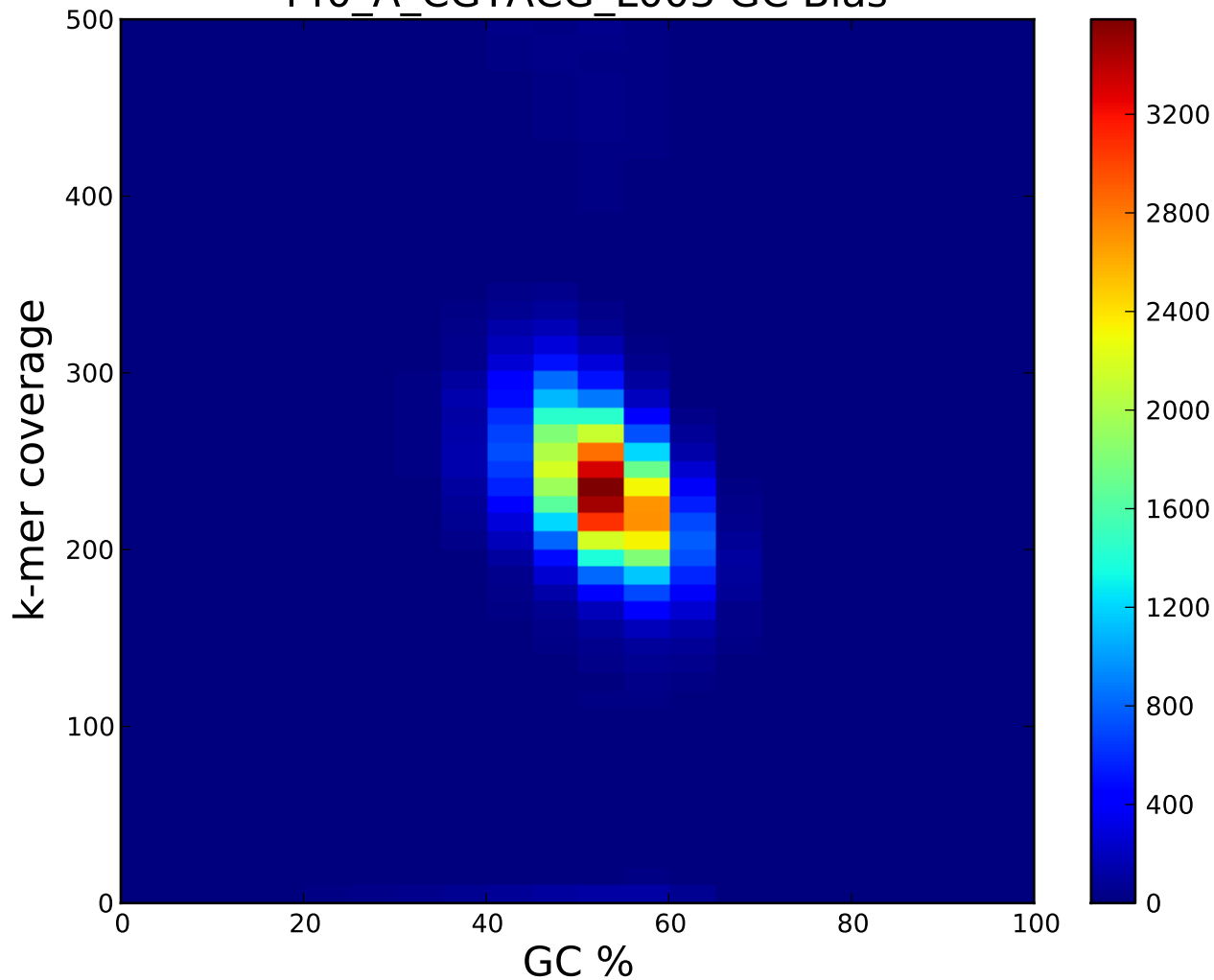




oyster GC Bias



# 440\_A\_CGTACG\_L003 GC Bias



Simulated contig lengths in the k-de Bruijn graph

