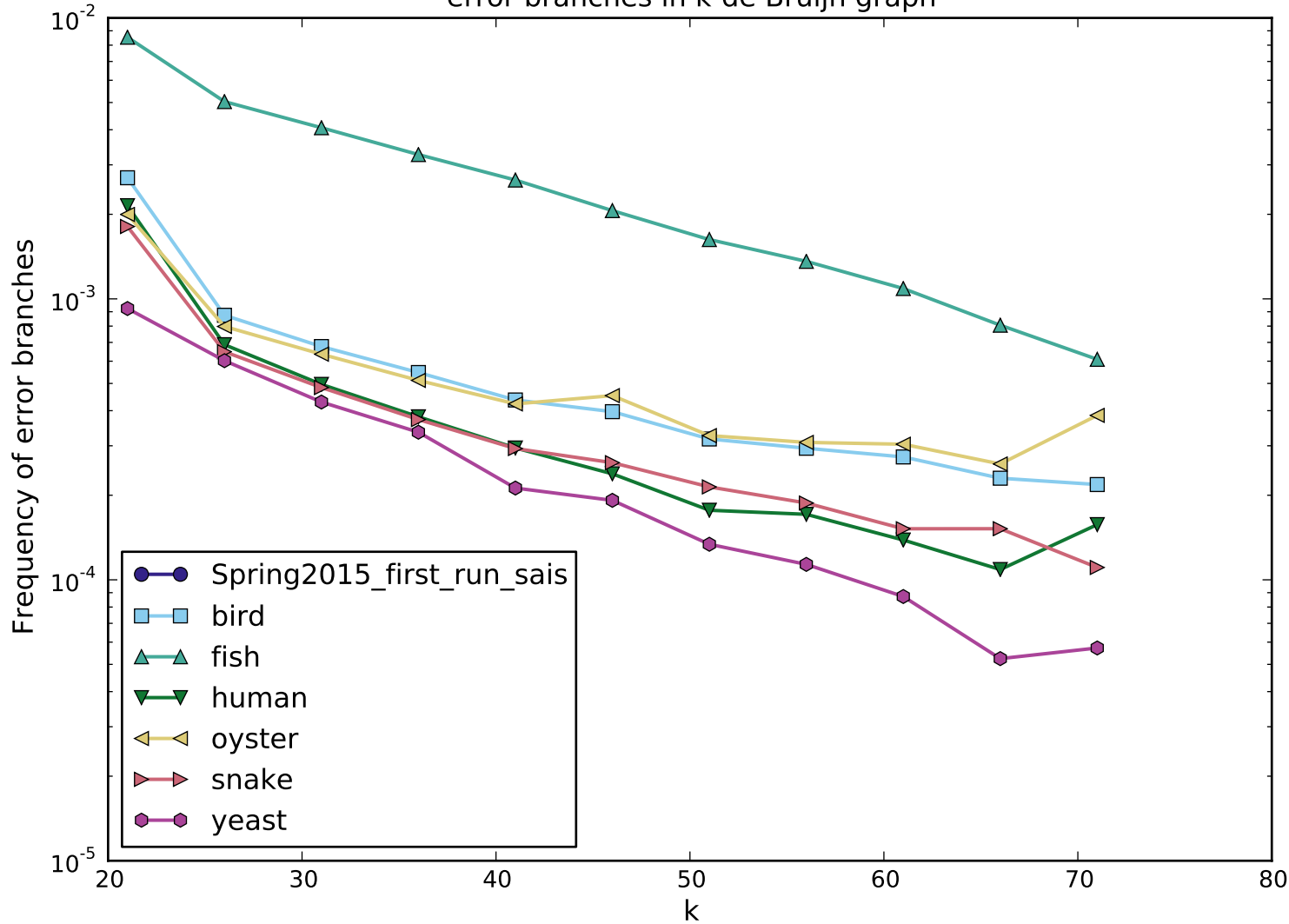
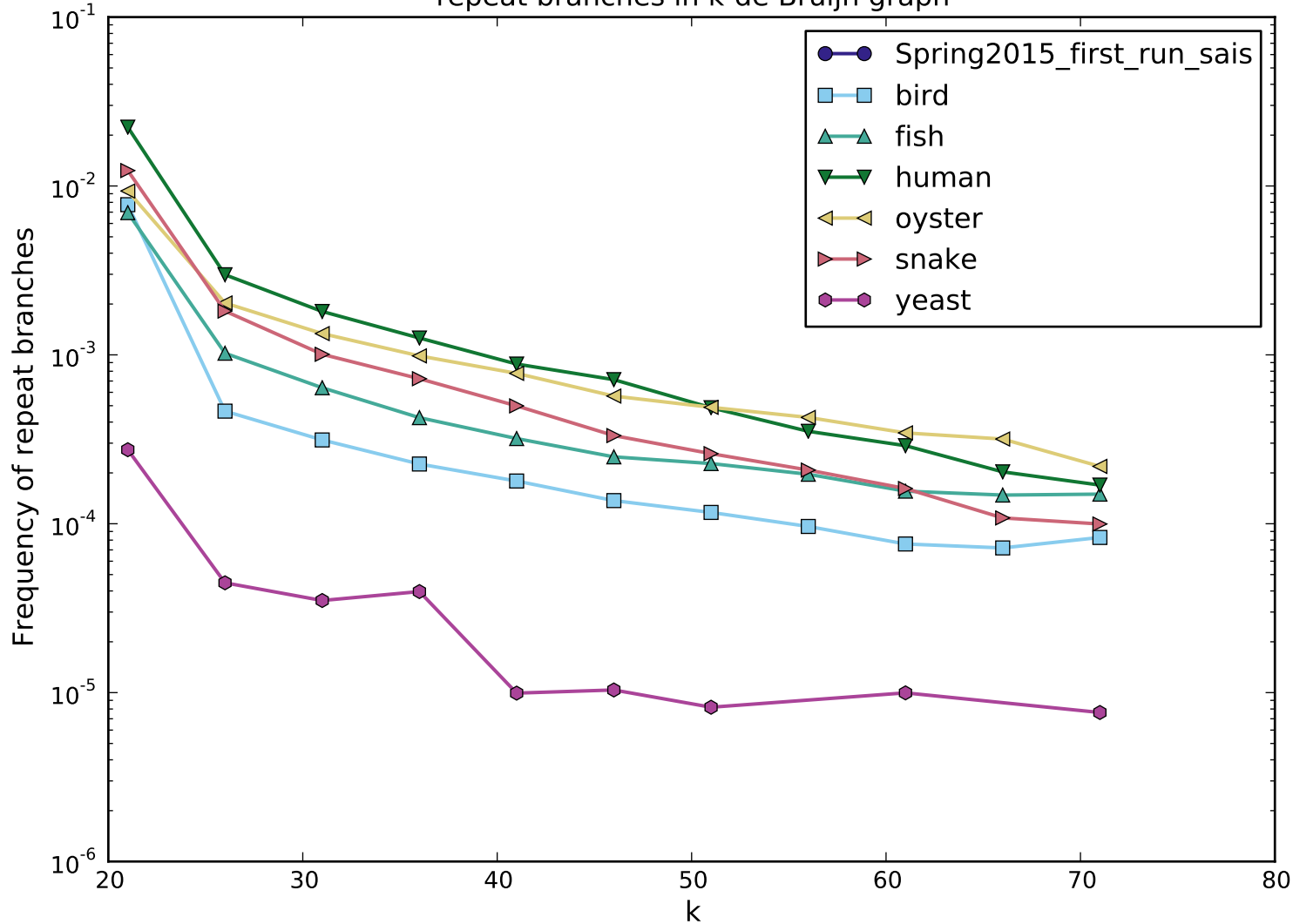


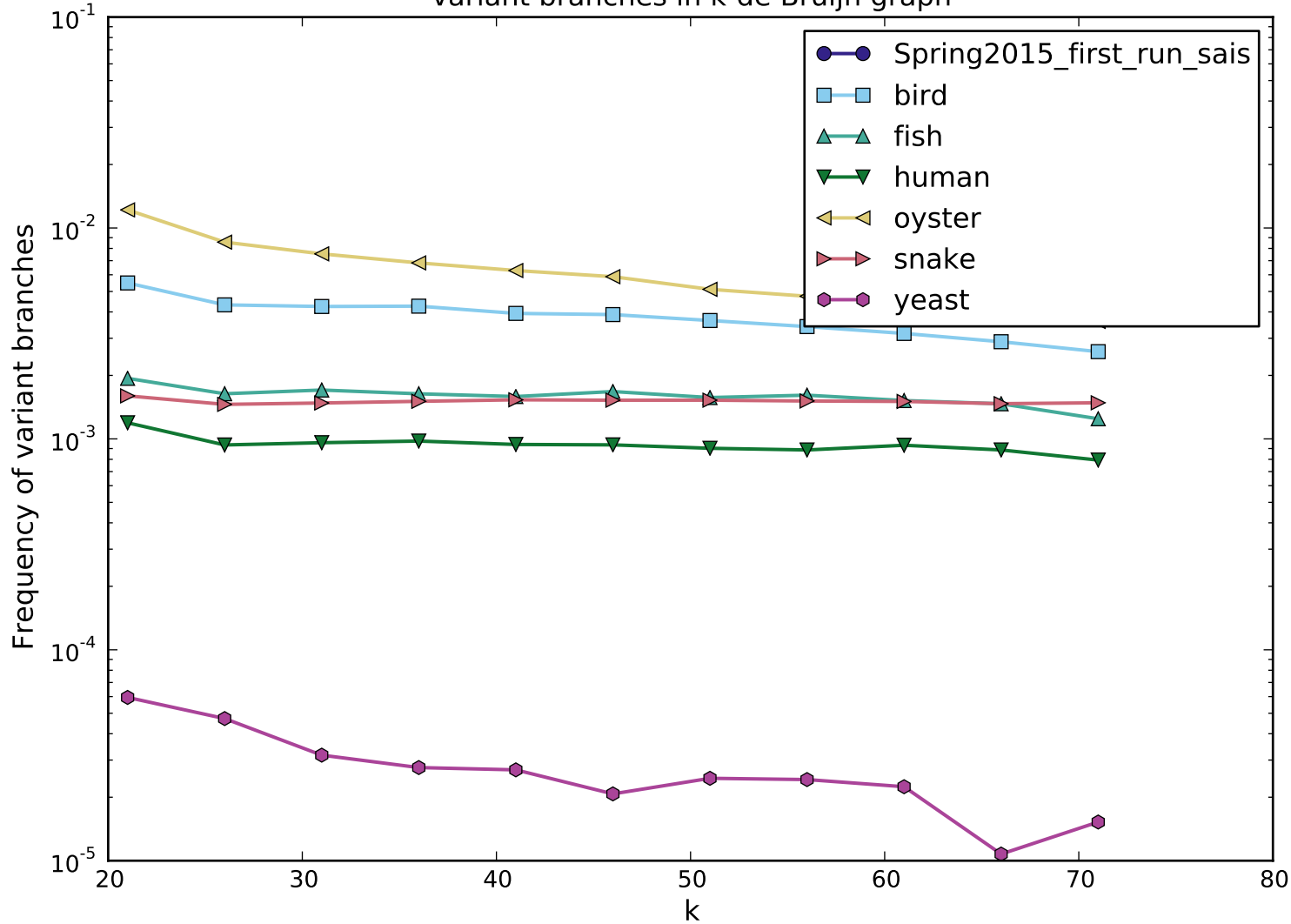
error branches in k-de Bruijn graph



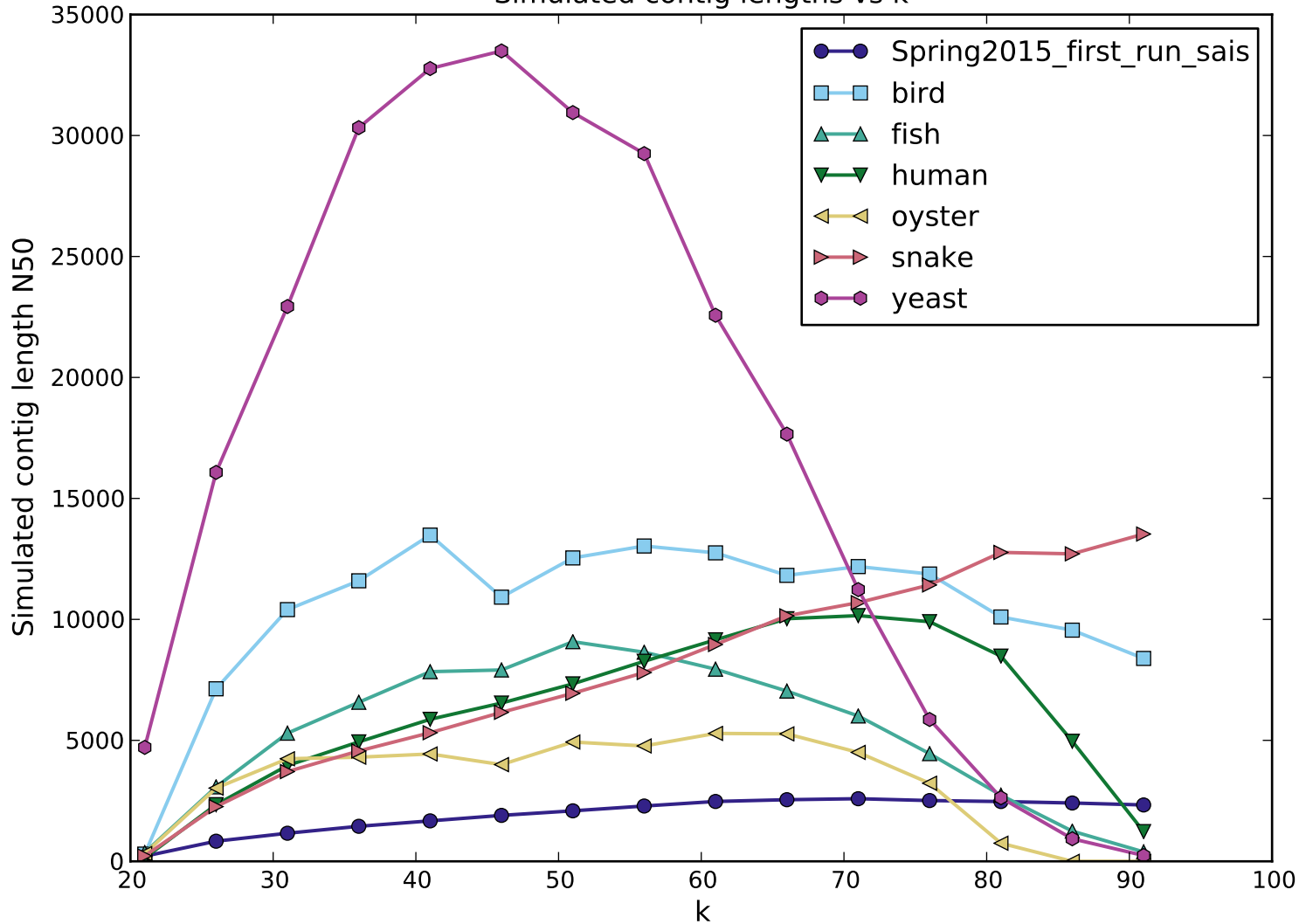
repeat branches in k-de Bruijn graph



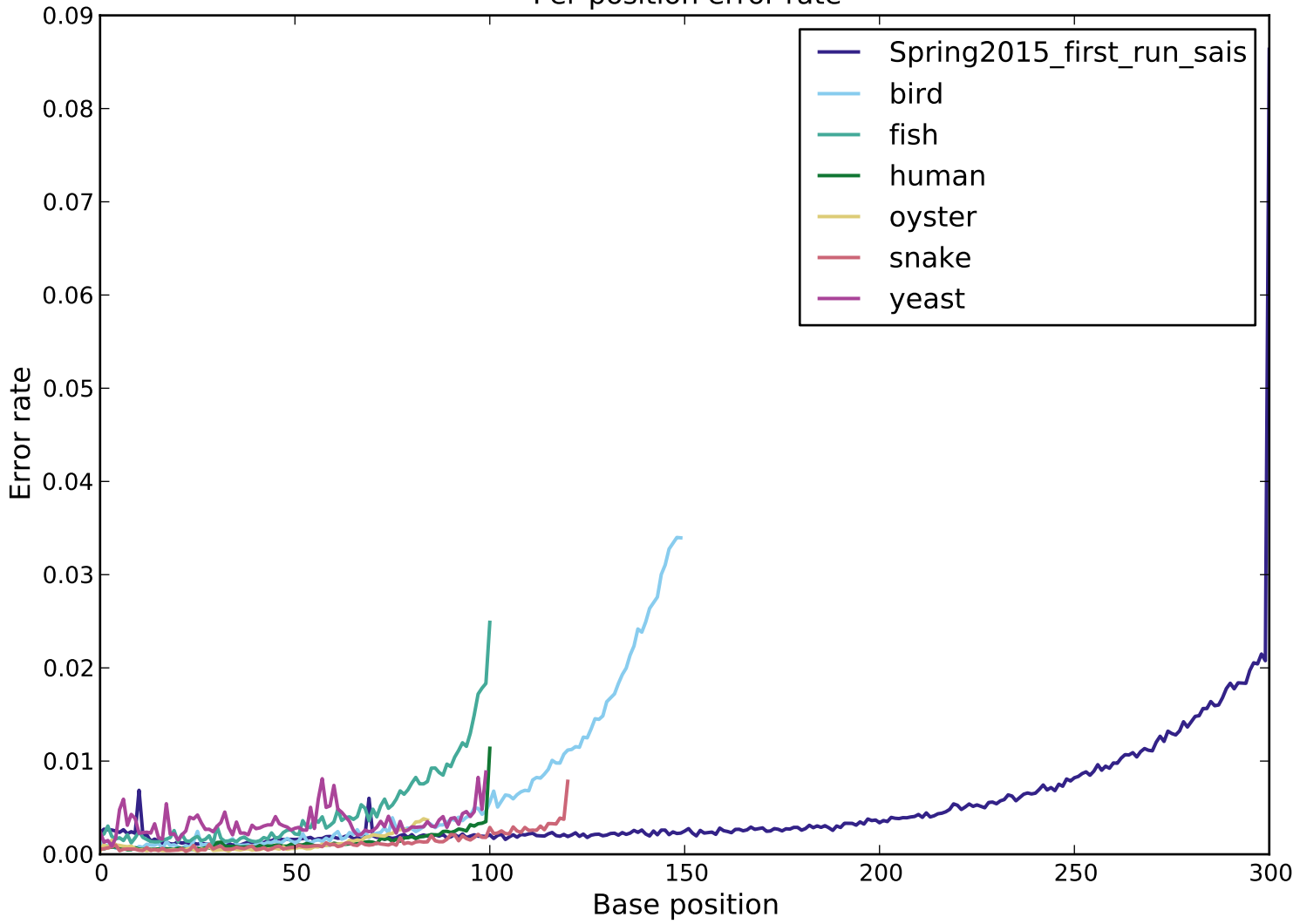
variant branches in k-de Bruijn graph



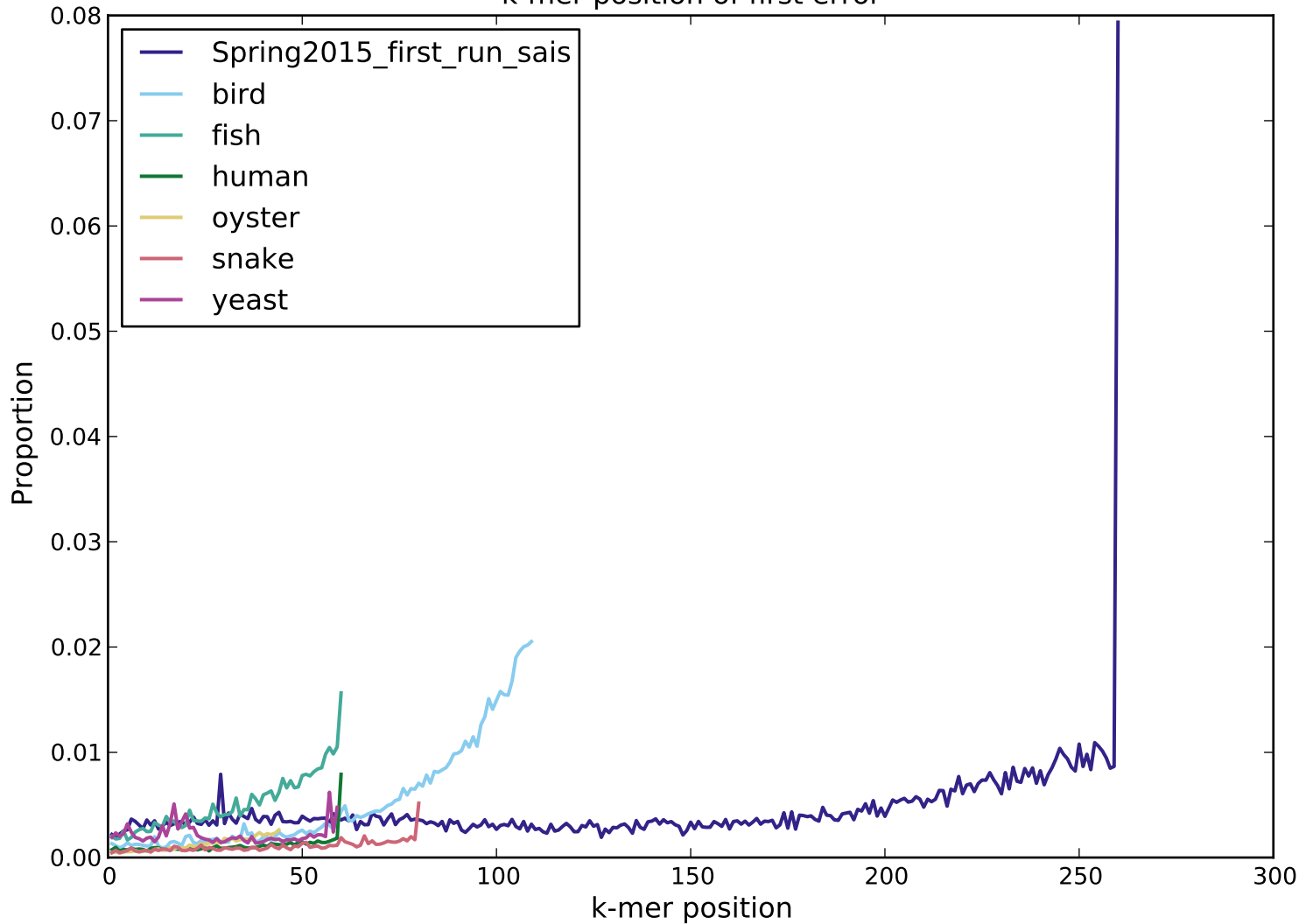
Simulated contig lengths vs k



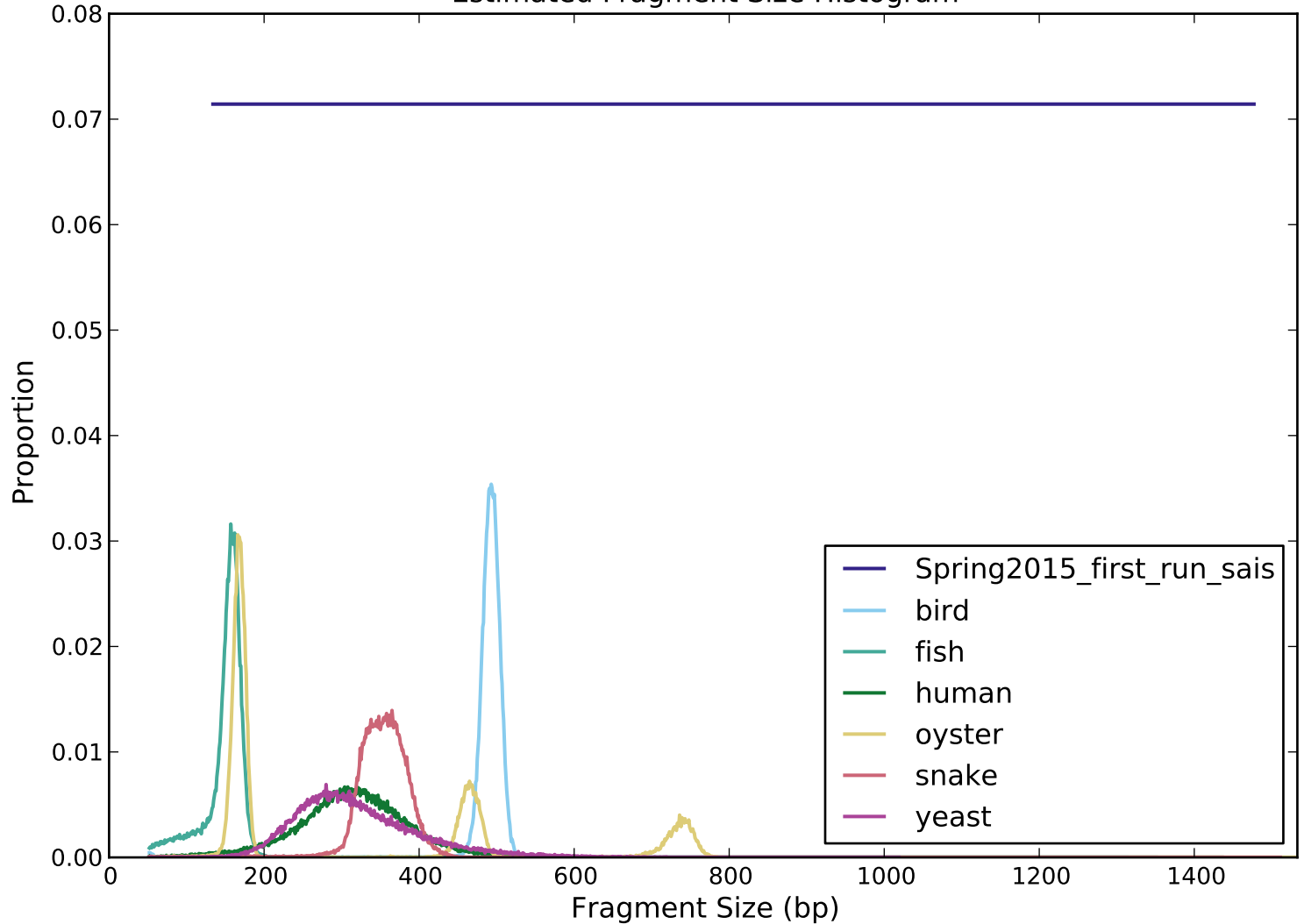
Per-position error rate



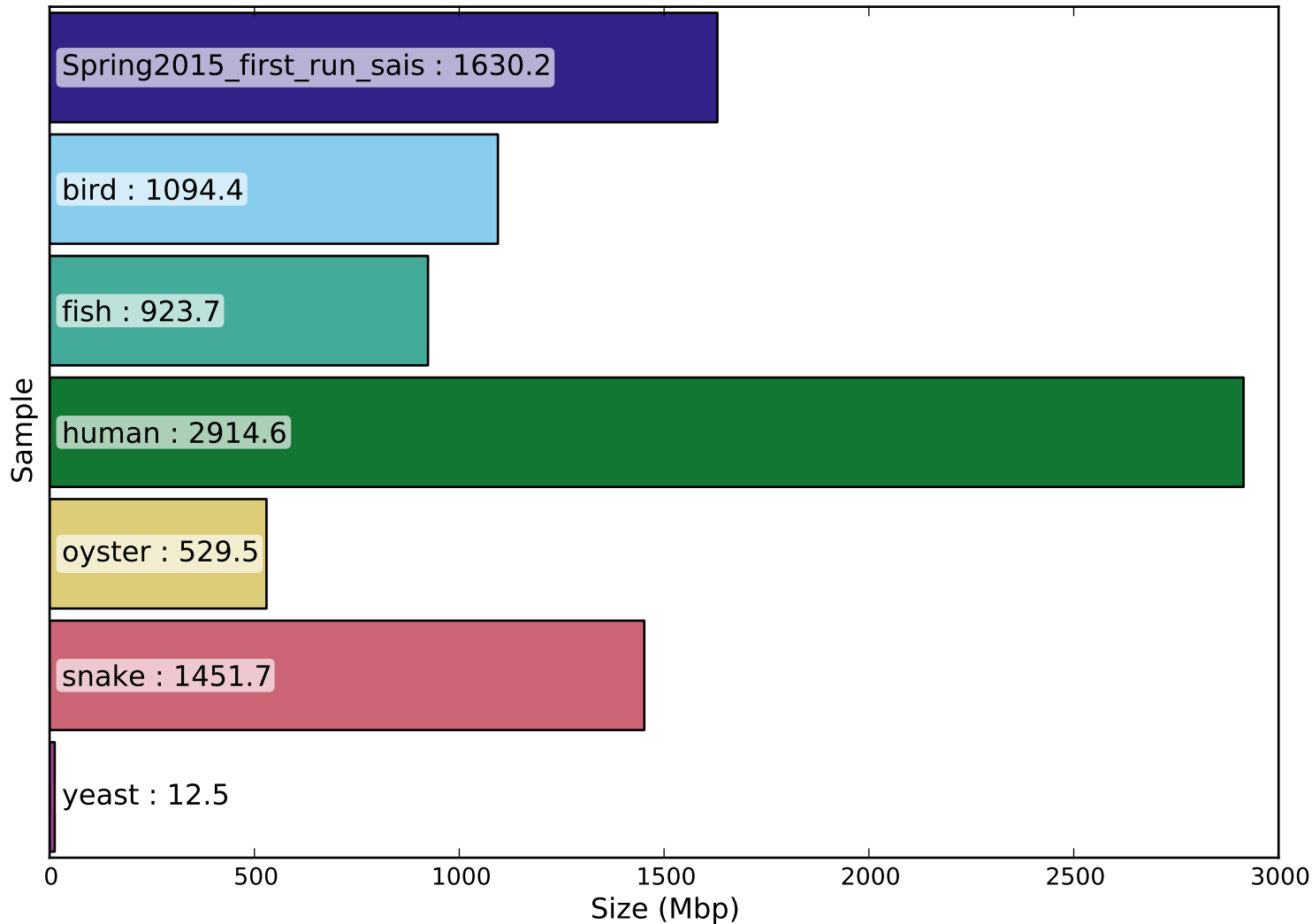
k-mer position of first error



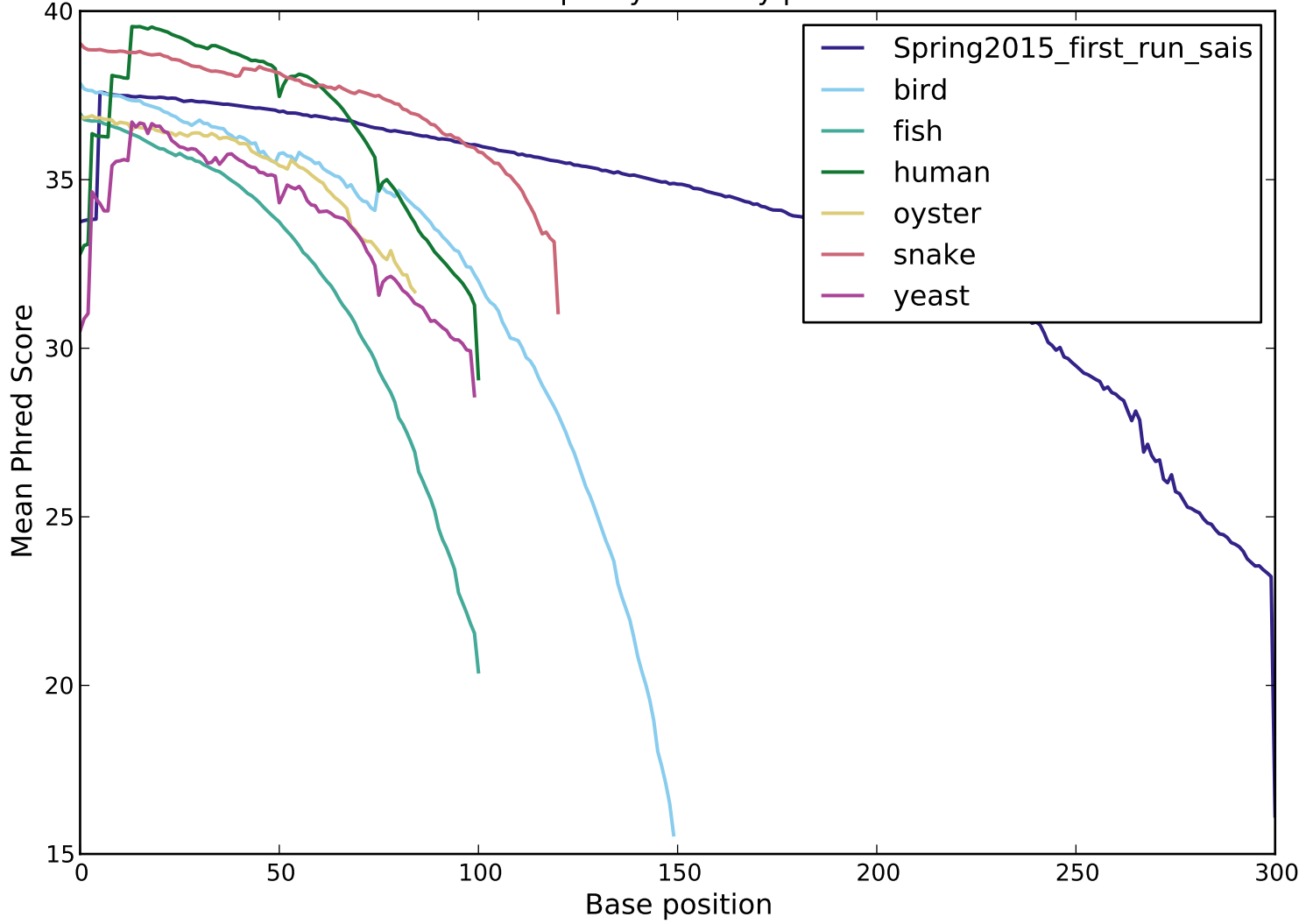
Estimated Fragment Size Histogram



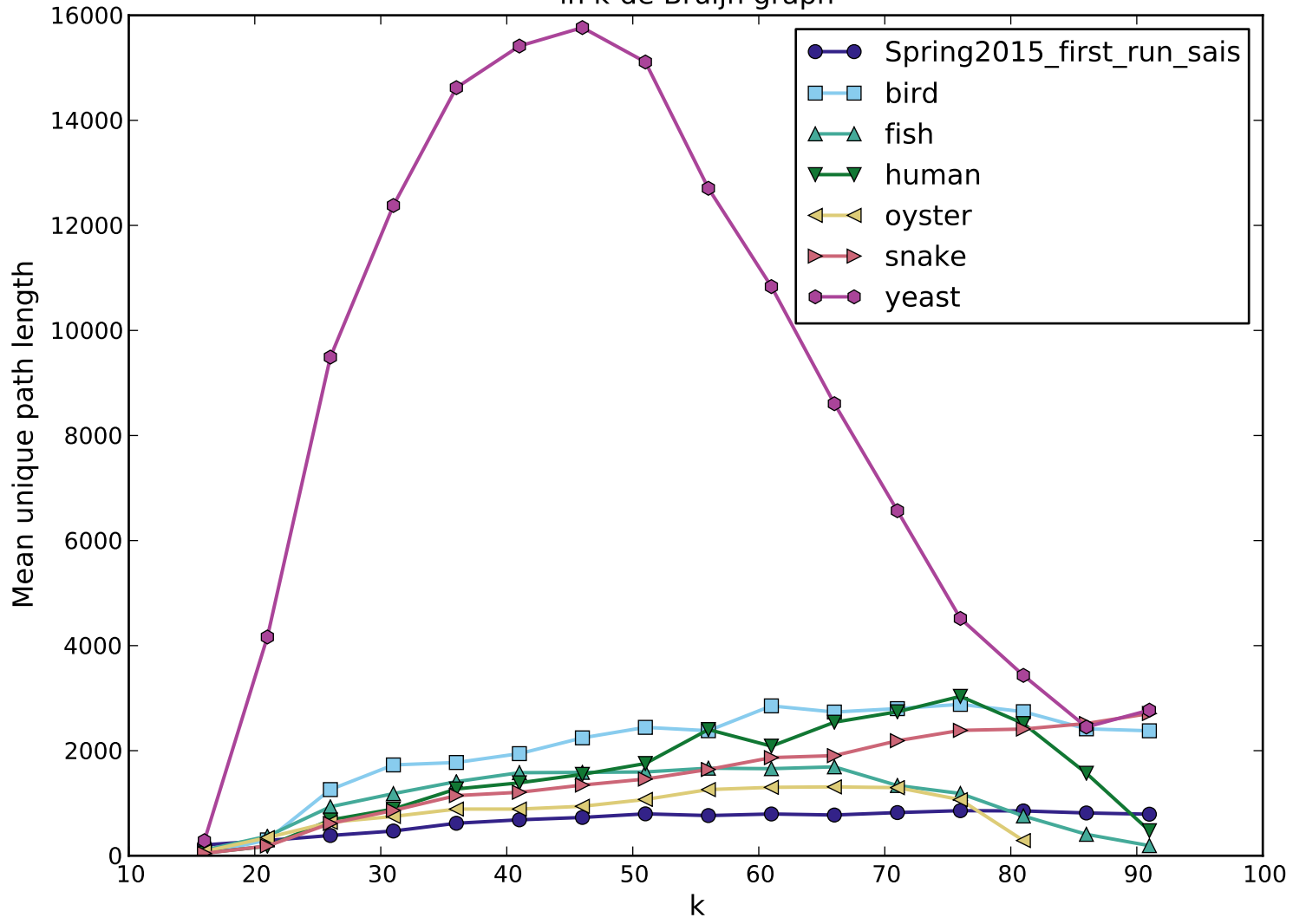
Est. Genome Size



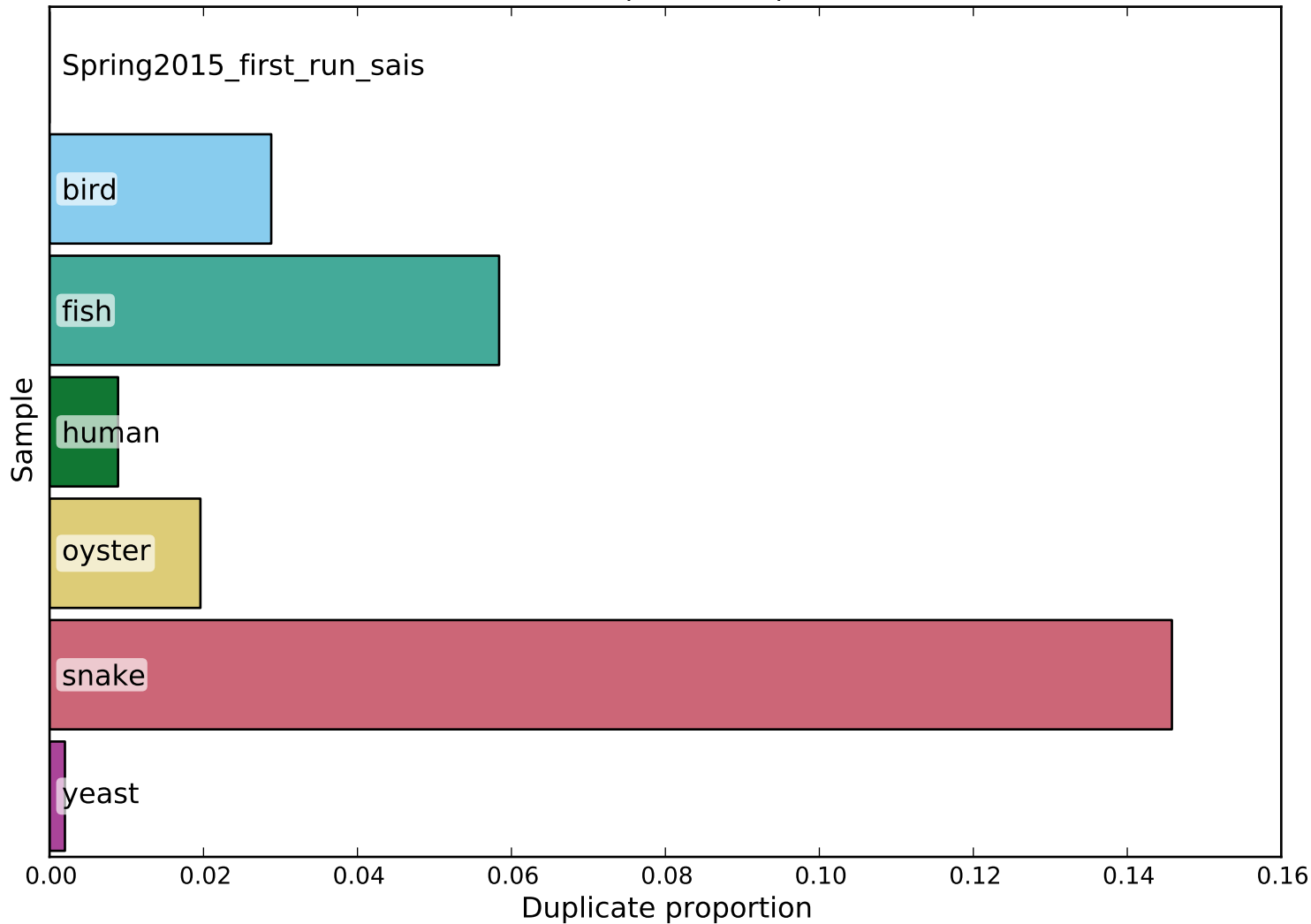
Mean quality score by position



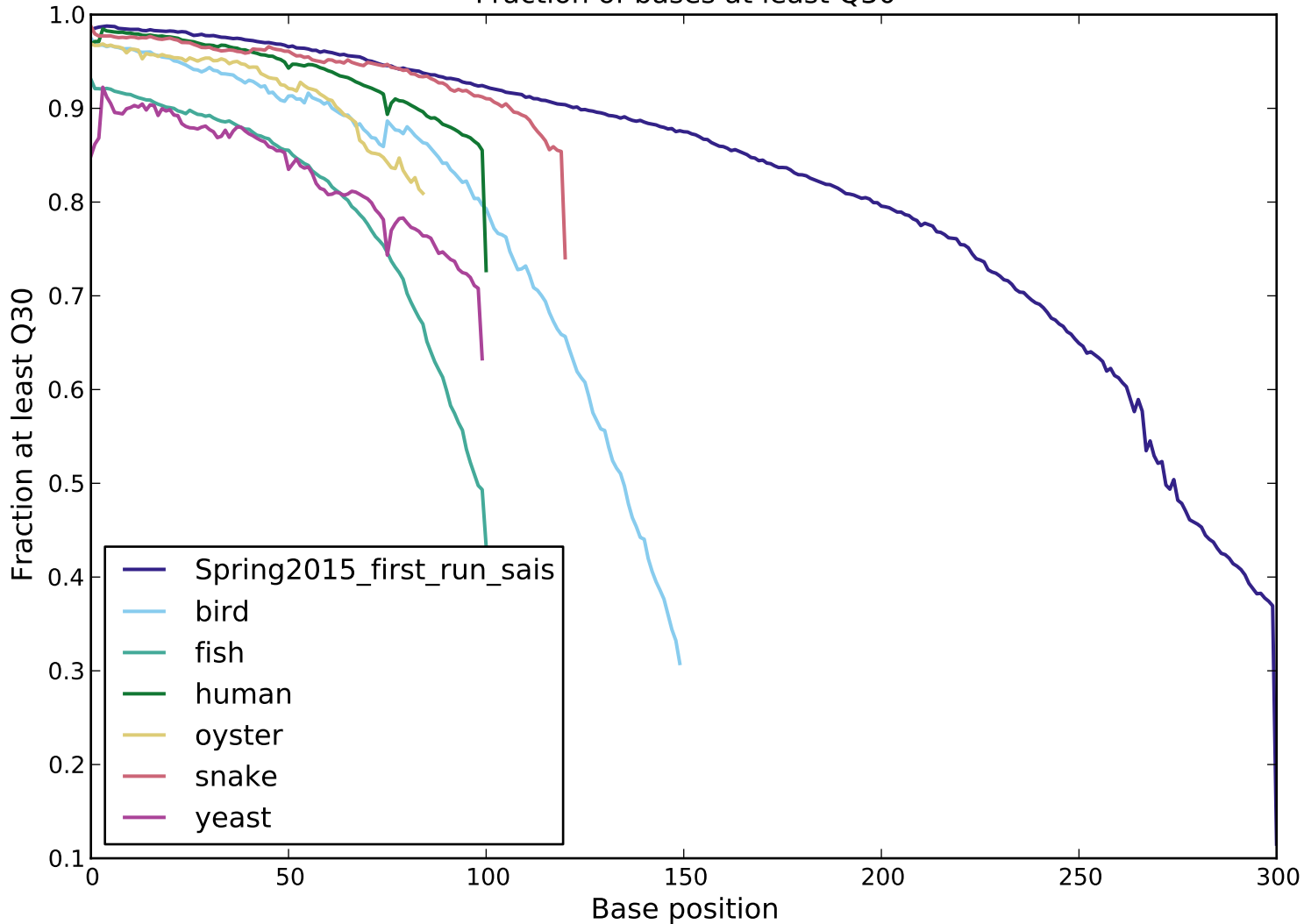
Mean length of unambiguous segments
in k-de Bruijn graph



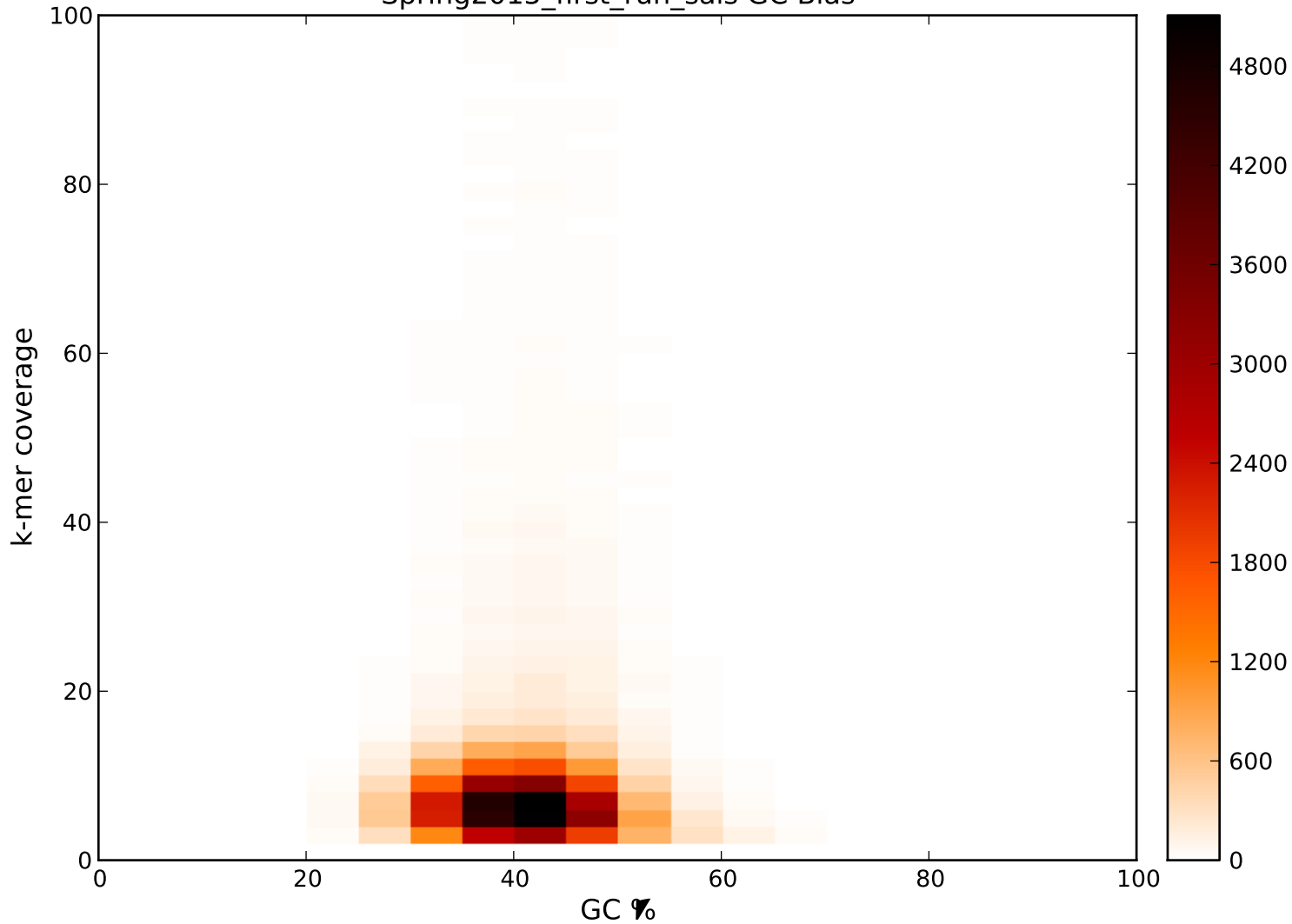
Est. PCR Duplicate Proportion



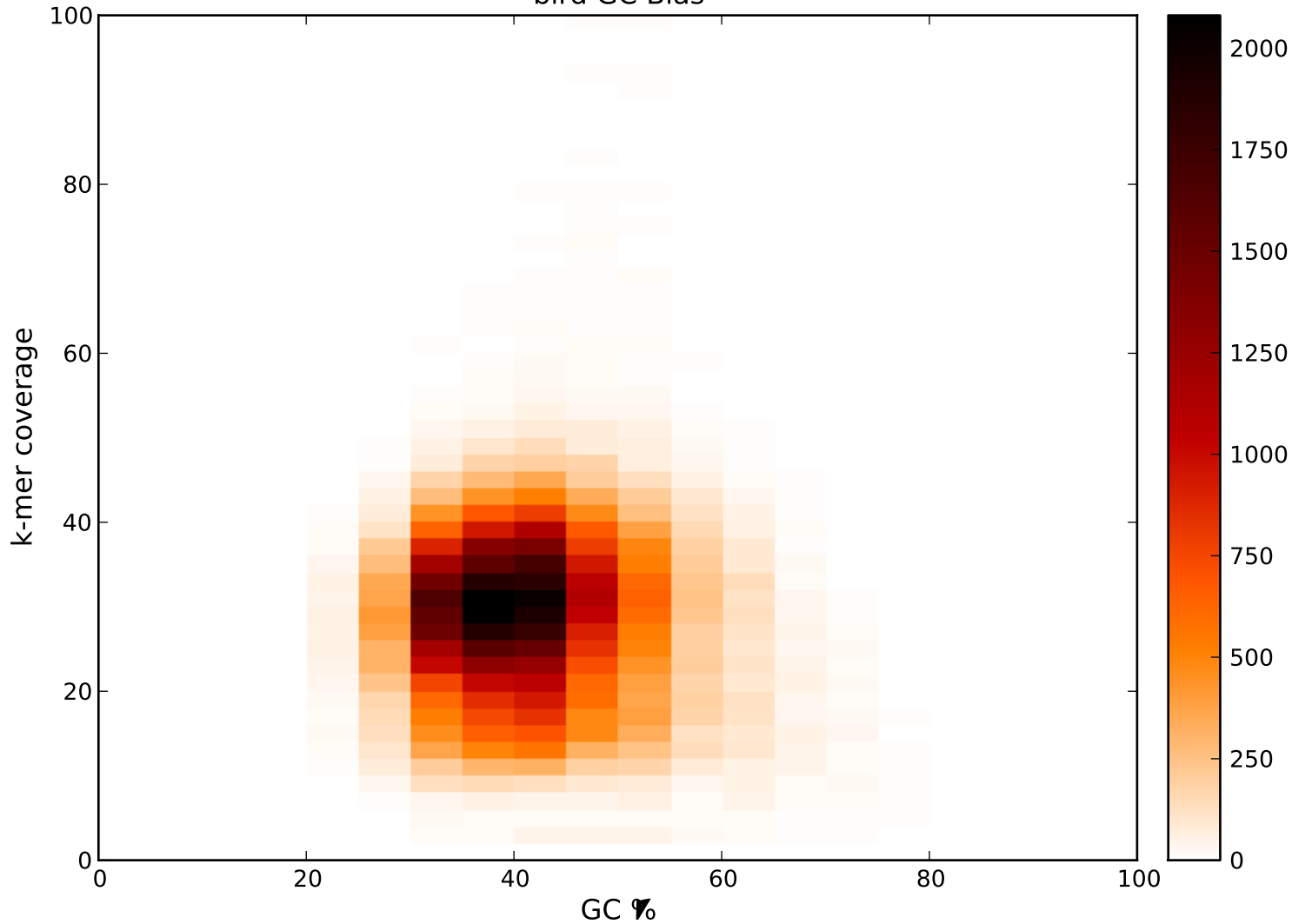
Fraction of bases at least Q30



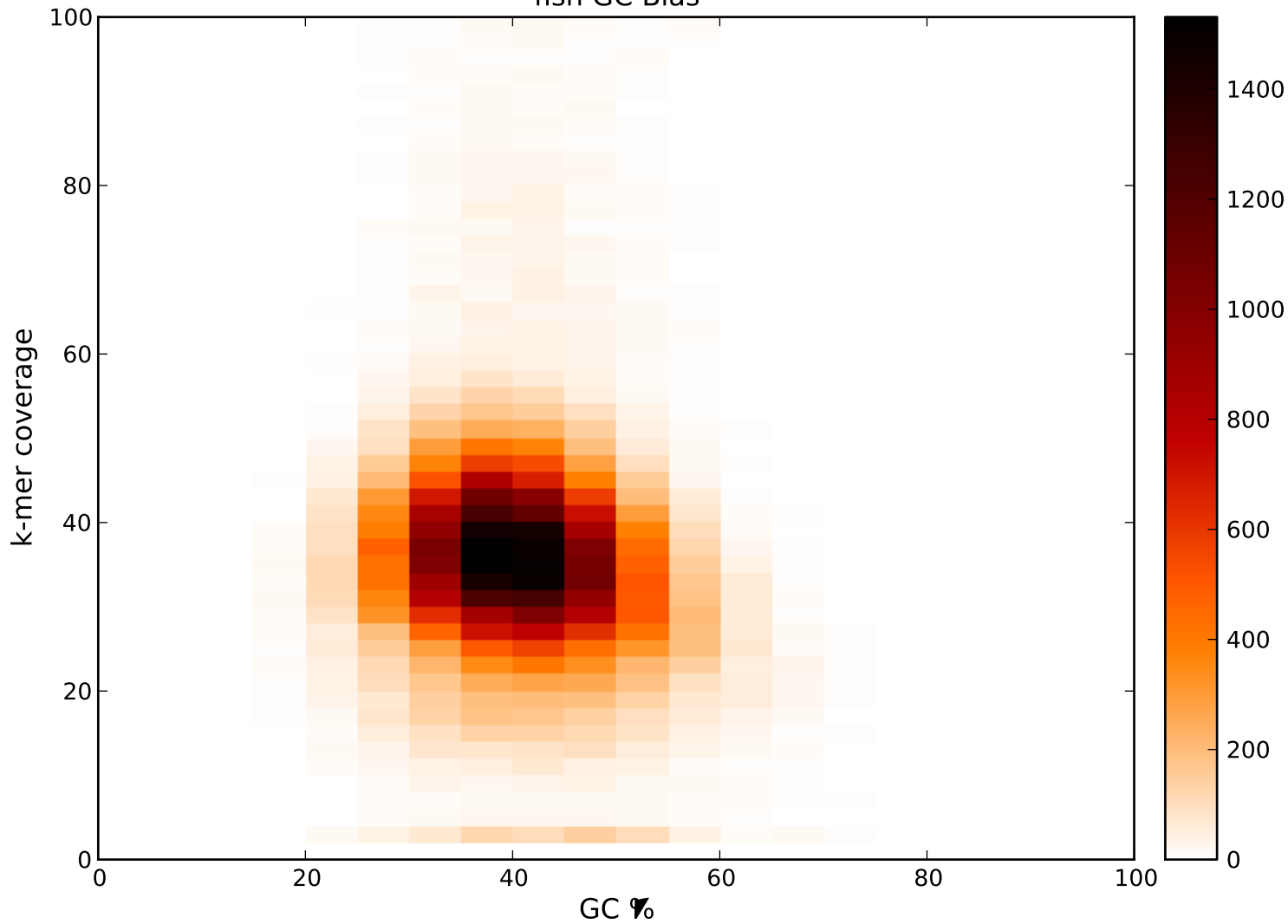
Spring2015_first_run_sais GC Bias



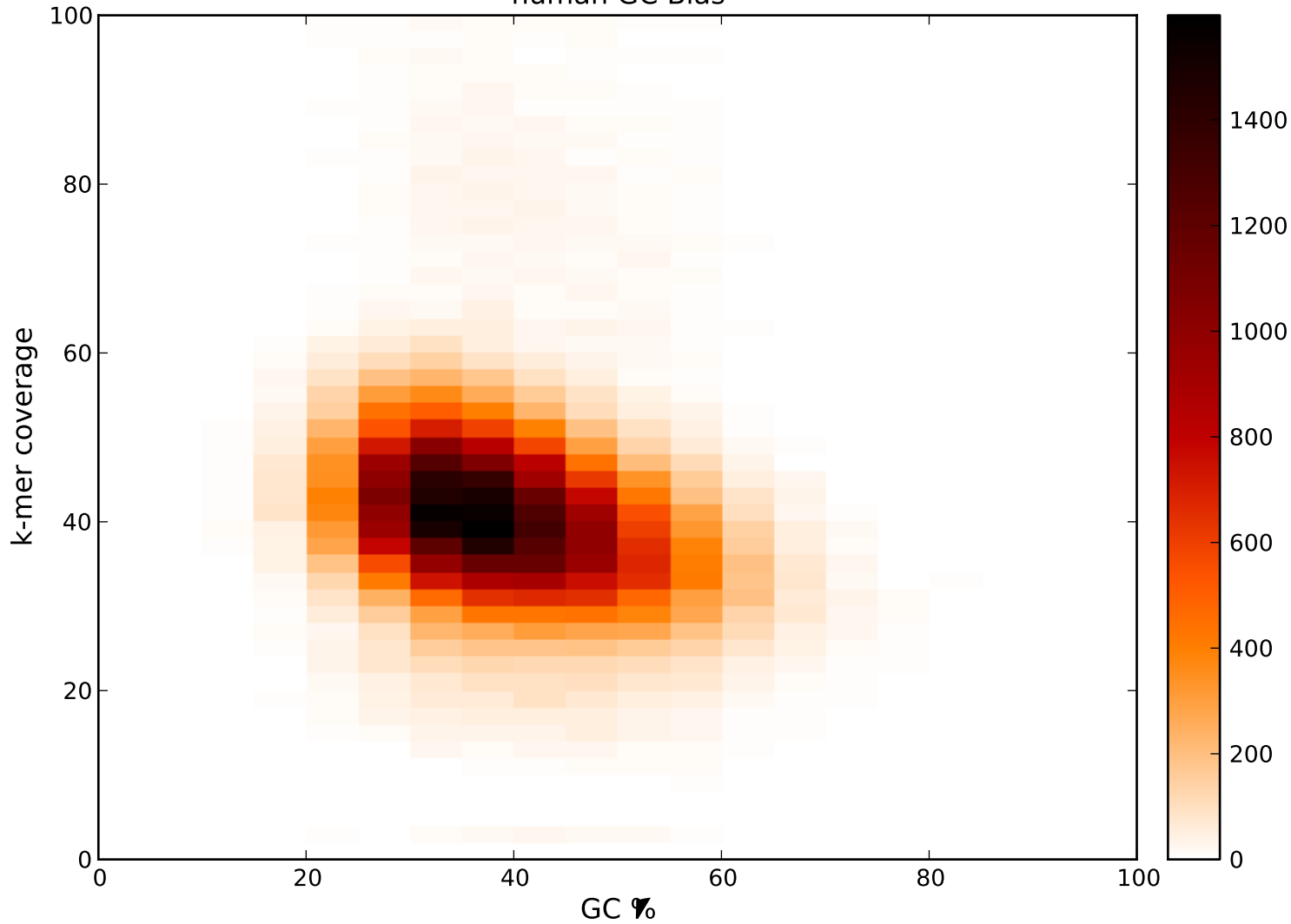
bird GC Bias



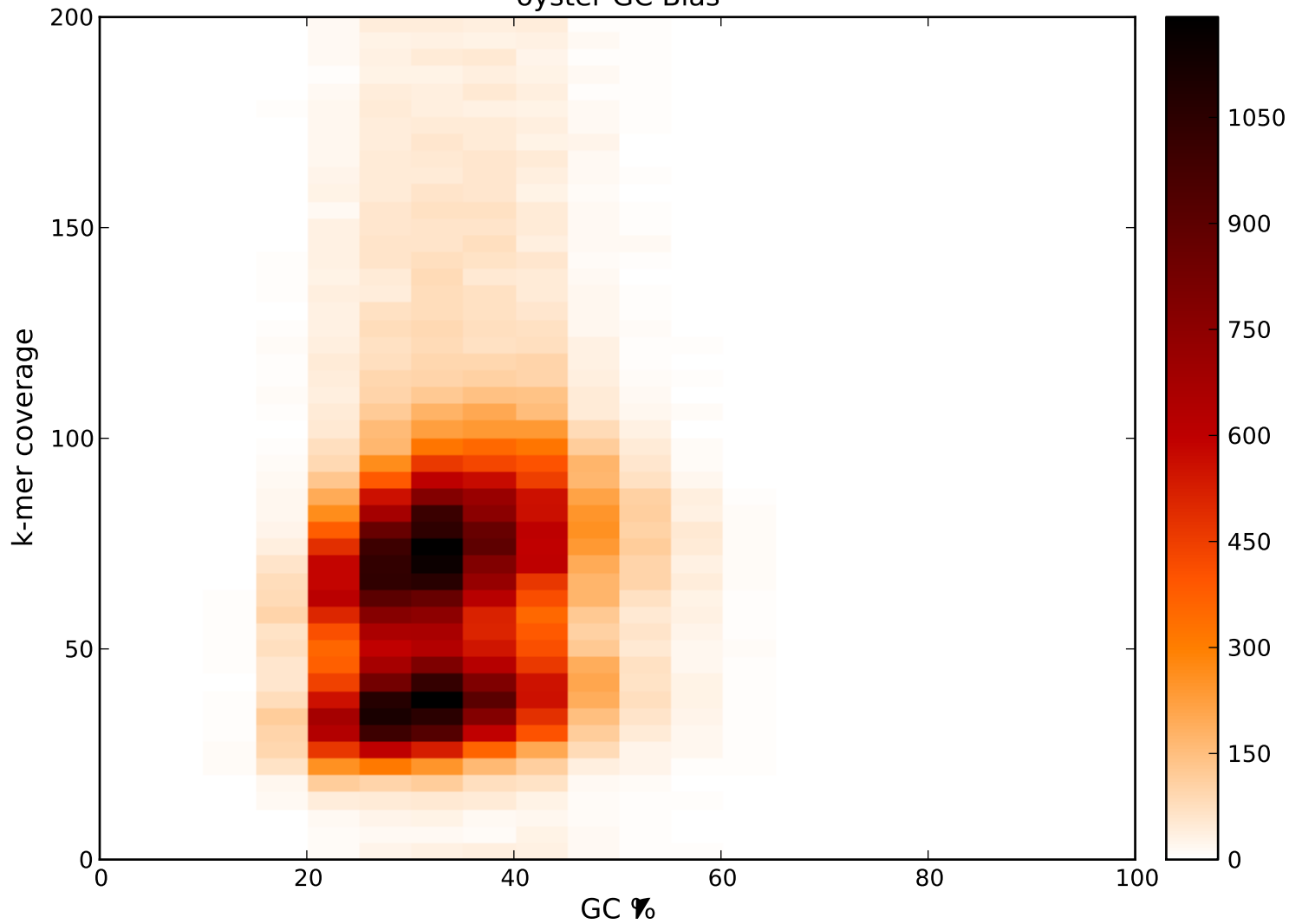
fish GC Bias



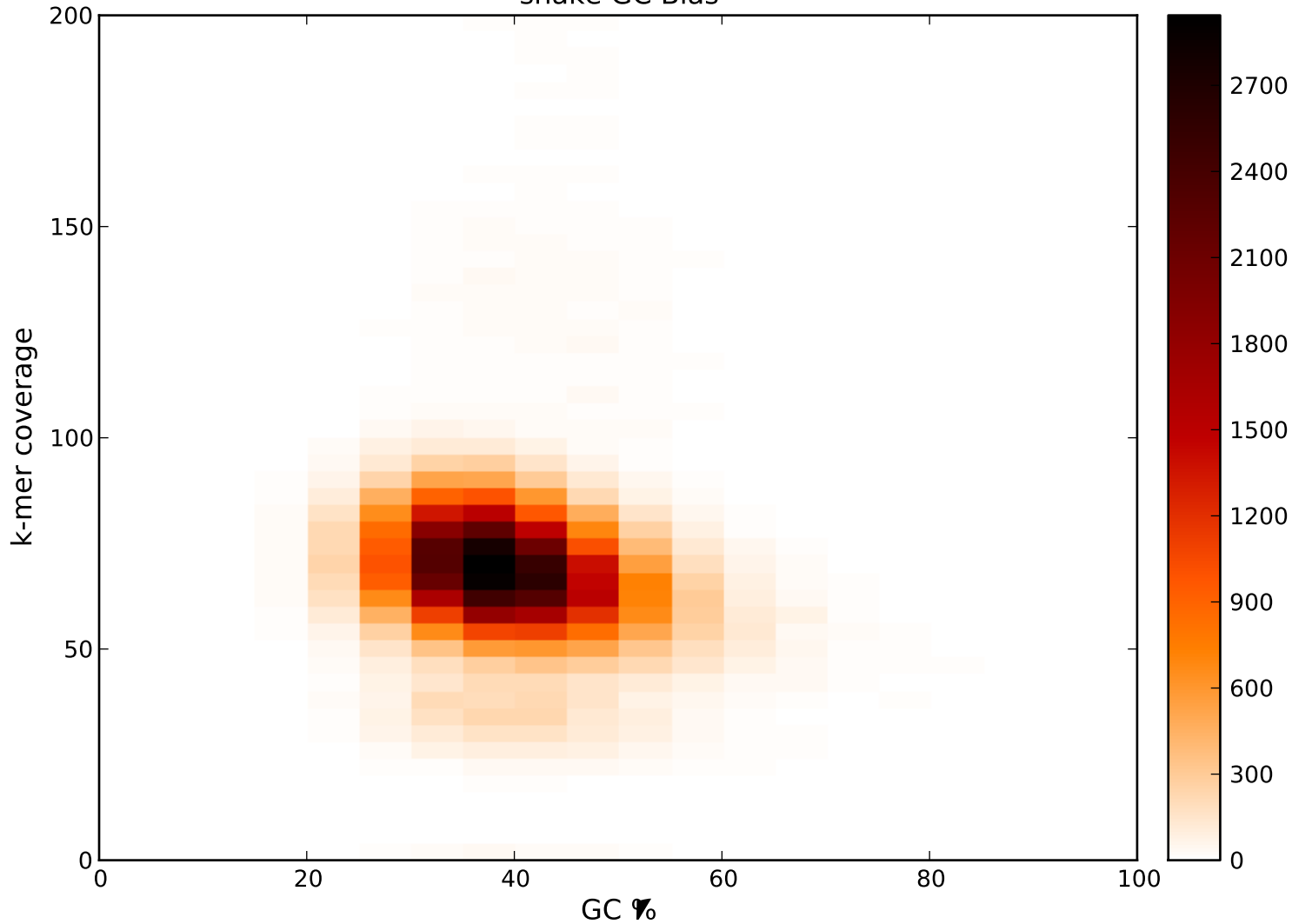
human GC Bias



oyster GC Bias



snake GC Bias



yeast GC Bias

