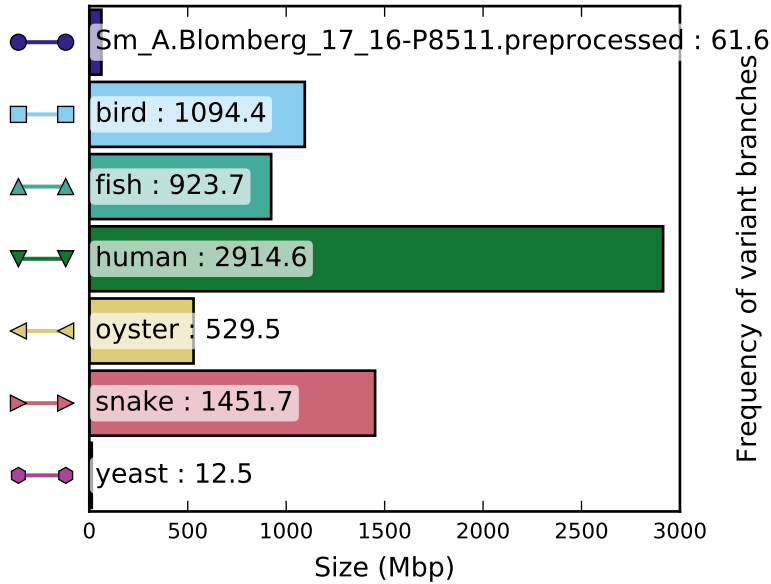
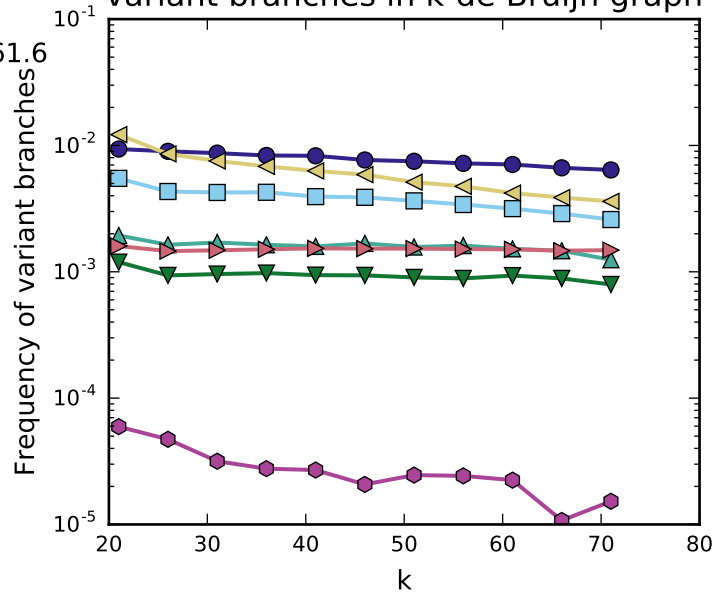


SGA Preqc Results : fig1

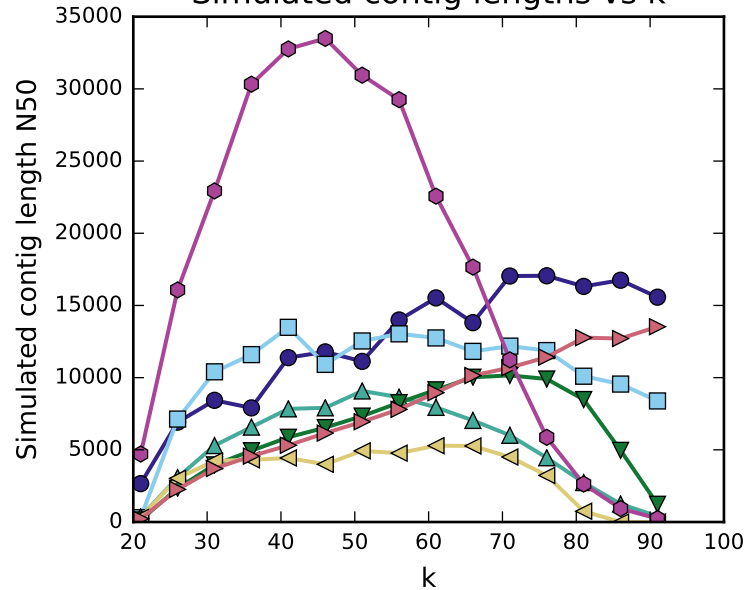
Est. Genome Size



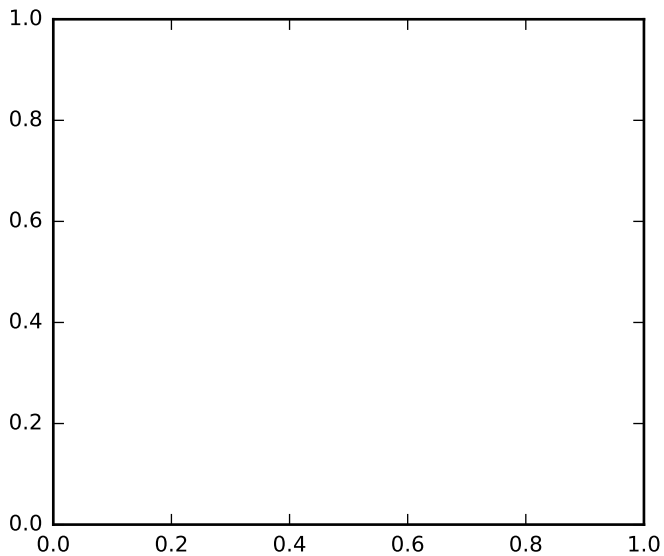
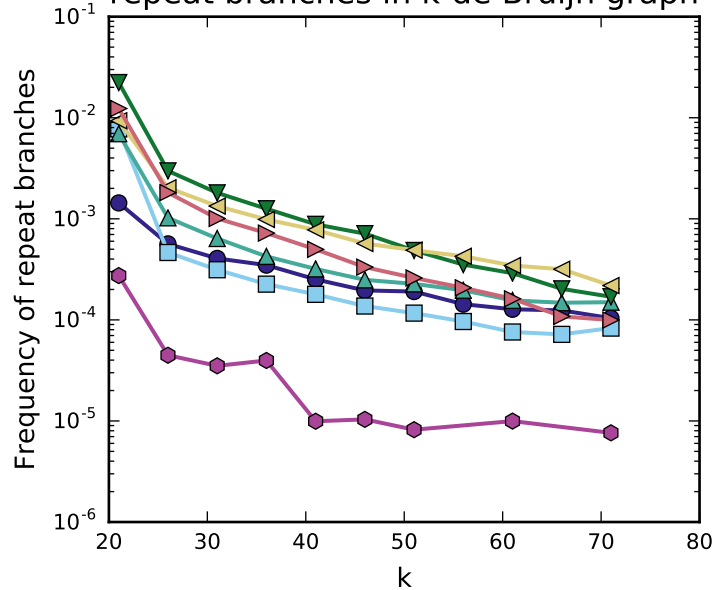
variant branches in k-de Bruijn graph



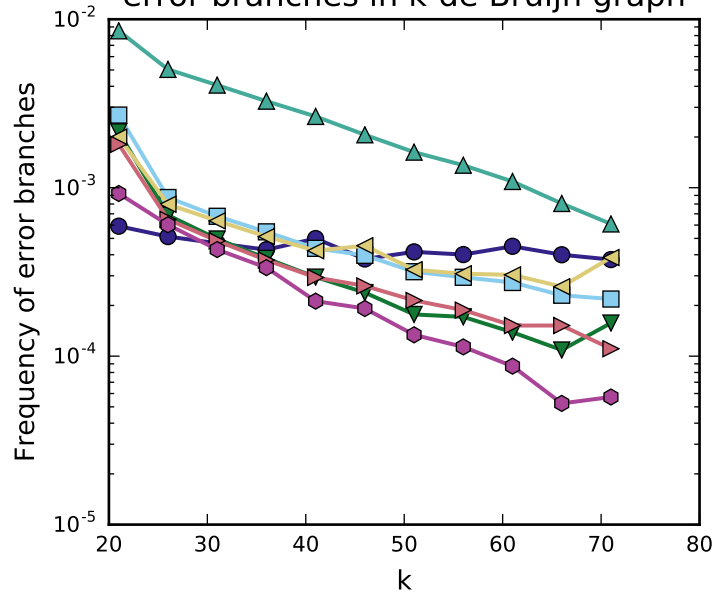
Simulated contig lengths vs k



repeat branches in k-de Bruijn graph

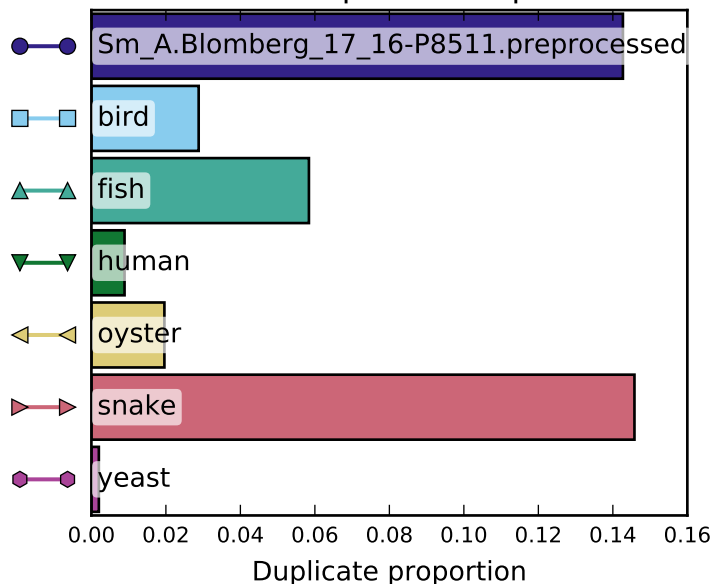


error branches in k-de Bruijn graph

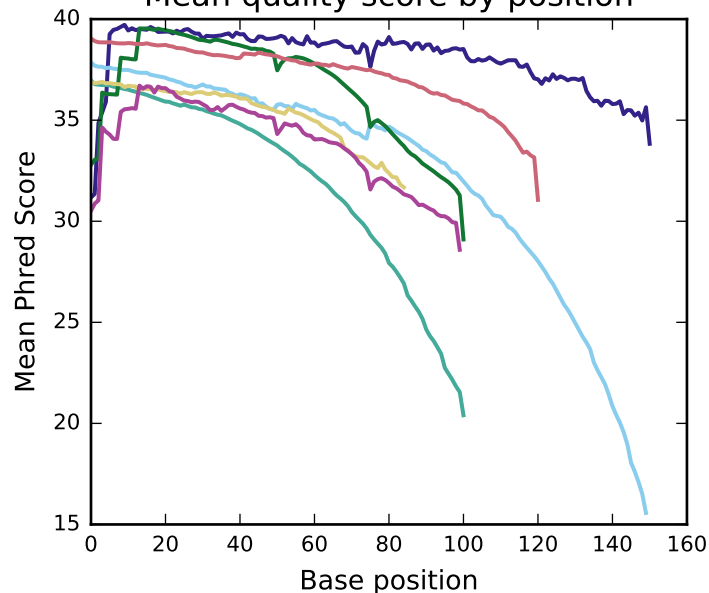


SGA Preqc Results : fig2

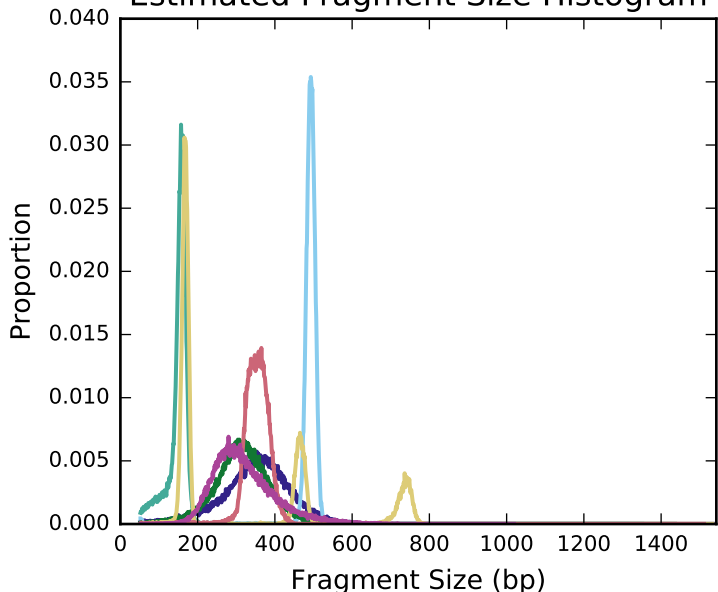
Est. PCR Duplicate Proportion



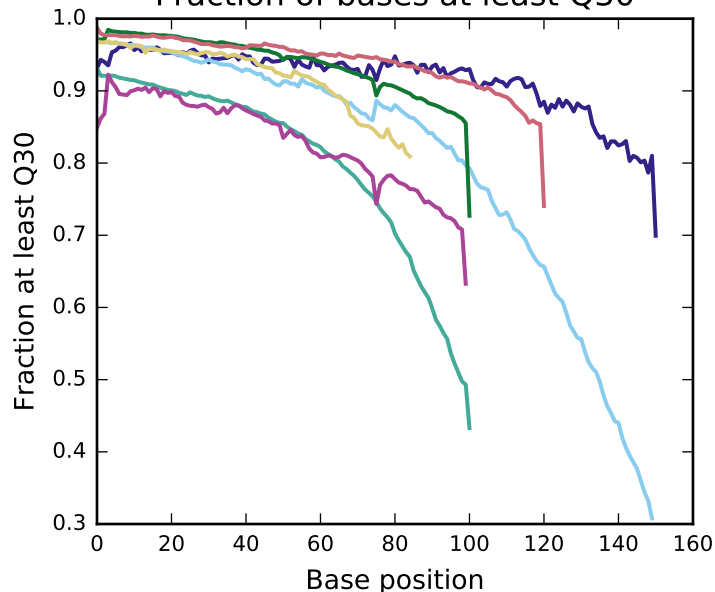
Mean quality score by position



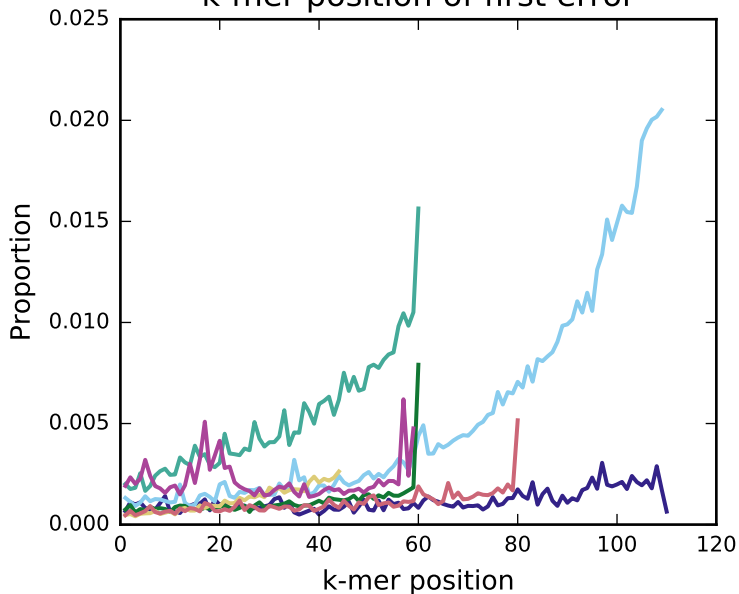
Estimated Fragment Size Histogram



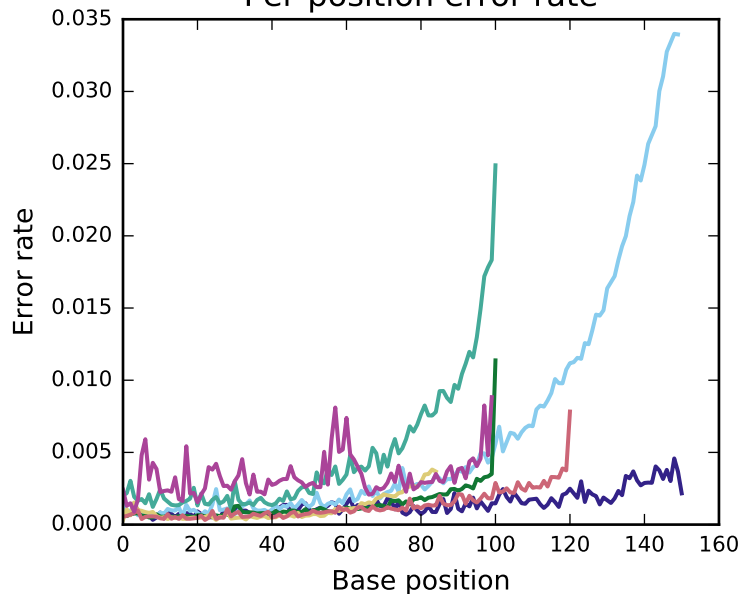
Fraction of bases at least Q30



k-mer position of first error

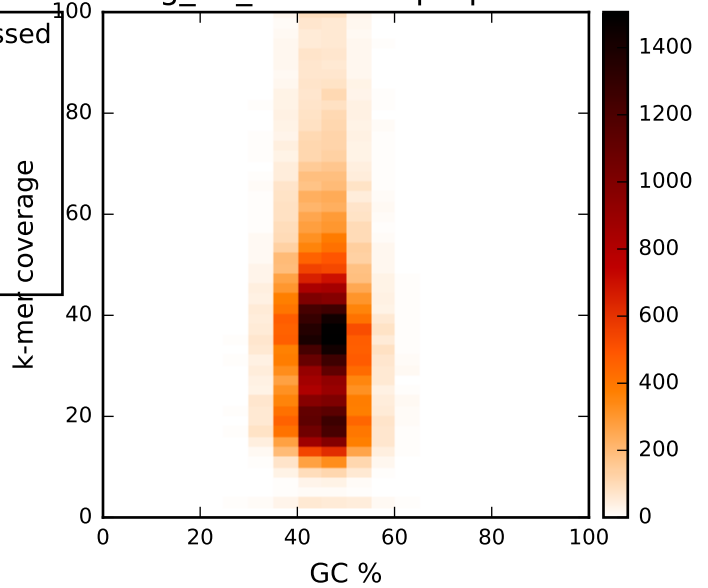
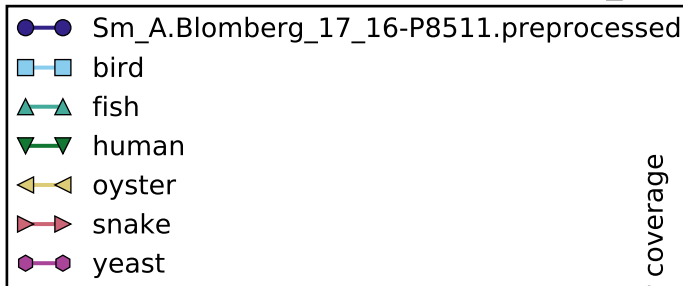


Per-position error rate

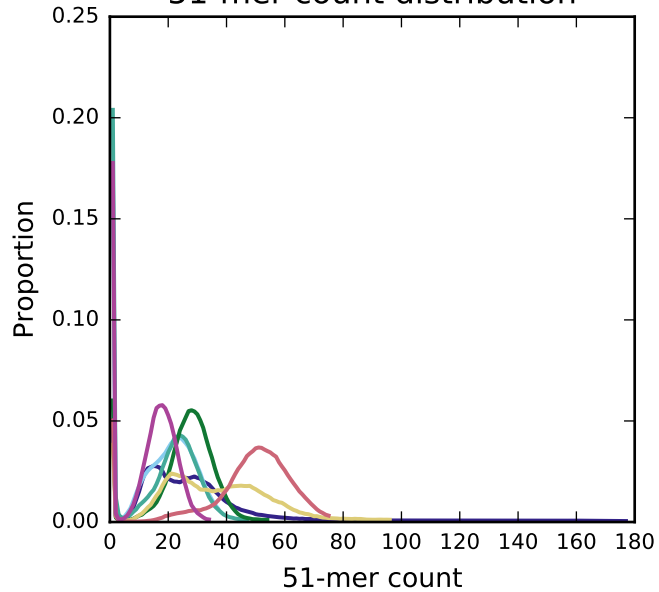


SGA Preqc Results : fig3

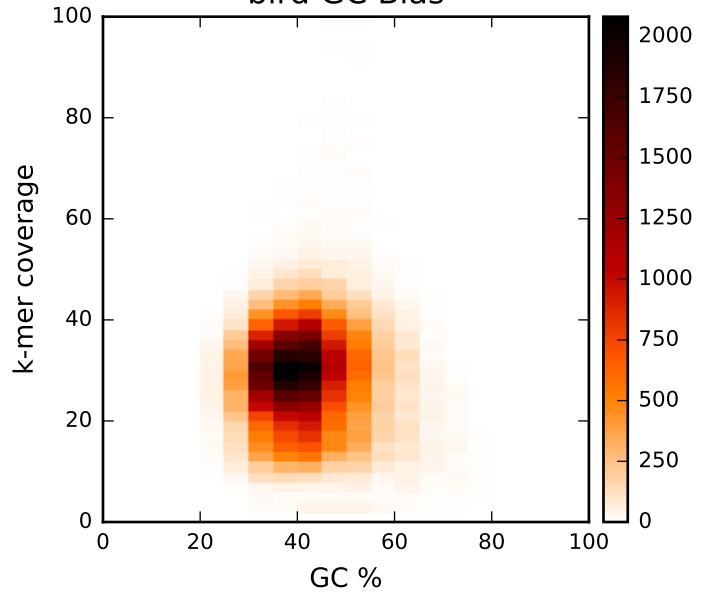
Sm_A.Blomberg_17_16-P8511.preprocessed GC Bias



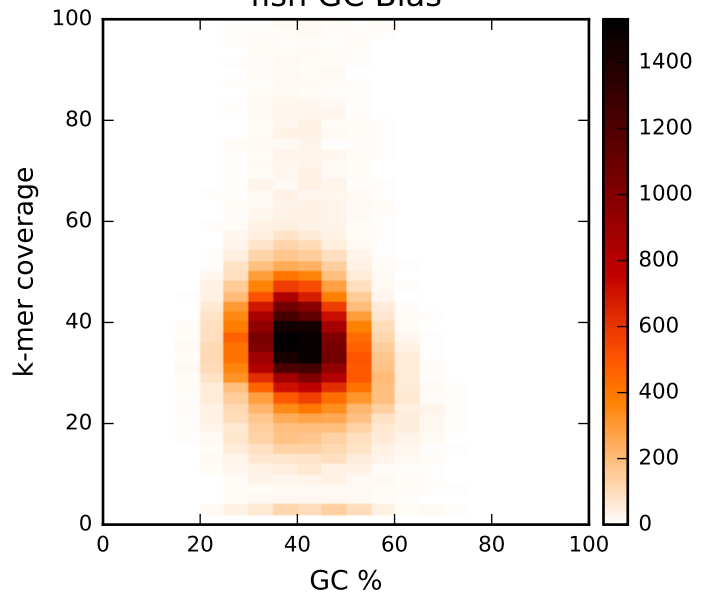
51-mer count distribution



bird GC Bias

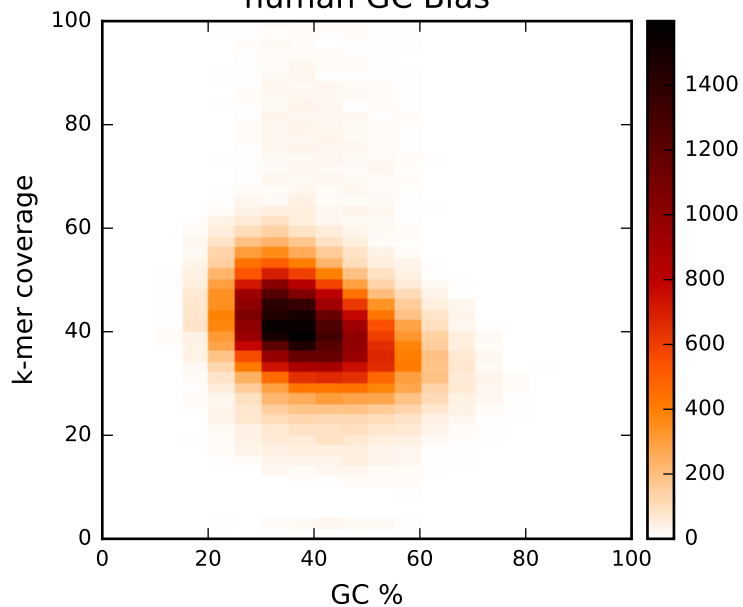


fish GC Bias

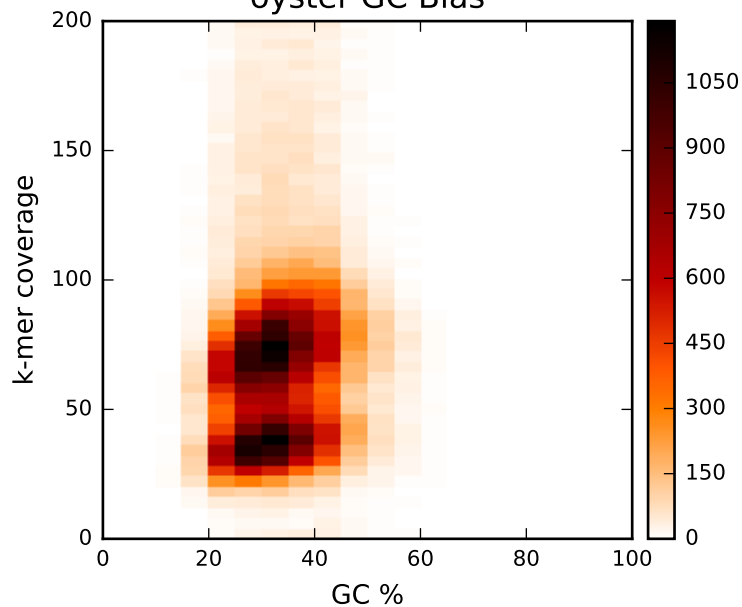


SGA Preqc Results : fig4

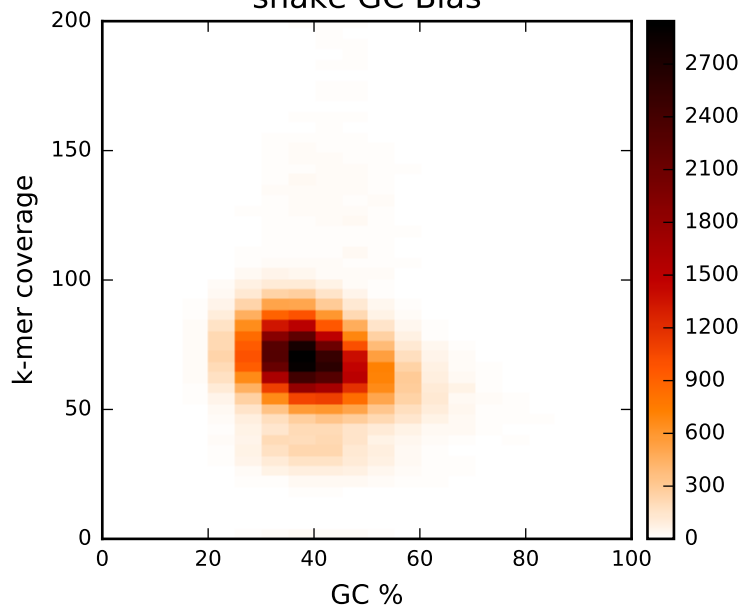
human GC Bias



oyster GC Bias



snake GC Bias



yeast GC Bias

