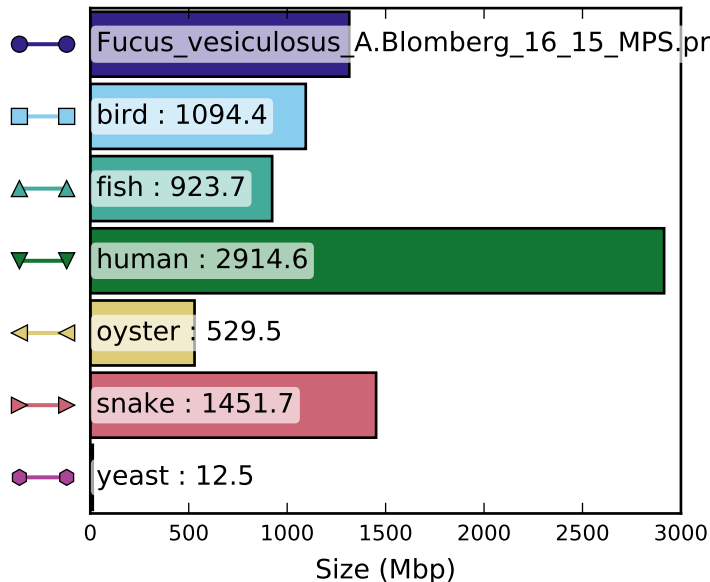
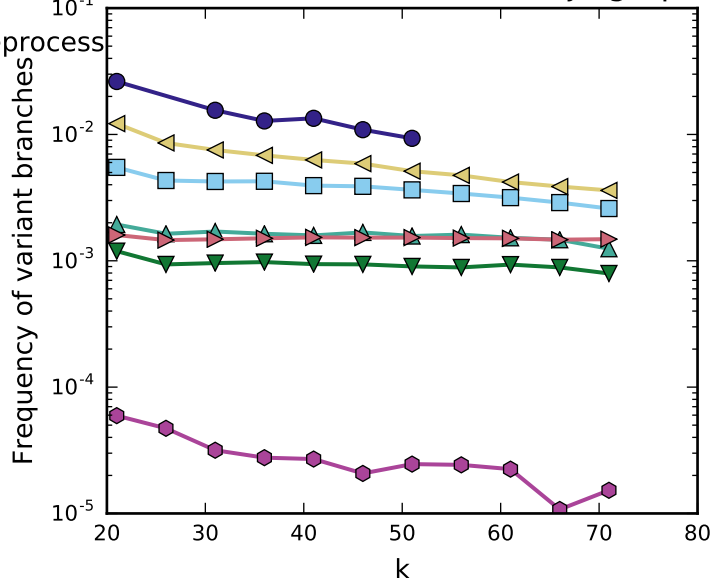


SGA Preqc Results : fig1

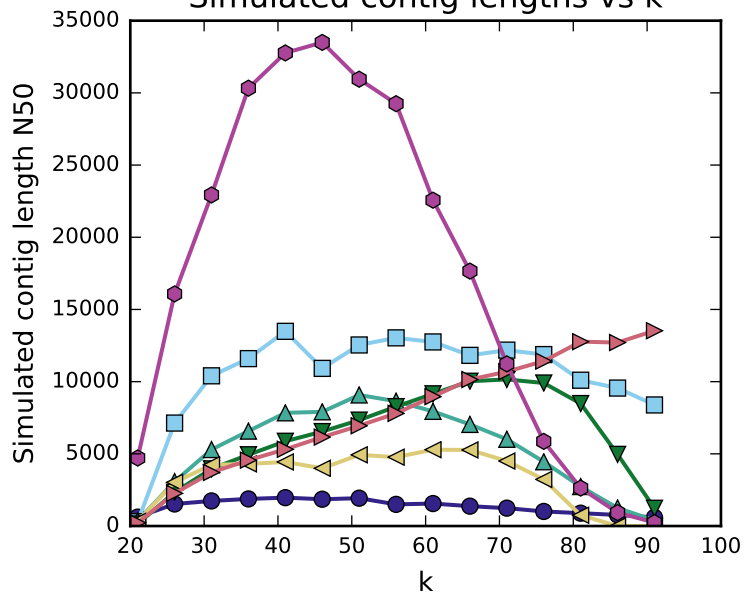
Est. Genome Size



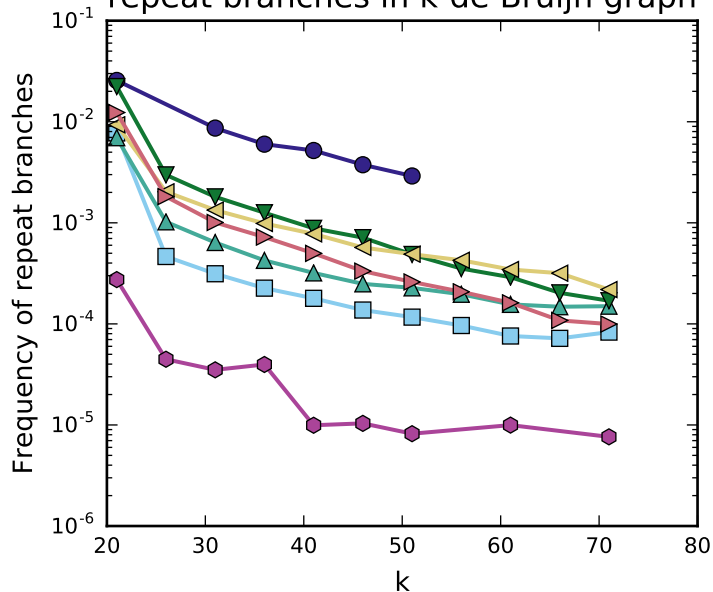
variant branches in k-de Bruijn graph



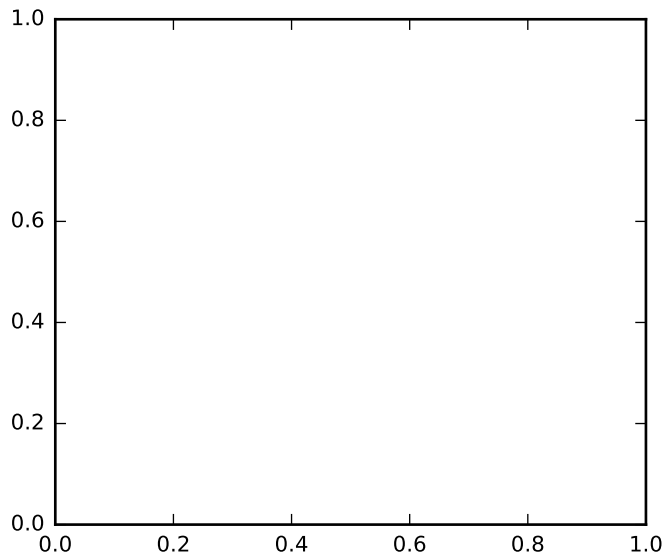
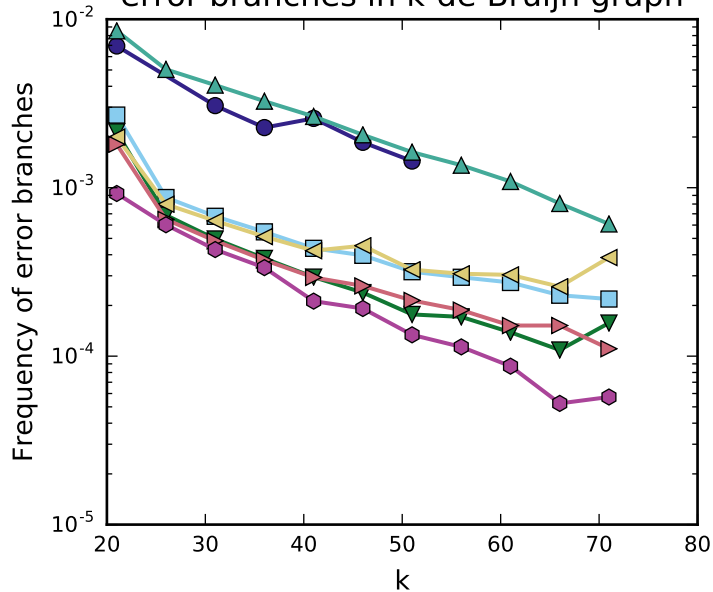
Simulated contig lengths vs k



repeat branches in k-de Bruijn graph

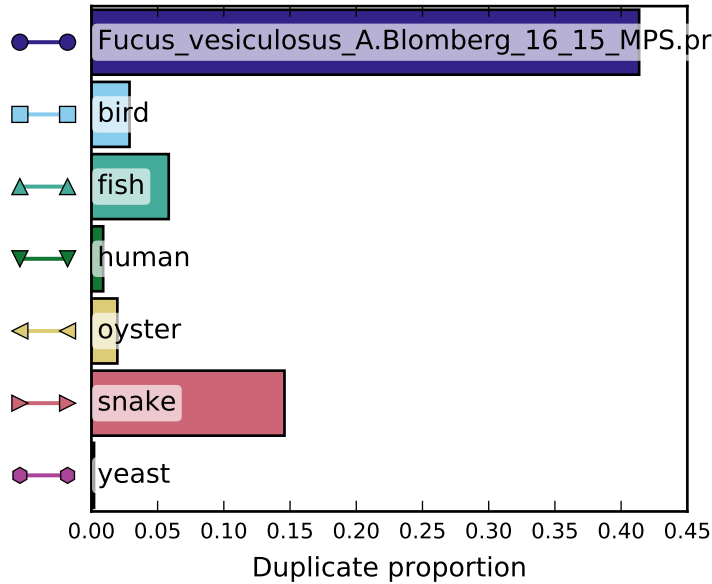


error branches in k-de Bruijn graph

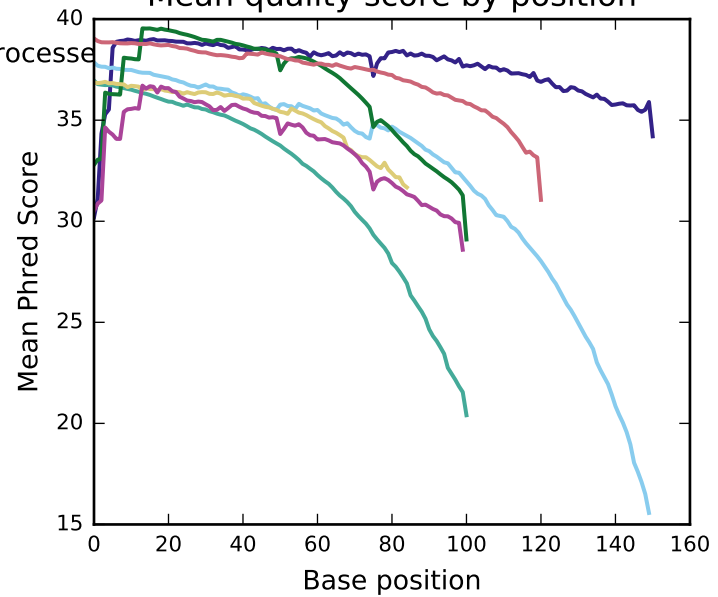


SGA Preqc Results : fig2

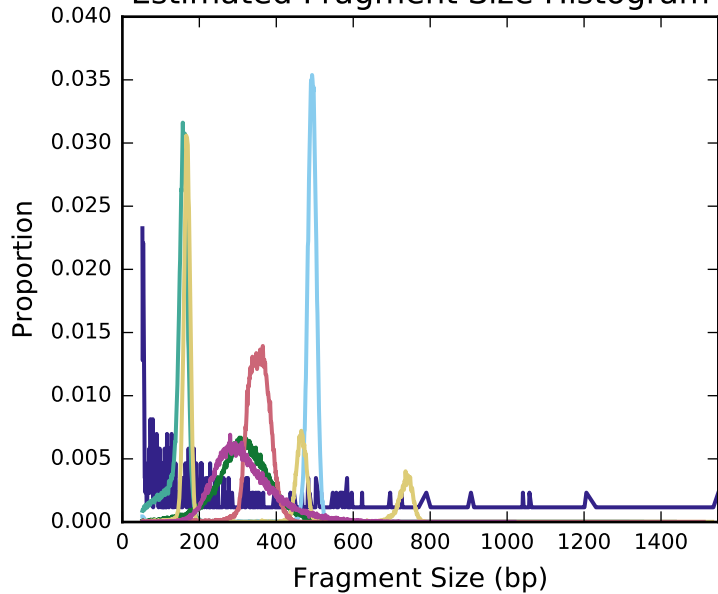
Est. PCR Duplicate Proportion



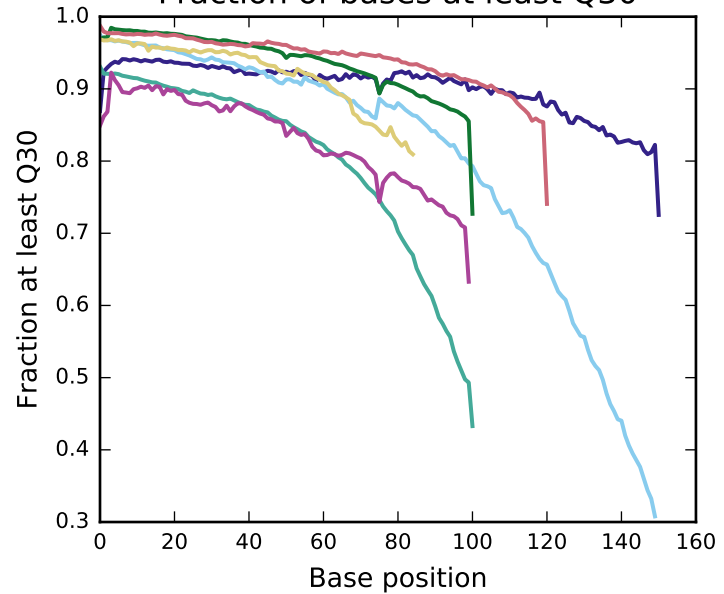
Mean quality score by position



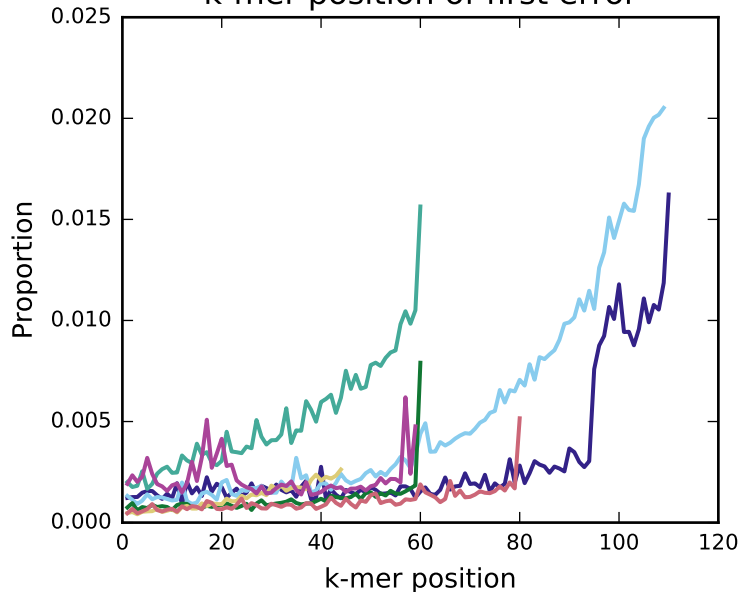
Estimated Fragment Size Histogram



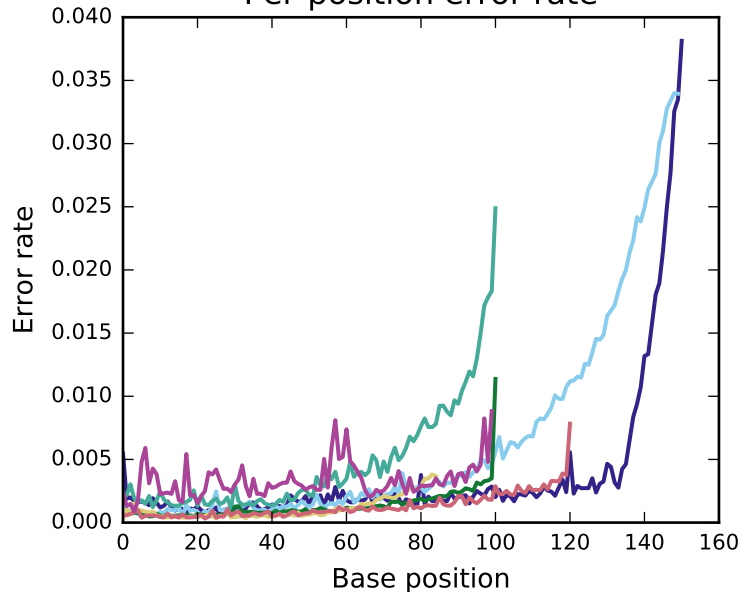
Fraction of bases at least Q30



k-mer position of first error

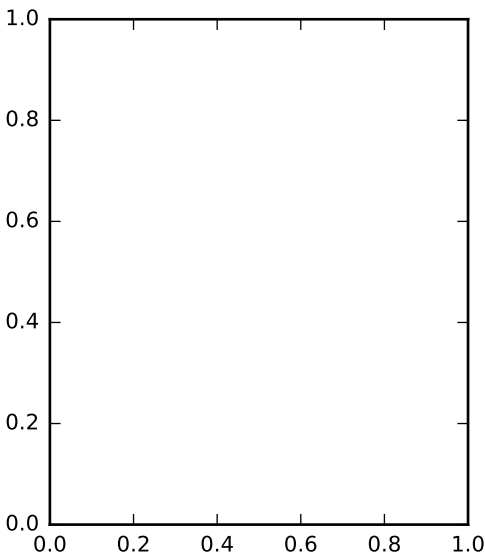
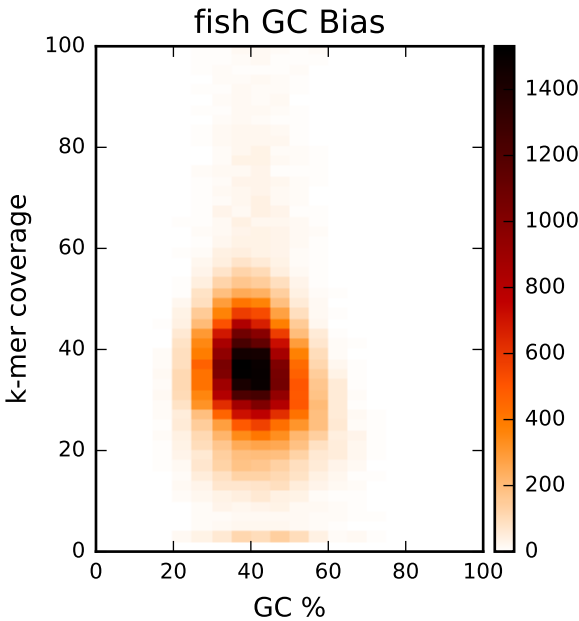
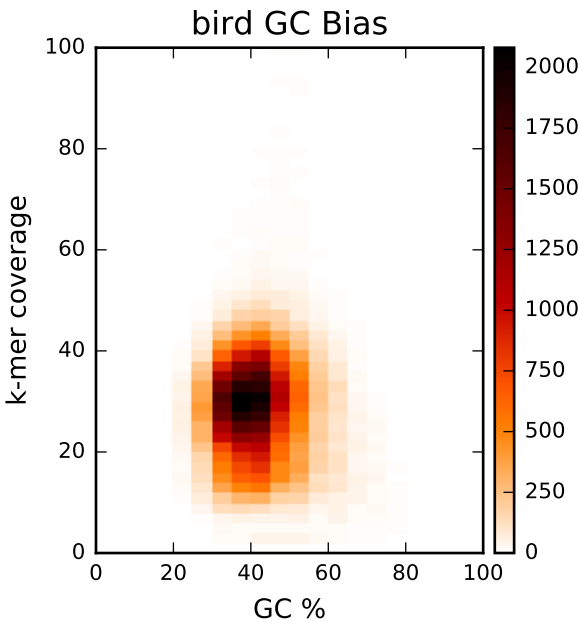
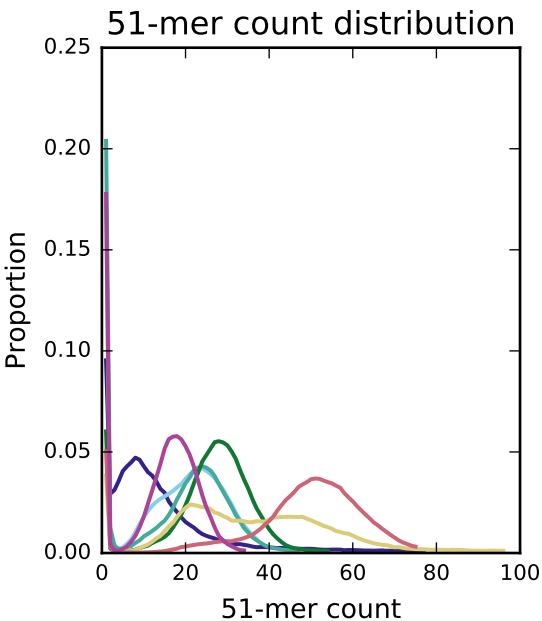
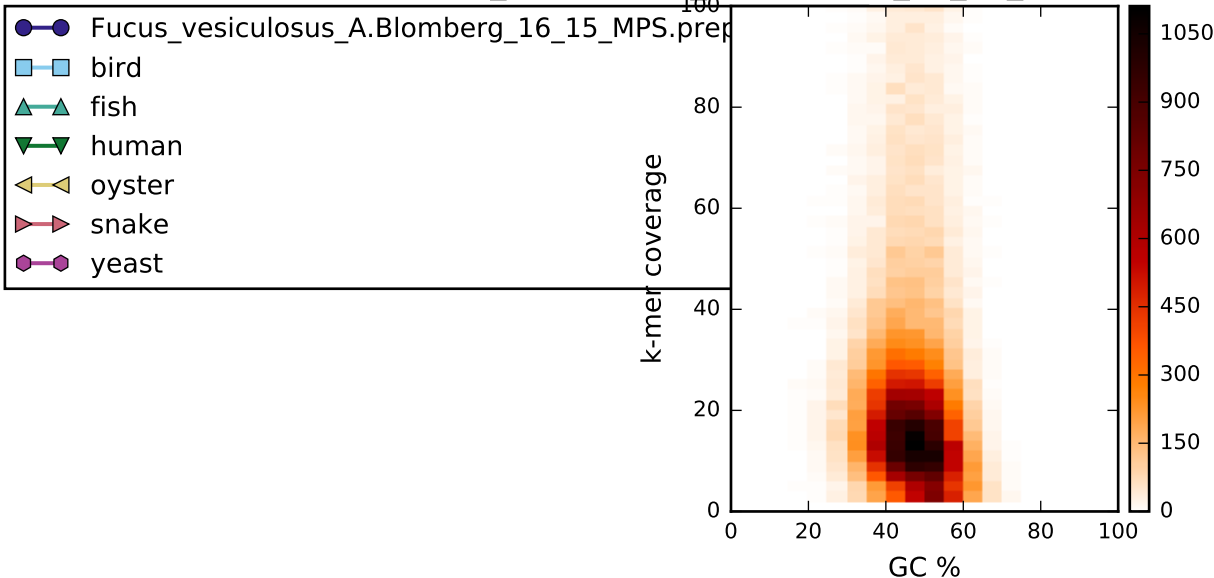


Per-position error rate



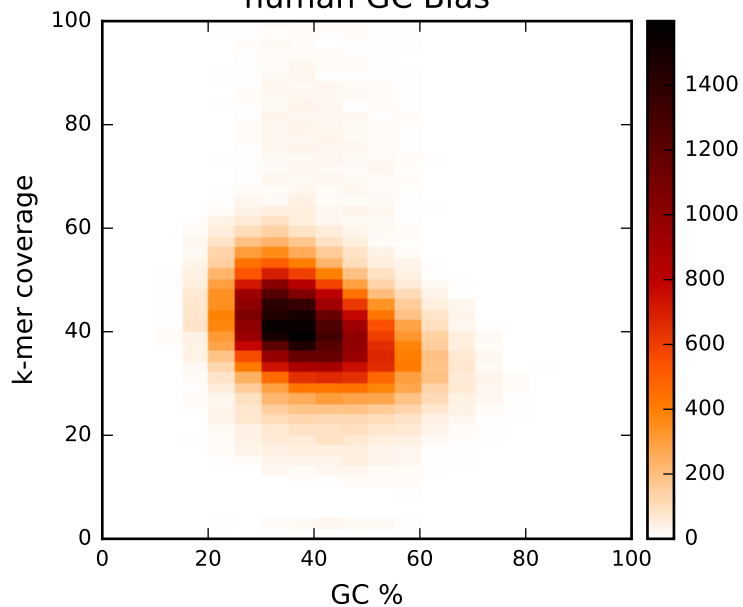
SGA Preqc Results : fig3

Fucus_vesiculosus_A.Blomberg_16_15_MPS.preprocessed GC Bi

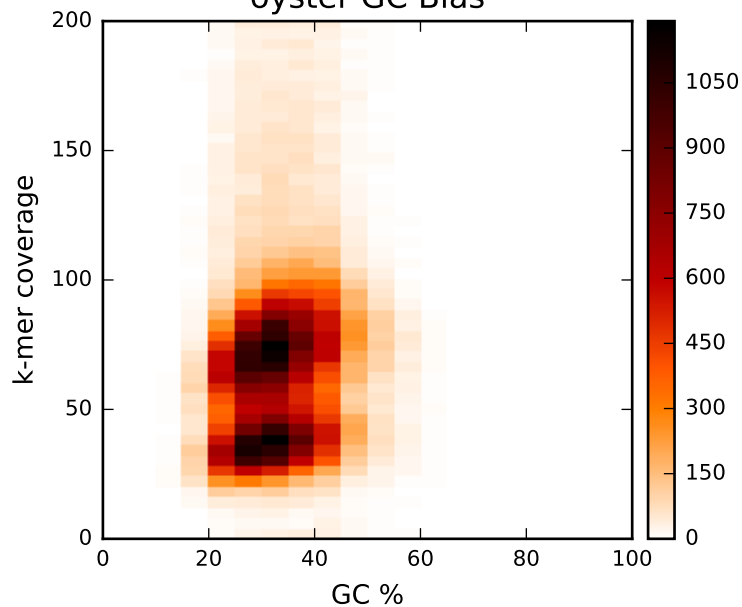


SGA Preqc Results : fig4

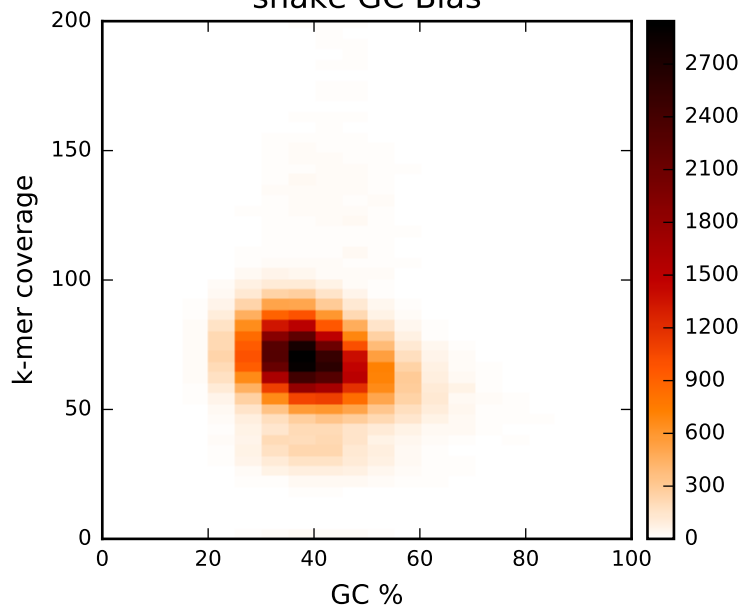
human GC Bias



oyster GC Bias



snake GC Bias



yeast GC Bias

