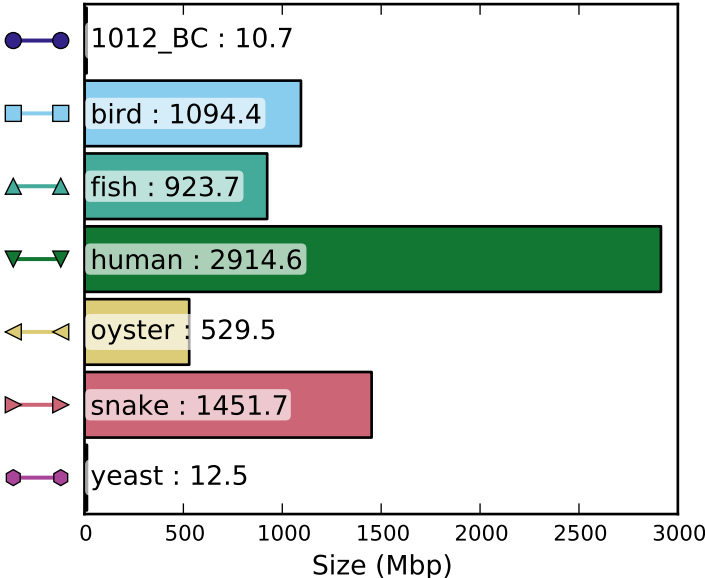
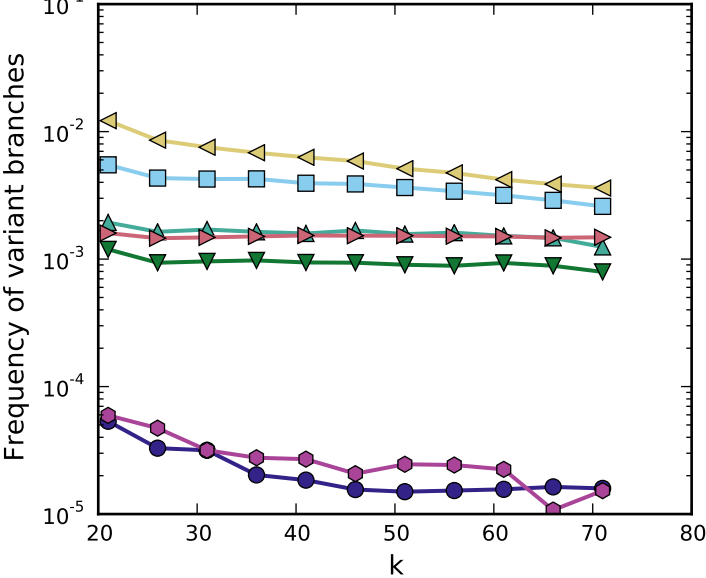


SGA Preqc Results : fig1

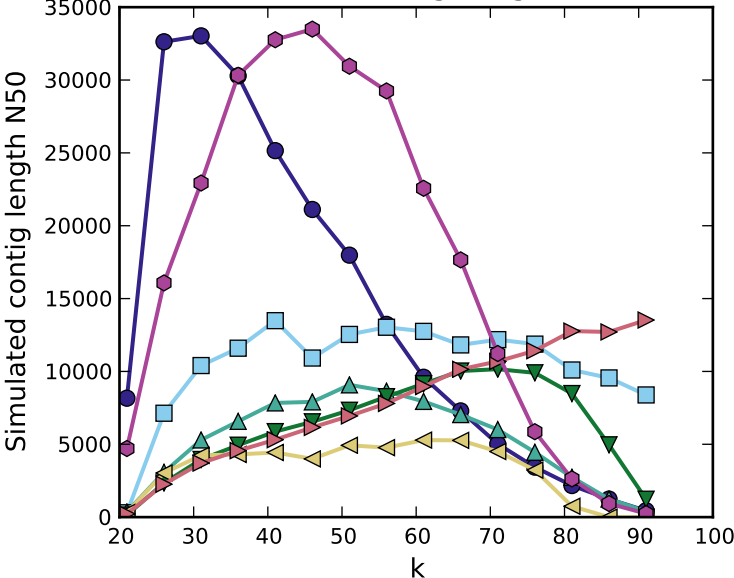
Est. Genome Size



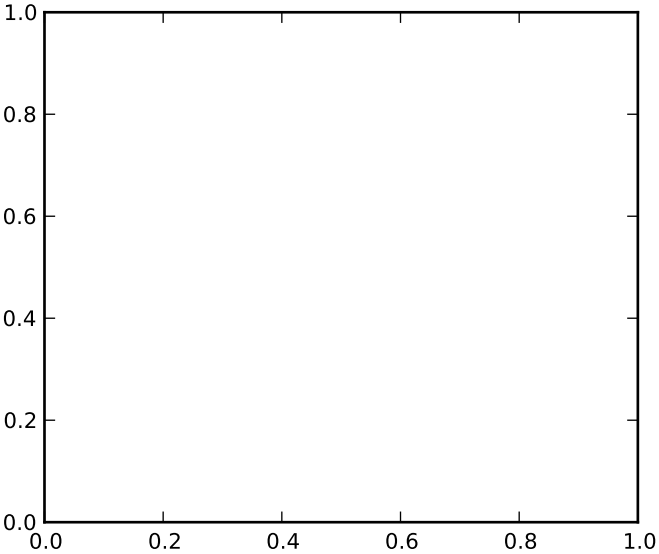
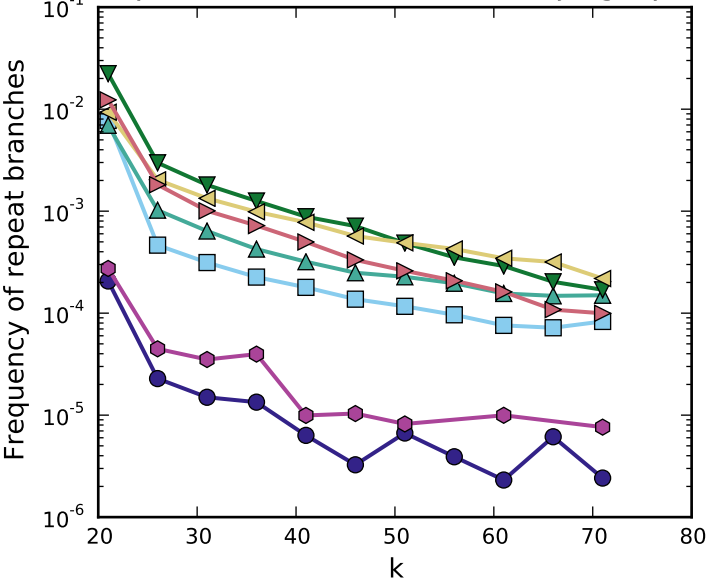
variant branches in k-de Bruijn graph



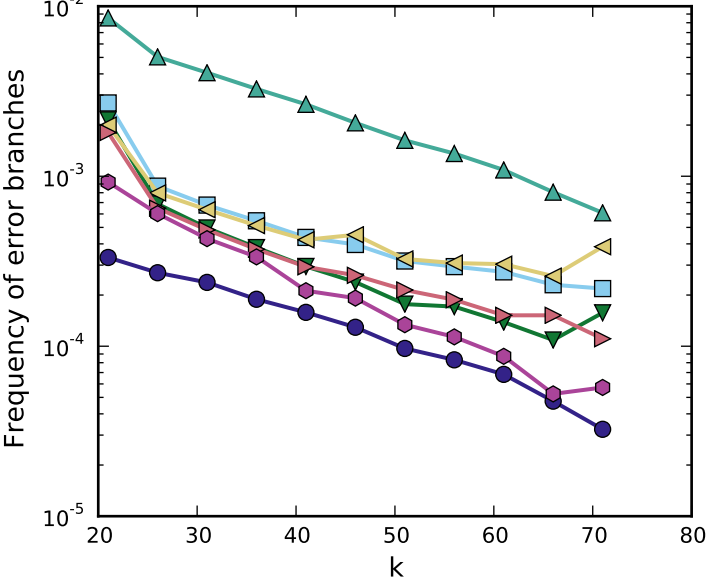
Simulated contig lengths vs k



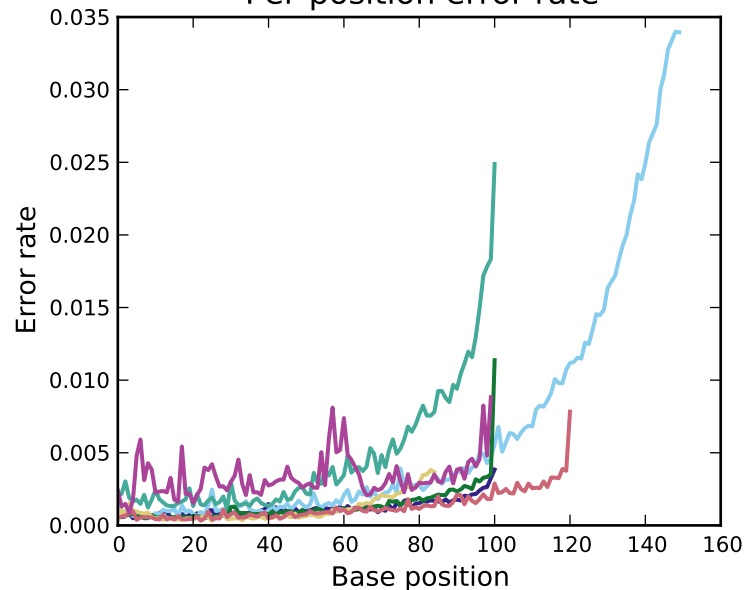
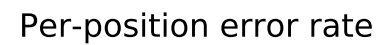
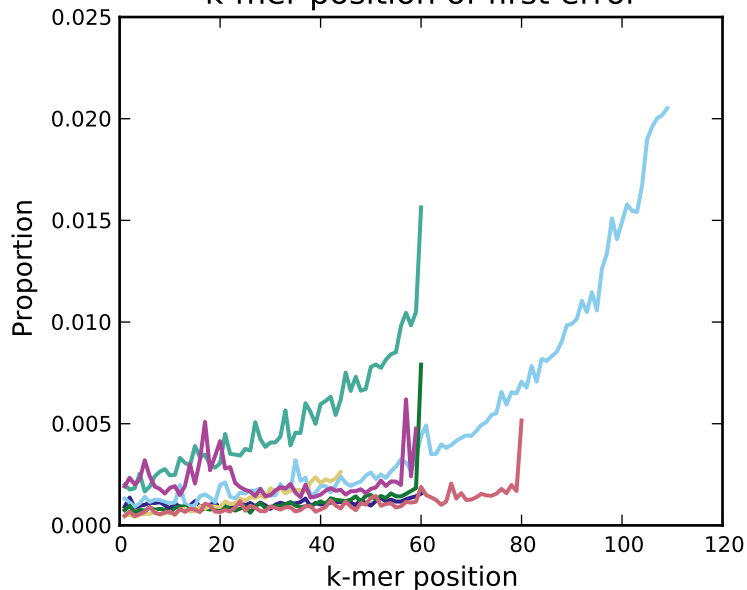
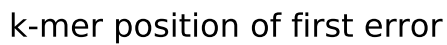
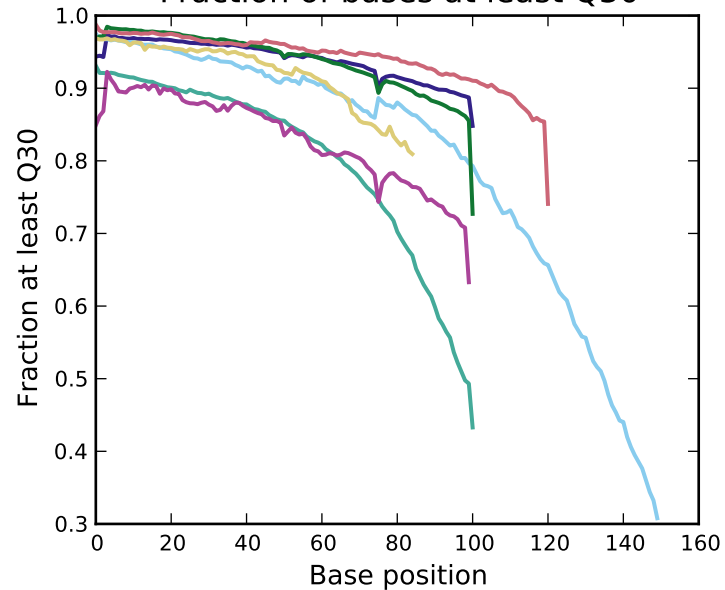
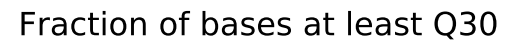
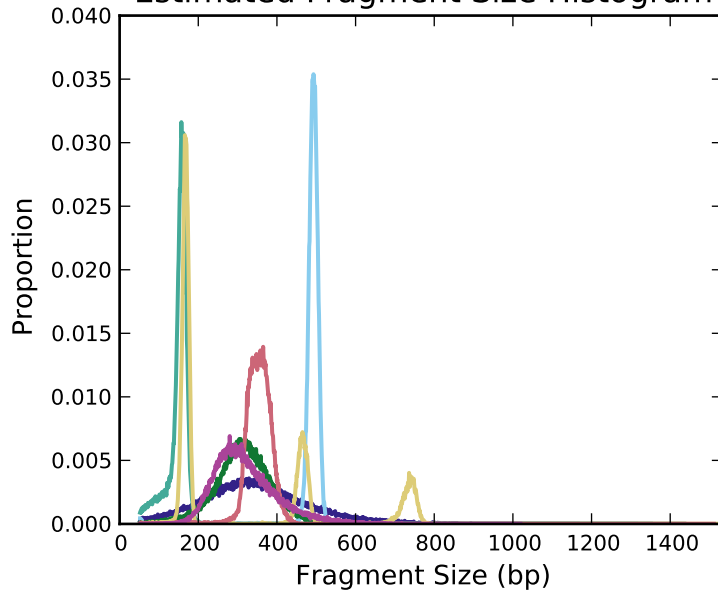
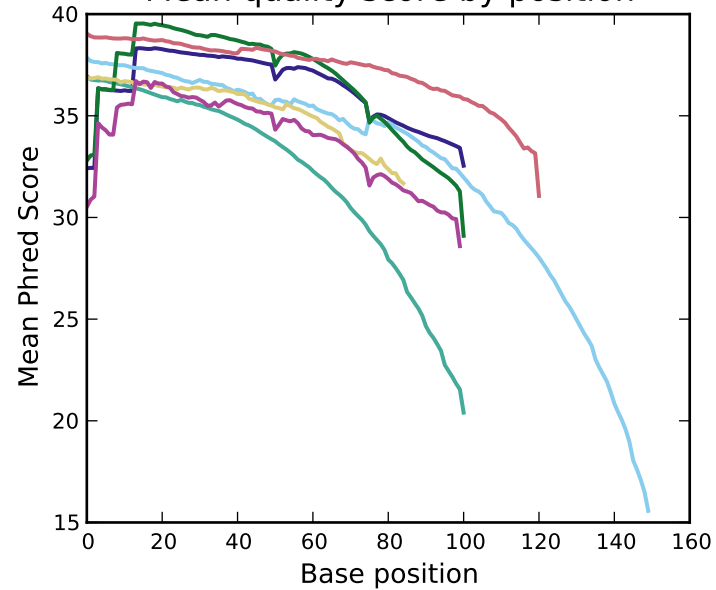
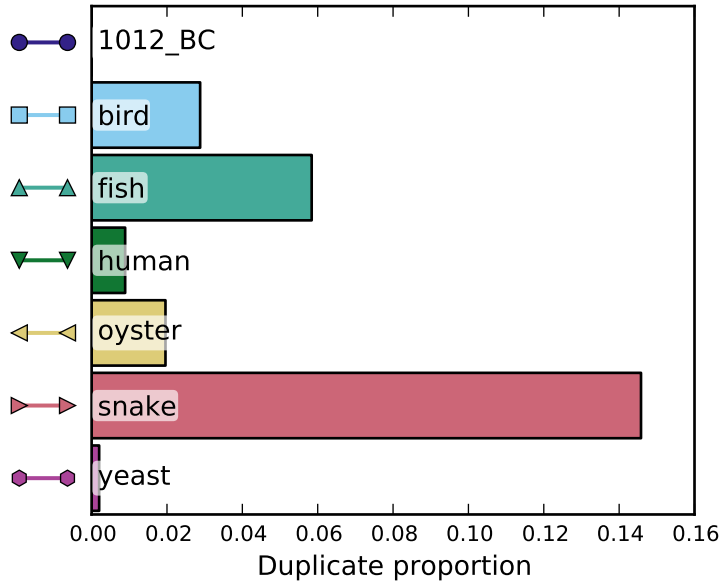
repeat branches in k-de Bruijn graph



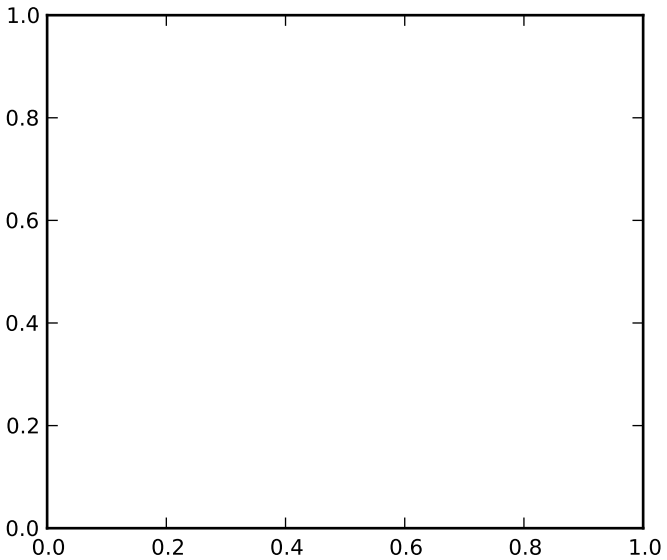
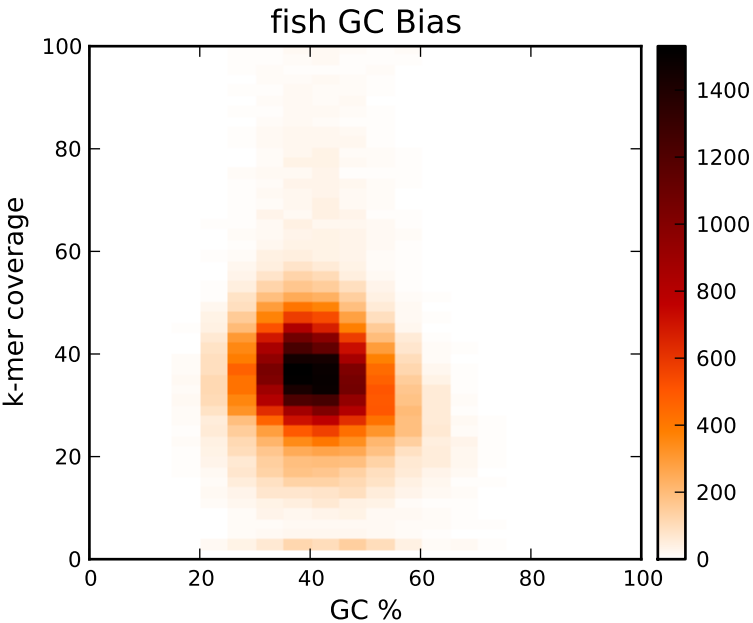
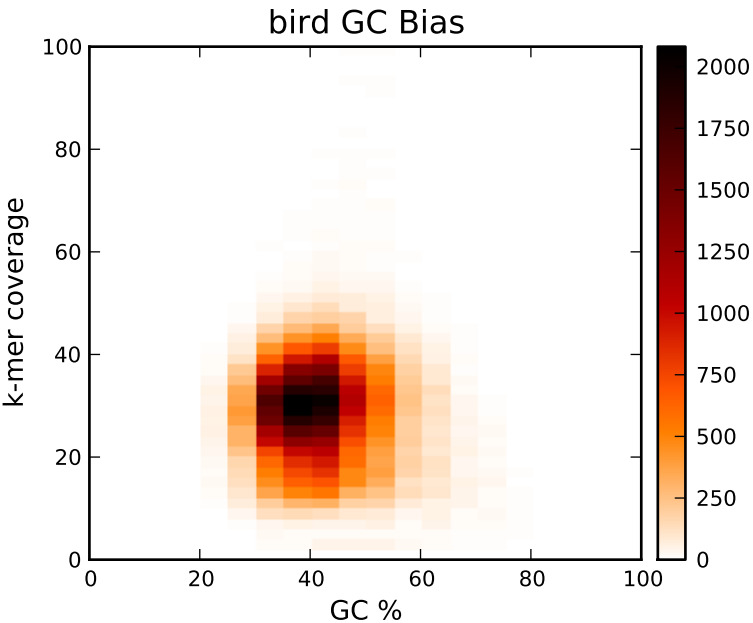
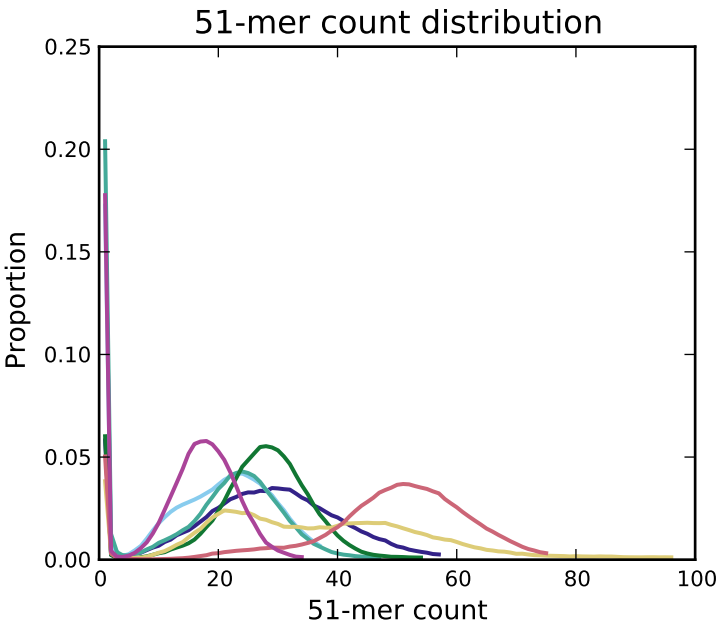
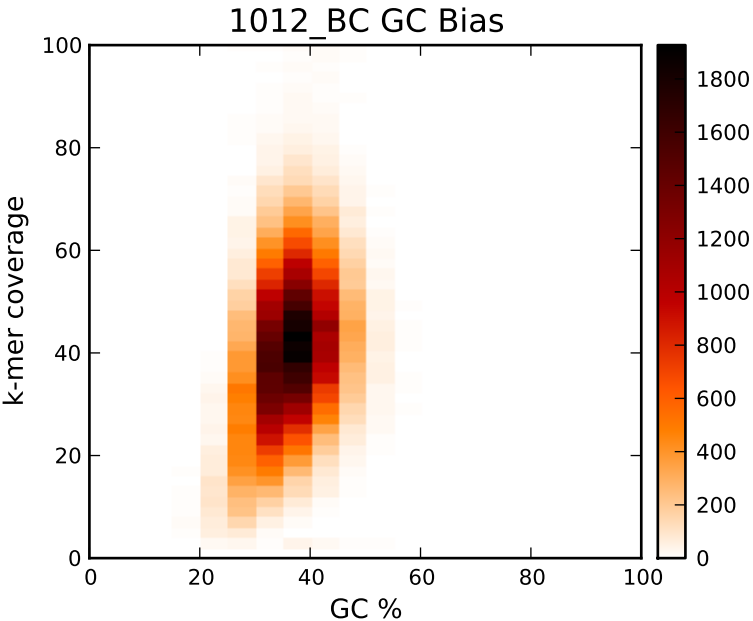
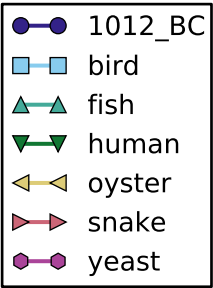
error branches in k-de Bruijn graph



SGA Preqc Results : fig2

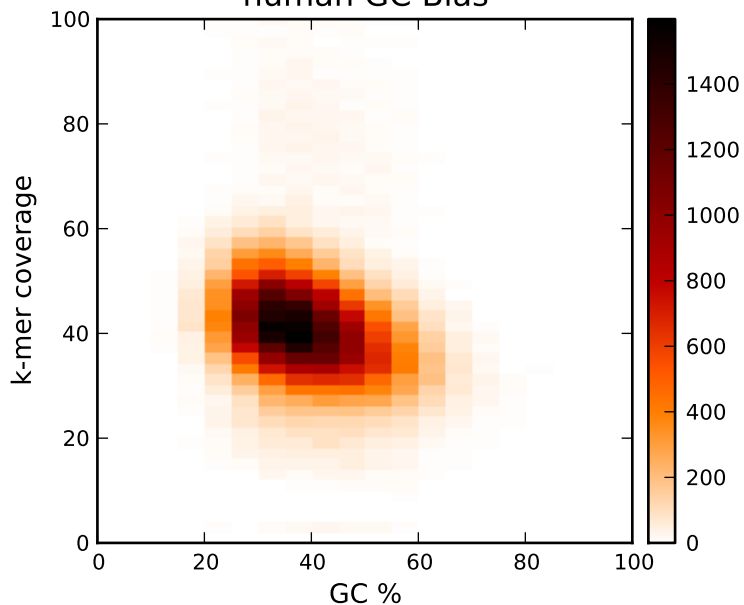


SGA Preqc Results : fig3

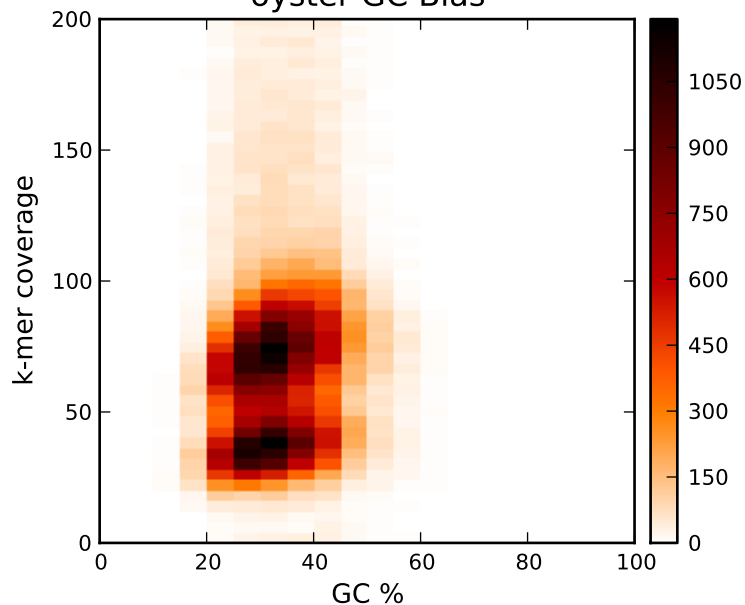


SGA Preqc Results : fig4

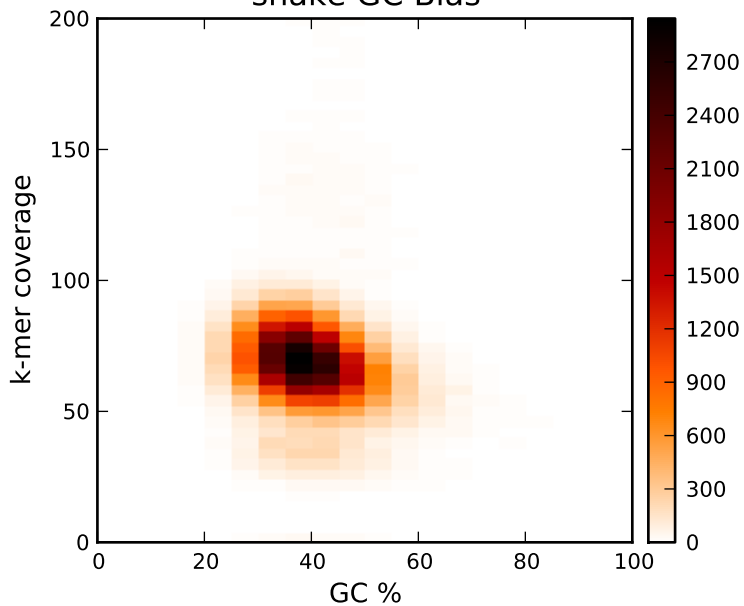
human GC Bias



oyster GC Bias



snake GC Bias



yeast GC Bias

