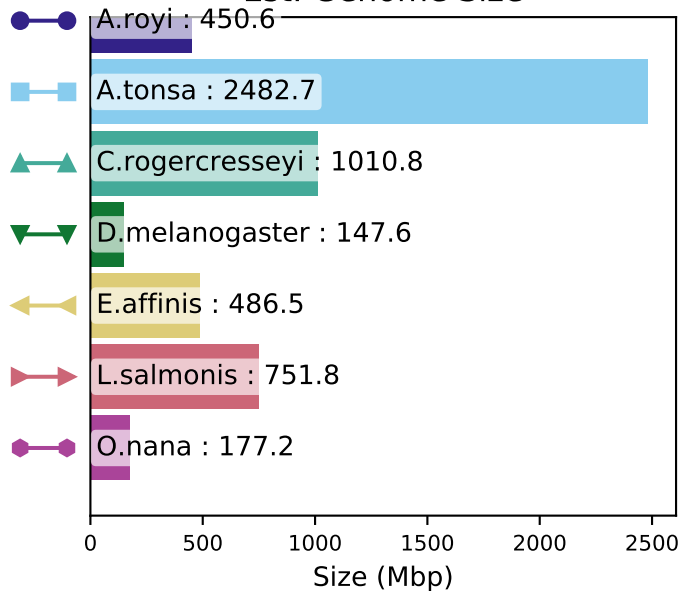
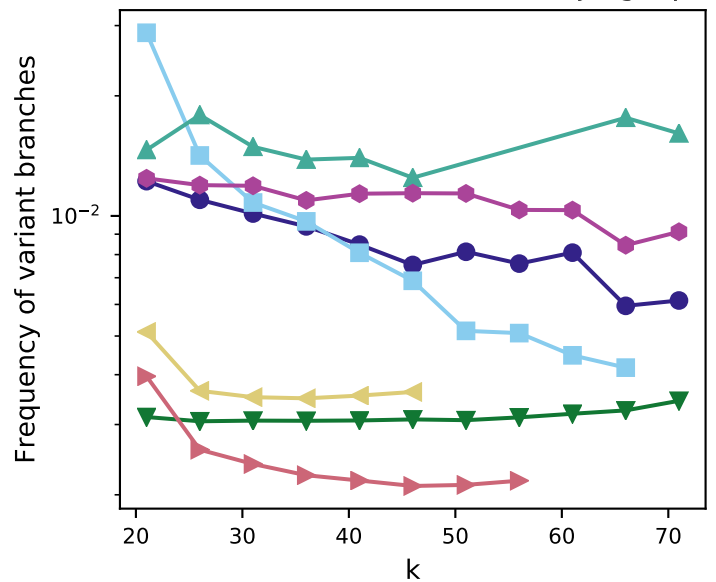


SGA Preqc Results : fig1

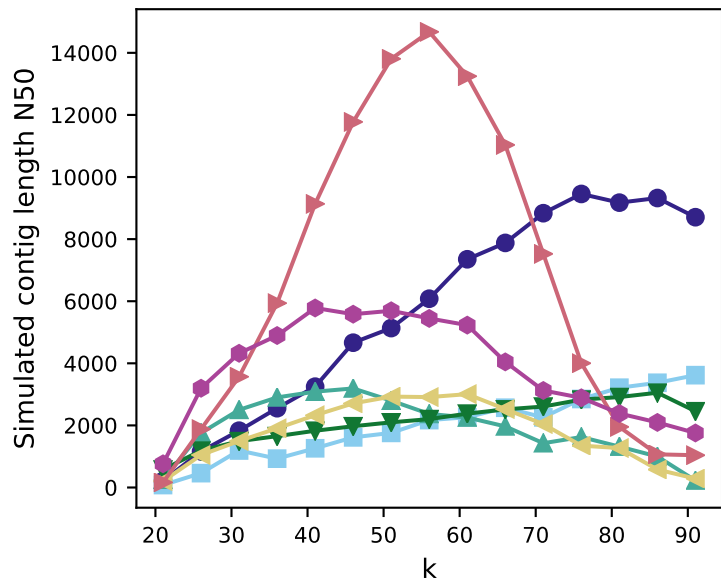
Est. Genome Size



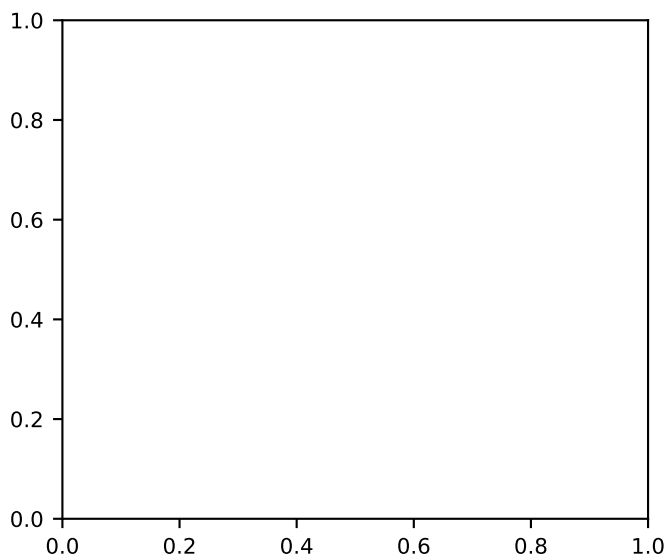
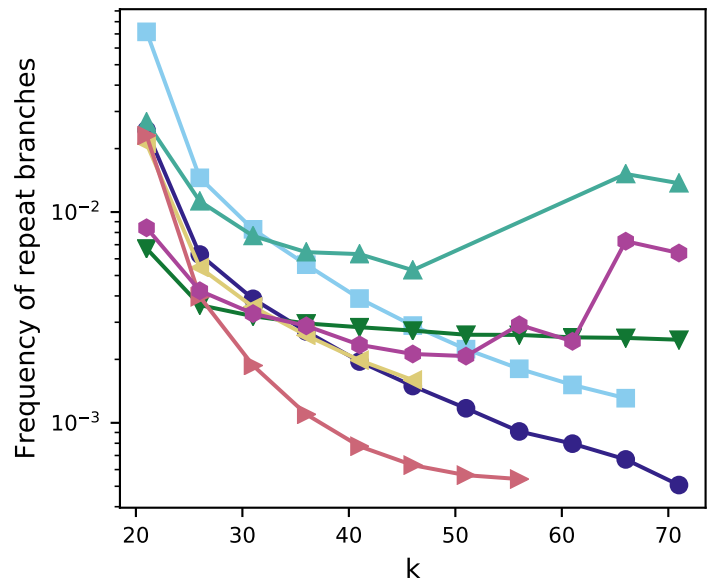
variant branches in k-de Bruijn graph



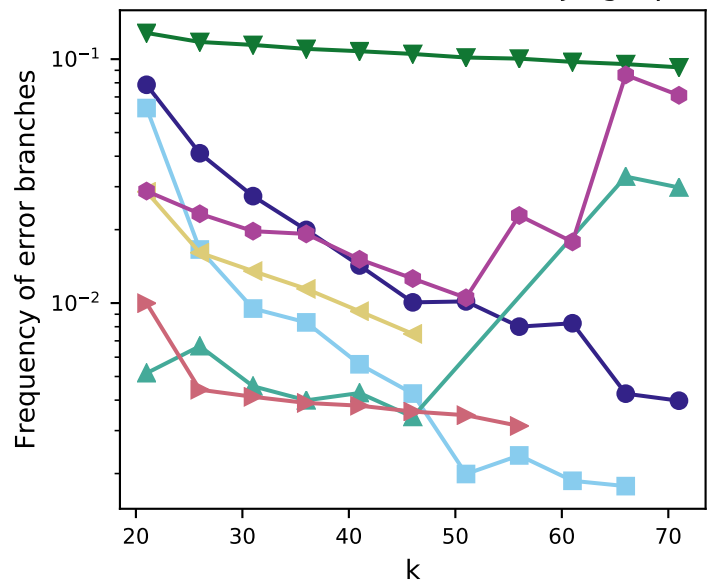
Simulated contig lengths vs k



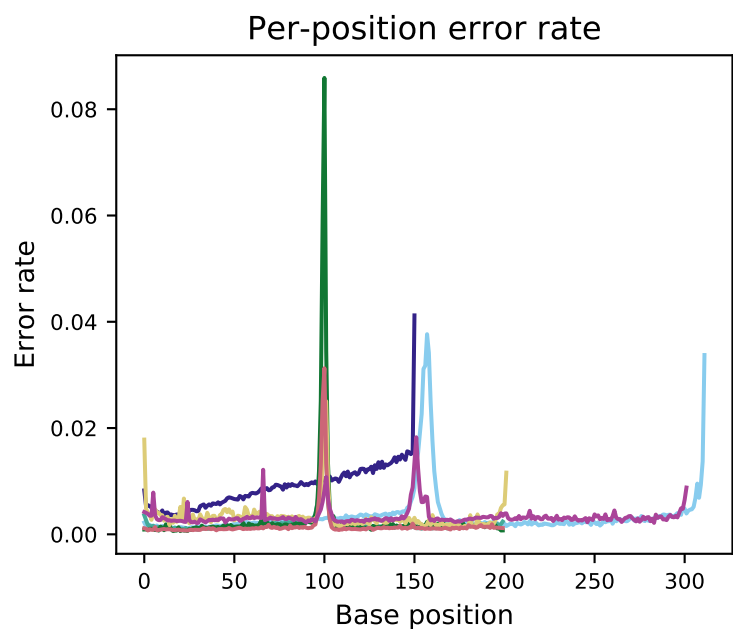
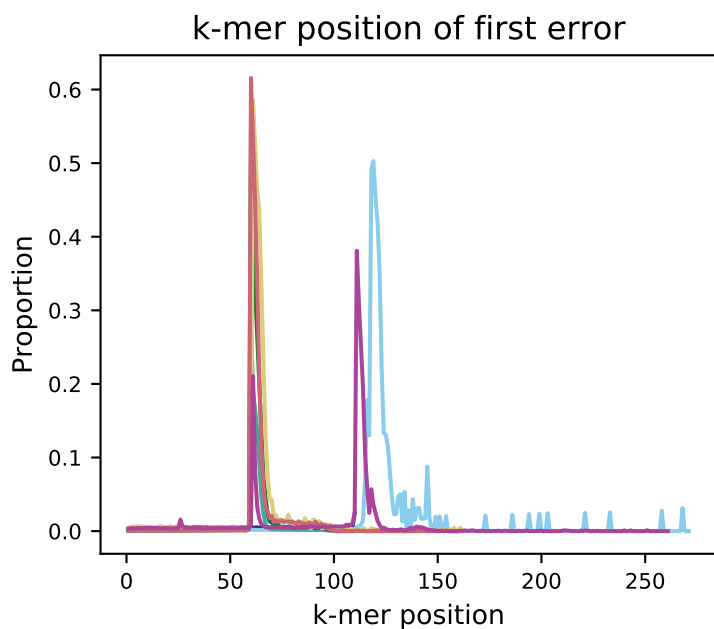
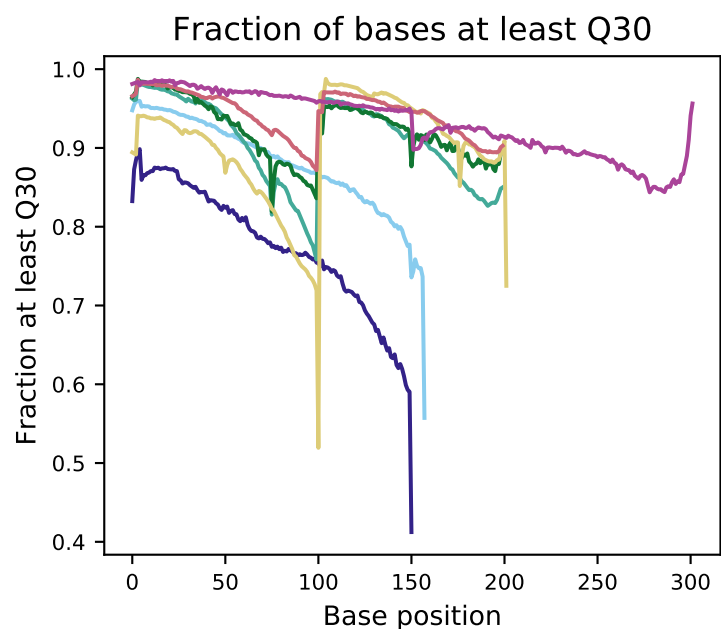
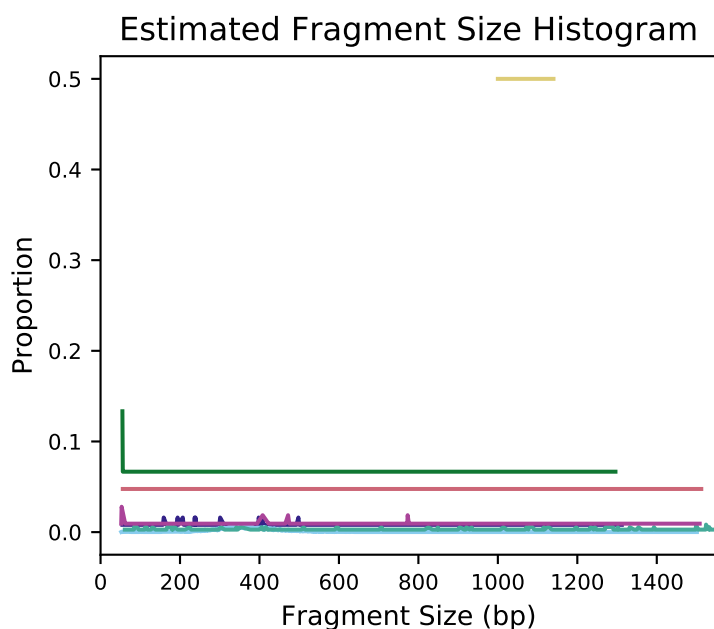
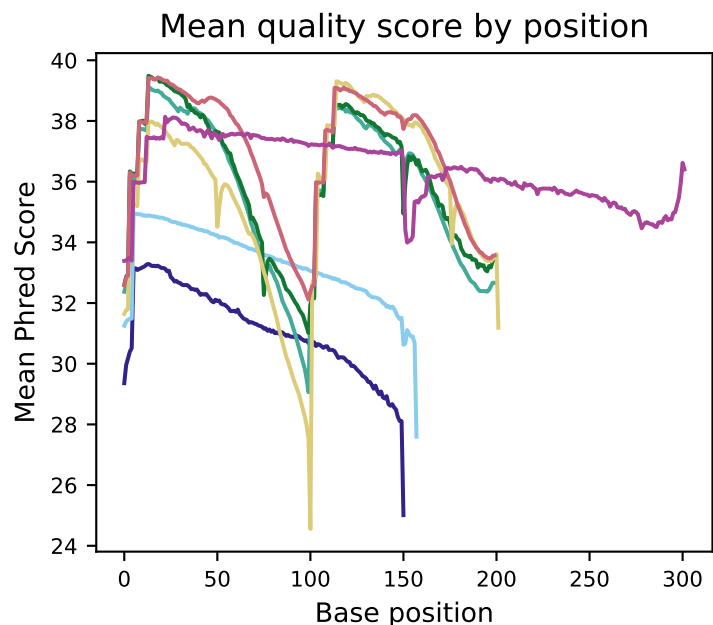
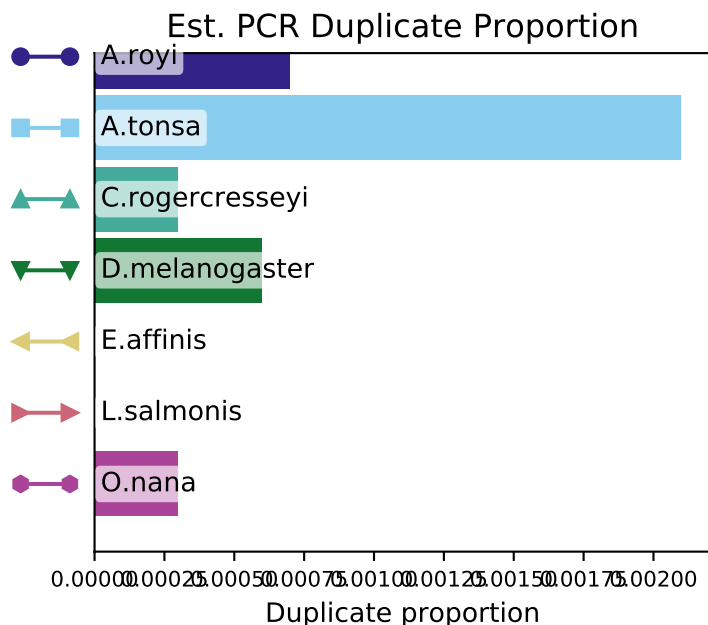
repeat branches in k-de Bruijn graph



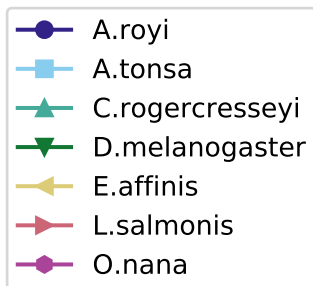
error branches in k-de Bruijn graph



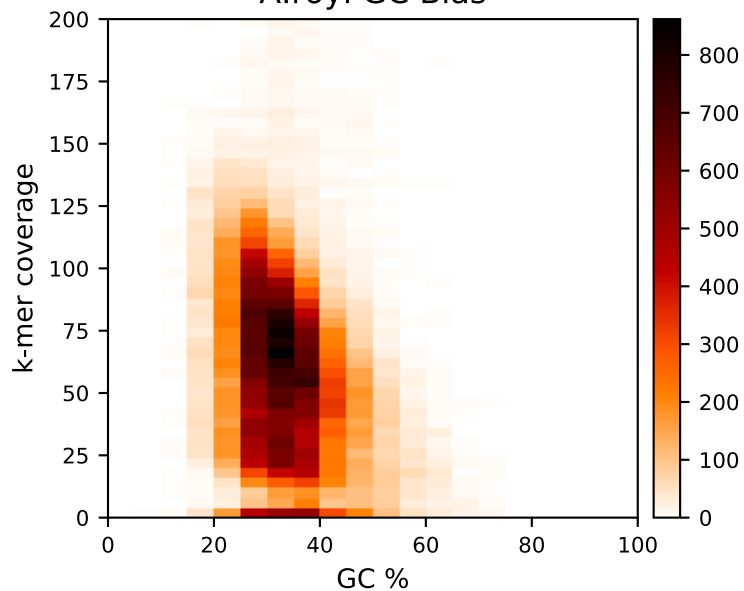
SGA Preqc Results : fig2



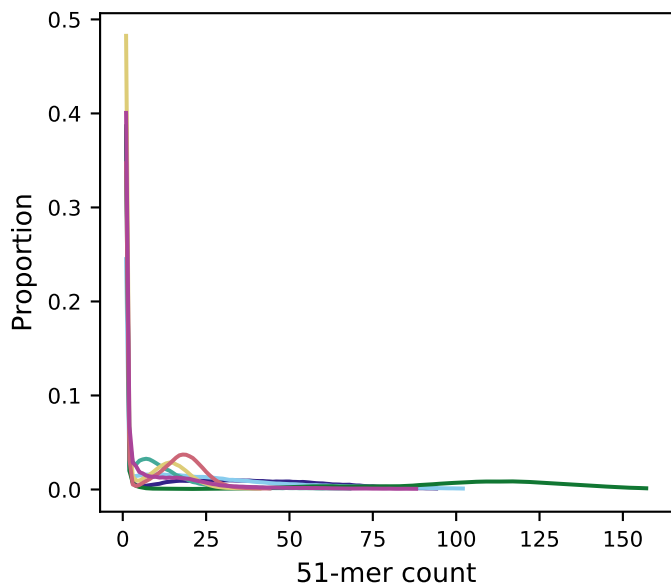
SGA Preqc Results : fig3



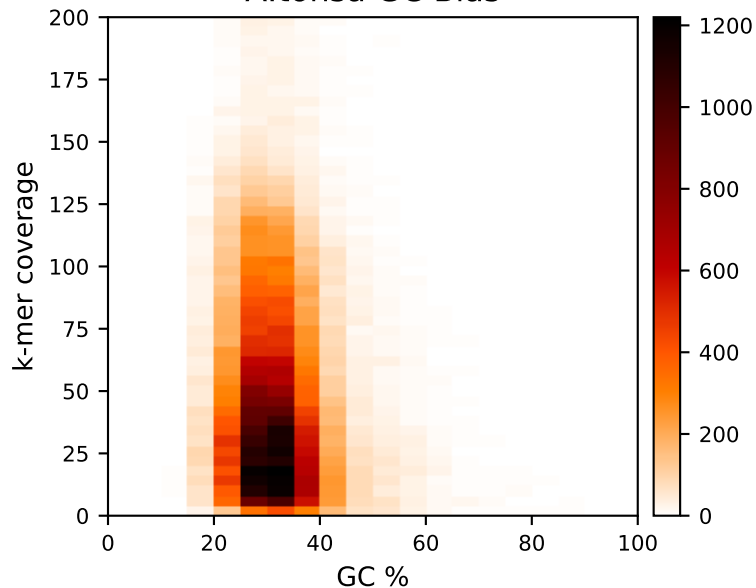
A.royi GC Bias



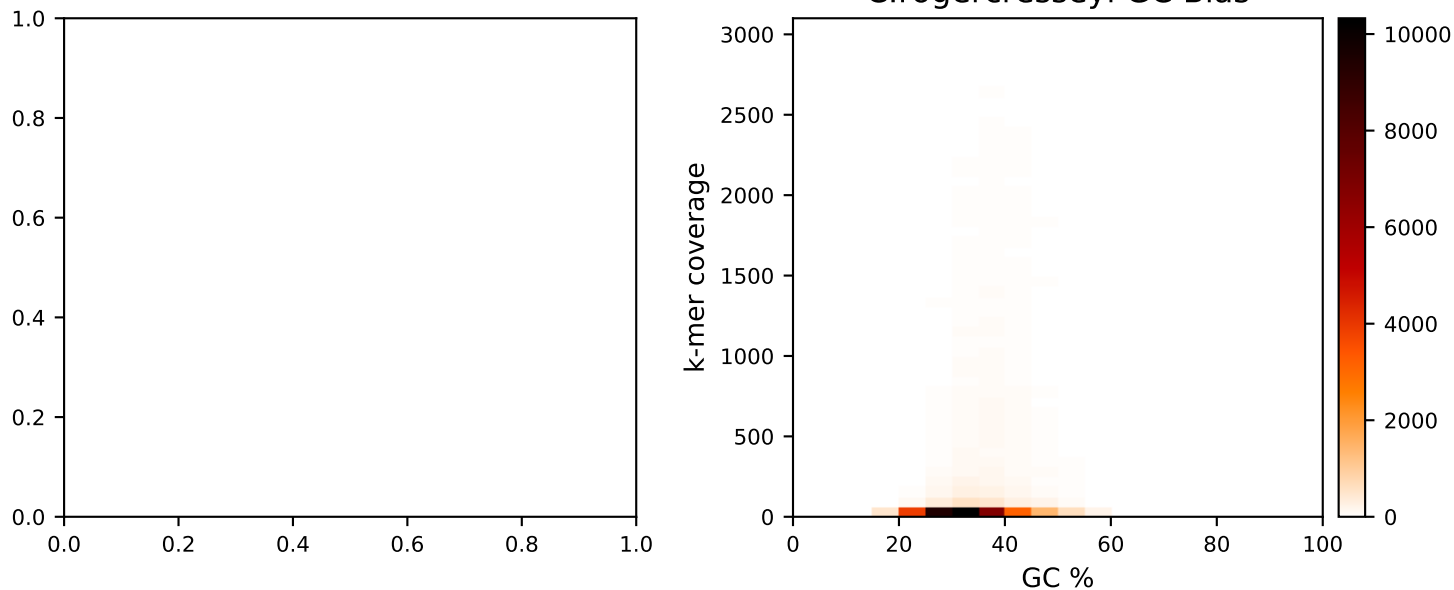
51-mer count distribution



A.tonsa GC Bias

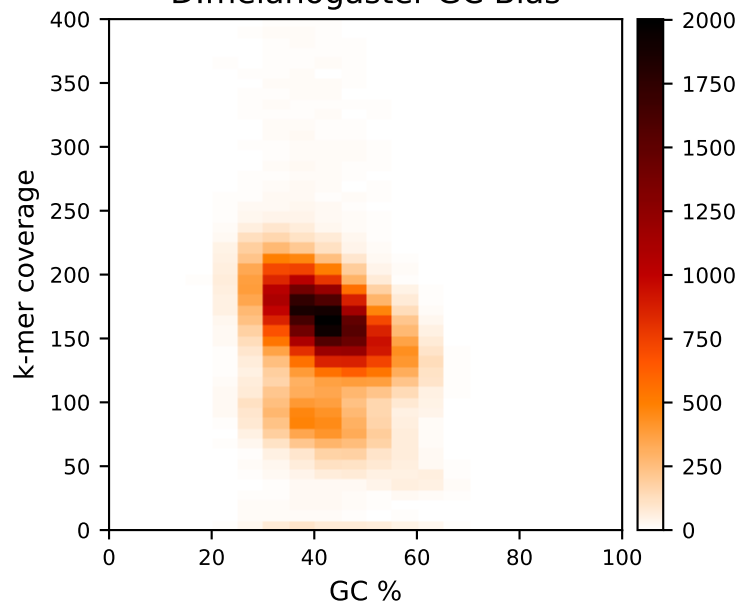


C.rogercresseyi GC Bias

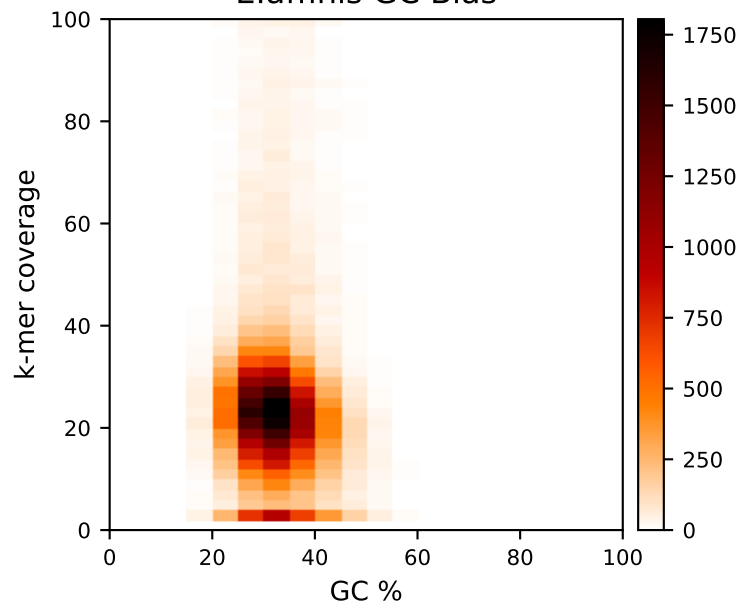


SGA Preqc Results : fig4

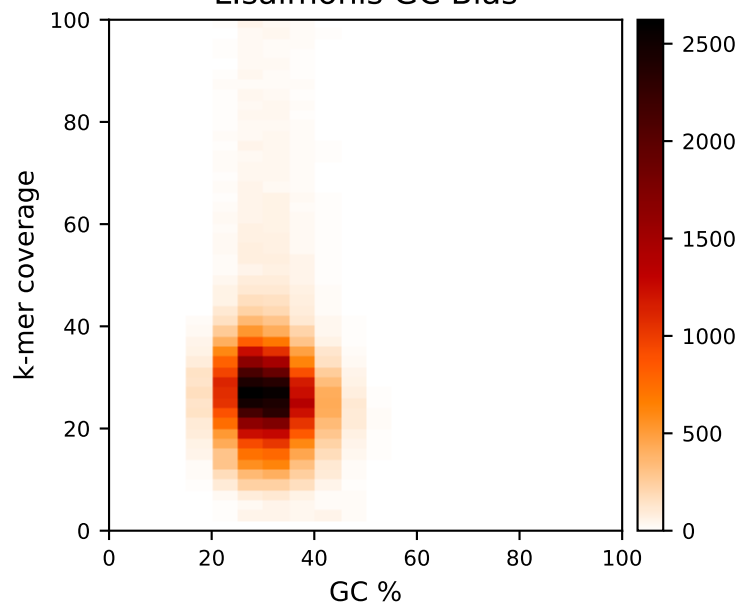
D.melanogaster GC Bias



E.affinis GC Bias



L.salmonis GC Bias



O.nana GC Bias

