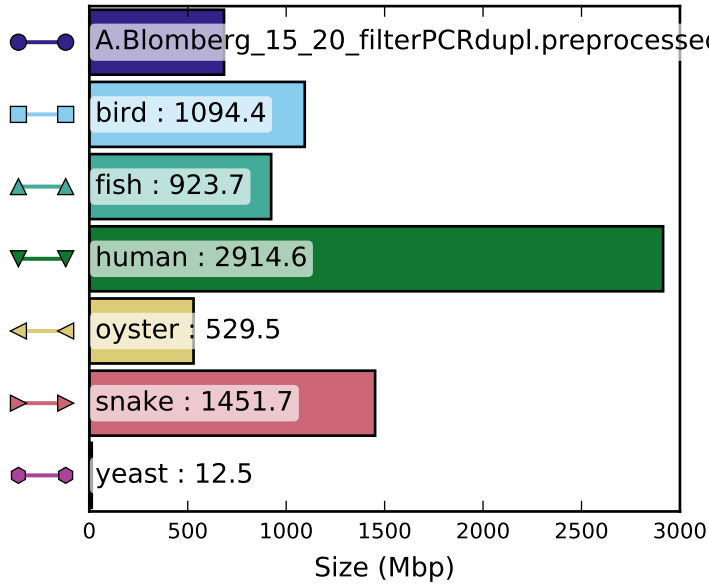
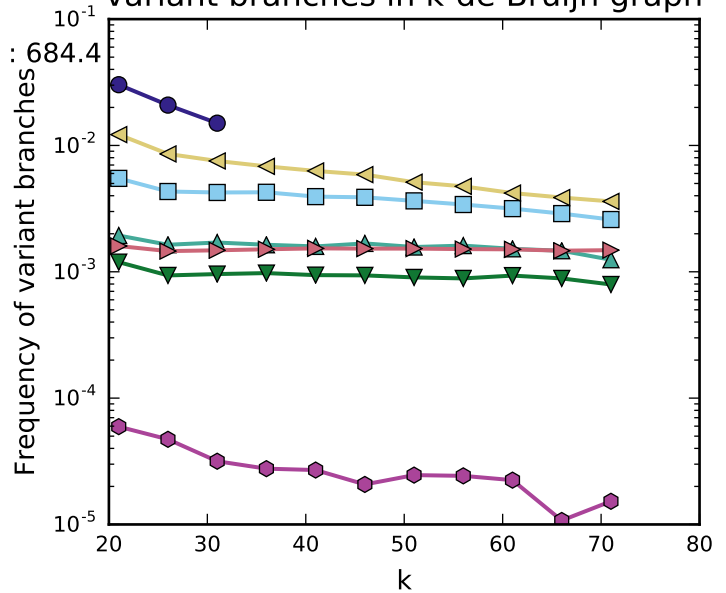


# SGA Preqc Results : fig1

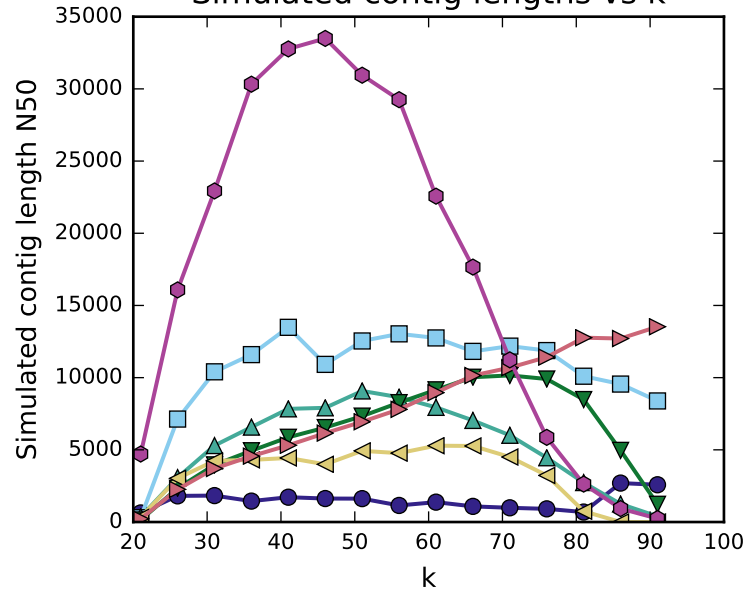
## Est. Genome Size



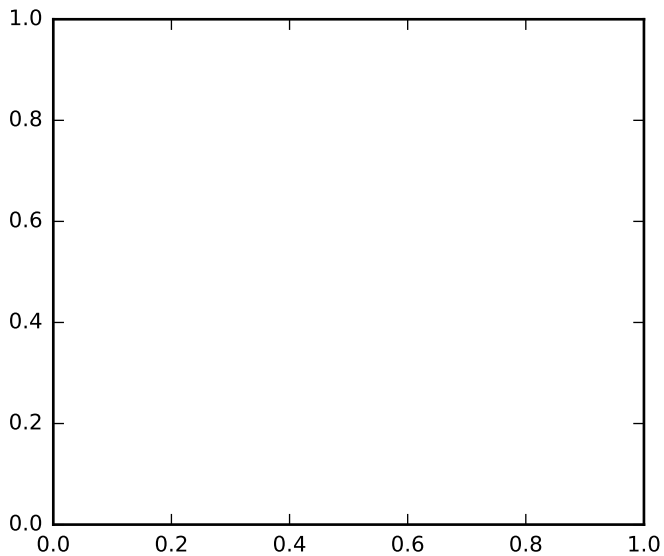
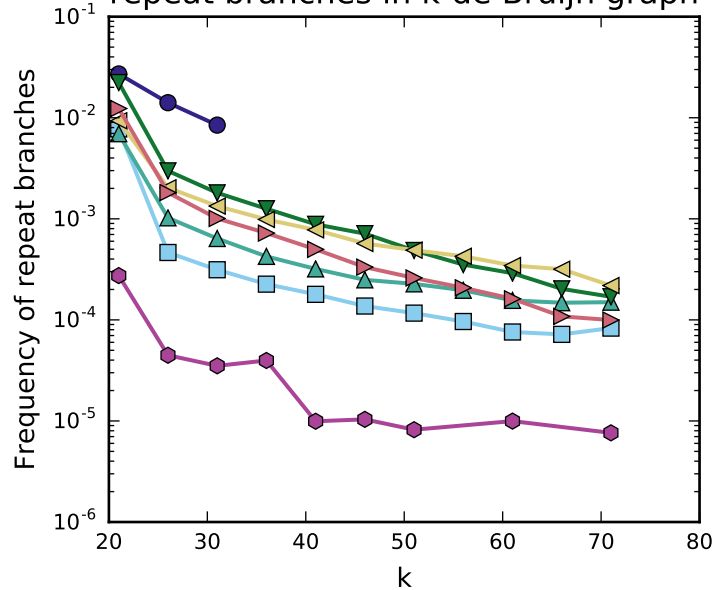
## variant branches in k-de Bruijn graph



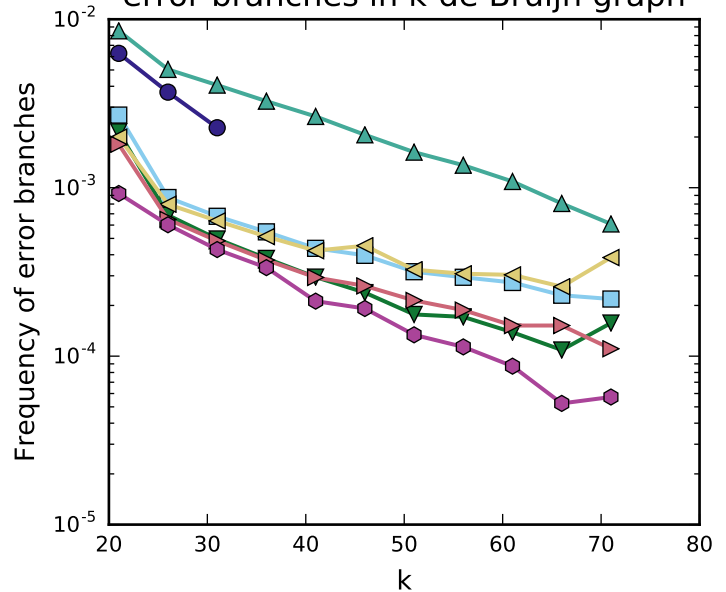
## Simulated contig lengths vs k



## repeat branches in k-de Bruijn graph

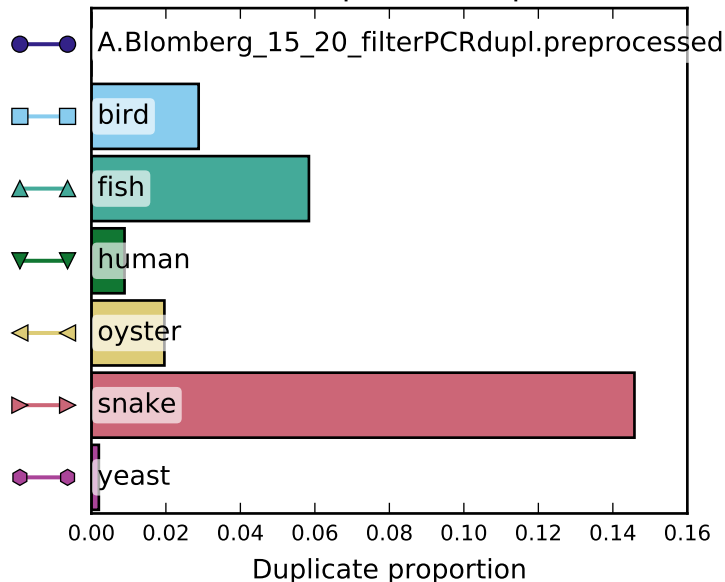


## error branches in k-de Bruijn graph

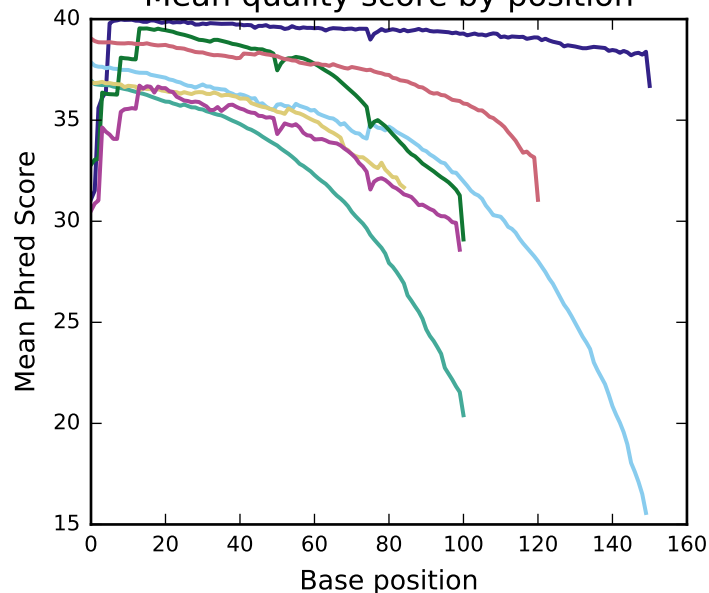


# SGA Preqc Results : fig2

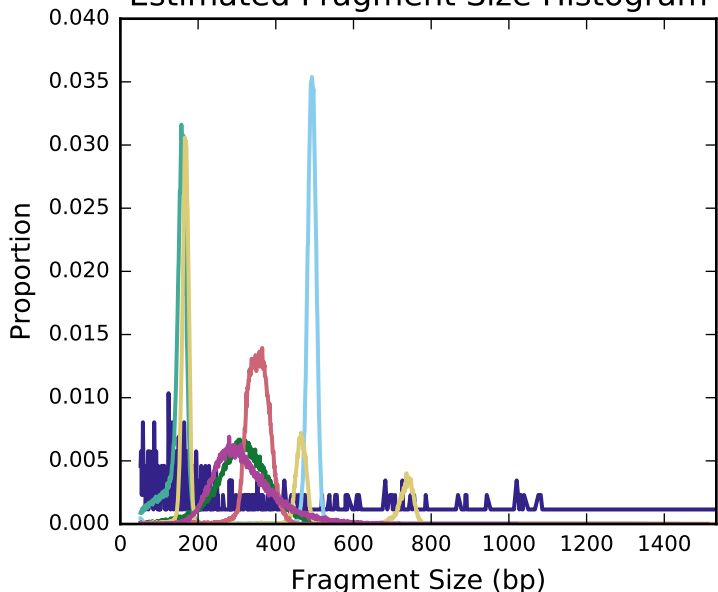
## Est. PCR Duplicate Proportion



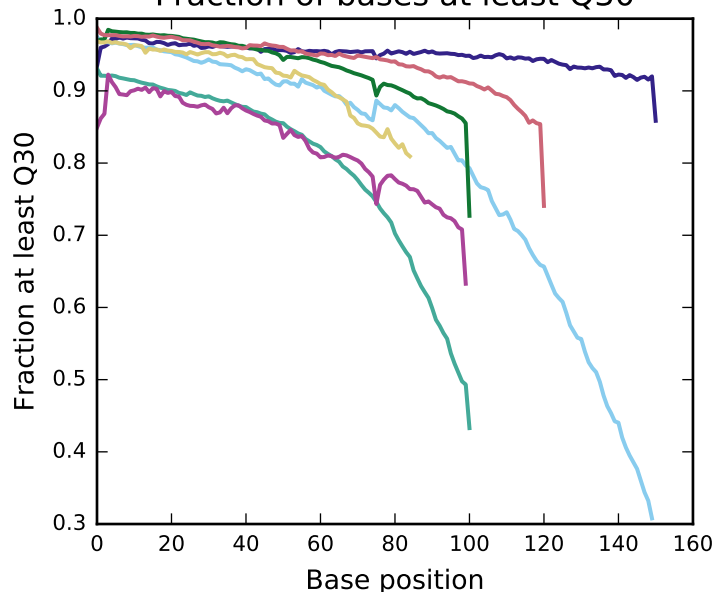
## Mean quality score by position



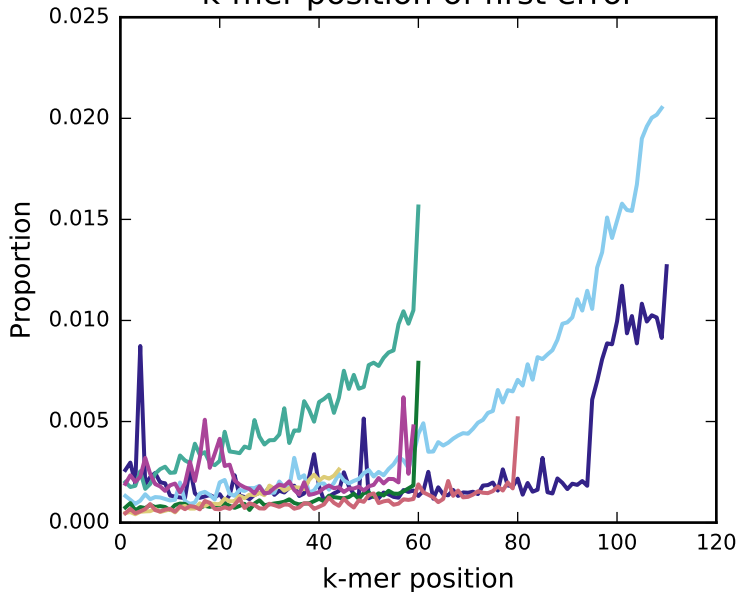
## Estimated Fragment Size Histogram



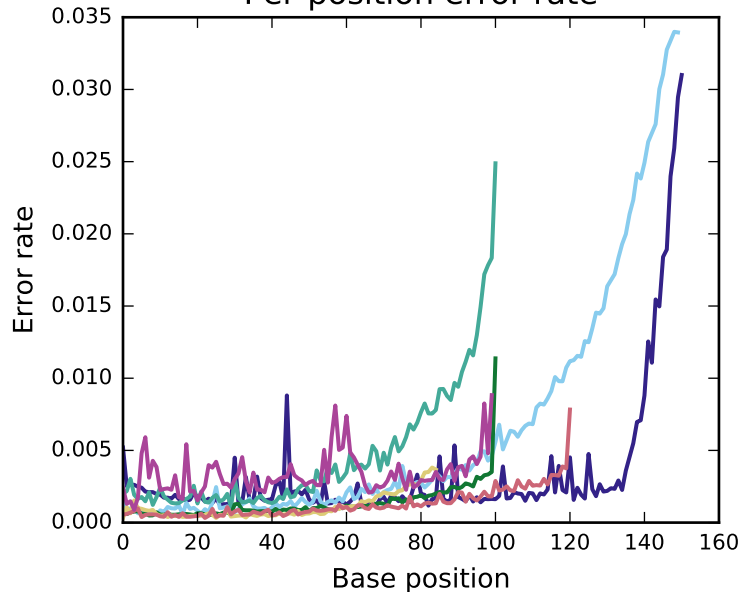
## Fraction of bases at least Q30



## k-mer position of first error

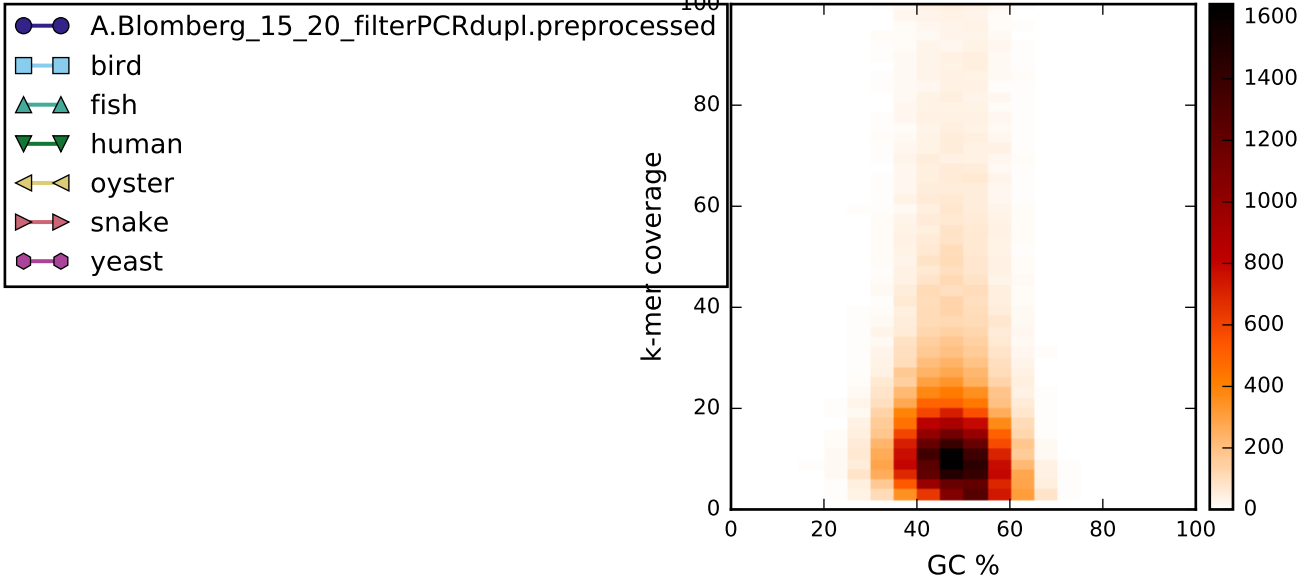


## Per-position error rate

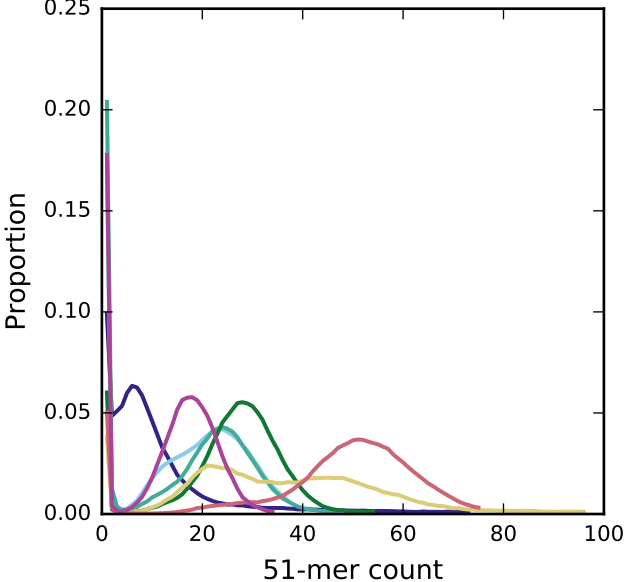


# SGA Preqc Results : fig3

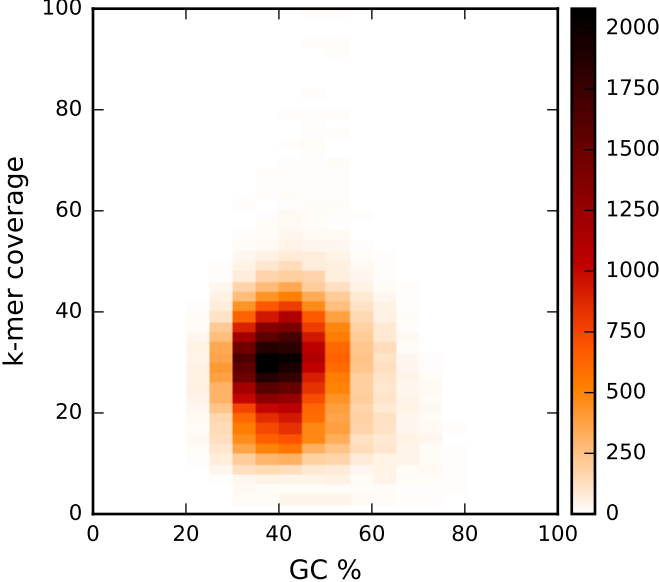
A.Blomberg\_15\_20\_filterPCRdupl.preprocessed GC Bias



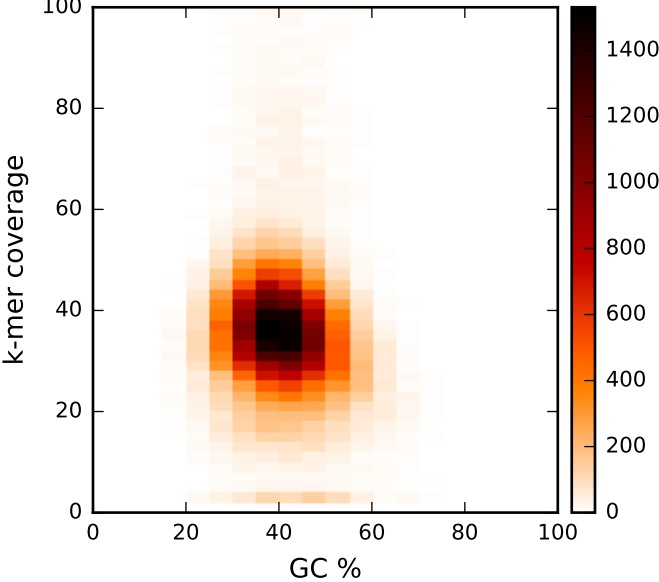
51-mer count distribution



bird GC Bias

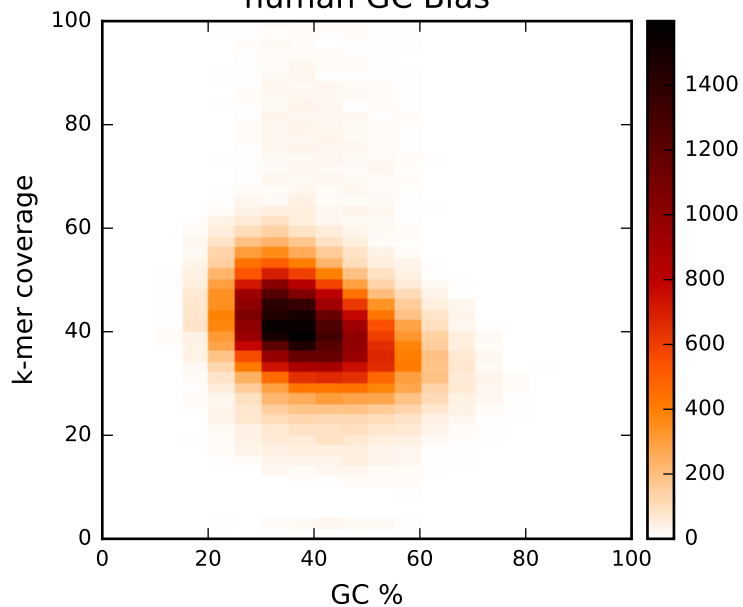


fish GC Bias

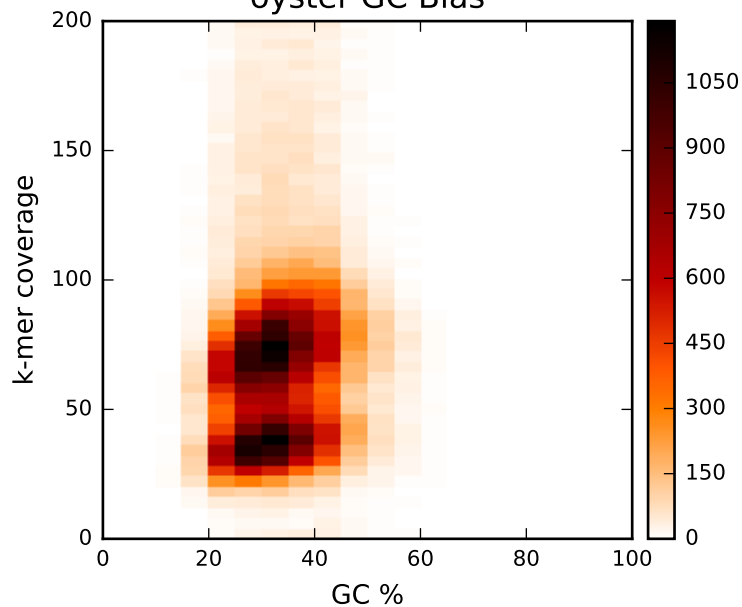


# SGA Preqc Results : fig4

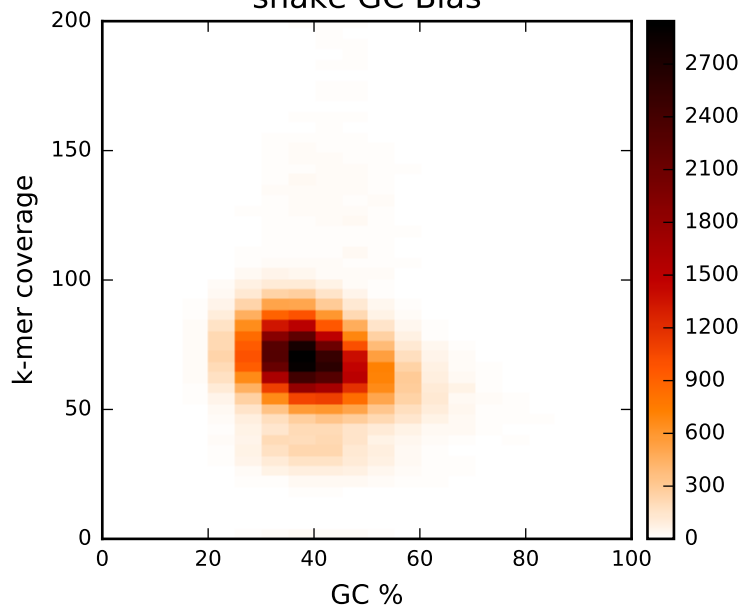
human GC Bias



oyster GC Bias



snake GC Bias



yeast GC Bias

