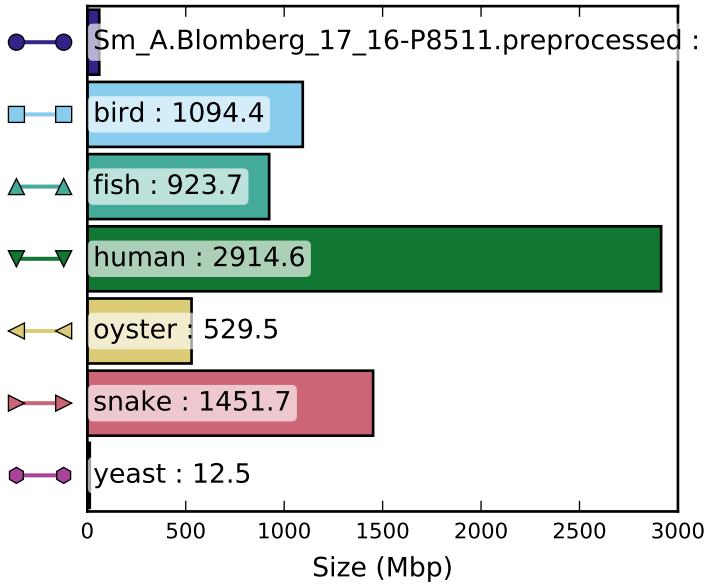
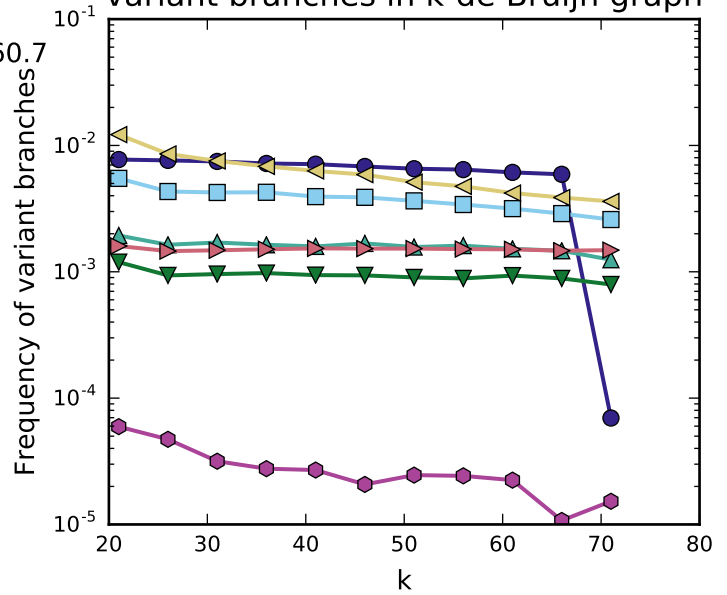


# SGA Preqc Results : fig1

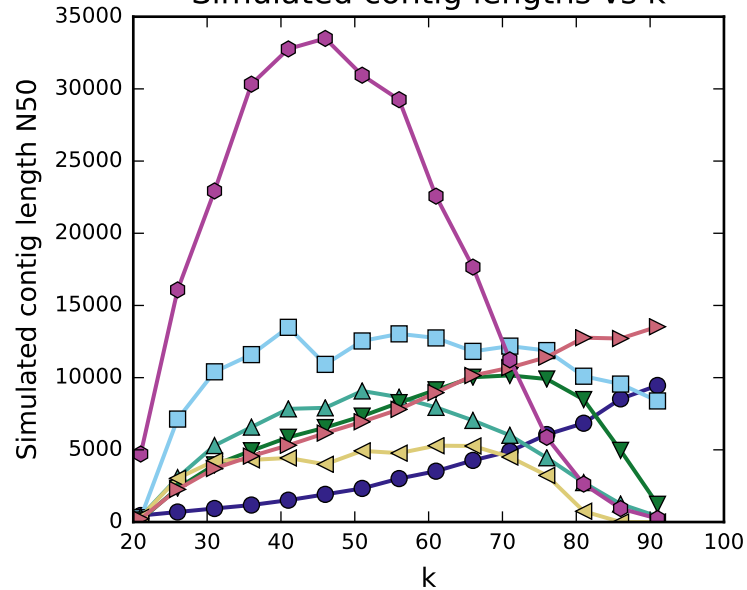
## Est. Genome Size



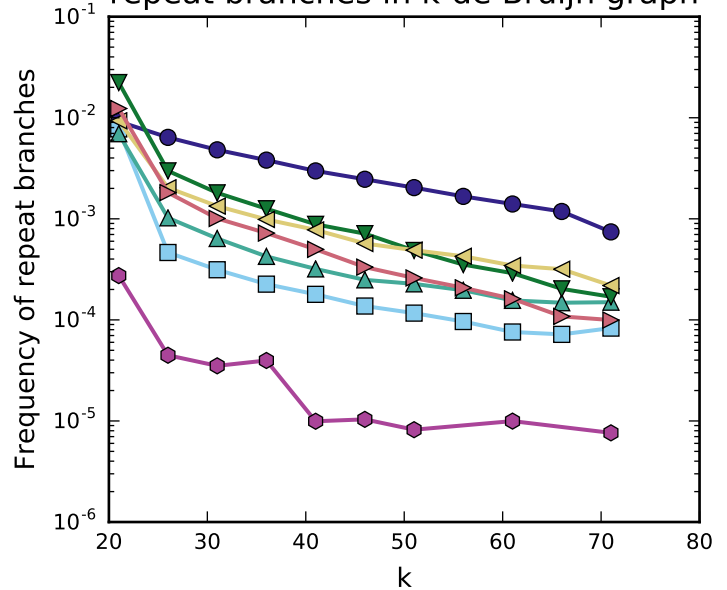
## variant branches in k-de Bruijn graph



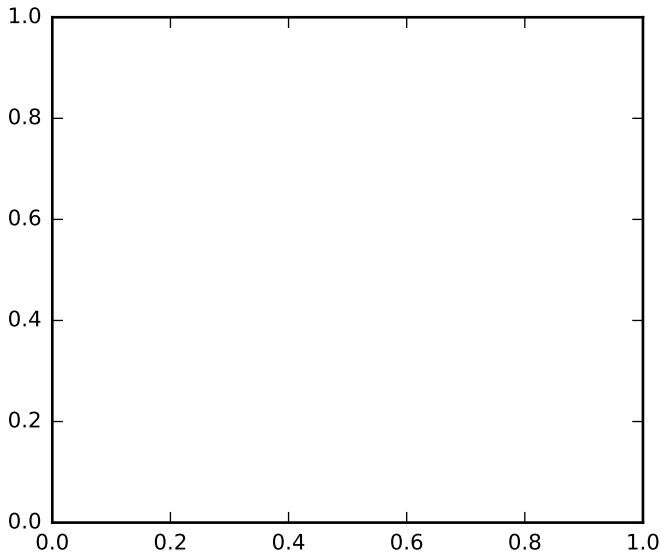
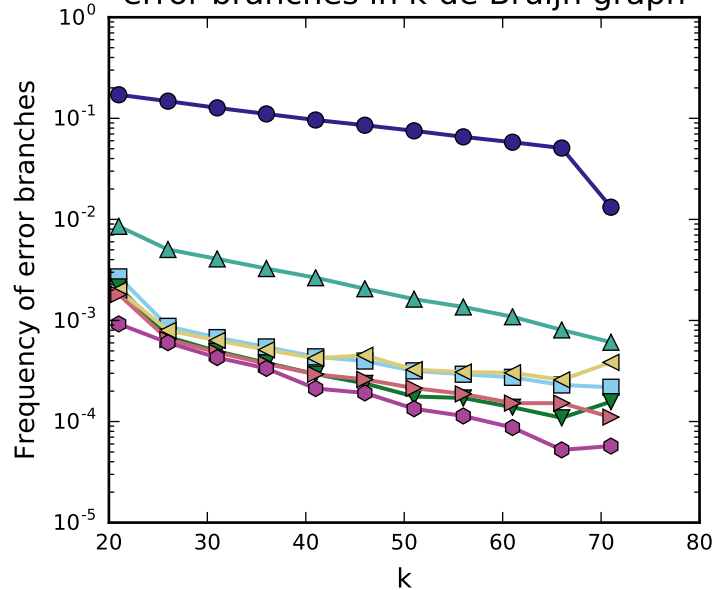
## Simulated contig lengths vs k



## repeat branches in k-de Bruijn graph

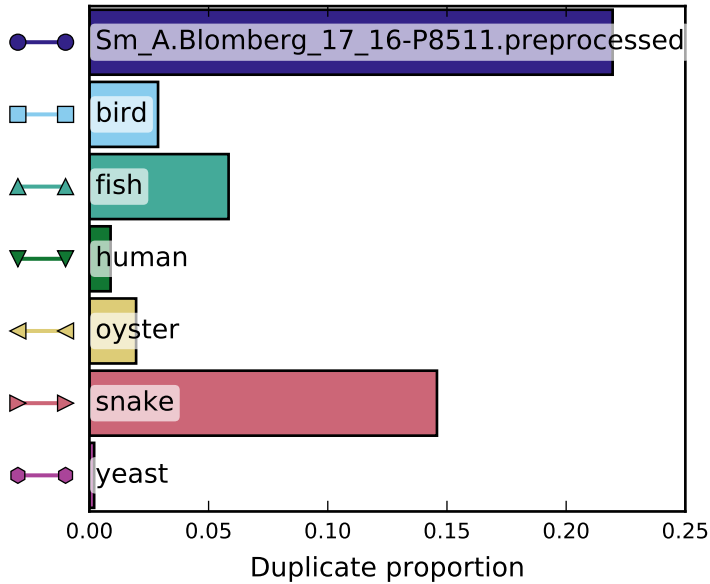


## error branches in k-de Bruijn graph

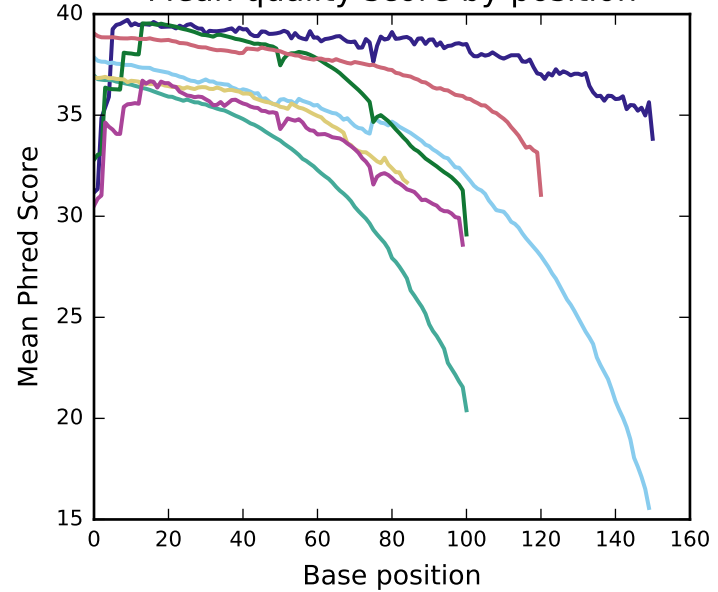


# SGA Preqc Results : fig2

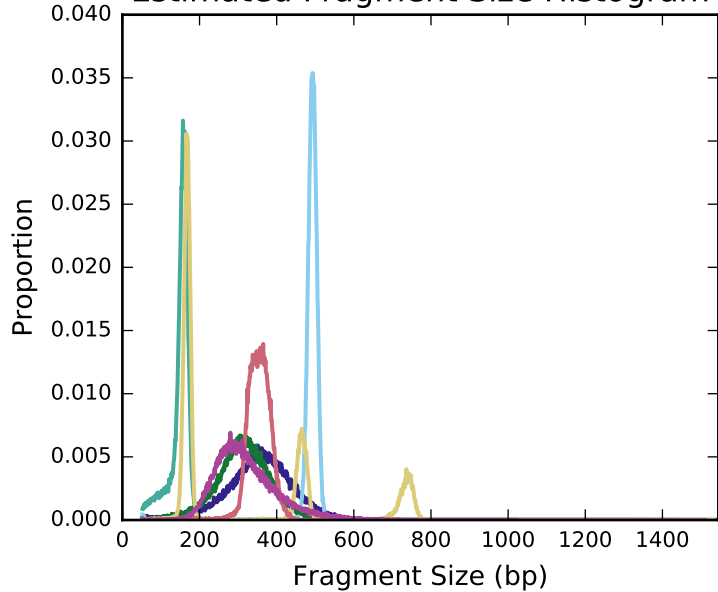
## Est. PCR Duplicate Proportion



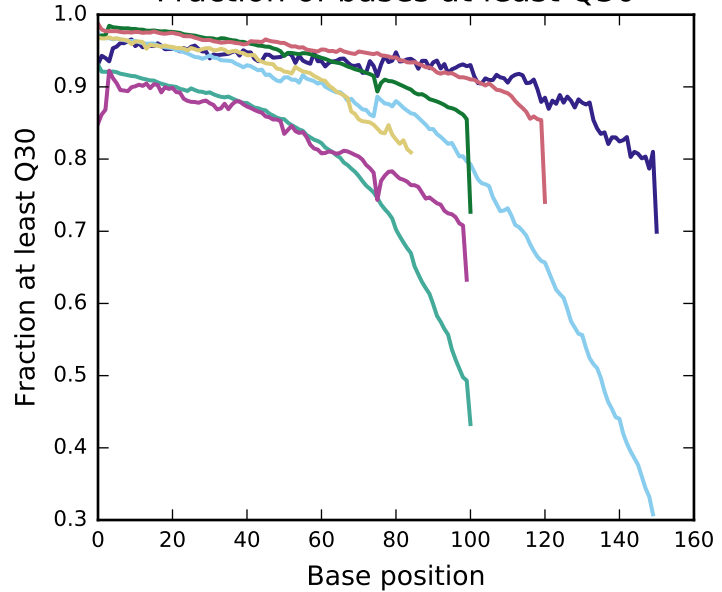
## Mean quality score by position



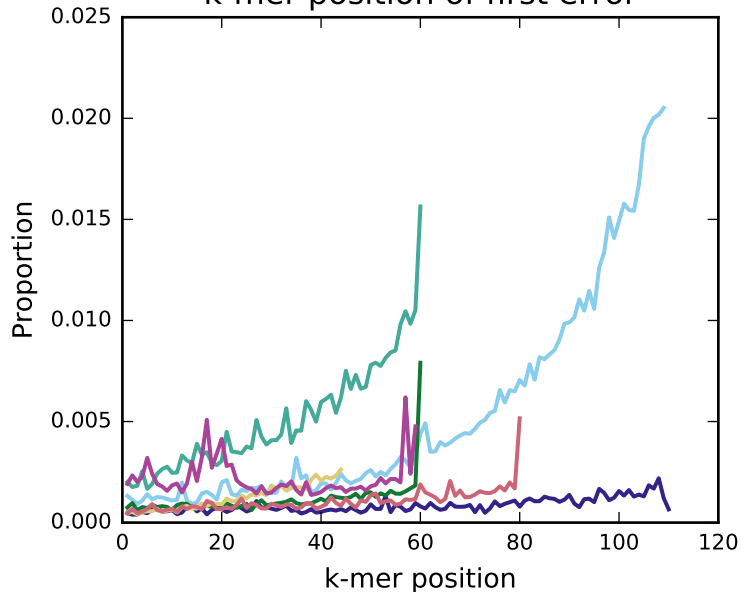
## Estimated Fragment Size Histogram



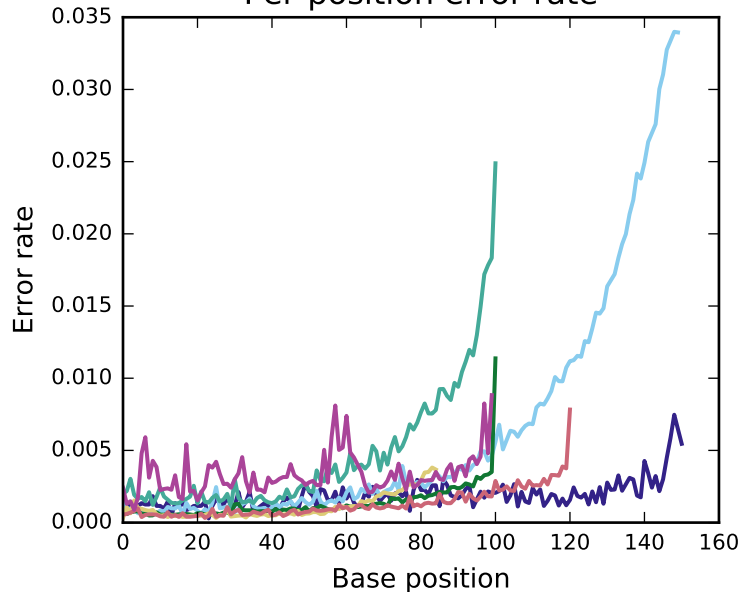
## Fraction of bases at least Q30



## k-mer position of first error

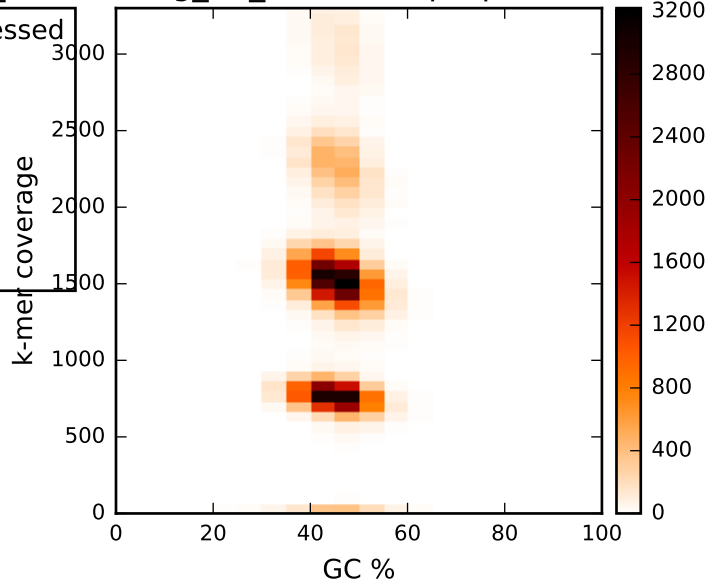
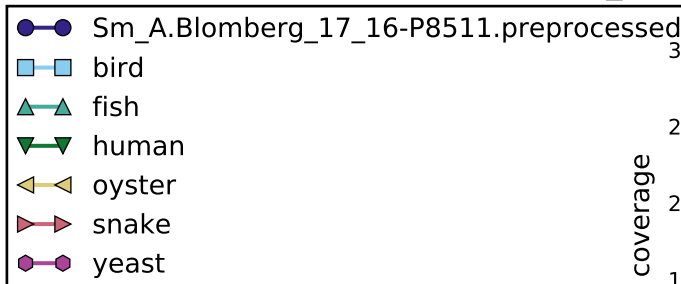


## Per-position error rate

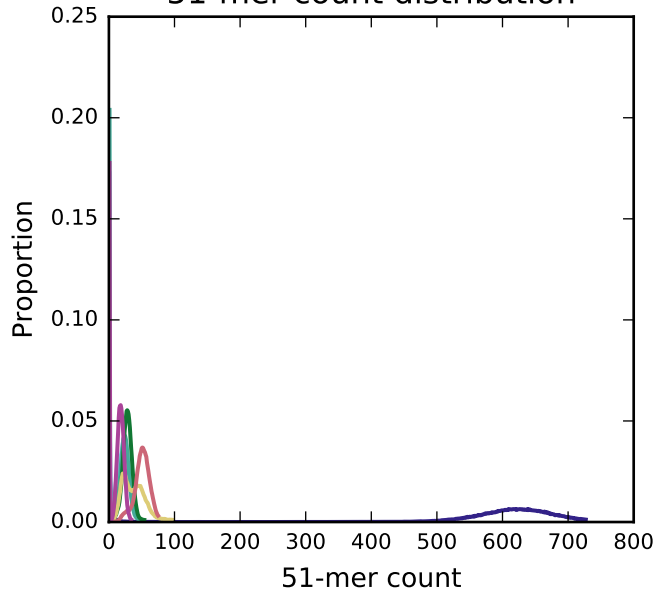


# SGA Preqc Results : fig3

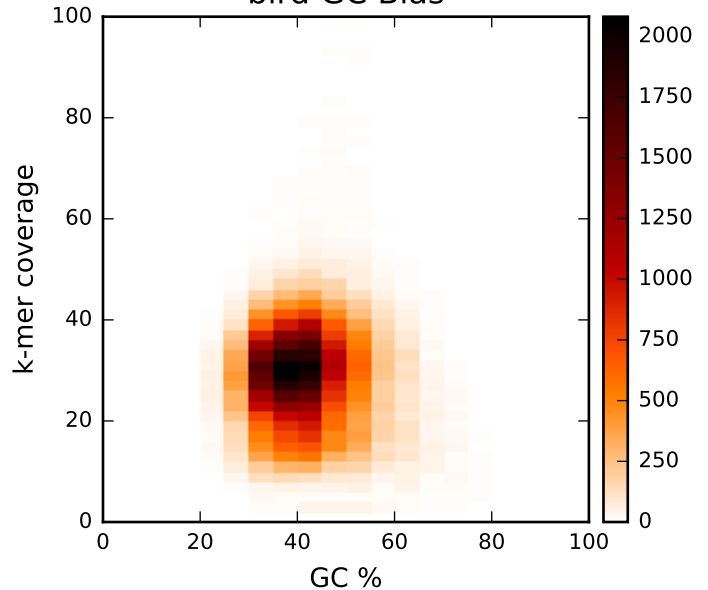
Sm\_A.Blomberg\_17\_16-P8511.preprocessed GC Bias



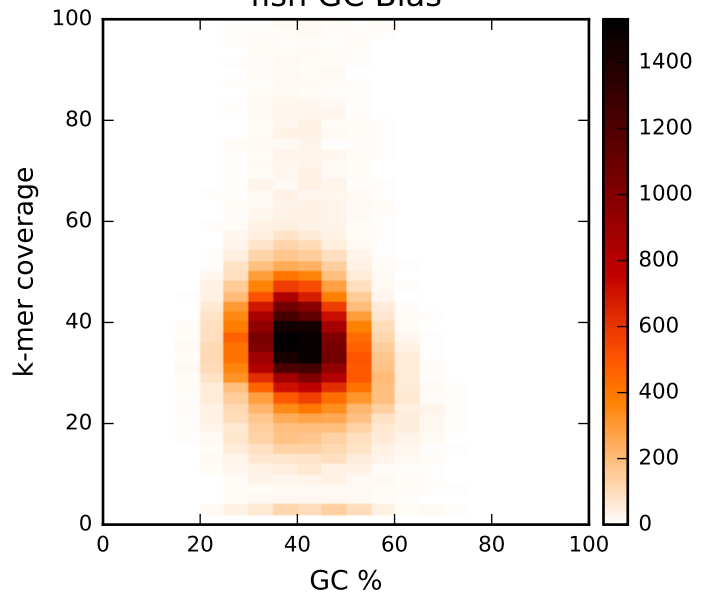
51-mer count distribution



bird GC Bias

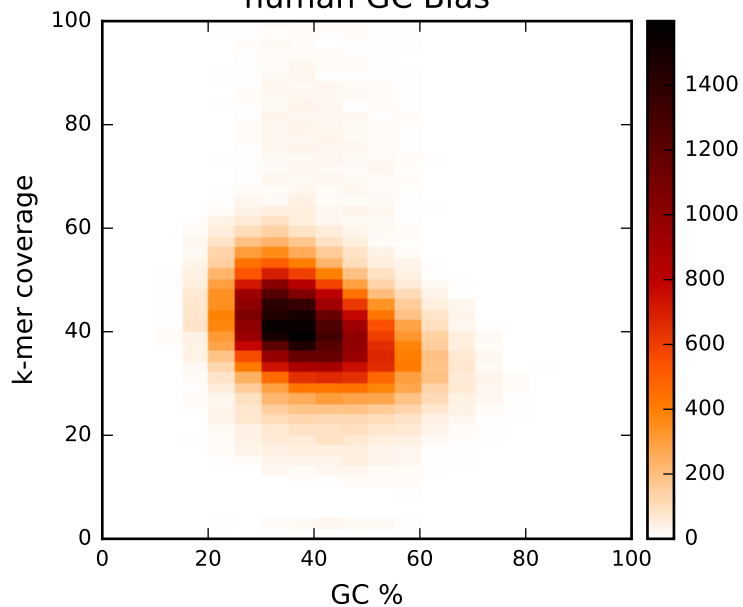


fish GC Bias

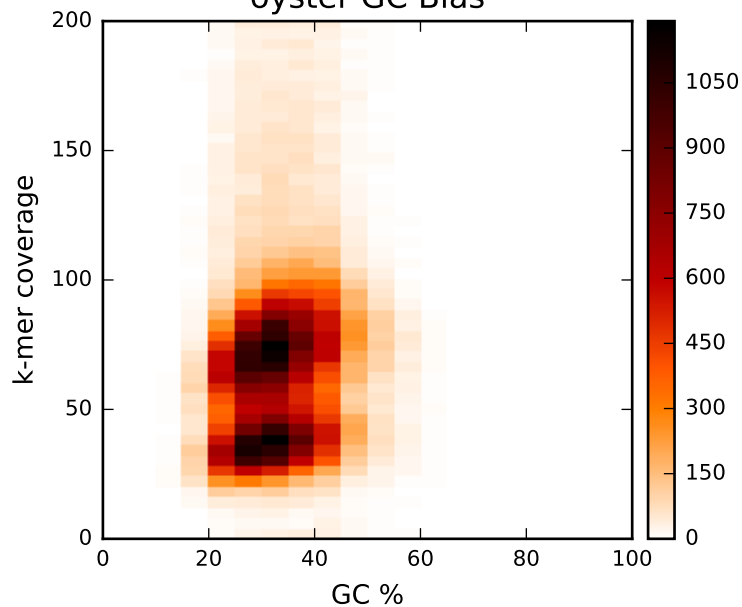


# SGA Preqc Results : fig4

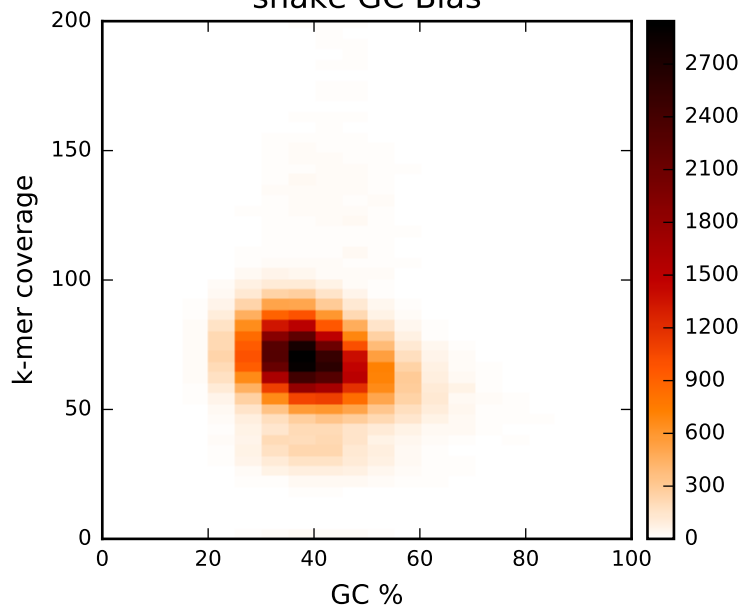
human GC Bias



oyster GC Bias



snake GC Bias



yeast GC Bias

