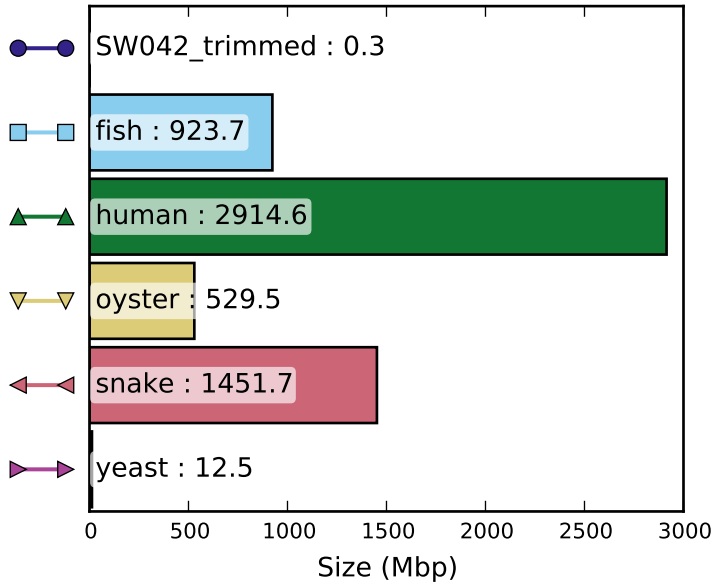
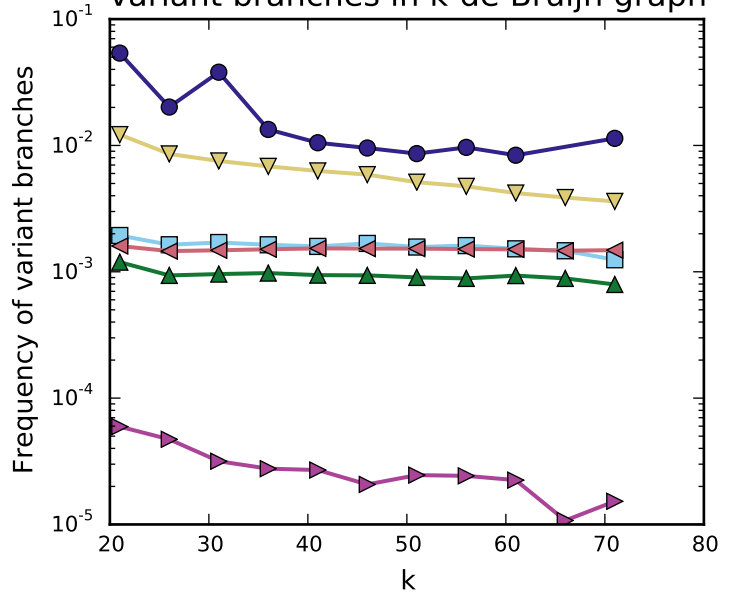


# SGA Preqc Results : fig1

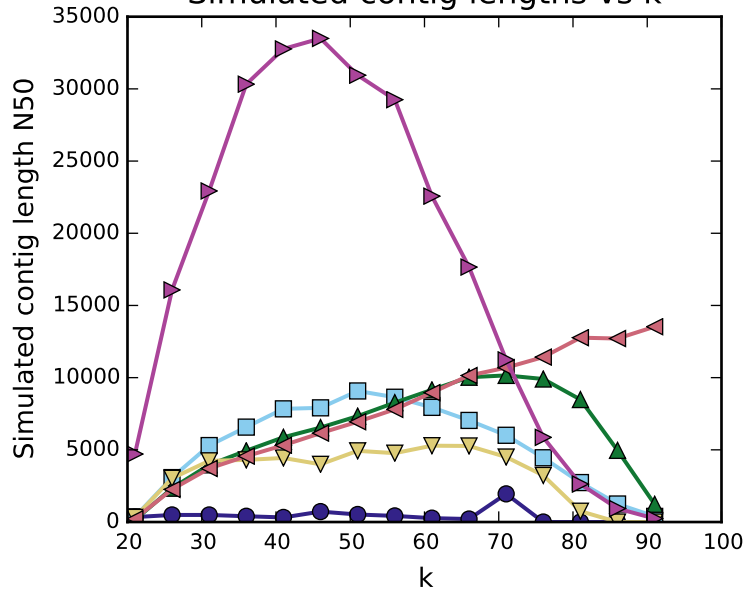
## Est. Genome Size



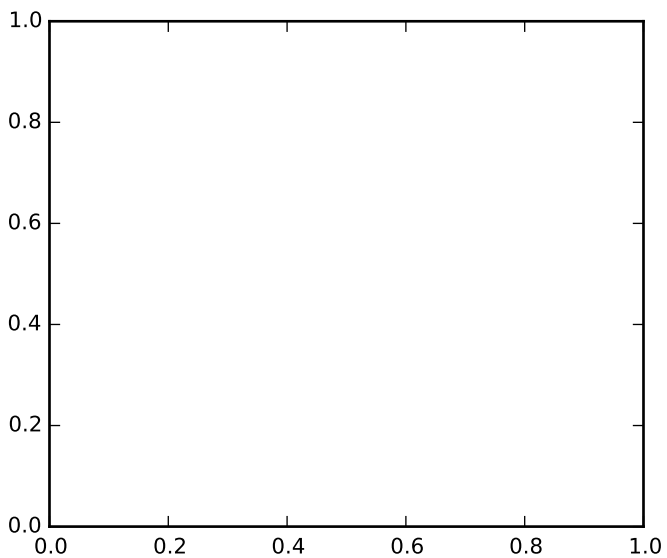
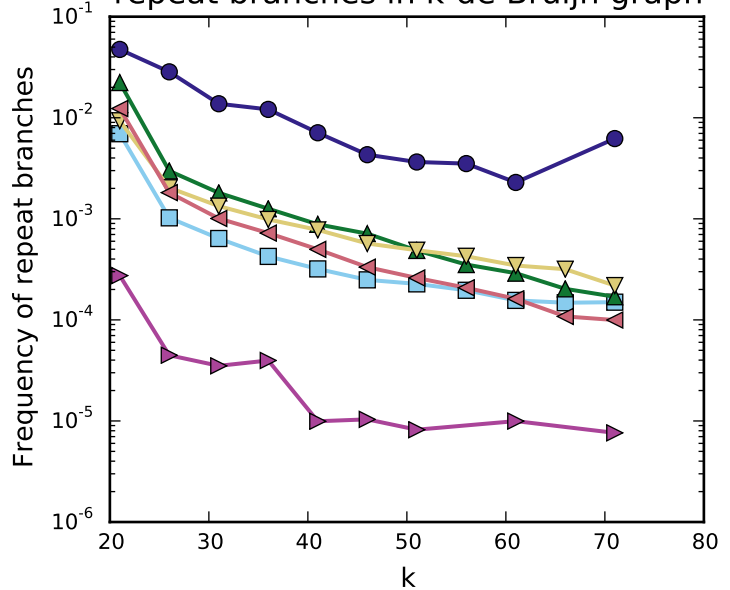
## variant branches in k-de Bruijn graph



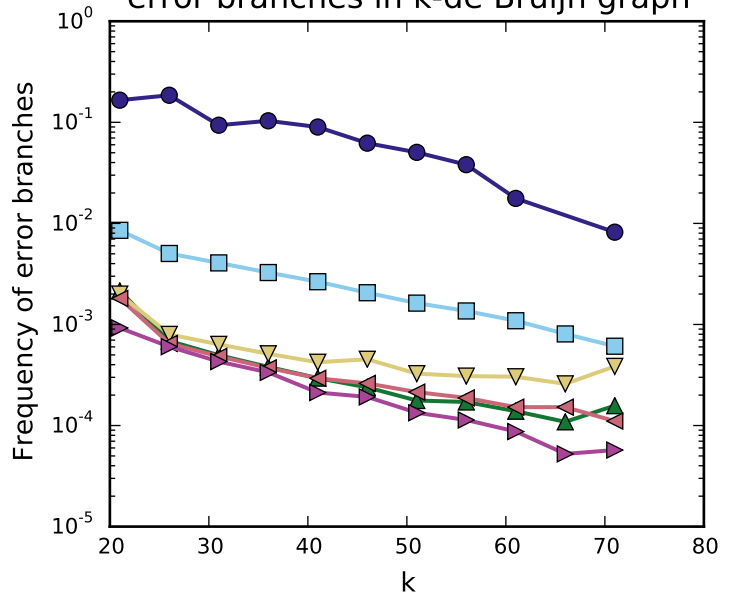
## Simulated contig lengths vs k



## repeat branches in k-de Bruijn graph

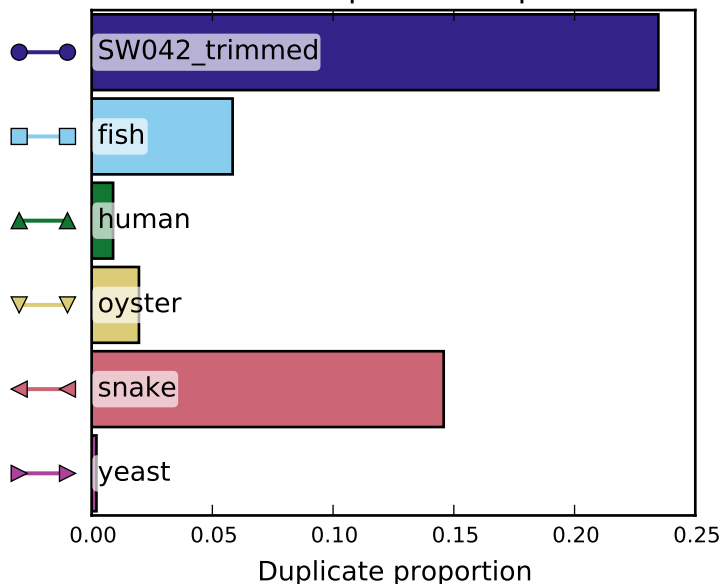


## error branches in k-de Bruijn graph

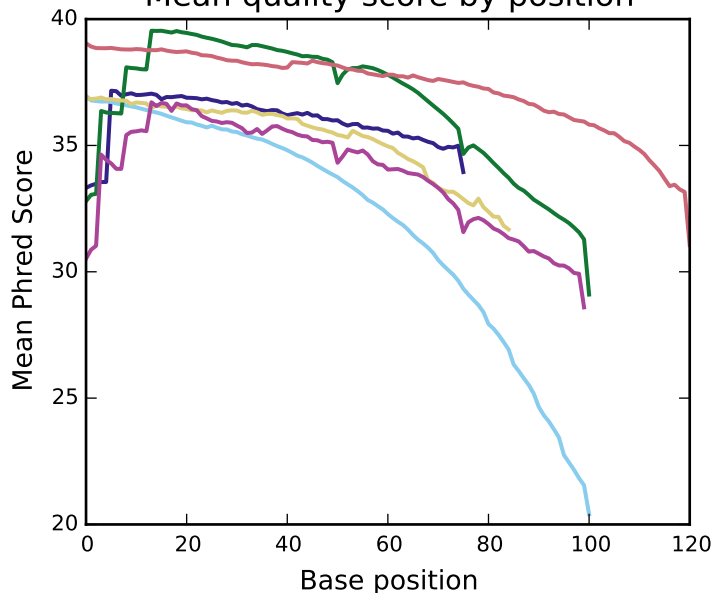


# SGA Preqc Results : fig2

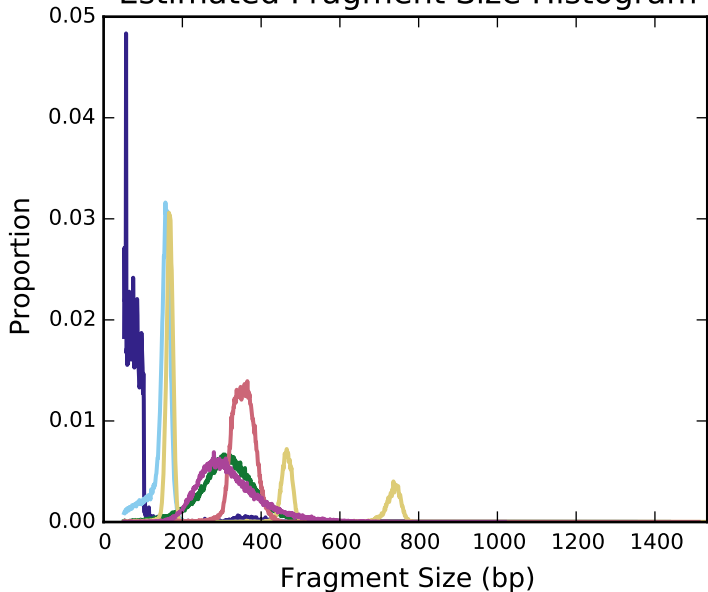
## Est. PCR Duplicate Proportion



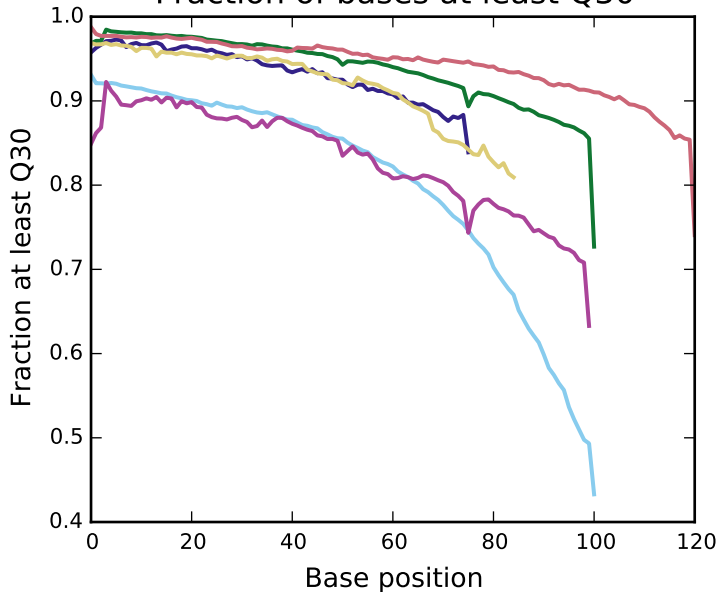
## Mean quality score by position



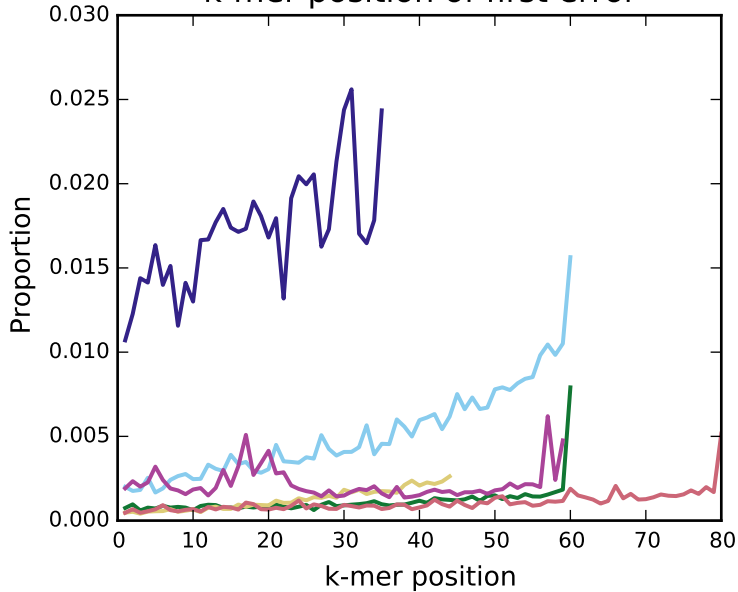
## Estimated Fragment Size Histogram



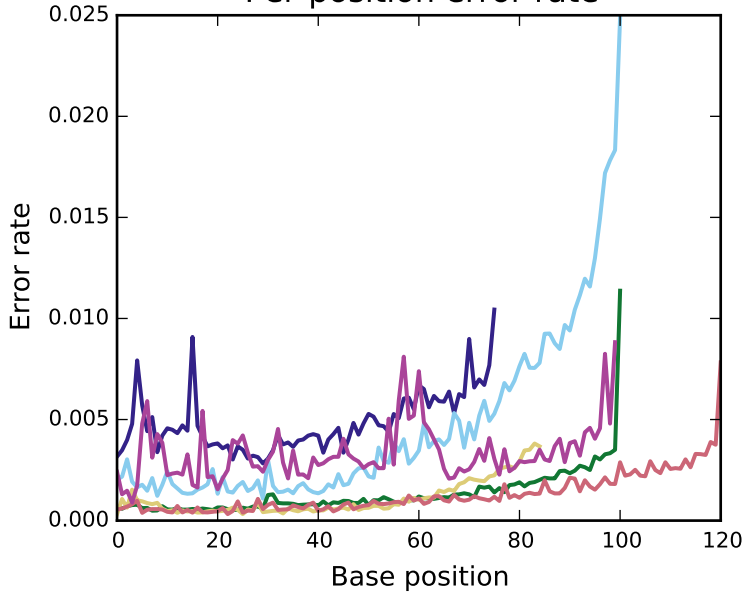
## Fraction of bases at least Q30



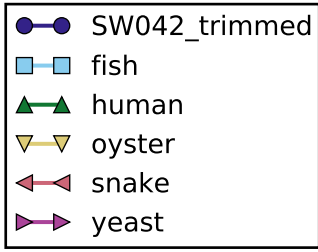
## k-mer position of first error



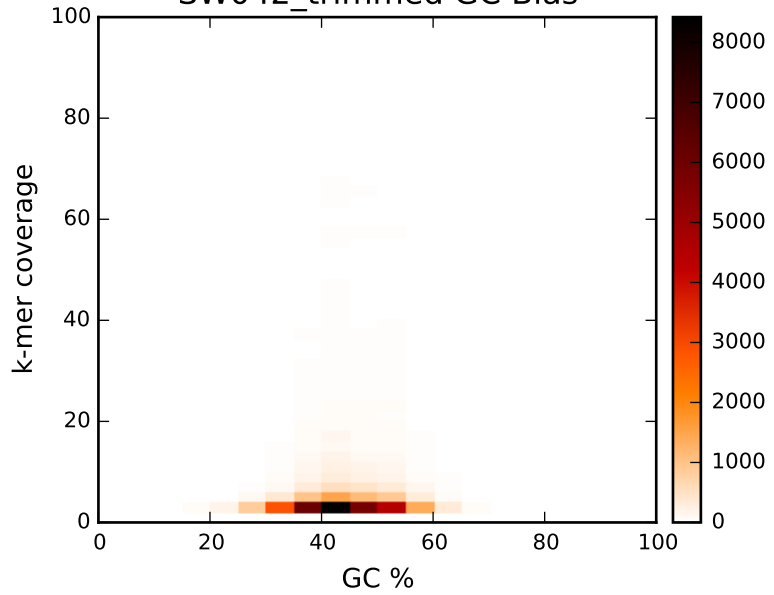
## Per-position error rate



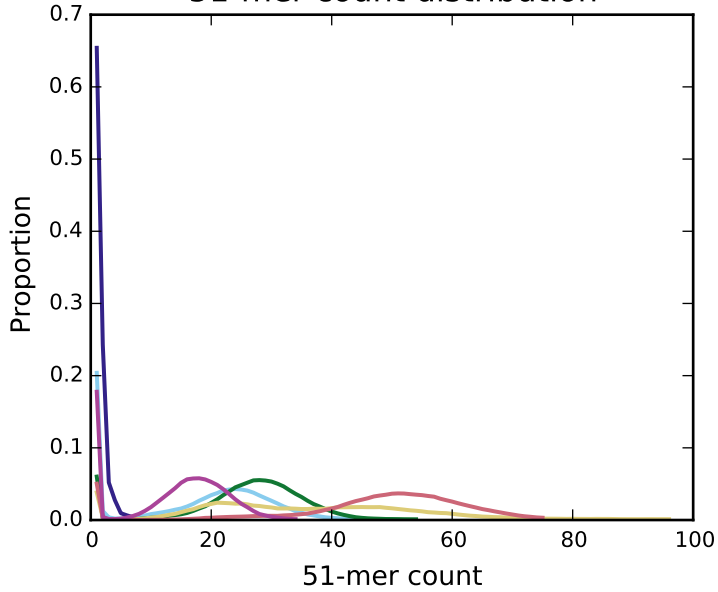
# SGA Preqc Results : fig3



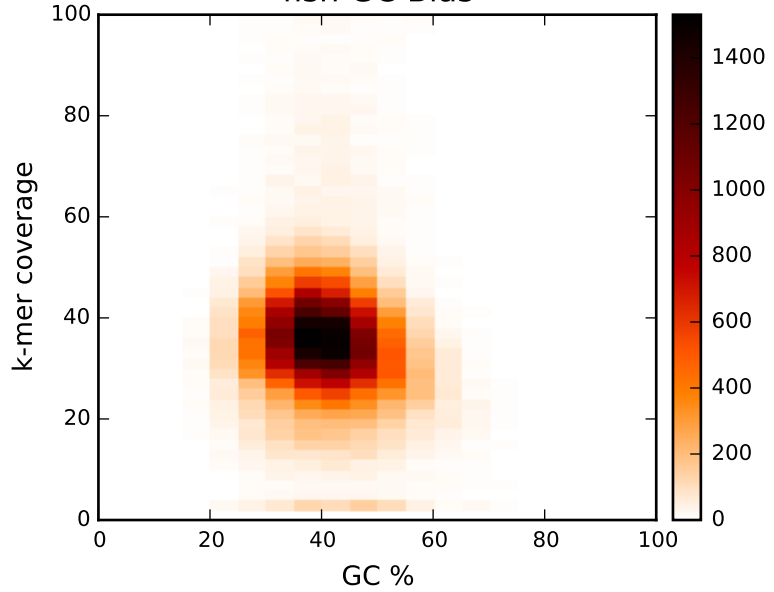
### SW042\_trimmed GC Bias



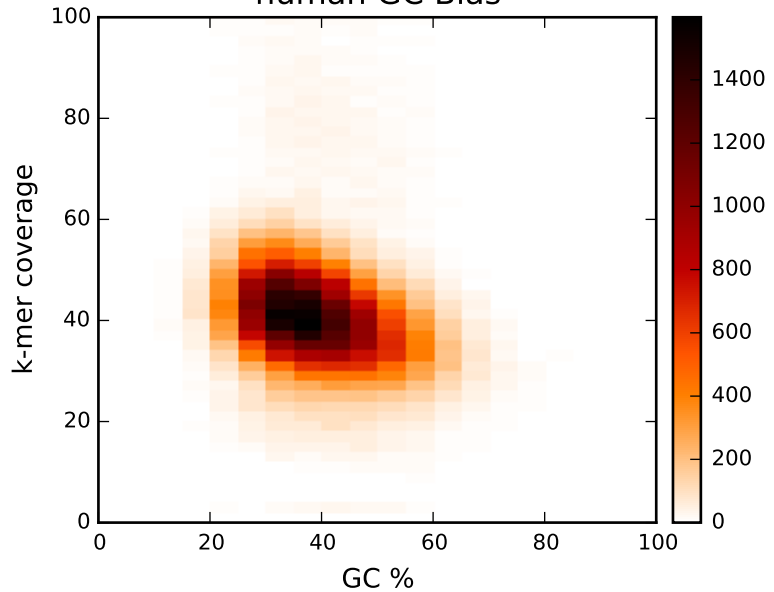
### 51-mer count distribution



### fish GC Bias

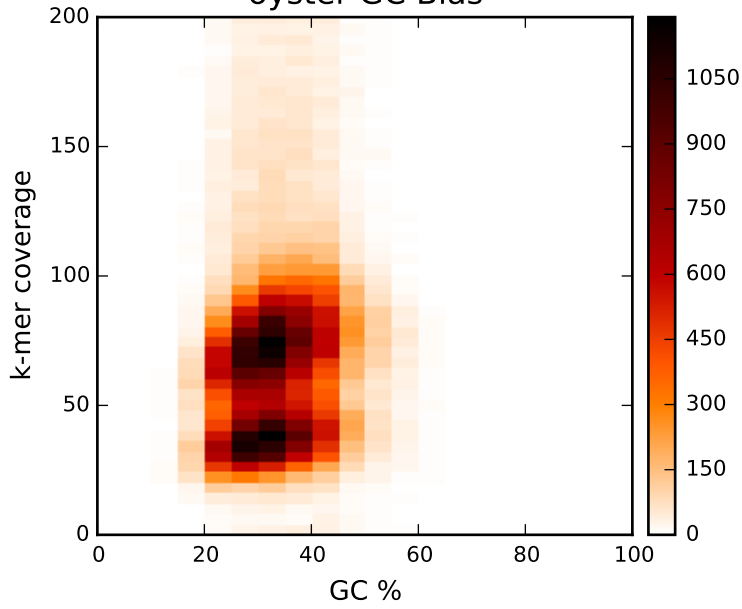


### human GC Bias

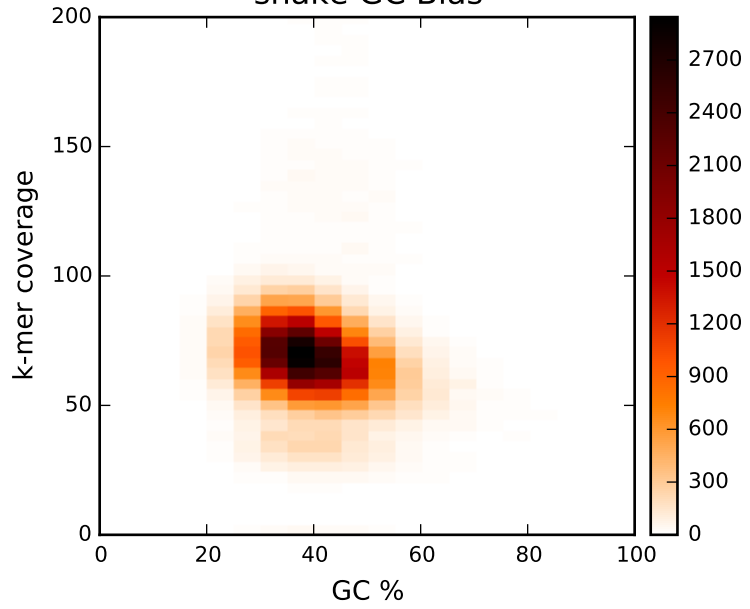


# SGA Preqc Results : fig4

## oyster GC Bias



## snake GC Bias



## yeast GC Bias

