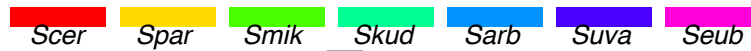


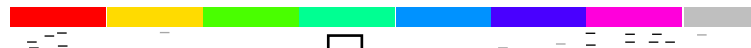
Combine Reference Genomes
combineRefGenomes.py



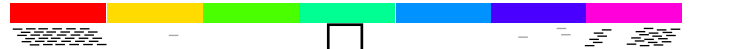
Map to Combination Reference
bwa mem



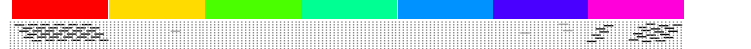
Keep MQ >3
samtools view



Sort to Reference Order
samtools sort



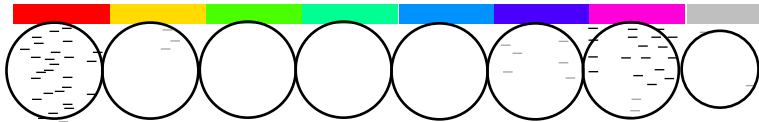
Get coverage by base pair or grouped
bedtools genomeCoverageBed



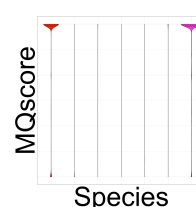
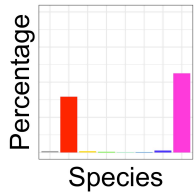
Average Coverage by Species and in Windows
meanDepth_sppIDer.R



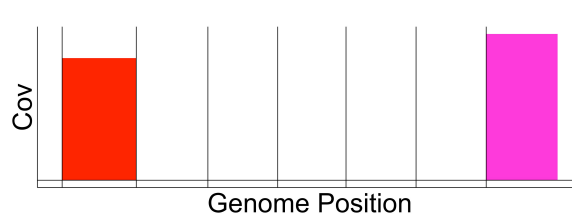
Count and analyze quality
parseSamFile.py



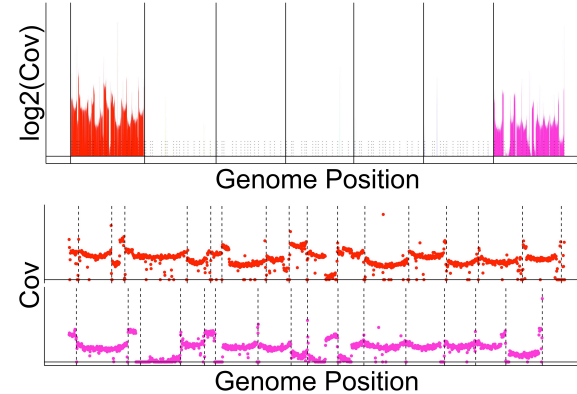
Plot and produce summary
MQscores_sumPlot.R



Plot Depth of Coverage by Species
sppIDer_depthPlot_forSpC.R



Plot Depth of Coverage by Window
sppIDer_depthPlot-d.R



Preparing for sppIDer

sppIDer

sppIDer output