

# dataPrepAutomate

## ↔ input

code/dataPrepAutomated.sh

## output →

aligned\_bam/{species}/{species}\_merged\_sorted.bam  
aligned\_bam/{species}/{species}\_merged\_sorted.bam.csi



# convertPrimaryBam

## ↔ input

aligned\_bam/{species}/{species}\_merged\_sorted.bam

## output →

aligned\_bam/{species}/{species}\_merged\_sorted\_primary.bam  
aligned\_bam/{species}/{species}\_merged\_sorted\_primary.bam.csi



# lociLocation

## ↔ input

/home1/zhuyixin/zhuyixin\_proj/AssmQuality/assemblies/{species}.alt.fasta  
/home1/zhuyixin/zhuyixin\_proj/AssmQuality/assemblies/{species}.pri.fasta  
code/refGene.sh

## output →

/home1/zhuyixin/zhuyixin\_proj/AssmQuality/gene\_position/{species}/Ig\_loci\_details.txt  
/home1/zhuyixin/zhuyixin\_proj/AssmQuality/gene\_position/{species}/ref\_loci\_details.txt  
gene\_position/{species}/final.Ig\_loci.txt



# cigarProcessing

## ↔ input

aligned\_bam/{species}/{species}\_merged\_sorted\_primary.bam  
aligned\_bam/{species}/{species}\_merged\_sorted\_primary.bam.csi  
code/cigar\_processing\_region.py  
gene\_position/{species}/final.Ig\_loci.txt

## output →

errorStats/{species}/IGH.txt  
errorStats/{species}/IGK.txt  
errorStats/{species}/IGL.txt  
errorStats/{species}/nonIG.txt



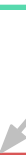
# coverageAnalysis

## ↔ input

aligned\_bam/{species}/{species}\_merged\_sorted\_primary.bam  
aligned\_bam/{species}/{species}\_merged\_sorted\_primary.bam.csi  
gene\_position/{species}/final.Ig\_loci.txt

## output →

errorStats/{species}/IGH\_alt\_pileup.txt  
errorStats/{species}/IGK\_alt\_pileup.txt  
errorStats/{species}/IGL\_alt\_pileup.txt



# all

## ↔ input

errorStats/mPumCon1/IGH.txt  
errorStats/mPumCon1/IGH\_alt\_pileup.txt  
errorStats/mPumCon1/IGK.txt  
errorStats/mPumCon1/IGK\_alt\_pileup.txt  
errorStats/mPumCon1/IGL.txt  
errorStats/mPumCon1/IGL\_alt\_pileup.txt  
errorStats/mPumCon1/nonIG.txt