dataPrepAutomate

↪ input

code/dataPrepAutomated.sh

output →

aligned_bam/{species}.corrected/{species}_merged_sorted.bam
aligned_bam/{species}.corrected/{species}_merged_sorted.bam.bai

runIGdetective_Corr

↪ input

/home1/zhuyixin/sc1/AssmQuality/assemblies/{species}.ljacorr.merged.fasta
code/igDetective.sh

output →

/home1/zhuyixin/sc1/AssmQuality/igGene/{species}.lja.igdetective/combined_genes_IGK.txt
/home1/zhuyixin/sc1/AssmQuality/igGene/{species}.lja.igdetective/combined_genes_IGL.txt

convertPrimaryBam

↪ input

aligned_bam/{species}.corrected/{species}_merged_sorted.bam

output →

aligned_bam/{species}.corrected/{species}_merged_sorted_primary.bam

geneLociAutomate

↪ input

/home1/zhuyixin/sc1/AssmQuality/igGene/{species}.lja.igdetective/combined_genes_IGK.txt
/home1/zhuyixin/sc1/AssmQuality/igGene/{species}.lja.igdetective/combined_genes_IGL.txt
code/geneLociAutomated.sh

output →

gene_position/{species}/lja/{species}_IGH_pos.sorted.bed
gene_position/{species}/lja/{species}_IGK_pos.sorted.bed
gene_position/{species}/lja/{species}_IGL_pos.sorted.bed

cigarProcessing

↪ input

aligned_bam/{species}.corrected/{species}_merged_sorted_primary.bam
code/cigar_processing.py
gene_position/{species}/lja/{species}_IGH_pos.sorted.bed
gene_position/{species}/lja/{species}_IGK_pos.sorted.bed
gene_position/{species}/lja/{species}_IGL_pos.sorted.bed

output →

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

all

↪ input

errorStats/mCanLor1.lja/IGH.txt
errorStats/mCanLor1.lja/IGK.txt
errorStats/mCanLor1.lja/IGL.txt
errorStats/mCanLor1.lja/nonIG.txt