$runlGdetective_noCorr$

→ input

/homel/zhuyixin/scl/AssmQuality/assemblies/{species}.alt.fasta/homel/zhuyixin/scl/AssmQuality/assemblies/{species}.pri.fastacode/igDetective.sh

output →

/homel/zhuyixin/scl/AssmQuality/igGene/{species}.alt.igdetective/combined_genes_IGL.txt /homel/zhuyixin/scl/AssmQuality/igGene/{species}.pri.igdetective/combined_genes_IGL.txt

dataPrepAutomate

→ input

code/dataPrepAutomated.sh

output →

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

geneLociAutomate

→ input

/homel/zhuyixin/scl/AssmQuality/igGene/{species}.alt.igdetective/combined_genes_IGL.txt /homel/zhuyixin/scl/AssmQuality/igGene/{species}.pri.igdetective/combined_genes_IGL.txt code/geneLociAutomated.sh

output →

gene_position/{species}/alt/{species}_IGK_pos.sorted.bed
gene_position/{species}/alt/{species}_IGL_pos.sorted.bed
gene_position/{species}/pri/{species}_IGL_pos.sorted.bed

convertPrimaryBam

→ input

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

output →

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

mergeLoci

→ input

code/mergePriAlt.sh

gene_position/{species}/alt/{species}_IGL_pos.sorted.bed
gene_position/{species}/pri/{species}_IGL_pos.sorted.bed

output →

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

cigarProcessing

→ input

aligned_bam/{species}/{species}_merged_sorted_primary.bam
code/cigar_processing.py

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

output →

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

all

→ input

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