seurat_preprocessing **→** input data/raw/aggregate/2021_083_Qinyu_agg/outs/atac_fragments.tsv.gz data/raw/aggregate/2021_083_Qinyu_agg/outs/filtered_feature_bc_matrix.h5 output → data/processed/snakemake/seurat_object_preprocessed.rds

seurat_processing

→ input

data/processed/snakemake/seurat_object_preprocessed.rds

output →

data/processed/snakemake/seurat_object_processed.rds

install_signac_environment_packages

download_TSS_reference

data/external/GREATv4.genes.mm10.tsv

→ input

data/processed/snakemake/seurat_object_processed.rds data/raw/genesig_HSCs.csv

data/raw/genesig_early_differentiation.csv

output →

→ input

data/processed/snakemake/seurat_object_with_gene_signatures.rds

add_gene_signatures

output →

.smk/signac_env_non_conda_pkgs_installed.marker

atac_processing

→ input

.smk/signac_env_non_conda_pkgs_installed.marker data/external/GREATv4.genes.mm10.tsv

data/processed/snakemake/seurat_object_with_gene_signatures.rds

data/processed/snakemake/seurat_object_atac_processed.rds

→ input

output →

 ${\tt data/processed/snakemake/seurat_object_with_gene_signatures.rds}$

plot_gene_signatures

output →

data/processed/snakemake/plots/is_HSC.svg data/processed/snakemake/plots/is_earlydiff.svg

output →

plot_motifs_genesig_groups

→ input

.smk/signac_env_non_conda_pkgs_installed.marker data/processed/snakemake/seurat_object_atac_processed.rds

output →

data/processed/snakemake/plots/motif plots genesig groups data/processed/snakemake/plots/umap_atac_genesig_group.svg data/processed/snakemake/plots/umap_rna_genesig_group.svg

plot motifs

→ input

.smk/signac_env_non_conda_pkgs_installed.marker data/processed/snakemake/seurat_object_atac_processed.rds

output →

data/processed/snakemake/plots/motif_plots

clean_annotations

output →

plot_integrated

output →

data/processed/snakemake/seurat_object_processed.rds

data/processed/snakemake/plots/integrated_ATAC_clusters.svg

data/processed/snakemake/plots/integrated_ATAC_origin.svg

data/processed/snakemake/plots/integrated_RNA_clusters.svg

data/processed/snakemake/plots/integrated_RNA_origin.svg

data/processed/snakemake/plots/integrated_ATAC_clusters_split.svg

data/processed/snakemake/plots/integrated_RNA_clusters_split.svg

data/processed/snakemake/plots/unintegrated_ATAC_clusters_split.svg

data/processed/snakemake/plots/unintegrated_RNA_clusters_split.svg

data/processed/snakemake/plots/unintegrated_ATAC_clusters.svg

data/processed/snakemake/plots/unintegrated_ATAC_origin.svg data/processed/snakemake/plots/unintegrated_RNA_clusters.svg

data/processed/snakemake/plots/unintegrated_RNA_origin.svg

data/interim/clean_annotations.bed

all

→ input

.smk/signac_env_non_conda_pkgs_installed.marker data/interim/clean_annotations.bed data/processed/snakemake/plots/integrated_RNA_origin.svg data/processed/snakemake/plots/is_HSC.svg data/processed/snakemake/plots/motif_plots data/processed/snakemake/plots/umap_rna_genesig_group.svg data/processed/snakemake/seurat_object_atac_processed.rds data/processed/snakemake/seurat_object_with_gene_signatures.rds