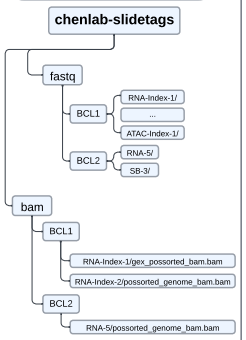
Sample Name	BCL	RNA Index	Lane	SB Index	SB Lane	Puck ID	ATAC Index	ATAC Lane	Merge RNA BCL	Add RNA Index	Merge SB Index	Add SB Index	Add Puck ID	Custom reference	species
tag_A	bcl1	RNA-Index-1	1	SB-Index-1	3	Puck_1	ATAC-Index-1	4	bcl2;bcl3	RNA-5					mouse
tag_B	bcl1	RNA-Index-2	1,2	SB-Index-2	3	Puck_2					bcl2	SB-3	Puck_2	GFP	mouse
tag_TCR	bcl1	RNA-Index-3-TR	2						bcl4	TR-5					mouse
tag_BCR	bcl1	RNA-Index-4-IG	2												mouse

Notes

1. ***cellranger mkfastq supported pattern of sequencing length:***
   cellranger-arc mkfastq
   Y50,I8,Y24,Y50
   cellranger mkfastq
   Y28n*,I10,I10,Y90n*
2. ***bcl2fastq supported patterns:***
   Y50,I8,Y24,Y50
   Y28n*,I10,I10,Y90n*
   Y170,I8n*,Y24,Y134
   Y150,I8n*,Y24,Y150 (ATAC mkfastq)
   Y150,I10,Y24,Y150 (ATAC mkfastq)
3. ***Double-check the index name****
   Pipeline can't check if index is right in a given BCL. It will generate an empty folder for mismatches in mkfastq.

   Supported Index name list:
   reference/Index_Info/
   Dual_Index_NN.csv
   Dual_Index_NT.csv
   Dual_Index_TT.csv
   Single_Index_GA.csv
   Single_Index_NA.csv

storage structure in chenlab bucket



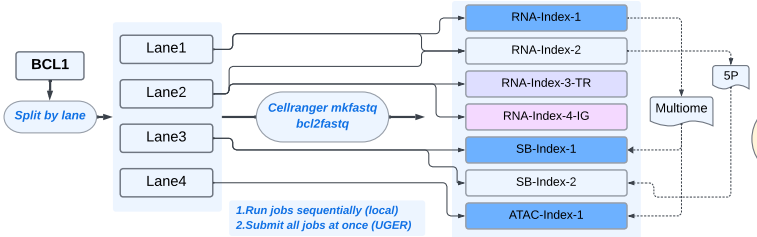
Input BCL (Set as main BCL)

Command: *slidetag_pipe.sh* ***-b bcl1 -mk -cr -mc -cb -sb -sp -gb***

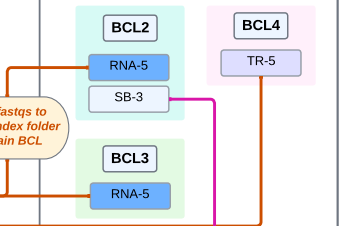
Additional BCLs exist

Mkfastq

Folders to store fastqs named by index provided in google sheet

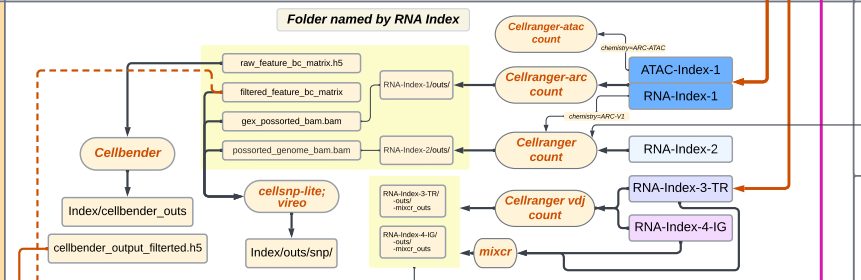


Ensure mkfastq completion for extra BCLs.

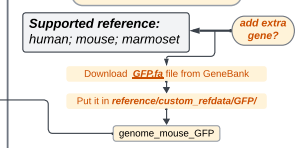


Cellranger Count & Cellbender & Mixcr & cellsnp;vireo

Folder named by RNA Index



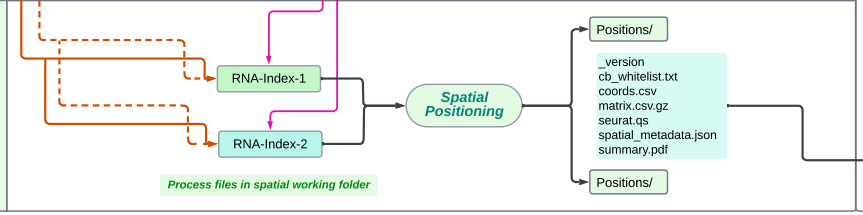
Make custom reference



SBcounts

Folder named by paired RNA Index

Spatial analysis



Copy results to personal store path

tag_TCR/
- align.report.txt
- assembleContigs.report.txt
- chainUsage.pdf
- consensus_annotations.csv
- refine.report.txt
- all_contig_annotations.csv
- assemblePartial.report.txt
- clones.tsv
- filtered_contig_annotations.csv
- web_summary.html
- assemble.report.txt
- barcodesFiltering.pdf
- clonotypes.csv
- metrics_summary.csv

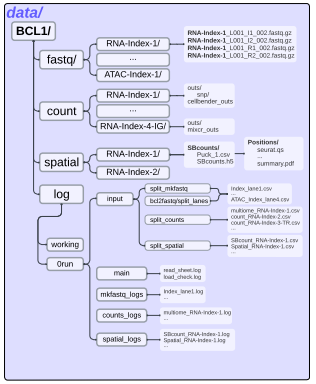
tag_A/
- Positions/
- cellbender_output_filtered.h5
- filtered_feature_bc_matrix.h5
- web_summary.html

Structure of pipeline folder

Main working folder

UGER */broad/thechenlab/pipeline_slidetag*

Local Server */mnt/slidetag/*



env/
- *main/*
- *cellbender2/*
- *cellsnp/*
- *SComatic/*

workflow/
- *config*
- *rules*
- *scripts*
- *slidetag_pipe.sh*

pkgs/
- *bcftools_1.20*
- *bcl2fastq2_v2.20.0*
- *CellBender-0.2.2*
- *cellranger-7.2.0*
- *cellranger-8.0.1*
- *cellranger-arc-2.0.2*
- *cellranger-atac-2.1.0*
- *google-cloud-sdk*

reference/
- *Index_Info*
- *custom_refdata*
- *probesets*
- *refdata-arc-GRCh38-2020-A*
- *refdata-cellranger-vdj-GRCh38*
- *refdata-gex-GRCh38-2024-A*
- *refdata-gex-marmoset*
- *refdata-arc-mm10-2020-A*
- *refdata-cellranger-vdj-GRCm38*
- *refdata-gex-GRCm39-2024-A*
- *refdata-gex-mm10-2020-A*