FNA transcriptomics

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Example code

Example code collected from orignal bash scripts, are shown for single samples.

cellranger v 5.0.0.

Reference files from 10x Genomics: - refdata-cellranger-GRCh38-1.2.0 (transcriptome) - refdata-cellranger-vdj-GRCh38-alts-ensembl-5.0.0 (vdj)

Seurat import onwards in later Rmd files.

1. Download the scRNAseq and Ig BCR libraries from SRA

```
## From http://SRAexplorer.info

#!/bin/bash
curl -L ftp://ftp.sra.ebi.ac.uk/vol1/fastq/SRR112/056/SRR11233656/SRR11233656_1.fastq.gz -o SRR11233656
curl -L ftp://ftp.sra.ebi.ac.uk/vol1/fastq/SRR112/056/SRR11233656/SRR11233656_2.fastq.gz -o SRR11233656

## All transcriptomic fq moved into a directory called 'fq_dir'

## All vdj fq moved into a directory called 'vdj_fqdir'.
```

2. Transcriptomic fq counting

```
module load cellranger

cellranger count --id TurnerSRR11233645 --fastqs fq_dir --sample SRR11233645_scRNA-seq_of_Homo_sapiens_a
```

3. VDJ fq cellranger

```
module load cellranger

cellranger vdj --id Turner_VDJ_SRR11233622 --fastqs vdj_fqdir --sample SRR11233622_single_cell_VDJ_of_H
```

SessionInfo

```
## R version 3.6.1 (2019-07-05)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: CentOS Linux 7 (Core)
##
## Matrix products: default
## BLAS:   /bi/apps/R/3.6.1/lib64/R/lib/libRblas.so
## LAPACK: /bi/apps/R/3.6.1/lib64/R/lib/libRlapack.so
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8 LC_NUMERIC=C         LC_TIME=C
##  [4] LC_COLLATE=C         LC_MONETARY=C        LC_MESSAGES=C
##  [7] LC_PAPER=C           LC_NAME=C            LC_ADDRESS=C
## [10] LC_TELEPHONE=C       LC_MEASUREMENT=C     LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## loaded via a namespace (and not attached):
##  [1] compiler_3.6.1  magrittr_1.5    tools_3.6.1     htmltools_0.4.0
##  [5] yaml_2.2.0      Rcpp_1.0.3      stringi_1.4.3   rmarkdown_2.0
##  [9] knitr_1.26      stringr_1.4.0   xfun_0.11       digest_0.6.23
## [13] rlang_0.4.10    evaluate_0.14
```