

PAPER TITLE TO BE DEFINED (in common.yaml)

2-scRNAseq mapping and counts

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Abstract

Lung interstitium macrophages (IMs) are non-alveolar resident tissue macrophages which contribute to the lung homeostasis. These cells were reported to be heterogeneous by our group and other teams, which contains two main distinct subpopulations: CD206+ IMs and CD206- IMs. However, the exact origin of IMs and the transcriptional programs that control IM differentiation remains unclear. In recent report, we analyzed the refilled IMs in the course of time after induced IM depletion with single-cell RNA sequencing (10X Genomics Chromium) and bulk RNA sequencing.

Contents

1	Description	2
2	CellRanger count from fastq	2
3	Session information	2
4	References	3

1 Description

The Cell Ranger (v3.0.2) application (10x Genomics) was then used to demultiplex the BCL files into FASTQ files (cellranger mkfastq), to perform alignment (to Cell Ranger mouse genome references GRCh38/Ensembl97), barcode filtering, UMI counting and to produce gene—barcode matrices (cellranger count).

2 CellRanger count from fastq

The script below was used to do the mapping and counting with Cellranger.

```
#!/usr/bin/env bash
cellranger count --id=${id} \
                  --fastqs="${FastqDir}/${id}" \
                  --transcriptome=$REF
```

Here, \$id, \$FastqDir and \$REF are the sample ID, the directory containing fastq files and transcriptome reference directory (mouse genome references GRCh38/Ensembl97).

3 Session information

```
sessionInfo()
## R version 4.0.3 (2020-10-10)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 20.04.3 LTS
##
## Matrix products: default
## BLAS: /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
## LAPACK: /usr/lib/x86_64-linux-gnu/openblas-pthread/liblapack.so.3
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8 LC_NUMERIC=C
##  [3] LC_TIME=en_GB.UTF-8 LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=en_GB.UTF-8 LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_GB.UTF-8 LC_NAME=C
##  [9] LC_ADDRESS=C LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_GB.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats graphics grDevices utils datasets methods base
##
## loaded via a namespace (and not attached):
##  [1] fansi_0.5.0 crayon_1.4.1 digest_0.6.27 utf8_1.2.2
##  [5] lifecycle_1.0.0 magrittr_2.0.1 evaluate_0.14 pillar_1.6.2
##  [9] stringi_1.7.3 rlang_0.4.11 vctrs_0.3.8 ellipsis_0
## [13] rmarkdown_2.9 tools_4.0.3 stringr_1.4.0 xfun_0.24
## [17] yaml_2.2.1 compiler_4.0.3 pkgconfig_2.0.3 htmltools_0
## [21] knitr_1.33 tibble_3.1.3
```

4 References