Supplemental Materials

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1.   Cellranger bash commands and parameter files

Bash commands:

```
cellranger count --id=10X_20_010_GE_HTO --
transcriptome=/home/david.mentrup/cellRanger/refdata-cellranger-hg19-3.0.0 --libraries
GE_010_HTO_Hash_library.csv -- feature-ref GE_010_HTO_Hash_feature_ref.csv --expect-
cells=10000 --localcores=24 --localmem=64

cellranger count --id=10X_20_011_GE_HTO --
transcriptome=/home/david.mentrup/cellRanger/refdata-cellranger-hg19-3.0.0 --libraries
GE_011_HTO_Hash_library.csv -- feature-ref GE_011_HTO_Hash_feature_ref.csv --expect-
cells=5100 --localcores=24 --localmem=64

cellranger count --id=10X_20_010_GE_Epi --transcriptome=/home/david.mentrup/cellRanger/refdata-
cellranger-hg19-3.0.0 --libraries GE_010_Epi_CITE__library.csv --feature-ref
GE_010_EPI_CITE_feature_ref.csv --expect-cells=10000 --localcores=24 --localmem=64
```

GE_010_HTO_Hash_library.csv

```
fastqs,sample,library_type
/home/david.mentrup/ProjectCITE/data/Run01/10X_20_OK_05_R59/fastq_files/P16358_1001/02-
FASTQ/200403_A00621_0207_AHKYCGDRXX,P16358_1001,Gene Expression
/home/david.mentrup/ProjectCITE/data/Run01/10X_20_OK_05_R59/fastq_files/P16358_1003/02-
FASTQ/200403_A00621_0207_AHKYCGDRXX,P16358_1003,Antibody Capture
```

GE_011_HTO_Hash_library.csv

```
fastqs,sample,library_type
/home/david.mentrup/ProjectCITE/data/Run01/10X_20_OK_05_R59/fastq_files/P16358_1002/02-
FASTQ/200403_A00621_0207_AHKYCGDRXX/,P16358_1002,Gene Expression
/home/david.mentrup/ProjectCITE/data/Run01/10X_20_OK_05_R59/fastq_files/P16358_1004/02-
FASTQ/200403_A00621_0207_AHKYCGDRXX/,P16358_1004,Antibody Capture
```

GE_010_Epi_CITE__library.csv

```
fastqs,sample,library_type
/home/david.mentrup/ProjectCITE/data/Run01/10X_20_OK_05_R59/fastq_files/P16358_1001/02-
FASTQ/200403_A00621_0207_AHKYCGDRXX/,P16358_1001,Gene Expression
/home/david.mentrup/ProjectCITE/data/Run01/10X_20_OK_05_R59/fastq_files/P16358_1005/02-
FASTQ/200403_A00621_0207_AHKYCGDRXX/,P16358_1005,Antibody Capture
```

GE_010_HTO_Hash_feature_ref.csv

```
id,name,read,pattern,sequence,feature_type
```

```
H1,Hash1_TotalSeqB,R2,5PNNNNNNNNNN(BC)NNNNNNNNN,GTCAACTCTTTAGCG,Antibody
Capture
H2,Hash2_TotalSeqB,R2,5PNNNNNNNNNN(BC)NNNNNNNNN,TGATGGCCTATTGGG,Antibody
Capture
H3,Hash3_TotalSeqB,R2,5PNNNNNNNNNN(BC)NNNNNNNNN,TTCCGCCTCTCTTTG,Antibody
Capture
```

GE_011_HTO_Hash_feature_ref.csv

```
id,name,read,pattern,sequence,feature_type
H3,Hash3_TotalSeqB,R2,5PNNNNNNNNNN(BC)NNNNNNNNN,TTCCGCCTCTCTTTG,Antibody
Capture
```

GE_010_Epi_CITE__library.csv

```
id,name,read,pattern,sequence,feature_type
CD19,CD19_TotalA,R2,^(BC),CTGGGCAATTACTCG,Antibody Capture
CD3,CD3_TotalA,R2,^(BC),CTCATTGTAACTCCT,Antibody Capture
CD16,CD16_TotalA,R2,^(BC),AAGTTCACTCTTTGC,Antibody Capture
CD4,CD4_TotalA,R2,^(BC),TGTTCCCGCTCAACT,Antibody Capture
CD11c,CD11c_TotalA,R2,^(BC),TACGCCTATAACTTG,Antibody Capture
CD56_NCAM,CD56_TotalA,R2,^(BC),TCCTTTCCTGATAGG,Antibody Capture
CD14,CD14_TotalA,R2,^(BC),TCTCAGACCTCCGTA,Antibody Capture
CD8,CD8_TotalA,R2,^(BC),GCGCAACTTGATGAT,Antibody Capture
CD45,CD45_TotalA,R2,^(BC),TCCCTTGCGATTTAC,Antibody Capture
CD34,CD34_TotalA,R2,^(BC),GCAGAAATCTCCCTT,Antibody Capture
CD15,CD15_TotalA,R2,^(BC),TCACCAGTACCTAGT,Antibody Capture
```

2.　　ScRNA Benchmarking bash command and parameter file

Bash command:

```
snakemake --configfile BMMC_small_config.yml --cores 16 --use-singularity
```

BMMC_small_config.yml

```
output_dir: BMMC_small/Output
datafile: BMMC_small/BMMC_Ref_count.csv
labfile: BMMC_small/BMMC_Ref_Label.csv
column: 1
number_of_features: 2000
tools_to_run:
 - singleCellNet
 - SingleR
 - kNN9
 - kNN50
 - scVI
 - scmapcell
 - Seurat_CCA
 - Seurat_PCA
 - SVM
 - SVM_rejection
 - LDA
 - LDA_rejection
 - RF
 - CHETAH
 - scmapcluster
 - scID
```

```
  - SingleR
  - NMC
```

3.   ClubAC bash command and parameter file

Bash command:

```
snakemake --configfile BMMC_AML_5000genes_config.yml --cores 16 --use-singularity
```

BMMC_AML_5000genes_config.yml

```
output_dir: BMMC_AML/output_5000genes
refdatafile: BMMC_AML/bmmc_Ref
reflabelfile: BMMC_AML/BMMC_Ref_Label.csv
testdatafile: BMMC_AML/AML_S01_CITE
testclusterfile: BMMC_AML/AML_Cluster.csv
column: 1
number_of_features: 5000
tools_to_run:
  - scmapcell
  - Seurat_CCA
  - Seurat_PCA
  - SVM
  - SVM_rejection
  - LDA
  - LDA_rejection
  - RF
  - CHETAH
  - scmapcluster
  - scID
  - SingleR
```