

# Quality Control for scRNA and scATAC seq data

Load and Merge the data

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```
library(tibble)
library(tidyr)
library(dplyr)
library(rtracklayer)

## Loading required package: GenomicRanges
## Warning: package 'GenomicRanges' was built under R version 4.4.1
## Loading required package: stats4
## Loading required package: BiocGenerics
##
## Attaching package: 'BiocGenerics'
## The following objects are masked from 'package:lubridate':
##     intersect, setdiff, union
## The following objects are masked from 'package:dplyr':
##     combine, intersect, setdiff, union
## The following objects are masked from 'package:stats':
##     IQR, mad, sd, var, xtabs
## The following objects are masked from 'package:base':
##     anyDuplicated, aperm, append, as.data.frame, basename, cbind,
##     colnames, dirname, do.call, duplicated, eval, evalq, Filter, Find,
##     get, grep, grepl, intersect, is.unsorted, lapply, Map, mapply,
##     match, mget, order, paste, pmax, pmax.int, pmin, pmin.int,
##     Position, rank, rbind, Reduce, rownames, sapply, setdiff, table,
##     tapply, union, unique, unsplit, which.max, which.min
## Loading required package: S4Vectors
## Warning: package 'S4Vectors' was built under R version 4.4.1
```

```

## 
## Attaching package: 'S4Vectors'
## The following objects are masked from 'package:lubridate':
## 
##     second, second<-
## 
## The following objects are masked from 'package:dplyr':
## 
##     first, rename
## 
## The following object is masked from 'package:tidyverse':
## 
##     expand
## 
## The following object is masked from 'package:utils':
## 
##     findMatches
## 
## The following objects are masked from 'package:base':
## 
##     expand.grid, I, unname
## 
## Loading required package: IRanges
## Warning: package 'IRanges' was built under R version 4.4.1
## 
## Attaching package: 'IRanges'
## 
## The following object is masked from 'package:lubridate':
## 
##     %within%
## 
## The following objects are masked from 'package:dplyr':
## 
##     collapse, desc, slice
## 
## The following object is masked from 'package:purrr':
## 
##     reduce
## 
## Loading required package: GenomeInfoDb
library(dplyr)
library(Seurat)

## Warning: package 'Seurat' was built under R version 4.4.1
## Loading required package: SeuratObject
## Loading required package: sp
## Warning: package 'sp' was built under R version 4.4.1
## 
## Attaching package: 'sp'
## 
## The following object is masked from 'package:IRanges':
## 
##     %over%
## 
## 'SeuratObject' was built with package 'Matrix' 1.7.0 but the current
## version is 1.7.3; it is recommended that you reinstall 'SeuratObject' as

```

```

## the ABI for 'Matrix' may have changed
##
## Attaching package: 'SeuratObject'
## The following object is masked from 'package:GenomicRanges':
##     intersect
## The following object is masked from 'package:GenomeInfoDb':
##     intersect
## The following object is masked from 'package:IRanges':
##     intersect
## The following object is masked from 'package:S4Vectors':
##     intersect
## The following object is masked from 'package:BiocGenerics':
##     intersect
## The following objects are masked from 'package:base':
##     intersect, t
library(Signac)

## Warning: package 'Signac' was built under R version 4.4.1
library(EnsDb.Hsapiens.v86)

## Loading required package: ensemblldb
## Warning: package 'ensemblldb' was built under R version 4.4.1
## Loading required package: GenomicFeatures
## Loading required package: AnnotationDbi
## Loading required package: Biobase
## Welcome to Bioconductor
##
##     Vignettes contain introductory material; view with
##     'browseVignettes()'. To cite Bioconductor, see
##     'citation("Biobase")', and for packages 'citation("pkgname")'.

## Attaching package: 'AnnotationDbi'
## The following object is masked from 'package:dplyr':
##     select
## Loading required package: AnnotationFilter
##
## Attaching package: 'ensemblldb'

```

```

## The following object is masked from 'package:dplyr':
##
##     filter

## The following object is masked from 'package:stats':
##
##     filter

library(ggplot2)
library(cowplot)

##
## Attaching package: 'cowplot'

## The following object is masked from 'package:lubridate':
##
##     stamp

library(simspec)
library(cowplot)
library(AnnotationHub)

## Loading required package: BiocFileCache

## Loading required package: dbplyr

##
## Attaching package: 'dbplyr'

## The following objects are masked from 'package:dplyr':
##
##     ident, sql

##
## Attaching package: 'AnnotationHub'

## The following object is masked from 'package:Biobase':
##
##     cache

## The following object is masked from 'package:rtracklayer':
##
##     hubUrl

# load function from local files

# load data from local files
library(Signac)
library(Seurat)
library(EnsDb.Hsapiens.v86)
library(BSgenome.Hsapiens.UCSC.hg38)

## Loading required package: BSgenome

## Loading required package: Biostrings

## Loading required package: XVector

##
## Attaching package: 'XVector'

## The following object is masked from 'package:purrr':

```

```

## compact
## Attaching package: 'Biostrings'
## The following object is masked from 'package:base':
## strsplit
## Loading required package: BiocIO
## Attaching package: 'BiocIO'
## The following object is masked from 'package:rtracklayer':
## FileForFormat
# # This folling code only need to run once
# annotations <- GetGRangesFromEnsDb(ensdb = EnsDb.Hsapiens.v86)
# seqlevelsStyle(annotations) <- "UCSC"    # e.g. "chr1", "chr2", ...
# genome(annotations)      <- "hg38"
# saveRDS(annotations, file = here::here("data", "reference", "annotations_ATAC_2025_05_01.rds"))

# load the annotation from a rds file
annotations <- readRDS(here::here("data", "reference", "annotations_ATAC_2025_05_01.rds"))

# load(here::here("data", "reference", "annotations_ATAC.rdata")) # load the annotations

```

## 1. Read the Raw Data

In this section, we will read the raw data from the cellranger-arc output files. We have 4 samples: PSZ-6, TSC-tube, TSC-edge, and CTRL. We will rename the samples as CTRL, TSC-tuber, TSC-edge, and TSC-outside, respectively.

```
# load data from cellranger and perform basic QC
library(Seurat)
library(tidyverse)
library(data.table)

## Warning: package 'data.table' was built under R version 4.4.1

##
## Attaching package: 'data.table'

## The following object is masked from 'package:GenomicRanges':
##
##      shift

## The following object is masked from 'package:IRanges':
##
##      shift

## The following objects are masked from 'package:S4Vectors':
##
##      first, second

## The following objects are masked from 'package:lubridate':
##
##      hour, isoweek, mday, minute, month, quarter, second, wday, week,
##      yday, year

## The following objects are masked from 'package:dplyr':
##
##      between, first, last

## The following object is masked from 'package:purrr':
##
##      transpose

library(scDblFinder)

## Loading required package: SingleCellExperiment
## Loading required package: SummarizedExperiment
## Loading required package: MatrixGenerics
## Loading required package: matrixStats

## Warning: package 'matrixStats' was built under R version 4.4.1

##
## Attaching package: 'matrixStats'

## The following objects are masked from 'package:Biobase':
##
##      anyMissing, rowMedians

## The following object is masked from 'package:dplyr':
##
##      count
```

```

## 
## Attaching package: 'MatrixGenerics'

## The following objects are masked from 'package:matrixStats':
## 

##     colAlls, colAnyNAs, colAnyNs, colAvgsPerRowSet, colCollapse,
##     colCounts, colCummaxs, colCummins, colCumprods, colCumsums,
##     colDiffs, colIQRDiffs, colIQRs, colLogSumExps, colMadDiffs,
##     colMads, colMaxs, colMeans2, colMedians, colMins, colOrderStats,
##     colProds, colQuantiles, colRanges, colRanks, colSdDiffs, colSds,
##     colSums2, colTabulates, colVarDiffs, colVars, colWeightedMads,
##     colWeightedMeans, colWeightedMedians, colWeightedSds,
##     colWeightedVars, rowAlls, rowAnyNAs, rowAnyNs, rowAvgsPerColSet,
##     rowCollapse, rowCounts, rowCummaxs, rowCummins, rowCumprods,
##     rowCumsums, rowDiffs, rowIQRDiffs, rowIQRs, rowLogSumExps,
##     rowMadDiffs, rowMads, rowMaxs, rowMeans2, rowMedians, rowMins,
##     rowOrderStats, rowProds, rowQuantiles, rowRanges, rowRanks,
##     rowSdDiffs, rowSds, rowSums2, rowTabulates, rowVarDiffs, rowVars,
##     rowWeightedMads, rowWeightedMeans, rowWeightedMedians,
##     rowWeightedSds, rowWeightedVars

## The following object is masked from 'package:Biobase':
## 

##     rowMedians

## 
## Attaching package: 'SummarizedExperiment'

## The following object is masked from 'package:Seurat':
## 

##     Assays

## The following object is masked from 'package:SeuratObject':
## 

##     Assays

options(Seurat.object.assay.version = "v5")

### read sample meta information
sample_meta <- c('CTRL', 'TSC_edge', 'TSC_tuber', 'TSC_outside')

### read cellranger out into Seurat object
lapply(1:length(sample_meta), function(i) {
  print(i)
  h5 <- sprintf(
    "../../data/raw-data/cellrange-arc-out/%s/filtered_feature_bc_matrix.h5",
    sample_meta[i])
  print(h5)

  obj_count <- Read10X_h5(h5)

  obj <- CreateSeuratObject(
    counts = obj_count ,
    project = sample_meta[i] ,
    assay = "RNA"
  )
  fragments_path <- sprintf(

```

```

"../../data/raw-data/cellrange-arc-out/%s/atac_fragments.tsv.gz",
sample_meta[i])
print(fragments_path)

obj [['ATAC']] <- CreateChromatinAssay(counts = obj_count$`Peaks`,
                                         annotation = annotations,
                                         fragments = fragments_path,
                                         sep = c(":", "-"),
                                         genome = 'hg38')

obj$group <- sample_meta[i]
# # add sample name to cell id
obj <- RenameCells(obj, add.cell.id = sample_meta[i])
obj
}) -> sample_seurat_list

## [1] 1
## [1] "../../data/raw-data/cellrange-arc-out/CTRL/filtered_feature_bc_matrix.h5"
## Genome matrix has multiple modalities, returning a list of matrices for this genome
## [1] "../../data/raw-data/cellrange-arc-out/CTRL/atac_fragments.tsv.gz"
## Computing hash
## [1] 2
## [1] "../../data/raw-data/cellrange-arc-out/TSC_edge/filtered_feature_bc_matrix.h5"
## Genome matrix has multiple modalities, returning a list of matrices for this genome
## [1] "../../data/raw-data/cellrange-arc-out/TSC_edge/atac_fragments.tsv.gz"
## Computing hash
## [1] 3
## [1] "../../data/raw-data/cellrange-arc-out/TSC_tuber/filtered_feature_bc_matrix.h5"
## Genome matrix has multiple modalities, returning a list of matrices for this genome
## [1] "../../data/raw-data/cellrange-arc-out/TSC_tuber/atac_fragments.tsv.gz"
## Computing hash
## [1] 4
## [1] "../../data/raw-data/cellrange-arc-out/TSC_outside/filtered_feature_bc_matrix.h5"
## Genome matrix has multiple modalities, returning a list of matrices for this genome
## [1] "../../data/raw-data/cellrange-arc-out/TSC_outside/atac_fragments.tsv.gz"
## Computing hash
names(sample_seurat_list) <- sample_meta

```

## 2. QC for data

```
### Data QC
lapply(1:length(sample_seurat_list), function(i) {
  print(i)
  obj <- sample_seurat_list[[i]]
  print(sample_meta[i])
  # show how many cells are in the object
  print(paste0("Number of cells before QC: ", ncol(obj)))
  obj$percent.mt <- PercentageFeatureSet(obj, pattern = "^\u00c9MT-")

  # before QC plot
  p<-VlnPlot(obj,
    features = c("nFeature_RNA", "nCount_RNA", "percent.mt", "nCount_ATAC"),
    ncol = 4
  )
  print(p)
  ggsave(sprintf("./results/%s_before_QC.png", sample_meta[i]),p,
    height = 5, width = 8
  )

  # pull out the raw count matrix from your Seurat object
  raw_counts <- obj[["RNA"]]$counts

  # build a minimal SCE
  sce <- SingleCellExperiment(
    assays = list(counts = raw_counts)
  )

  # now run doublet detection
  sce <- scDblFinder(sce)

  assertthat::are_equal(colnames(sce), colnames(obj))
  obj$scDblFinder.class <- sce$scDblFinder.class

  # QC for RNA
  obj <- subset(obj,
    subset =
      nFeature_RNA > 200 &
      nFeature_RNA < 10000 &
      percent.mt < 20 &
      scDblFinder.class == "singlet"
  )

  # QC for ATAC
  # REF: https://satijalab.org/seurat/archive/v3.1/atacseq\_integration\_vignette
  obj <- subset( obj , subset = nCount_ATAC > 30 &
    nCount_ATAC < 10000)

  # after QC plot
  p<-VlnPlot(obj,
    features = c("nFeature_RNA", "nCount_RNA", "percent.mt", "nCount_ATAC"),
    ncol = 4
```

```

    )
print(p)

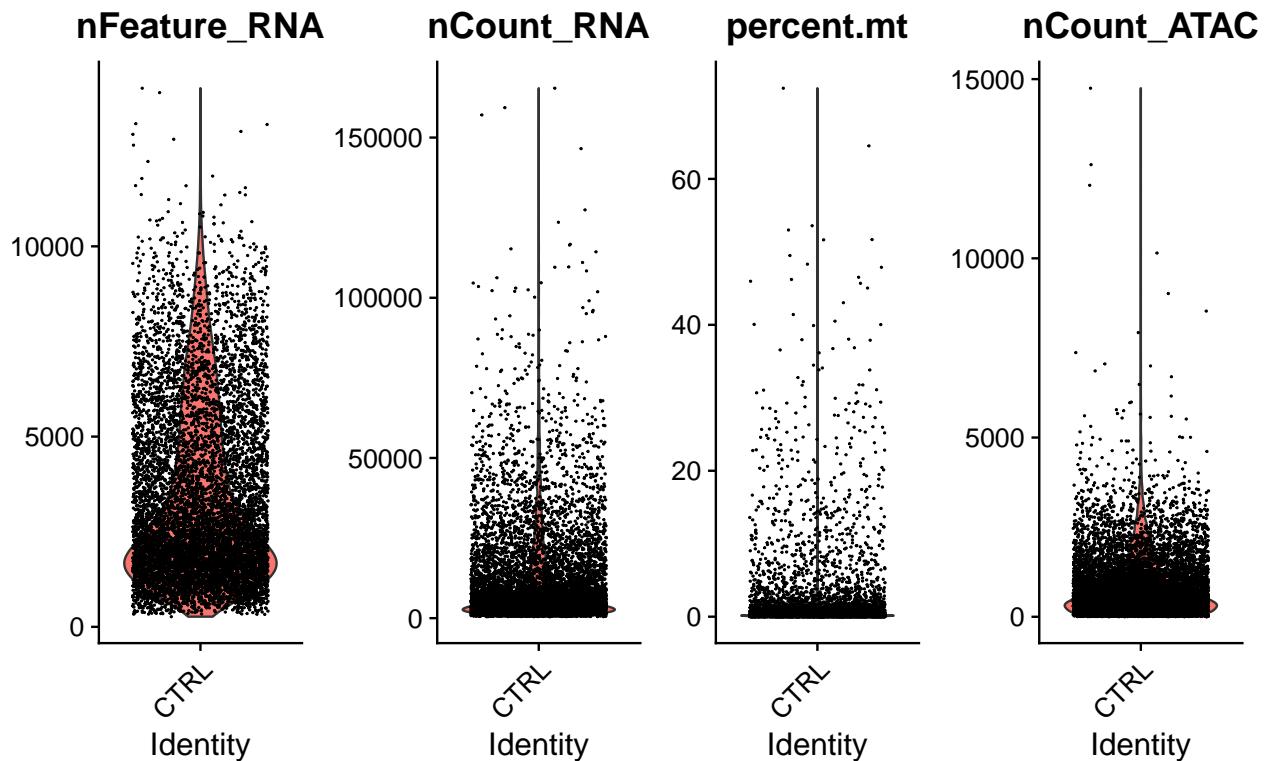
# show how many cells are left after QC
print(paste0("Number of cells after QC: ", ncol(obj)))
ggsave(sprintf("./results/%s_after_QC.png", sample_meta[i]), p,
       height = 5, width = 8
)
obj
}) -> sample_seurat_list

```

```

## [1] 1
## [1] "CTRL"
## [1] "Number of cells before QC: 8654"
## Warning: Default search for "data" layer in "RNA" assay yielded no results;
## utilizing "counts" layer instead.

```



```

## Warning in LayerData.Assay5(object = x, layer = i): multiple layers are identified by counts.Gene Expr
## only the first layer is used

## Warning in .checkSCE(sce): Some cells in `sce` have an extremely low read
## counts; note that these could trigger errors and might best be filtered out

## Creating ~6924 artificial doublets...

## Dimensional reduction

## Evaluating kNN...

## Training model...

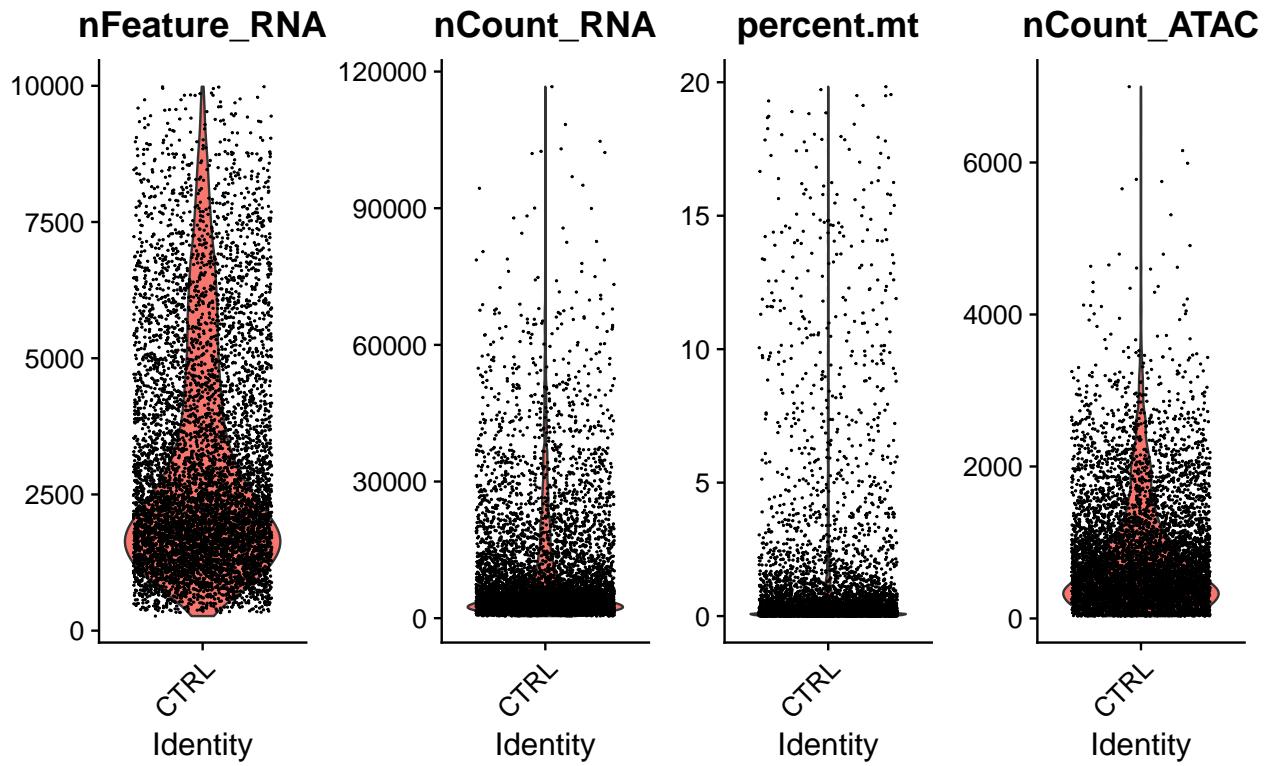
## iter=0, 1773 cells excluded from training.

```

```

## Warning in seq.default(along = y): partial argument match of 'along' to
## 'along.with'
## iter=1, 1960 cells excluded from training.
## Warning in seq.default(along = y): partial argument match of 'along' to
## 'along.with'
## iter=2, 1966 cells excluded from training.
## Warning in seq.default(along = y): partial argument match of 'along' to
## 'along.with'
## Threshold found:0.618
## 1201 (13.9%) doublets called
## Warning: Default search for "data" layer in "RNA" assay yielded no results;
## utilizing "counts" layer instead.
## [1] "Number of cells after QC: 7044"

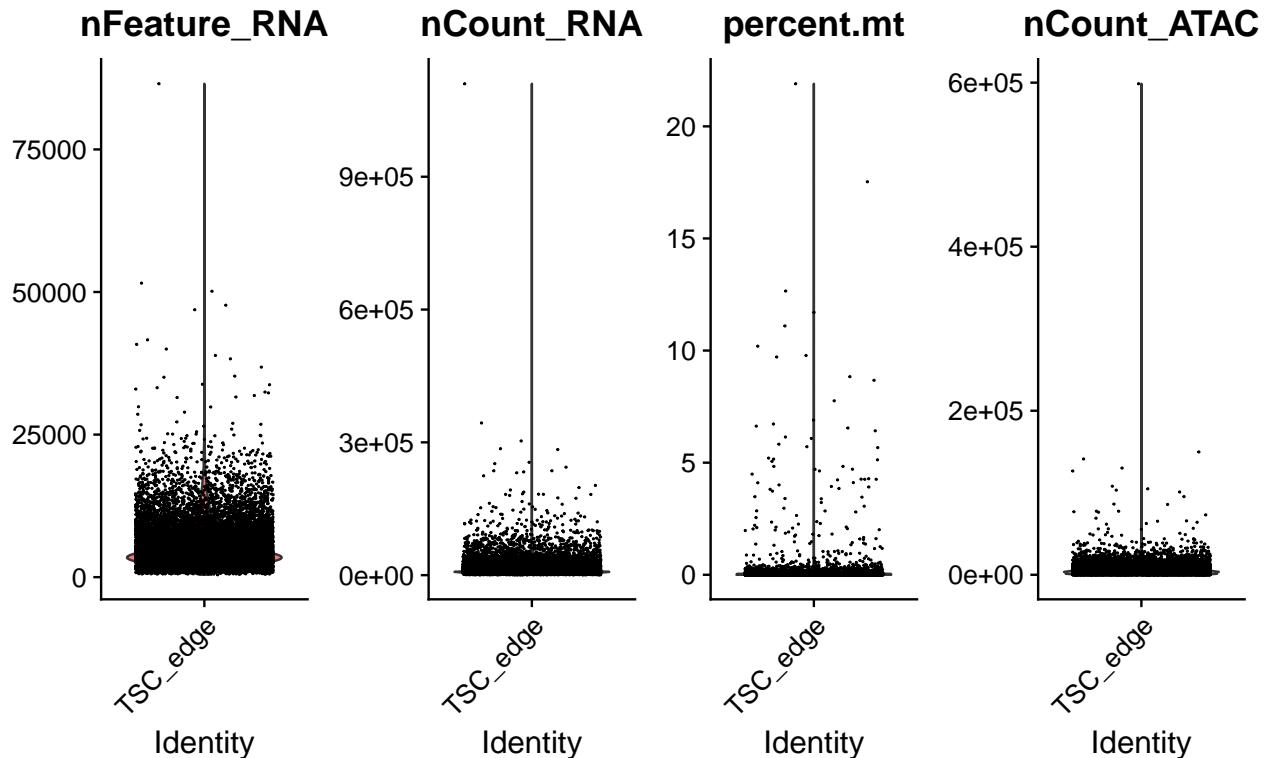
```



```

## [1] 2
## [1] "TSC_edge"
## [1] "Number of cells before QC: 16701"
## Warning: Default search for "data" layer in "RNA" assay yielded no results;
## utilizing "counts" layer instead.

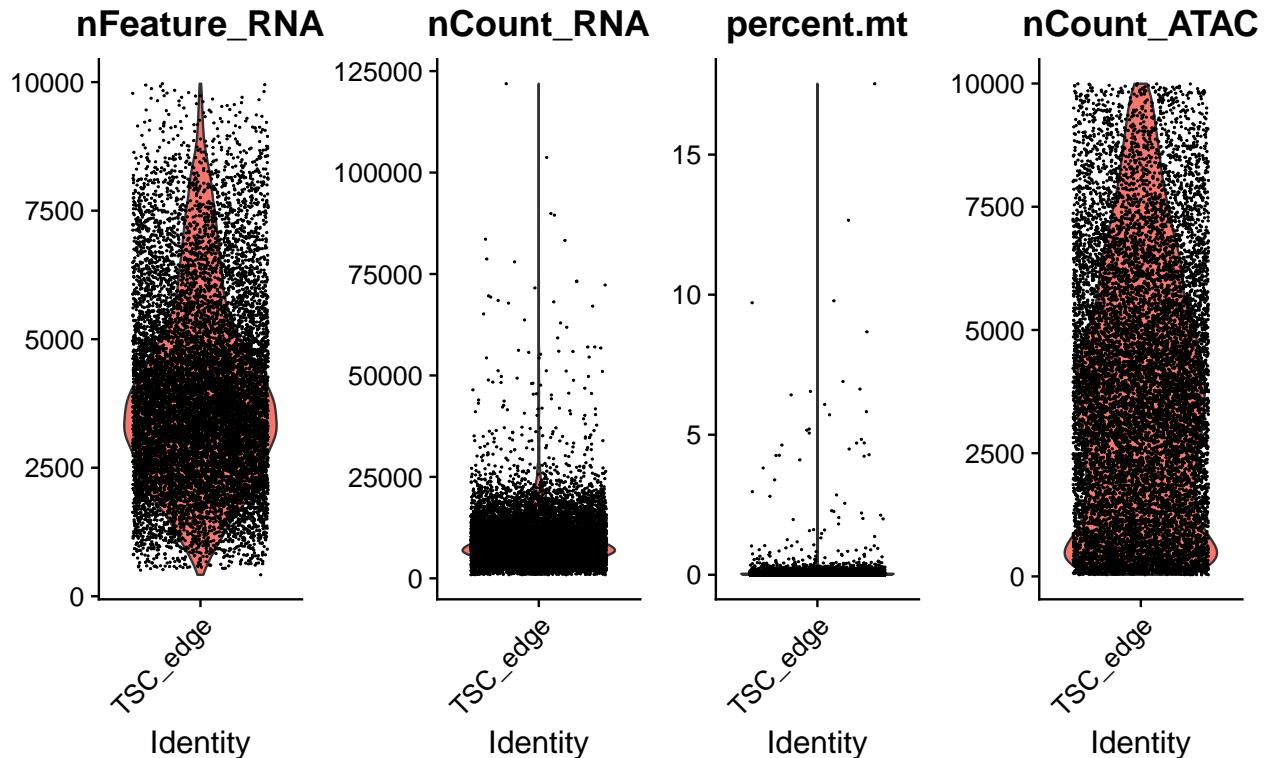
```



```

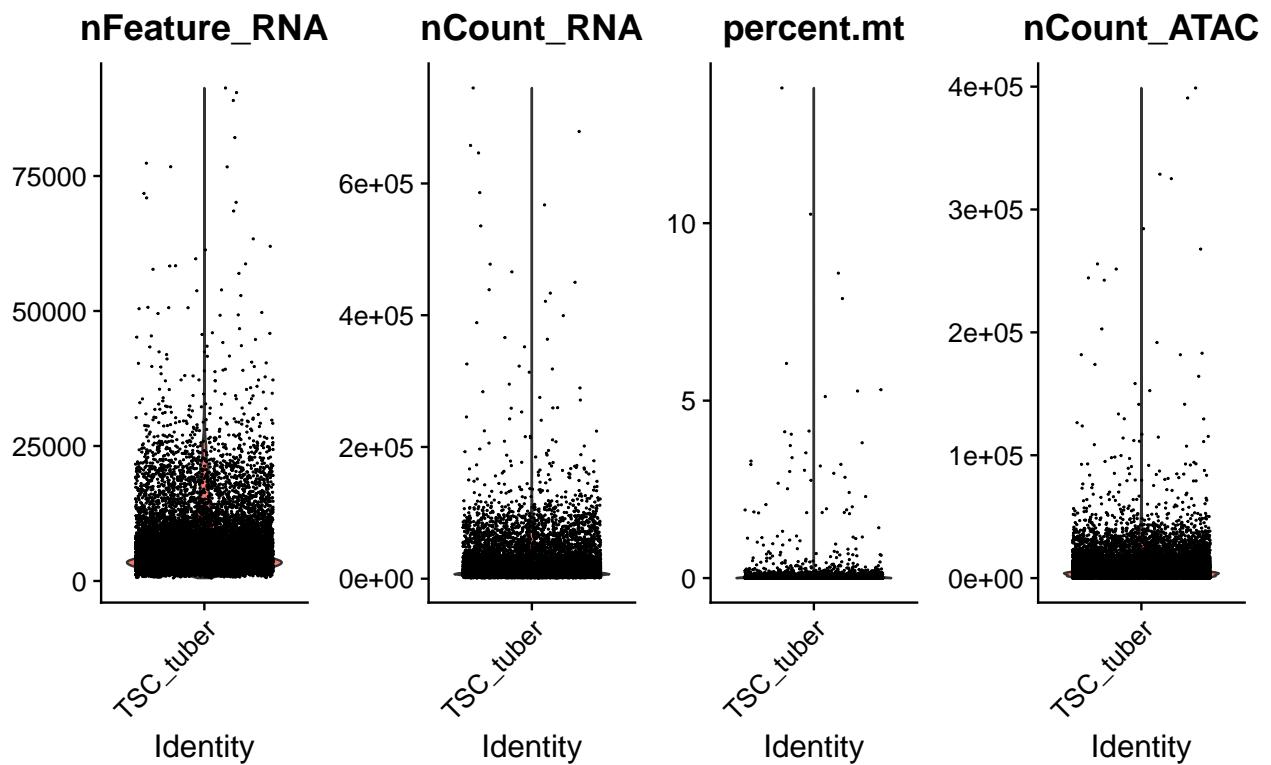
## Warning in LayerData.Assay5(object = x, layer = i): multiple layers are identified by counts.Gene Expr
##   only the first layer is used
## Warning in LayerData.Assay5(object = x, layer = i): Some cells in `sce` have an extremely low read co
## Creating ~13361 artificial doublets...
## Dimensional reduction
## Evaluating kNN...
## Training model...
## iter=0, 4330 cells excluded from training.
## Warning in seq.default(along = y): partial argument match of 'along' to
##   'along.with'
## iter=1, 4365 cells excluded from training.
## Warning in seq.default(along = y): partial argument match of 'along' to
##   'along.with'
## iter=2, 4424 cells excluded from training.
## Warning in seq.default(along = y): partial argument match of 'along' to
##   'along.with'
## Threshold found:0.545
## 3090 (18.5%) doublets called
## Warning: Default search for "data" layer in "RNA" assay yielded no results;
## utilizing "counts" layer instead.
## [1] "Number of cells after QC: 12327"

```



```
## [1] 3
## [1] "TSC_tuber"
## [1] "Number of cells before QC: 12764"

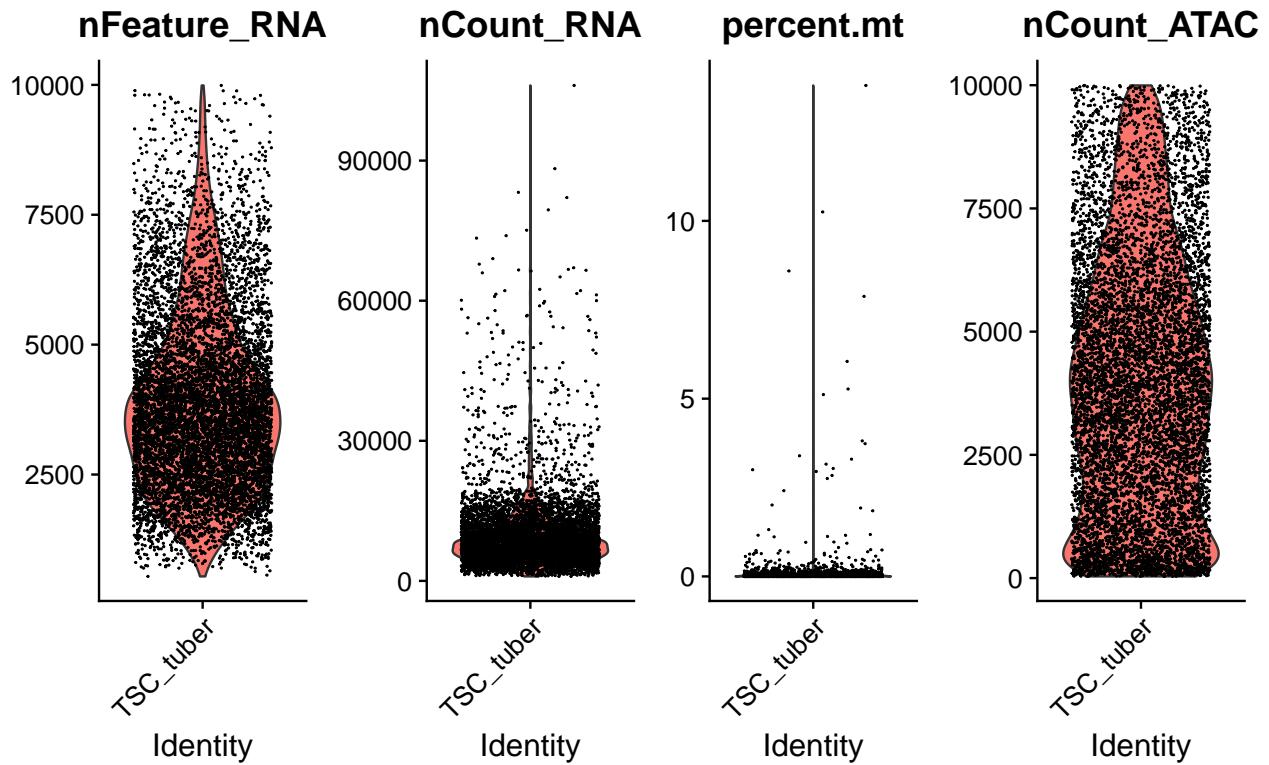
## Warning: Default search for "data" layer in "RNA" assay yielded no results;
## utilizing "counts" layer instead.
```



```

## Warning in LayerData.Assay5(object = x, layer = i): multiple layers are identified by counts.Gene Expr
## only the first layer is used
## Warning in LayerData.Assay5(object = x, layer = i): Some cells in `sce` have an extremely low read co
## Creating ~10212 artificial doublets...
## Dimensional reduction
## Evaluating kNN...
## Training model...
## iter=0, 2951 cells excluded from training.
## Warning in seq.default(along = y): partial argument match of 'along' to
## 'along.with'
## iter=1, 3042 cells excluded from training.
## Warning in seq.default(along = y): partial argument match of 'along' to
## 'along.with'
## iter=2, 3019 cells excluded from training.
## Warning in seq.default(along = y): partial argument match of 'along' to
## 'along.with'
## Threshold found:0.521
## 2016 (15.8%) doublets called
## Warning: Default search for "data" layer in "RNA" assay yielded no results;
## utilizing "counts" layer instead.
## [1] "Number of cells after QC: 8329"

```



```

## [1] 4

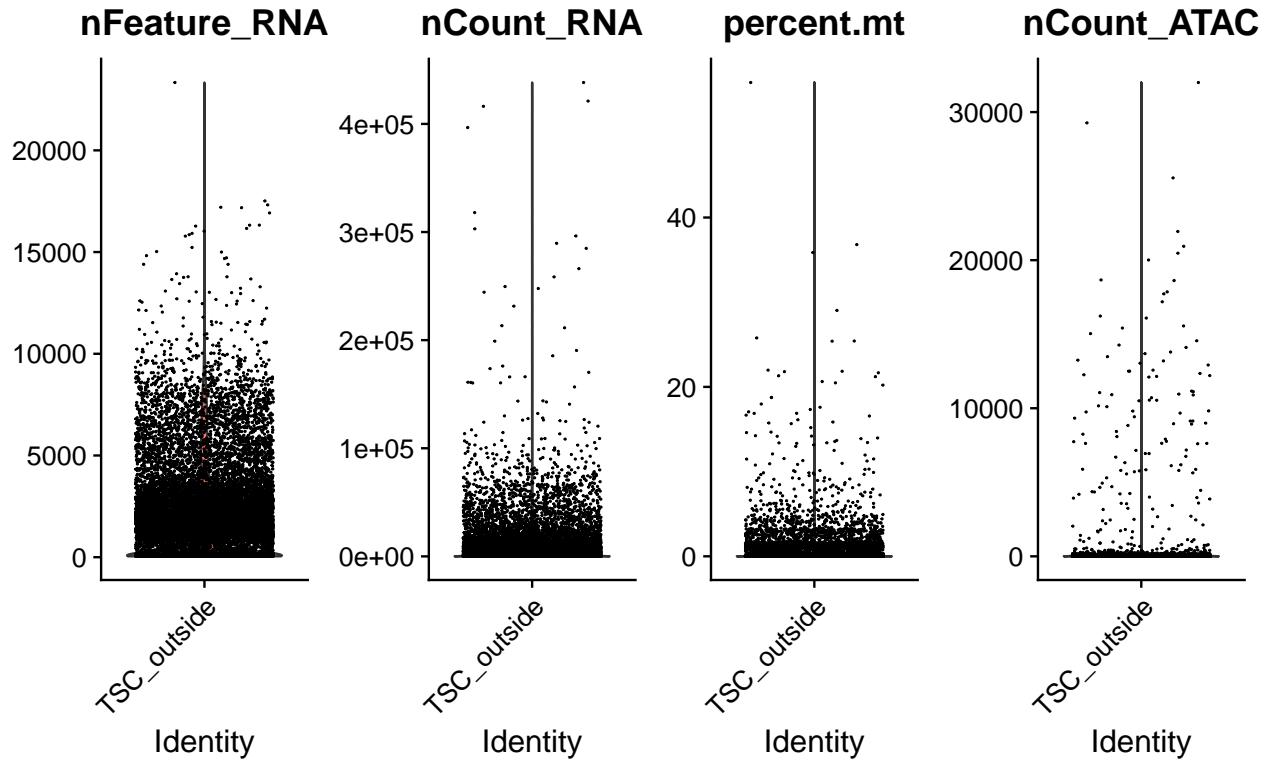
```

```

## [1] "TSC_outside"
## [1] "Number of cells before QC: 20000"

## Warning: Default search for "data" layer in "RNA" assay yielded no results;
## utilizing "counts" layer instead.

```



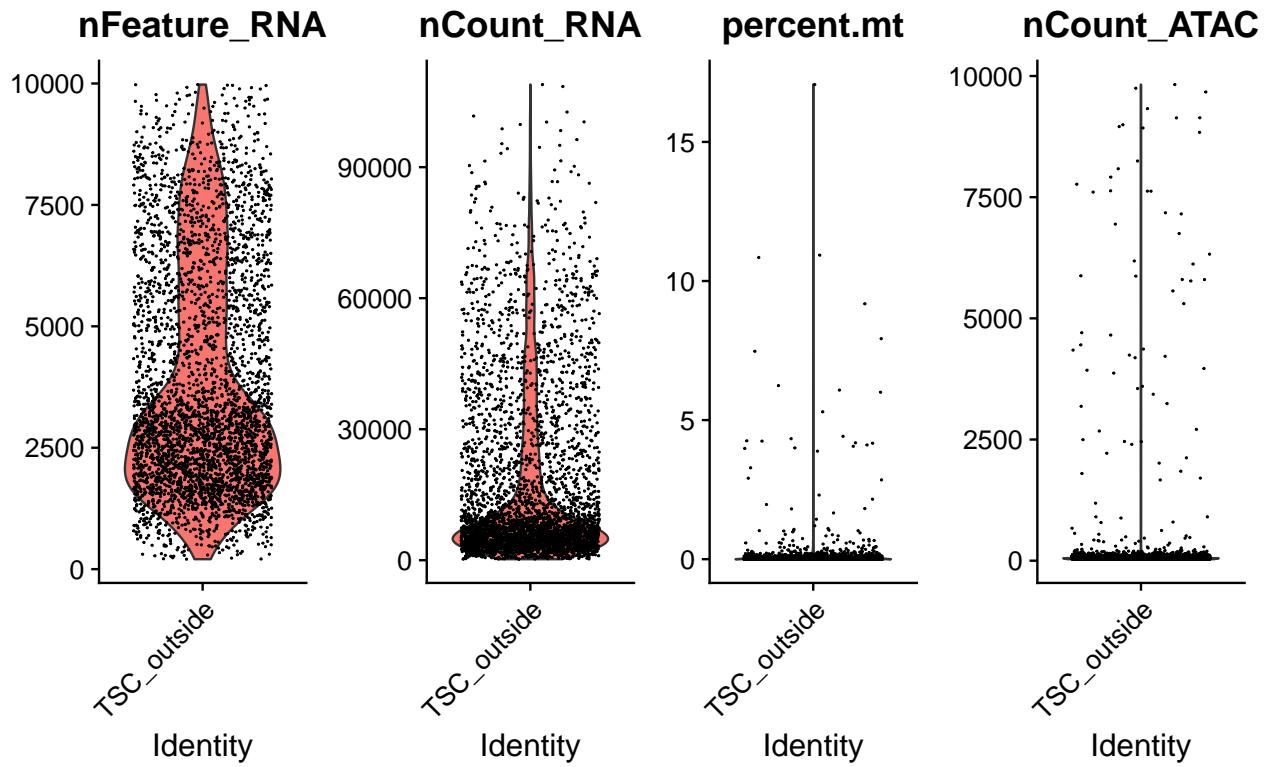
```

## Warning in LayerData.Assay5(object = x, layer = i): multiple layers are identified by counts.Gene Expr
## only the first layer is used
## Warning in LayerData.Assay5(object = x, layer = i): Some cells in `sce` have an extremely low read co
## Creating ~16000 artificial doublets...
## Dimensional reduction
## Evaluating kNN...
## Training model...
## iter=0, 3591 cells excluded from training.
## Warning in seq.default(along = y): partial argument match of 'along' to
## 'along.with'
## iter=1, 3553 cells excluded from training.
## Warning in seq.default(along = y): partial argument match of 'along' to
## 'along.with'
## iter=2, 3716 cells excluded from training.
## Warning in seq.default(along = y): partial argument match of 'along' to
## 'along.with'
## Threshold found:0.487
## 2336 (11.7%) doublets called

```

```
## Warning: Default search for "data" layer in "RNA" assay yielded no results;  
## utilizing "counts" layer instead.
```

```
## [1] "Number of cells after QC: 3703"
```



```
names(sample_seurat_list) <- sample_meta
```

```
# save clean data  
saveRDS(sample_seurat_list,  
        file = here::here("data", "processed-data",  
                           "sample_seurat_list_2025-05-01.rds"),  
        compress = F,  
)  
  
saveRDS(sample_meta,  
        file = here::here("data", "processed-data",  
                           "sample_meta_2025-05-01.rds"),  
)
```

```

sessionInfo()

## R version 4.4.0 (2024-04-24)
## Platform: aarch64-apple-darwin20
## Running under: macOS 15.4
##
## Matrix products: default
## BLAS:    /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRblas.0.dylib
## LAPACK:  /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRlapack.dylib;  LAPACK v
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## time zone: America/New_York
## tzcode source: internal
##
## attached base packages:
## [1] stats4      stats       graphics   grDevices  utils      datasets   methods
## [8] base
##
## other attached packages:
## [1] scDbxFinder_1.18.0           SingleCellExperiment_1.26.0
## [3] SummarizedExperiment_1.34.0  MatrixGenerics_1.16.0
## [5] matrixStats_1.5.0            data.table_1.17.0
## [7] BSgenome.Hsapiens.UCSC.hg38_1.4.5 BSgenome_1.72.0
## [9] BiocIO_1.14.0                Biostrings_2.72.1
## [11] XVector_0.44.0              AnnotationHub_3.12.0
## [13] BiocFileCache_2.12.0         dbplyr_2.5.0
## [15] simspec_0.0.0.9000          cowplot_1.1.3
## [17] EnsDb.Hsapiens.v86_2.99.0    ensemblDb_2.28.1
## [19] AnnotationFilter_1.28.0      GenomicFeatures_1.56.0
## [21] AnnotationDbi_1.66.0         Biobase_2.64.0
## [23] Signac_1.14.0               Seurat_5.2.1
## [25] SeuratObject_5.0.2          sp_2.2-0
## [27] rtracklayer_1.64.0          GenomicRanges_1.56.2
## [29] GenomeInfoDb_1.40.1         IRanges_2.38.1
## [31] S4Vectors_0.42.1            BiocGenerics_0.50.0
## [33] knitr_1.50                  lubridate_1.9.4
## [35]forcats_1.0.0               stringr_1.5.1
## [37] dplyr_1.1.4                 purrr_1.0.4
## [39] readr_2.1.5                 tidyR_1.3.1
## [41] tibble_3.2.1                ggplot2_3.5.2
## [43] tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
## [1] ProtGenerics_1.36.0          spatstat.sparse_3.1-0
## [3] bitops_1.0-9                 httr_1.4.7
## [5] RColorBrewer_1.1-3           tools_4.4.0
## [7] sctransform_0.4.1            R6_2.6.1
## [9] lazyeval_0.2.2               uwot_0.2.3
## [11] withr_3.0.2                 gridExtra_2.3
## [13] progressr_0.15.1            textshaping_1.0.0
## [15] cli_3.6.4                   spatstat.explore_3.4-2
## [17] fastDummies_1.7.5           labeling_0.4.3

```

```

## [19] spatstat.data_3.1-6      ggridges_0.5.6
## [21] pbapply_1.7-2           systemfonts_1.2.2
## [23] Rsamtools_2.20.0        scater_1.32.1
## [25] parallelly_1.43.0       limma_3.60.6
## [27] rstudioapi_0.17.1       RSQLite_2.3.9
## [29] generics_0.1.3          ica_1.0-3
## [31] spatstat.random_3.3-3   Matrix_1.7-3
## [33] ggbeeswarm_0.7.2        abind_1.4-8
## [35] lifecycle_1.0.4         edgeR_4.2.2
## [37] yaml_2.3.10            SparseArray_1.4.8
## [39] Rtsne_0.17              grid_4.4.0
## [41] blob_1.2.4              dqrng_0.4.1
## [43] promises_1.3.2          crayon_1.5.3
## [45] miniUI_0.1.2           lattice_0.22-7
## [47] beachmat_2.20.0         KEGGREST_1.44.1
## [49] metapod_1.12.0          pillar_1.10.2
## [51] rjson_0.2.23            xgboost_1.7.9.1
## [53] future.apply_1.11.3     codetools_0.2-20
## [55] fastmatch_1.1-6         glue_1.8.0
## [57] spatstat.univar_3.1-2   vctrs_0.6.5
## [59] png_0.1-8               spam_2.11-1
## [61] gtable_0.3.6             assertthat_0.2.1
## [63] cachem_1.1.0            xfun_0.52
## [65] S4Arrays_1.4.1          mime_0.13
## [67] survival_3.8-3          RcppRoll_0.3.1
## [69] tinytex_0.57             statmod_1.5.0
## [71] bluster_1.14.0          fitdistrplus_1.2-2
## [73] ROCR_1.0-11              nlme_3.1-168
## [75] bit64_4.6.0-1           filelock_1.0.3
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## [79] irlba_2.3.5.1           viper_0.4.7
## [81] KernSmooth_2.23-26       colorspace_2.1-1
## [83] DBI_1.2.3                ggrastr_1.0.2
## [85] tidyselect_1.2.1          bit_4.6.0
## [87] compiler_4.4.0            curl_6.2.2
## [89] BiocNeighbors_1.22.0     hdf5r_1.3.12
## [91] DelayedArray_0.30.1      plotly_4.10.4
## [93] scales_1.3.0              lmtest_0.9-40
## [95] rappdirs_0.3.3           digest_0.6.37
## [97] goftest_1.2-3            spatstat.utils_3.1-3
## [99] rmarkdown_2.29             htmltools_0.5.8.1
## [101] pkgconfig_2.0.3          sparseMatrixStats_1.16.0
## [103] fastmap_1.2.0            rlang_1.1.6
## [105] htmlwidgets_1.6.4        UCSC.utils_1.0.0
## [107] shiny_1.10.0             DelayedMatrixStats_1.26.0
## [109] farver_2.1.2             zoo_1.8-14
## [111] jsonlite_2.0.0           BiocParallel_1.38.0
## [113] BiocSingular_1.20.0       RCurl_1.98-1.17
## [115] magrittr_2.0.3            scuttle_1.14.0
## [117] GenomeInfoDbData_1.2.12  dotCall164_1.2
## [119] patchwork_1.3.0           munsell_0.5.1
## [121] Rcpp_1.0.14              viridis_0.6.5
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## [133] tensor_1.5                   hms_1.1.3
## [135] locfit_1.5-9.12              igraph_2.1.4
## [137] spatstat.geom_3.3-6          RcppHNSW_0.6.0
## [139] reshape2_1.4.4                ScaledMatrix_1.12.0
## [141] BiocVersion_3.19.1           XML_3.99-0.18
## [143] evaluate_1.0.3                scran_1.32.0
## [145] BiocManager_1.30.25          tzdb_0.5.0
## [147] httpuv_1.6.16                RANN_2.6.2
## [149] polyclip_1.10-7              future_1.40.0
## [151] scattermore_1.2              rsvd_1.0.5
## [153] xtable_1.8-4                restfulr_0.0.15
## [155] RSpectra_0.16-2             later_1.4.2
## [157] ragg_1.4.0                  viridisLite_0.4.2
## [159] beeswarm_0.4.0               memoise_2.0.1
## [161] GenomicAlignments_1.40.0     cluster_2.1.8.1
## [163] timechange_0.3.0              globals_0.17.0
## [165] here_1.0.1
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