Figrue for 2025-05-30

Ximing Ran

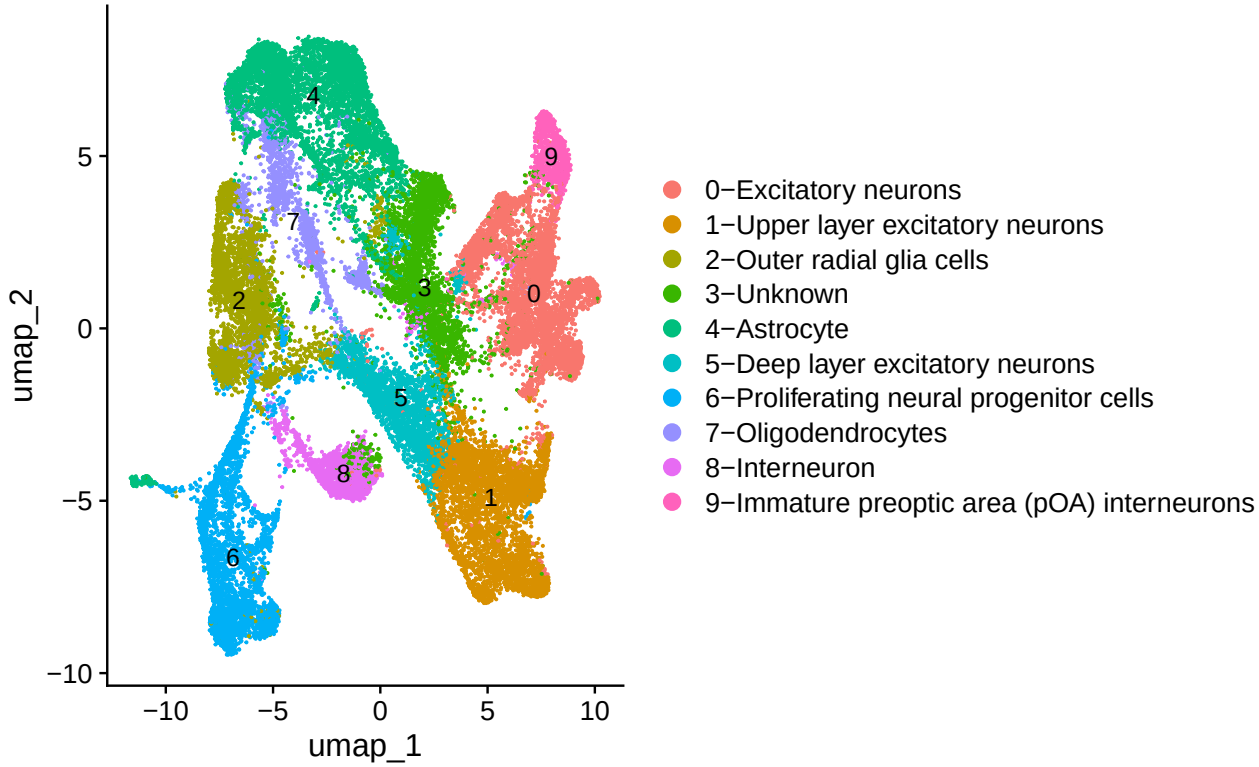
2025-05-30

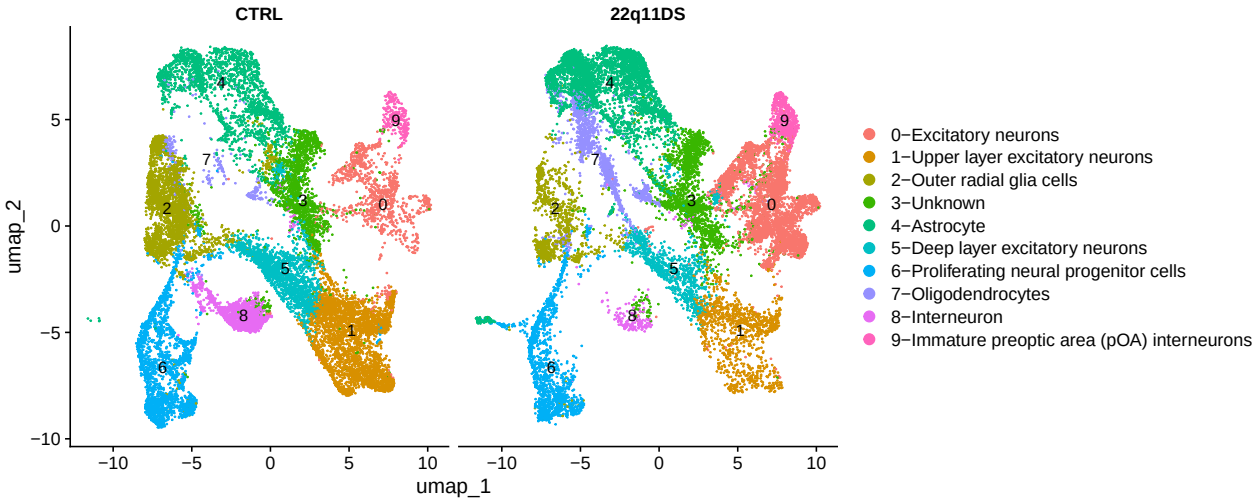
Contents

1. Read the merged Data

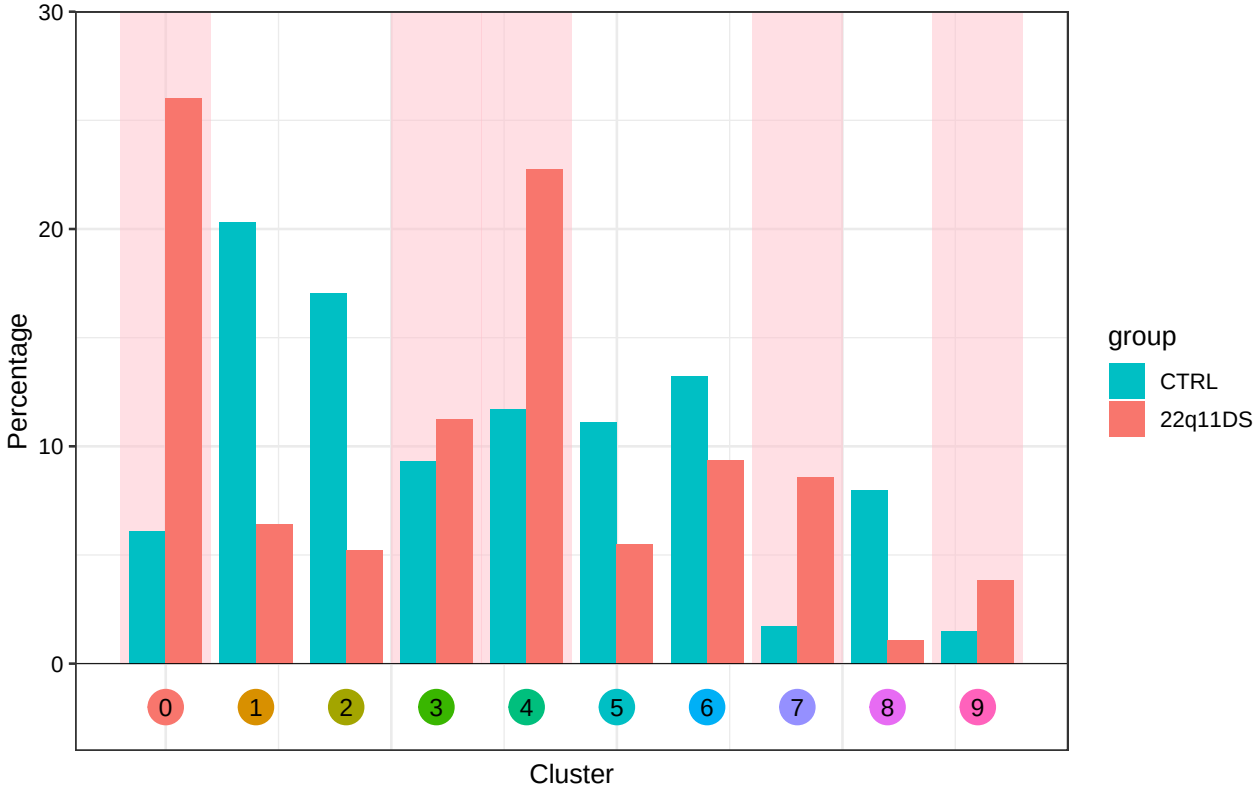
2. Plot the UMAP

```
##
##                         0-Excitatory neurons
##                                         5608
##             1-Upper layer excitatory neurons
##                                         4626
##                    2-Outer radial glia cells
##                                         3848
##                                   3-Unknown
##                                         3576
##                                 4-Astrocyte
##                                         6009
##              5-Deep layer excitatory neurons
##                                         2880
##     6-Proliferating neural progenitor cells
##                                         3923
##                           7-Oligodendrocytes
##                                         1802
##                                8-Interneuron
##                                         1563
## 9-Immature preoptic area (pOA) interneurons
##                                          930
```





3. Plot the cell_type proportion



4. DEG

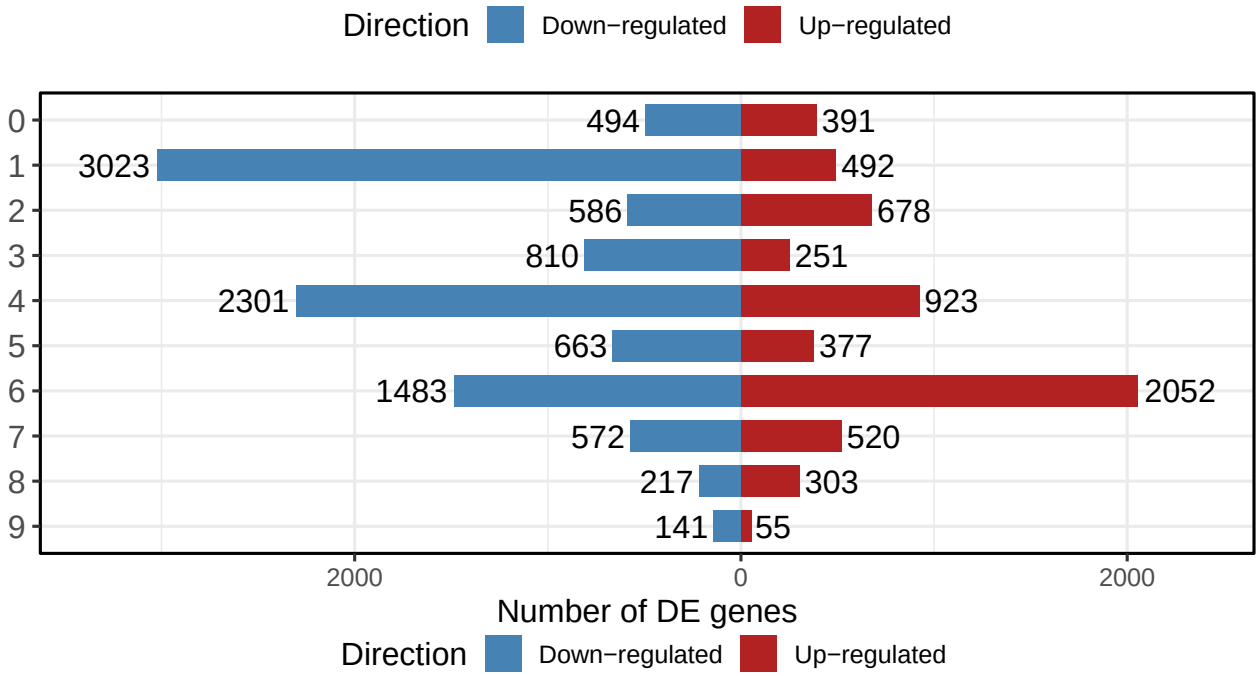
```
##
##                                22q_Astrocyte
##                                         3987
##              22q_Deep layer excitatory neurons
##                                          966
##                        22q_Excitatory neurons
```

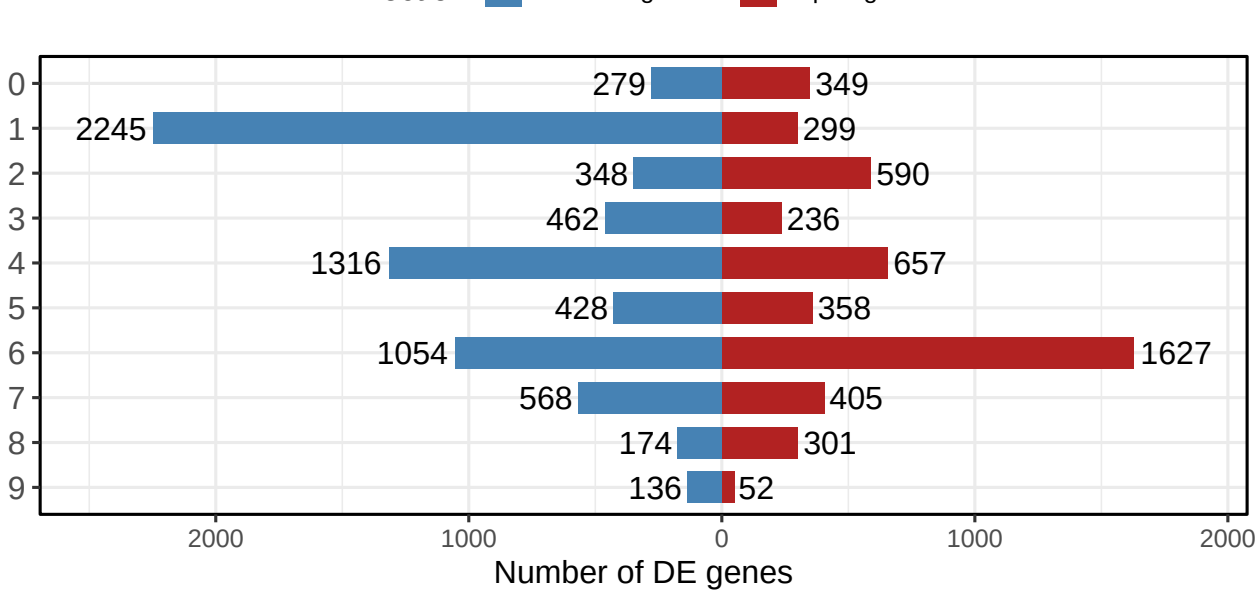
```
##                                          4560
##  22q_Immature preoptic area (pOA) interneurons
##                                           675
##                                 22q_Interneuron
##                                           188
##                           22q_Oligodendrocytes
##                                          1502
##                    22q_Outer radial glia cells
##                                           912
##      22q_Proliferating neural progenitor cells
##                                          1639
##                                   22q_Unknown
##                                          1973
##             22q_Upper layer excitatory neurons
##                                          1121
##                                CTRL_Astrocyte
##                                          2022
##             CTRL_Deep layer excitatory neurons
##                                          1914
##                         CTRL_Excitatory neurons
##                                          1048
## CTRL_Immature preoptic area (pOA) interneurons
##                                           255
##                               CTRL_Interneuron
##                                          1375
##                           CTRL_Oligodendrocytes
##                                           300
##                    CTRL_Outer radial glia cells
##                                          2936
##     CTRL_Proliferating neural progenitor cells
##                                          2284
##                                   CTRL_Unknown
##                                          1603
##            CTRL_Upper layer excitatory neurons
##                                          3505
```

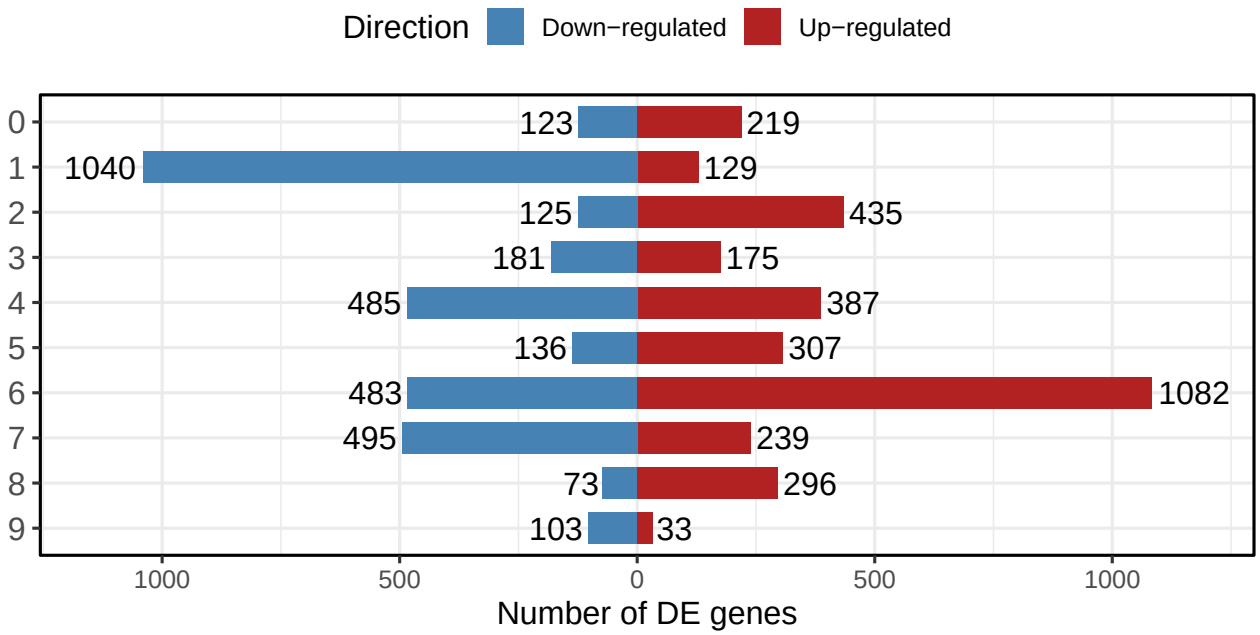
```
## [1] Astrocyte
## 10 Levels: Excitatory neurons ... Immature preoptic area (pOA) interneurons
```

```
## [1] Interneuron
## 10 Levels: Excitatory neurons ... Immature preoptic area (pOA) interneurons
## [1] Proliferating neural progenitor cells
## 10 Levels: Excitatory neurons ... Immature preoptic area (pOA) interneurons
## [1] Outer radial glia cells
## 10 Levels: Excitatory neurons ... Immature preoptic area (pOA) interneurons
## [1] Excitatory neurons
## 10 Levels: Excitatory neurons ... Immature preoptic area (pOA) interneurons
## [1] Immature preoptic area (pOA) interneurons
## 10 Levels: Excitatory neurons ... Immature preoptic area (pOA) interneurons
## [1] Upper layer excitatory neurons
## 10 Levels: Excitatory neurons ... Immature preoptic area (pOA) interneurons
## [1] Unknown
## 10 Levels: Excitatory neurons ... Immature preoptic area (pOA) interneurons
## [1] Oligodendrocytes
## 10 Levels: Excitatory neurons ... Immature preoptic area (pOA) interneurons
```

```
## [1] Deep layer excitatory neurons
## 10 Levels: Excitatory neurons ... Immature preoptic area (pOA) interneurons
```






Direction
Down−regulated
Up−regulated
0
1
2
3
4
5
6
7
8
9
123
219
1040
129
125
435
181
175
485
387
136
307
483
1082
495
239
73
296
103
33
1000
500
0
500
1000
Number of DE genes

Session Information

```
## R version 4.4.0 (2024-04-24)
## Platform: aarch64-apple-darwin20
## Running under: macOS 15.5
##
## 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] kableExtra_1.4.0          extrafont_0.19
##  [3] patchwork_1.3.0           pheatmap_1.0.12
##  [5] data.table_1.17.4         harmony_1.2.3
##  [7] Rcpp_1.0.14               conflicted_1.2.0
##  [9] openxlsx_4.2.8            Seurat_5.3.0
## [11] SeuratObject_5.1.0        sp_2.2-0
## [13] AnnotationHub_3.12.0      BiocFileCache_2.12.0
## [15] dbplyr_2.5.0              simspec_0.0.0.9000
## [17] cowplot_1.1.3             EnsDb.Hsapiens.v86_2.99.0
## [19] ensembldb_2.28.1          AnnotationFilter_1.28.0
## [21] GenomicFeatures_1.56.0    AnnotationDbi_1.66.0
## [23] Biobase_2.64.0            Signac_1.14.0
## [25] rtracklayer_1.64.0        GenomicRanges_1.56.2
## [27] GenomeInfoDb_1.40.1       IRanges_2.38.1
## [29] S4Vectors_0.42.1          BiocGenerics_0.50.0
## [31] knitr_1.50                lubridate_1.9.4
## [33] forcats_1.0.0             stringr_1.5.1
## [35] dplyr_1.1.4               purrr_1.0.4
## [37] readr_2.1.5               tidyr_1.3.1
## [39] tibble_3.2.1              ggplot2_3.5.2
## [41] tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
##   [1] RcppAnnoy_0.0.22           splines_4.4.0
##   [3] later_1.4.2                BiocIO_1.14.0
##   [5] bitops_1.0-9               filelock_1.0.3
##   [7] polyclip_1.10-7            XML_3.99-0.18
##   [9] fastDummies_1.7.5          lifecycle_1.0.4
##  [11] rprojroot_2.0.4            globals_0.18.0
##  [13] lattice_0.22-7             MASS_7.3-65
##  [15] magrittr_2.0.3             limma_3.60.6
##  [17] plotly_4.10.4              rmarkdown_2.29
##  [19] yaml_2.3.10                httpuv_1.6.16
```

```
##  [21] sctransform_0.4.2           zip_2.3.2
##  [23] spam_2.11-1                 spatstat.sparse_3.1-0
##  [25] reticulate_1.42.0           pbapply_1.7-2
##  [27] DBI_1.2.3                   RColorBrewer_1.1-3
##  [29] abind_1.4-8                 zlibbioc_1.50.0
##  [31] Rtsne_0.17                  presto_1.0.0
##  [33] RCurl_1.98-1.17             rappdirs_0.3.3
##  [35] GenomeInfoDbData_1.2.12     ggrepel_0.9.6
##  [37] irlba_2.3.5.1               spatstat.utils_3.1-4
##  [39] listenv_0.9.1               goftest_1.2-3
##  [41] RSpectra_0.16-2             spatstat.random_3.4-1
##  [43] fitdistrplus_1.2-2          parallelly_1.44.0
##  [45] svglite_2.2.1               codetools_0.2-20
##  [47] DelayedArray_0.30.1         RcppRoll_0.3.1
##  [49] xml2_1.3.8                  tidyselect_1.2.1
##  [51] UCSC.utils_1.0.0            farver_2.1.2
##  [53] spatstat.explore_3.4-3      matrixStats_1.5.0
##  [55] GenomicAlignments_1.40.0    jsonlite_2.0.0
##  [57] progressr_0.15.1            ggridges_0.5.6
##  [59] survival_3.8-3              systemfonts_1.2.3
##  [61] tools_4.4.0                 ragg_1.4.0
##  [63] ica_1.0-3                   glue_1.8.0
##  [65] Rttf2pt1_1.3.12             gridExtra_2.3
##  [67] SparseArray_1.4.8           here_1.0.1
##  [69] xfun_0.52                   MatrixGenerics_1.16.0
##  [71] withr_3.0.2                 BiocManager_1.30.25
##  [73] fastmap_1.2.0               digest_0.6.37
##  [75] timechange_0.3.0            R6_2.6.1
##  [77] mime_0.13                   textshaping_1.0.1
##  [79] colorspace_2.1-1            scattermore_1.2
##  [81] tensor_1.5                  spatstat.data_3.1-6
##  [83] dichromat_2.0-0.1           RSQLite_2.3.11
##  [85] generics_0.1.4              httr_1.4.7
##  [87] htmlwidgets_1.6.4           S4Arrays_1.4.1
##  [89] uwot_0.2.3                  pkgconfig_2.0.3
##  [91] gtable_0.3.6                blob_1.2.4
##  [93] lmtest_0.9-40               XVector_0.44.0
##  [95] htmltools_0.5.8.1           dotCall64_1.2
##  [97] ProtGenerics_1.36.0         scales_1.4.0
##  [99] png_0.1-8                   spatstat.univar_3.1-3
## [101] rstudioapi_0.17.1           tzdb_0.5.0
## [103] reshape2_1.4.4              rjson_0.2.23
## [105] nlme_3.1-168                curl_6.2.3
## [107] cachem_1.1.0                zoo_1.8-14
## [109] BiocVersion_3.19.1          KernSmooth_2.23-26
## [111] parallel_4.4.0              miniUI_0.1.2
## [113] restfulr_0.0.15             pillar_1.10.2
## [115] grid_4.4.0                  vctrs_0.6.5
## [117] RANN_2.6.2                  promises_1.3.3
## [119] xtable_1.8-4                cluster_2.1.8.1
## [121] extrafontdb_1.0             evaluate_1.0.3
## [123] tinytex_0.57                cli_3.6.5
## [125] compiler_4.4.0              Rsamtools_2.20.0
## [127] rlang_1.1.6                 crayon_1.5.3
```

```
## [129] future.apply_1.11.3         labeling_0.4.3
## [131] plyr_1.8.9                  stringi_1.8.7
## [133] deldir_2.0-4                viridisLite_0.4.2
## [135] BiocParallel_1.38.0         Biostrings_2.72.1
## [137] lazyeval_0.2.2              spatstat.geom_3.4-1
## [139] Matrix_1.7-3                RcppHNSW_0.6.0
## [141] hms_1.1.3                   bit64_4.6.0-1
## [143] future_1.49.0               statmod_1.5.0
## [145] KEGGREST_1.44.1             shiny_1.10.0
## [147] SummarizedExperiment_1.34.0 ROCR_1.0-11
## [149] igraph_2.1.4                memoise_2.0.1
## [151] fastmatch_1.1-6             bit_4.6.0
```