

Cell Type Anotation

Cluster Marker

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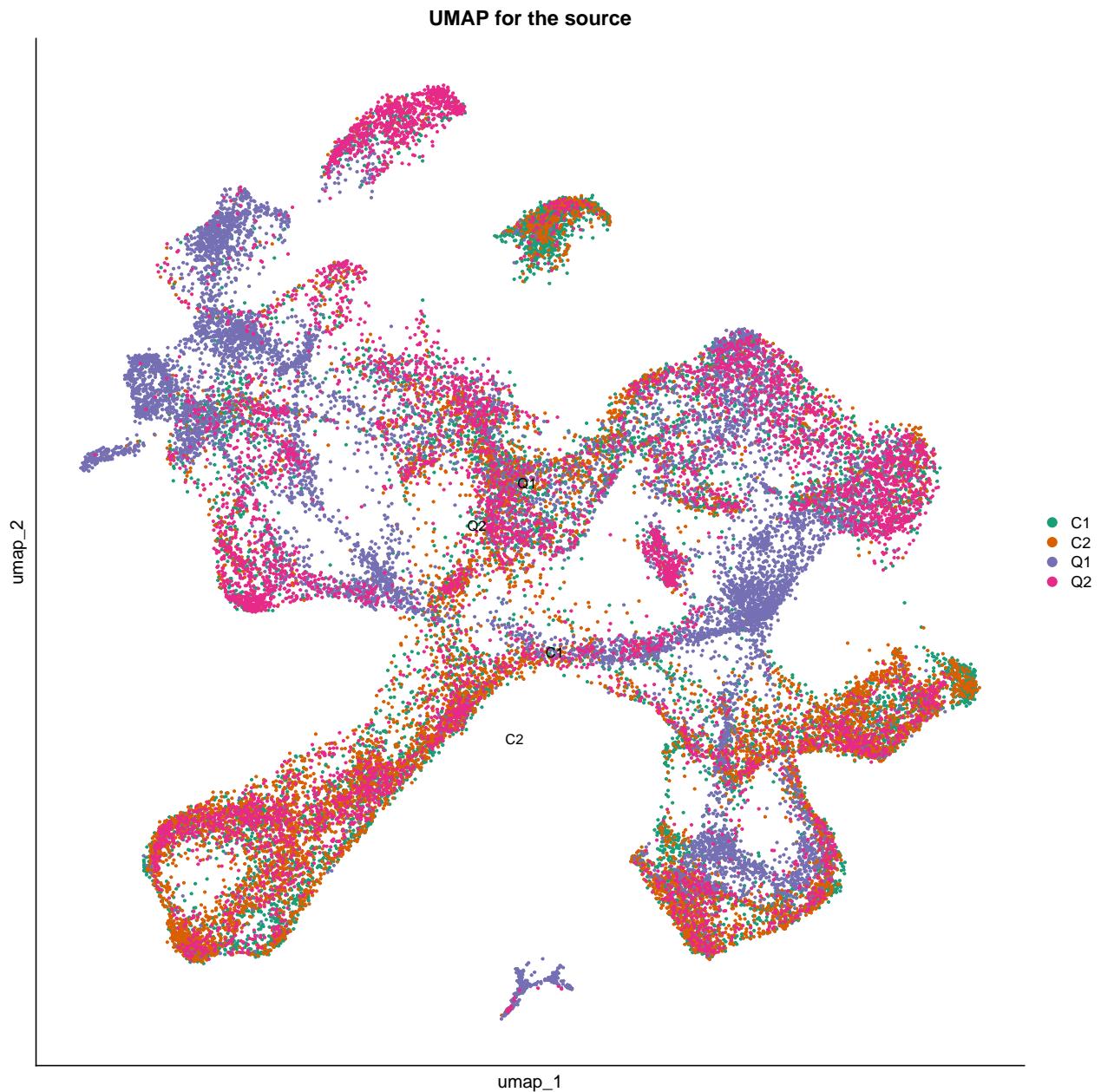
2025-05-15

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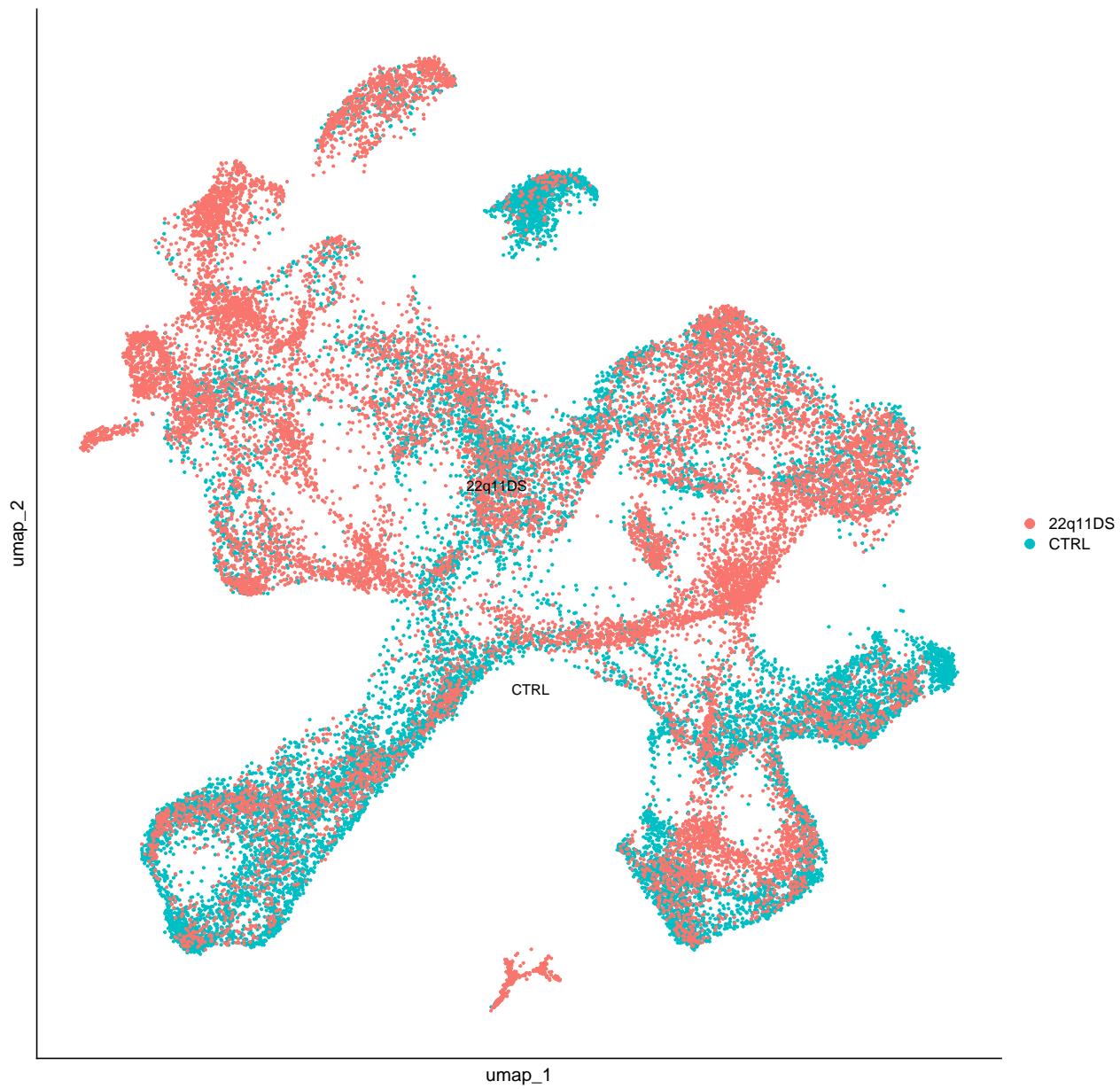
1. Read the merged Data

Plot the UMAP with source and Group

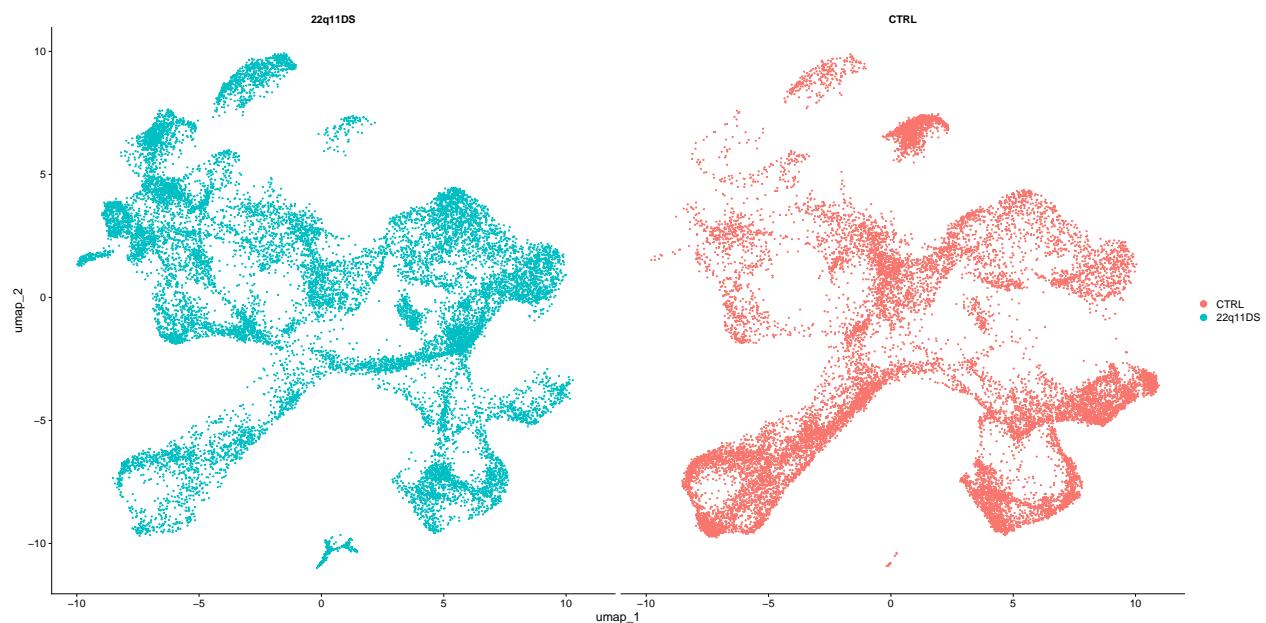


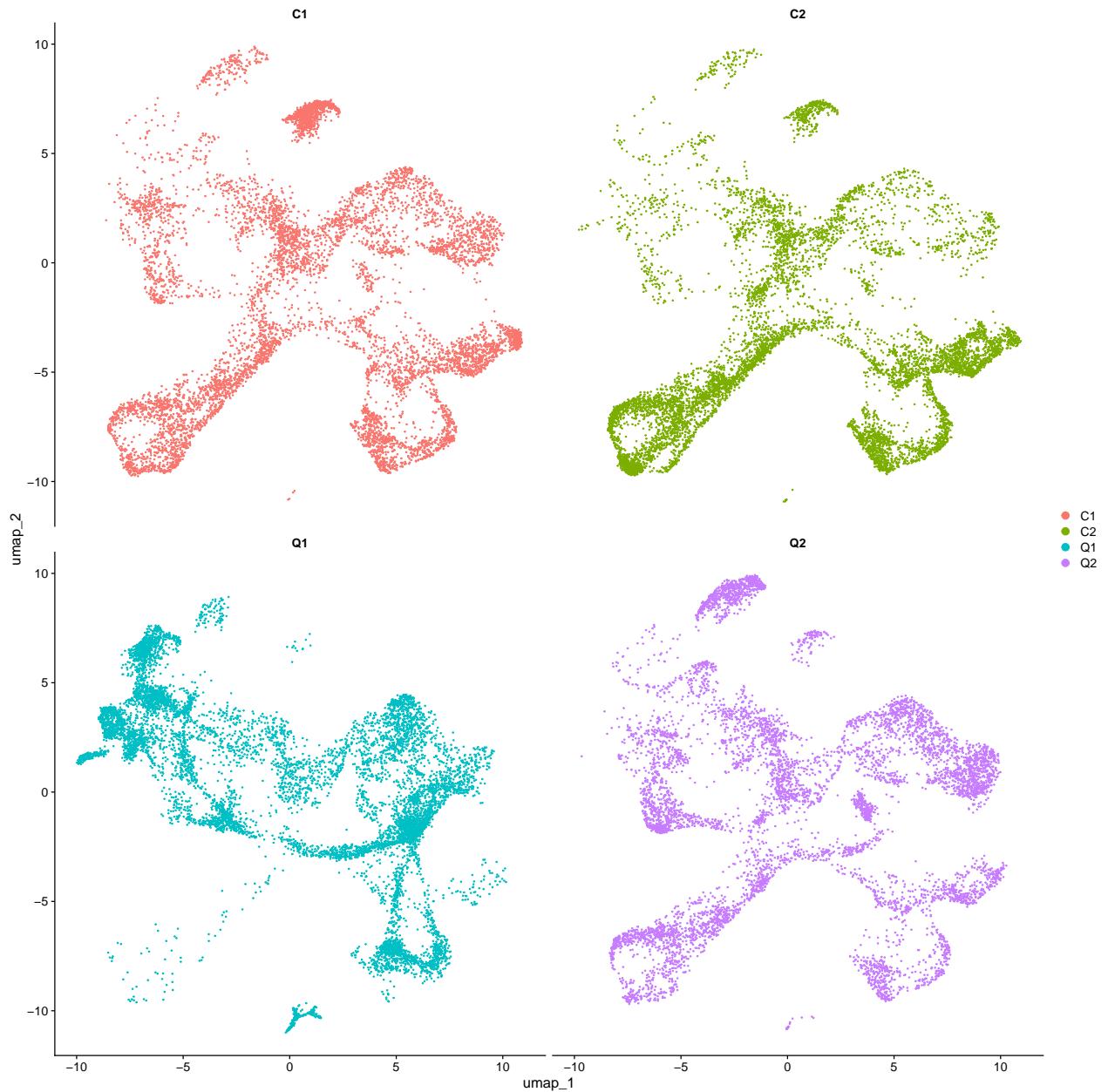
```
## [1] "UMAP for the source"
```

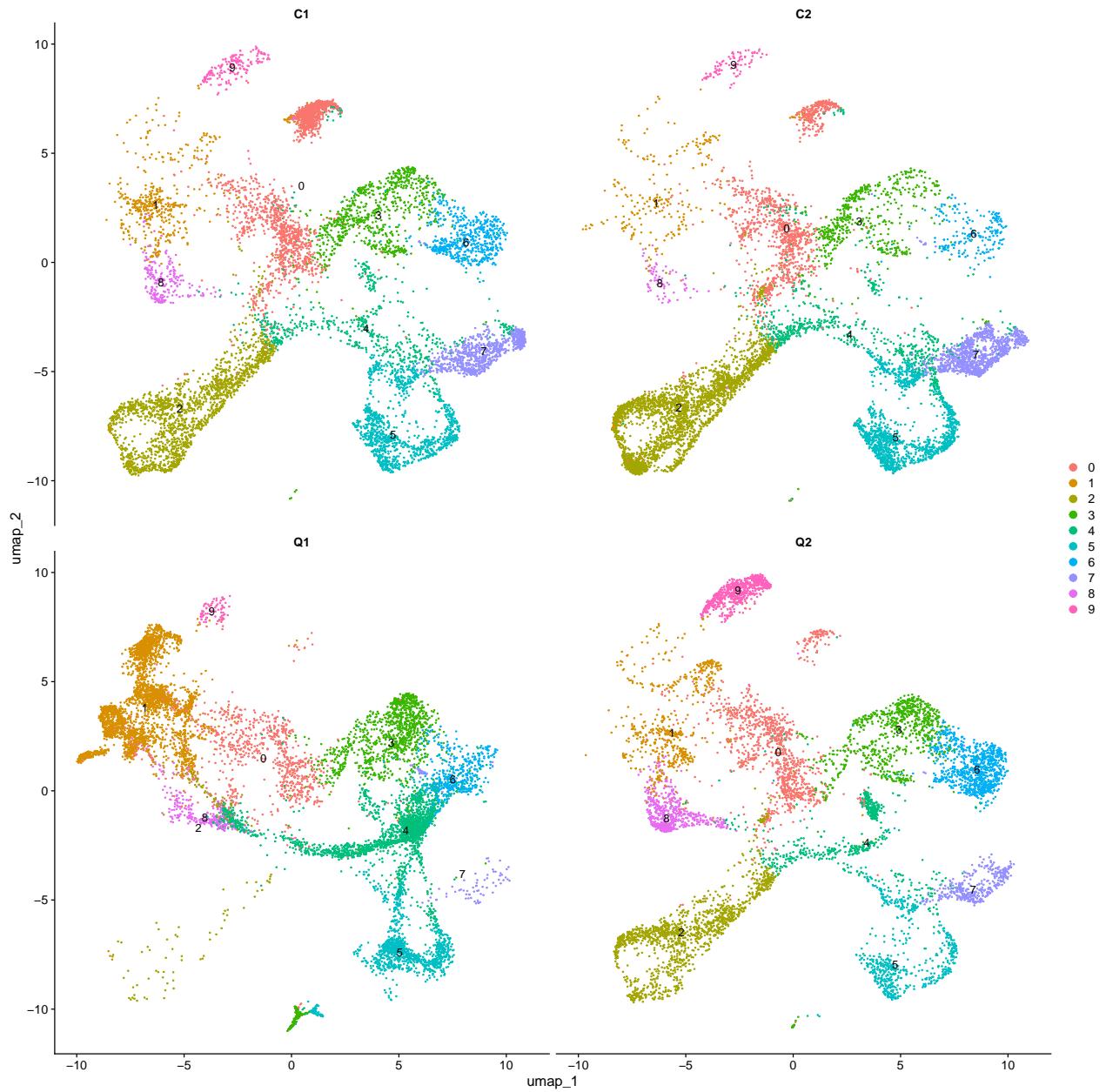
UMAP for the source



Plot the UMAP with source and Group

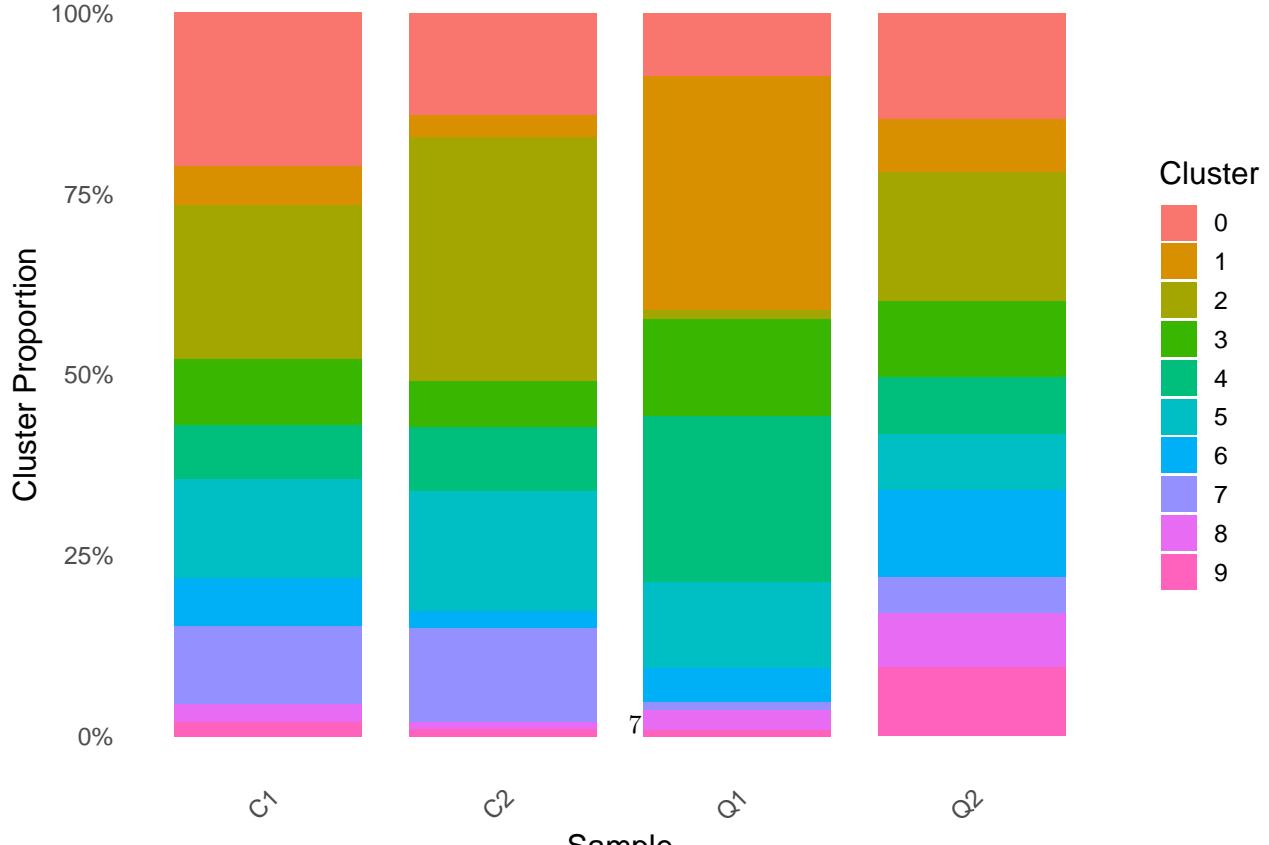
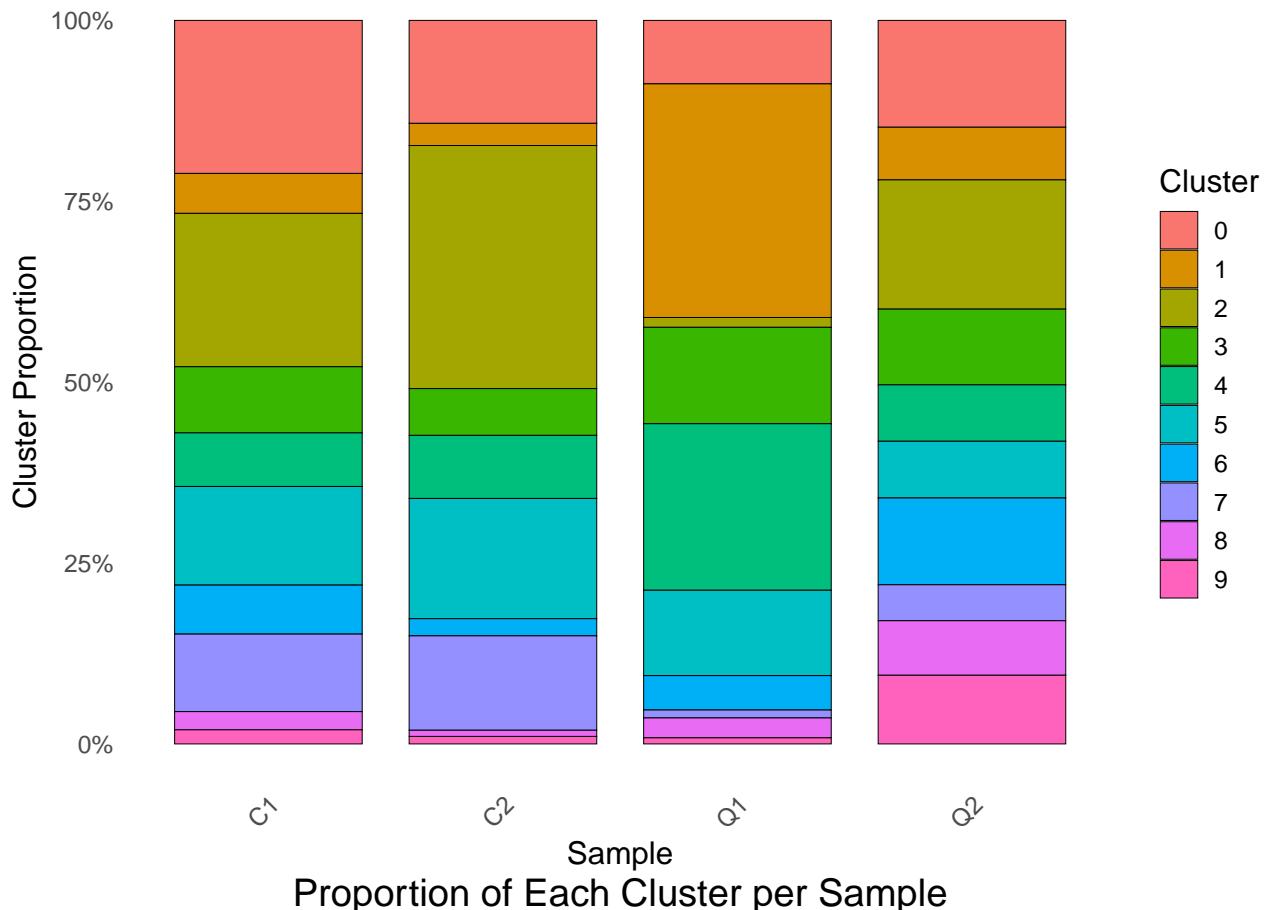




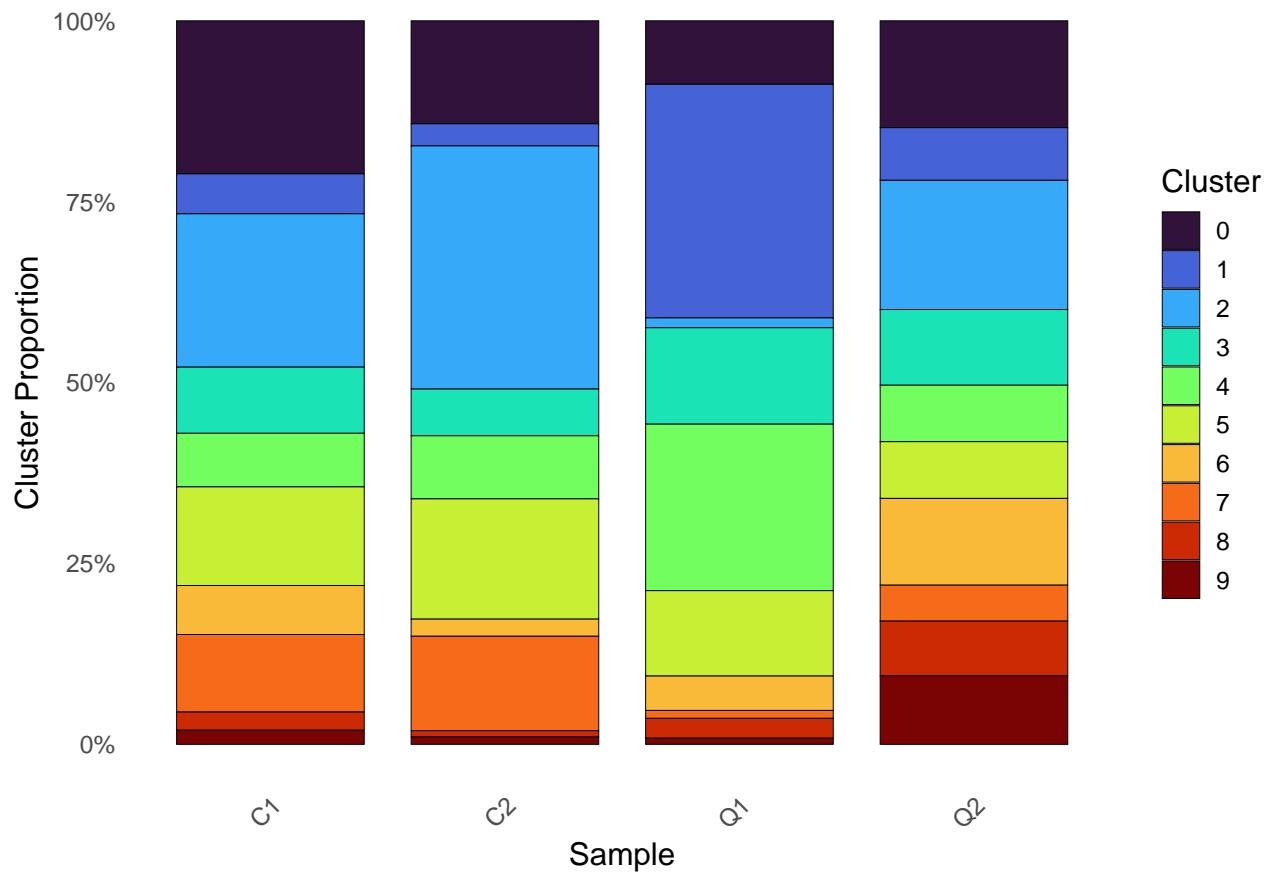


Plot the sample proportions of clusters

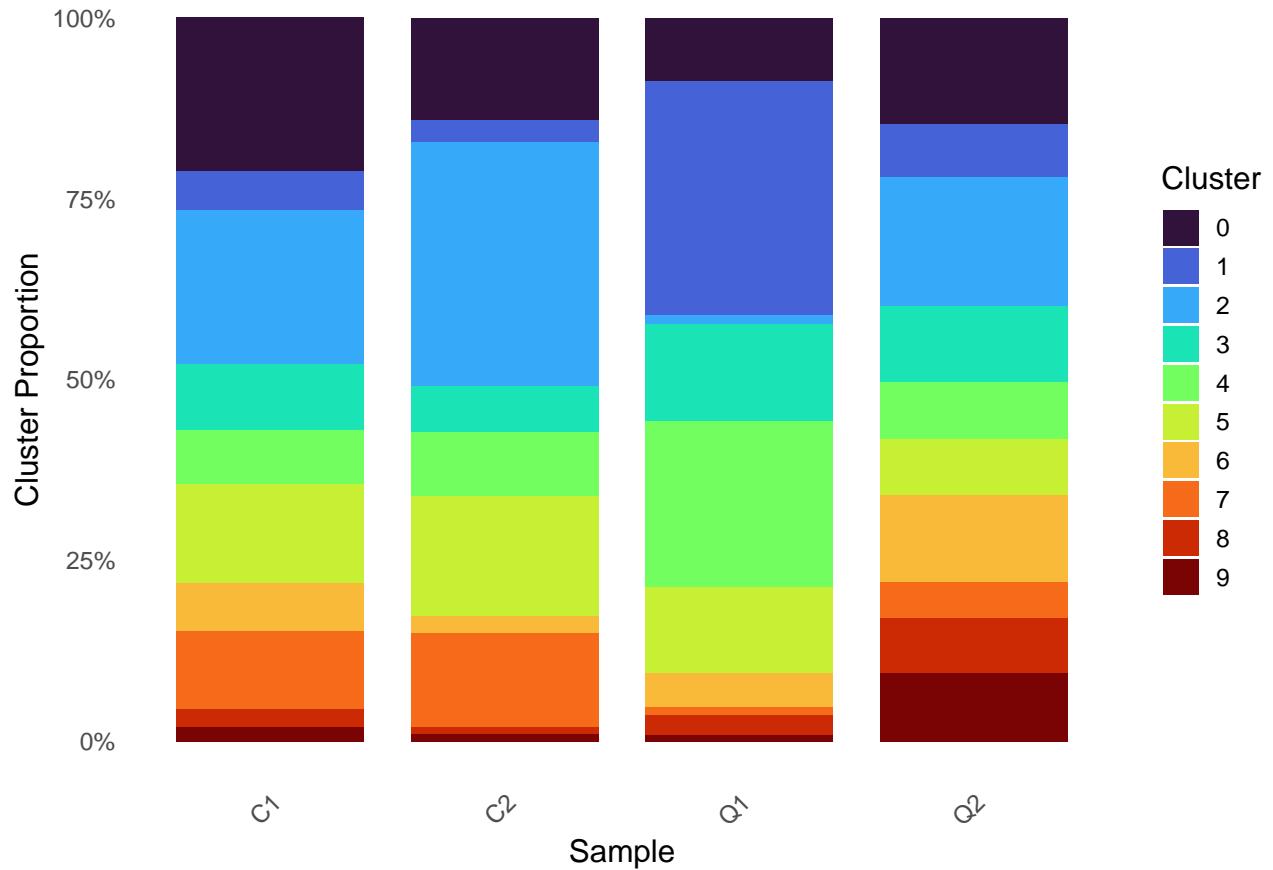
Proportion of Each Cluster per Sample



Proportion of Each Cluster per Sample



Proportion of Each Cluster per Sample



Heatmap of the cell type number in each sample

Cell Type Number in Each Sample

1828	477	1832	790	640	1178	585	926	218	168	C1
1213	261	2864	551	743	1417	202	1112	73	88	C2
865	3185	134	1314	2270	1164	469	108	271	83	Q1
1136	560	1374	805	600	603	923	382	580	730	Q2

Table 1: Cell Type Number in Each Sample

	0	1	2	3	4	5	6	7	8	9
C1	1828	477	1832	790	640	1178	585	926	218	168
C2	1213	261	2864	551	743	1417	202	1112	73	88
Q1	865	3185	134	1314	2270	1164	469	108	271	83
Q2	1136	560	1374	805	600	603	923	382	580	730

2. Find Maker Genes

```
## [1] "cluster marker genes loaded"
## [1] "processing resolution 0.1 cluster 0"
## [1] "processing resolution 0.1 cluster 2"
## [1] "processing resolution 0.1 cluster 3"
## [1] "processing resolution 0.1 cluster 4"
## [1] "processing resolution 0.1 cluster 5"
## [1] "processing resolution 0.1 cluster 6"
## [1] "processing resolution 0.1 cluster 7"
## [1] "cluster marker genes loaded"
## [1] "processing resolution 0.2 cluster 0"
## [1] "processing resolution 0.2 cluster 1"
## [1] "processing resolution 0.2 cluster 2"
## [1] "processing resolution 0.2 cluster 3"
## [1] "processing resolution 0.2 cluster 4"
## [1] "processing resolution 0.2 cluster 5"
## [1] "processing resolution 0.2 cluster 6"
## [1] "processing resolution 0.2 cluster 7"
## [1] "processing resolution 0.2 cluster 8"
## [1] "processing resolution 0.2 cluster 9"
## [1] "cluster marker genes loaded"
## [1] "processing resolution 0.3 cluster 0"
## [1] "processing resolution 0.3 cluster 1"
## [1] "processing resolution 0.3 cluster 2"
## [1] "processing resolution 0.3 cluster 3"
## [1] "processing resolution 0.3 cluster 4"
## [1] "processing resolution 0.3 cluster 5"
## [1] "processing resolution 0.3 cluster 6"
## [1] "processing resolution 0.3 cluster 7"
## [1] "processing resolution 0.3 cluster 8"
## [1] "processing resolution 0.3 cluster 9"
## [1] "processing resolution 0.3 cluster 10"
## [1] "processing resolution 0.3 cluster 11"
## [1] "processing resolution 0.3 cluster 12"
## [1] "cluster marker genes loaded"
## [1] "processing resolution 0.4 cluster 0"
## [1] "processing resolution 0.4 cluster 1"
```

```

## [1] "processing resolution 0.4 cluster 2"
## [1] "processing resolution 0.4 cluster 3"
## [1] "processing resolution 0.4 cluster 4"
## [1] "processing resolution 0.4 cluster 5"
## [1] "processing resolution 0.4 cluster 6"
## [1] "processing resolution 0.4 cluster 7"
## [1] "processing resolution 0.4 cluster 8"
## [1] "processing resolution 0.4 cluster 9"
## [1] "processing resolution 0.4 cluster 10"
## [1] "processing resolution 0.4 cluster 11"
## [1] "processing resolution 0.4 cluster 12"
## [1] "processing resolution 0.4 cluster 13"
## [1] "processing resolution 0.4 cluster 14"
## [1] "processing resolution 0.4 cluster 16"
## [1] "cluster marker genes loaded"
## [1] "processing resolution 0.5 cluster 0"
## [1] "processing resolution 0.5 cluster 1"
## [1] "processing resolution 0.5 cluster 2"
## [1] "processing resolution 0.5 cluster 3"
## [1] "processing resolution 0.5 cluster 4"
## [1] "processing resolution 0.5 cluster 5"
## [1] "processing resolution 0.5 cluster 6"
## [1] "processing resolution 0.5 cluster 7"
## [1] "processing resolution 0.5 cluster 8"
## [1] "processing resolution 0.5 cluster 9"
## [1] "processing resolution 0.5 cluster 10"
## [1] "processing resolution 0.5 cluster 11"
## [1] "processing resolution 0.5 cluster 12"
## [1] "processing resolution 0.5 cluster 13"
## [1] "processing resolution 0.5 cluster 14"
## [1] "processing resolution 0.5 cluster 15"
## [1] "processing resolution 0.5 cluster 16"
## [1] "processing resolution 0.5 cluster 17"

## An object of class Seurat
## 39606 features across 34722 samples within 2 assays
## Active assay: integrated (1000 features, 1000 variable features)
## 2 layers present: data, scale.data
## 1 other assay present: RNA

```

```

## 2 dimensional reductions calculated: pca, umap
## [1] "PCDH15"
## [1] "Upper layer excitatory neurons"
## [1] "plot PCDH15 for Upper layer excitatory neurons"
## [1] "SATB2"
## [1] "Excitatory neurons"
## [1] "plot SATB2 for Excitatory neurons"
## [1] "SLC17A7"
## [1] "Excitatory neurons"
## [1] "plot SLC17A7 for Excitatory neurons"
## [1] "STMN1"
## [1] "Excitatory neurons"
## [1] "plot STMN1 for Excitatory neurons"
## [1] "TUBB3"
## [1] "Excitatory neurons"
## [1] "plot TUBB3 for Excitatory neurons"
## [1] "CUX1"
## [1] "Excitatory neurons"
## [1] "plot CUX1 for Excitatory neurons"
## [1] "POU3F2"
## [1] "Excitatory neurons"
## [1] "plot POU3F2 for Excitatory neurons"
## [1] "CUX2"
## [1] "Excitatory neurons"
## [1] "plot CUX2 for Excitatory neurons"
## [1] "PAX6"
## [1] "Outer radial glia cells"
## [1] "plot PAX6 for Outer radial glia cells"
## [1] "HES1"
## [1] "Outer radial glia cells"
## [1] "plot HES1 for Outer radial glia cells"
## [1] "HOPX"
## [1] "Outer radial glia cells"
## [1] "plot HOPX for Outer radial glia cells"
## [1] "FAM107A"
## [1] "Outer radial glia cells"
## [1] "plot FAM107A for Outer radial glia cells"
## [1] "FABP7"
## [1] "Outer radial glia cells"
## [1] "plot FABP7 for Outer radial glia cells"
## [1] "SNAP25"
## [1] "Unknown"
## [1] "plot SNAP25 for Unknown"
## [1] "SLC32A1"
## [1] "Unknown"

```

```

## [1] "plot SLC32A1 for Unknown"
## [1] "TAC1"
## [1] "Unknown"

## [1] "plot TAC1 for Unknown"
## [1] "PTGDS"
## [1] "Astrocyte"

## [1] "plot PTGDS for Astrocyte"
## [1] "ALDH1L1"
## [1] "Astrocyte"

## [1] "plot ALDH1L1 for Astrocyte"
## [1] "APOE"
## [1] "Astrocyte"

## [1] "plot APOE for Astrocyte"
## [1] "BCL11B"
## [1] "Deep layer excitatory neurons"

## [1] "plot BCL11B for Deep layer excitatory neurons"
## [1] "SLC17A6"
## [1] "Deep layer excitatory neurons"

## [1] "plot SLC17A6 for Deep layer excitatory neurons"
## [1] "TBR1"
## [1] "Deep layer excitatory neurons"

## [1] "plot TBR1 for Deep layer excitatory neurons"
## [1] "SYT1"
## [1] "Deep layer excitatory neurons"

## [1] "plot SYT1 for Deep layer excitatory neurons"
## [1] "RELN"
## [1] "Deep layer excitatory neurons"

## [1] "plot RELN for Deep layer excitatory neurons"
## [1] "GRIN2B"
## [1] "Deep layer excitatory neurons"

## [1] "plot GRIN2B for Deep layer excitatory neurons"
## [1] "S100B"
## [1] "Astrocyte"

## [1] "plot S100B for Astrocyte"
## [1] "AQP4"
## [1] "Astrocyte"

## [1] "plot AQP4 for Astrocyte"
## [1] "S100B"
## [1] "Astrocyte"

## [1] "plot S100B for Astrocyte"
## [1] "APOE"
## [1] "Astrocyte"

## [1] "plot APOE for Astrocyte"
## [1] "TOP2A"
## [1] "Proliferating neural progenitor cells"

## [1] "plot TOP2A for Proliferating neural progenitor cells"

```

```

## [1] "MKI67"
## [1] "Proliferating neural progenitor cells"
## [1] "plot MKI67 for Proliferating neural progenitor cells"
## [1] "SOX2"
## [1] "Proliferating neural progenitor cells"
## [1] "plot SOX2 for Proliferating neural progenitor cells"
## [1] "OLIG1"
## [1] "Oligodendrocytes"
## [1] "plot OLIG1 for Oligodendrocytes"
## [1] "OLIG2"
## [1] "Oligodendrocytes"
## [1] "plot OLIG2 for Oligodendrocytes"
## [1] "GAD1"
## [1] "Interneuron"
## [1] "plot GAD1 for Interneuron"
## [1] "GAD2"
## [1] "Interneuron"
## [1] "plot GAD2 for Interneuron"
## [1] "ARX"
## [1] "Interneuron"
## [1] "plot ARX for Interneuron"
## [1] "NOS1"
## [1] "Interneuron"
## [1] "plot NOS1 for Interneuron"
## [1] "MKI67"
## [1] "Proliferating neural progenitor cells"
## [1] "plot MKI67 for Proliferating neural progenitor cells"
## [1] "TOP2A"
## [1] "Proliferating neural progenitor cells"
## [1] "plot TOP2A for Proliferating neural progenitor cells"
## [1] "SOX2"
## [1] "Proliferating neural progenitor cells"
## [1] "plot SOX2 for Proliferating neural progenitor cells"
## [1] "LHX1"
## [1] "Immature preoptic area (pOA) interneurons"
## [1] "plot LHX1 for Immature preoptic area (pOA) interneurons"

```

Session Information

```
## 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] viridis_0.6.5          viridisLite_0.4.2
##  [3] scales_1.4.0           kableExtra_1.4.0
##  [5] patchwork_1.3.0         pheatmap_1.0.12
##  [7] data.table_1.17.2       harmony_1.2.3
##  [9] Rcpp_1.0.14             conflicted_1.2.0
## [11] openxlsx_4.2.8          Seurat_5.3.0
## [13] SeuratObject_5.1.0     sp_2.2-0
## [15] AnnotationHub_3.12.0   BiocFileCache_2.12.0
## [17] dbplyr_2.5.0            simspec_0.0.0.9000
## [19] cowplot_1.1.3           EnsDb.Hsapiens.v86_2.99.0
## [21] ensemblDb_2.28.1        AnnotationFilter_1.28.0
## [23] GenomicFeatures_1.56.0  AnnotationDbi_1.66.0
## [25] Biobase_2.64.0          Signac_1.14.0
## [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              purrrr_1.0.4
## [39] readr_2.1.5              tidyrr_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] 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             plotly_4.10.4
## [17] rmarkdown_2.29              yaml_2.3.10
```

```

## [19] httpuv_1.6.16           sctransform_0.4.2
## [21] zip_2.3.2                spam_2.11-1
## [23] spatstat.sparse_3.1-0   reticulate_1.42.0
## [25] pbapply_1.7-2           DBI_1.2.3
## [27] RColorBrewer_1.1-3      abind_1.4-8
## [29] zlibbioc_1.50.0          Rtsne_0.17
## [31] RCurl_1.98-1.17         rappdirs_0.3.3
## [33] GenomeInfoDbData_1.2.12 ggrepel_0.9.6
## [35] irlba_2.3.5.1           spatstat.utils_3.1-3
## [37] listenv_0.9.1            goftest_1.2-3
## [39] RSpectra_0.16-2          spatstat.random_3.3-3
## [41] fitdistrplus_1.2-2       parallelly_1.44.0
## [43] svglite_2.2.1            codetools_0.2-20
## [45] DelayedArray_0.30.1     RcppRoll_0.3.1
## [47] xml2_1.3.8               tidyselect_1.2.1
## [49] UCSC.utils_1.0.0          farver_2.1.2
## [51] spatstat.explore_3.4-2    matrixStats_1.5.0
## [53] GenomicAlignments_1.40.0  jsonlite_2.0.0
## [55] progressr_0.15.1          ggridges_0.5.6
## [57] survival_3.8-3           systemfonts_1.2.3
## [59] tools_4.4.0                ragg_1.4.0
## [61] ica_1.0-3                 glue_1.8.0
## [63] gridExtra_2.3              SparseArray_1.4.8
## [65] here_1.0.1                xfun_0.52
## [67] MatrixGenerics_1.16.0    withr_3.0.2
## [69] BiocManager_1.30.25       fastmap_1.2.0
## [71] digest_0.6.37             timechange_0.3.0
## [73] R6_2.6.1                  mime_0.13
## [75] textshaping_1.0.1         colorspace_2.1-1
## [77] scattermore_1.2           tensor_1.5
## [79] spatstat.data_3.1-6       dichromat_2.0-0.1
## [81] RSQLite_2.3.11             generics_0.1.4
## [83] httr_1.4.7                htmlwidgets_1.6.4
## [85] S4Arrays_1.4.1             uwot_0.2.3
## [87] pkgconfig_2.0.3            gtable_0.3.6
## [89] blob_1.2.4                lmtest_0.9-40
## [91] XVector_0.44.0            htmltools_0.5.8.1
## [93] dotCall64_1.2              ProtGenerics_1.36.0
## [95] png_0.1-8                 spatstat.univar_3.1-3
## [97] rstudioapi_0.17.1         tzdb_0.5.0
## [99] reshape2_1.4.4             rjson_0.2.23
## [101] nlme_3.1-168             curl_6.2.2
## [103] cachem_1.1.0              zoo_1.8-14
## [105] BiocVersion_3.19.1        KernSmooth_2.23-26
## [107] vipor_0.4.7              parallel_4.4.0
## [109] miniUI_0.1.2              ggrastr_1.0.2
## [111] restfulr_0.0.15           pillar_1.10.2
## [113] grid_4.4.0                vctrs_0.6.5
## [115] RANN_2.6.2                promises_1.3.2
## [117] xtable_1.8-4              cluster_2.1.8.1
## [119] beeswarm_0.4.0             evaluate_1.0.3
## [121] tinytex_0.57               cli_3.6.5
## [123] compiler_4.4.0            Rsamtools_2.20.0
## [125] rlang_1.1.6                crayon_1.5.3

```

```
## [127] future.apply_1.11.3          labeling_0.4.3
## [129] ggbeeswarm_0.7.2            plyr_1.8.9
## [131] stringi_1.8.7              deldir_2.0-4
## [133] BiocParallel_1.38.0         Biostrings_2.72.1
## [135] lazyeval_0.2.2              spatstat.geom_3.3-6
## [137] Matrix_1.7-3                RcppHNSW_0.6.0
## [139] hms_1.1.3                  bit64_4.6.0-1
## [141] future_1.49.0               KEGGREST_1.44.1
## [143] shiny_1.10.0                SummarizedExperiment_1.34.0
## [145] ROCR_1.0-11                 igraph_2.1.4
## [147] memoise_2.0.1               fastmatch_1.1-6
## [149] bit_4.6.0
```