

Cell Type Anotation

Cluster Marker

Ximing Ran

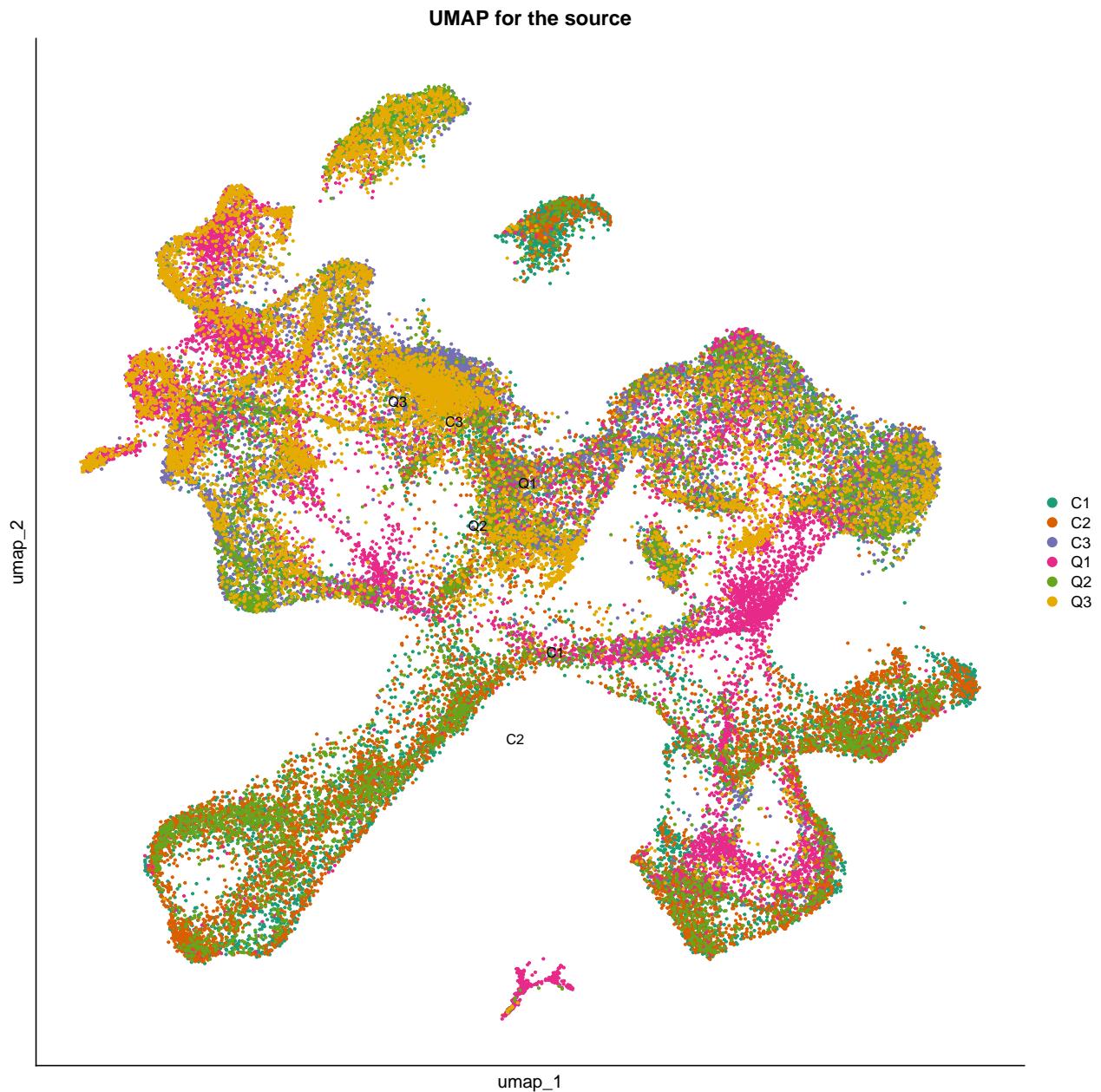
2025-05-15

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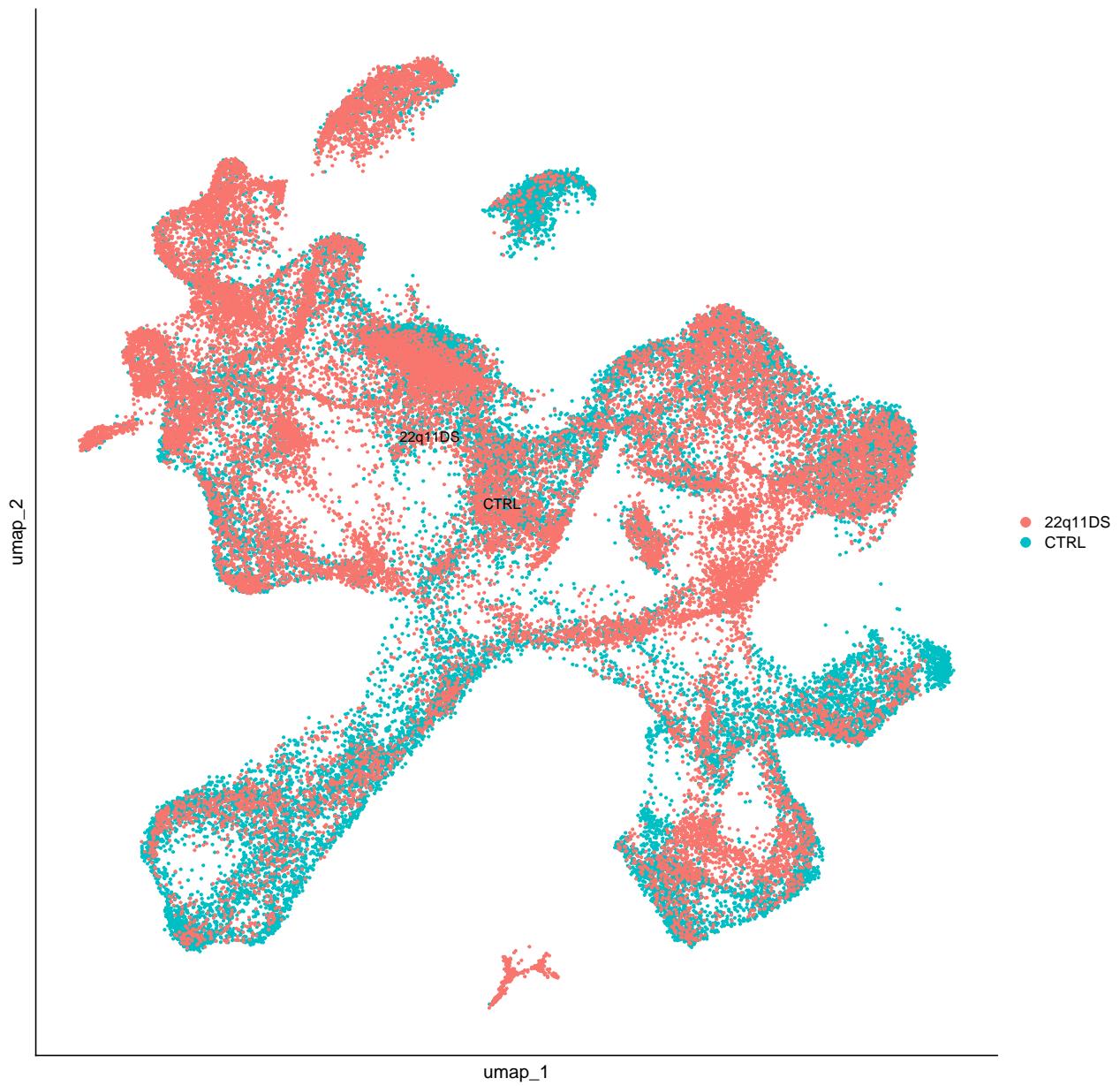
1. Read the merged Data

Plot the UMAP with source and Group

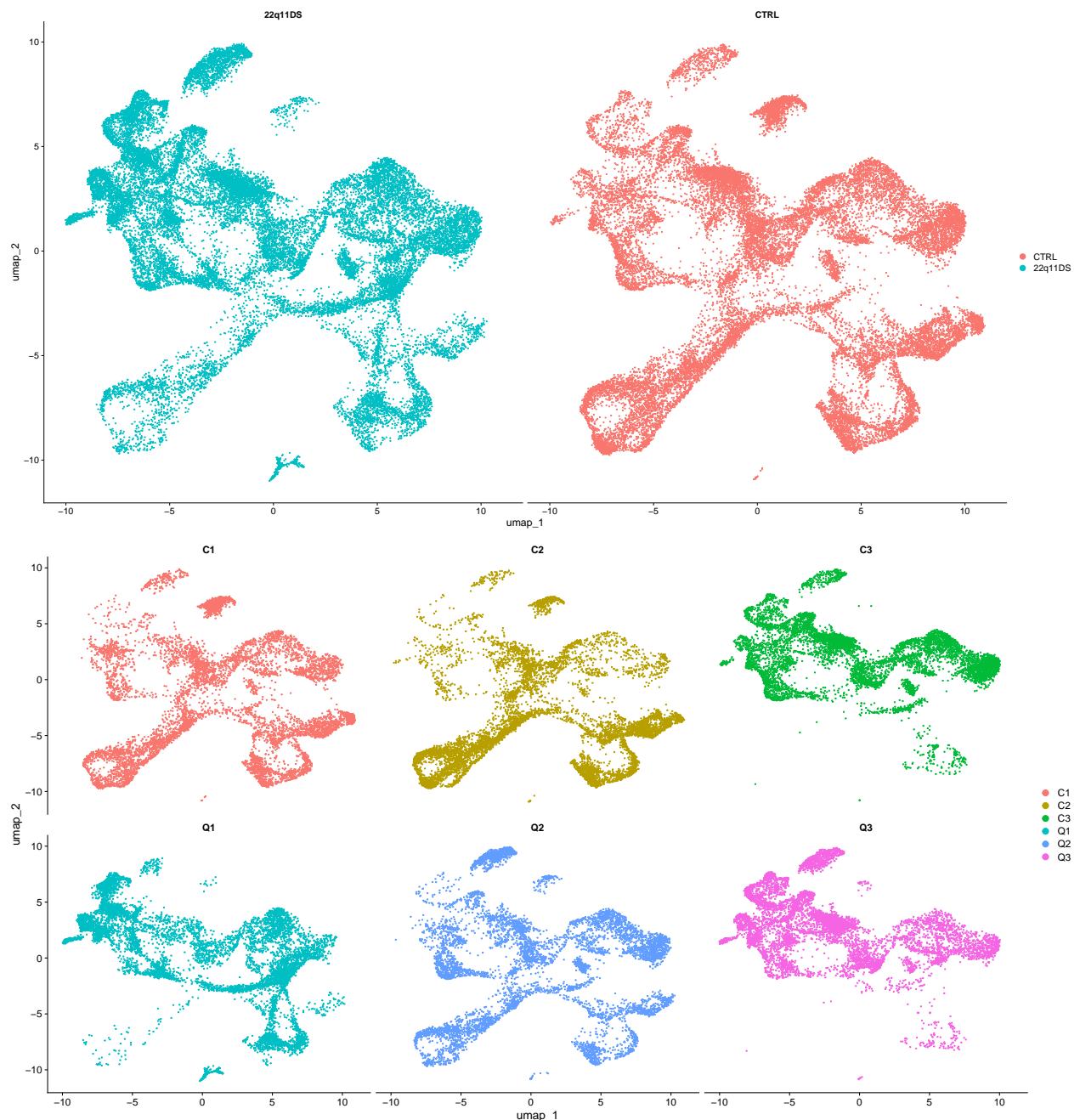


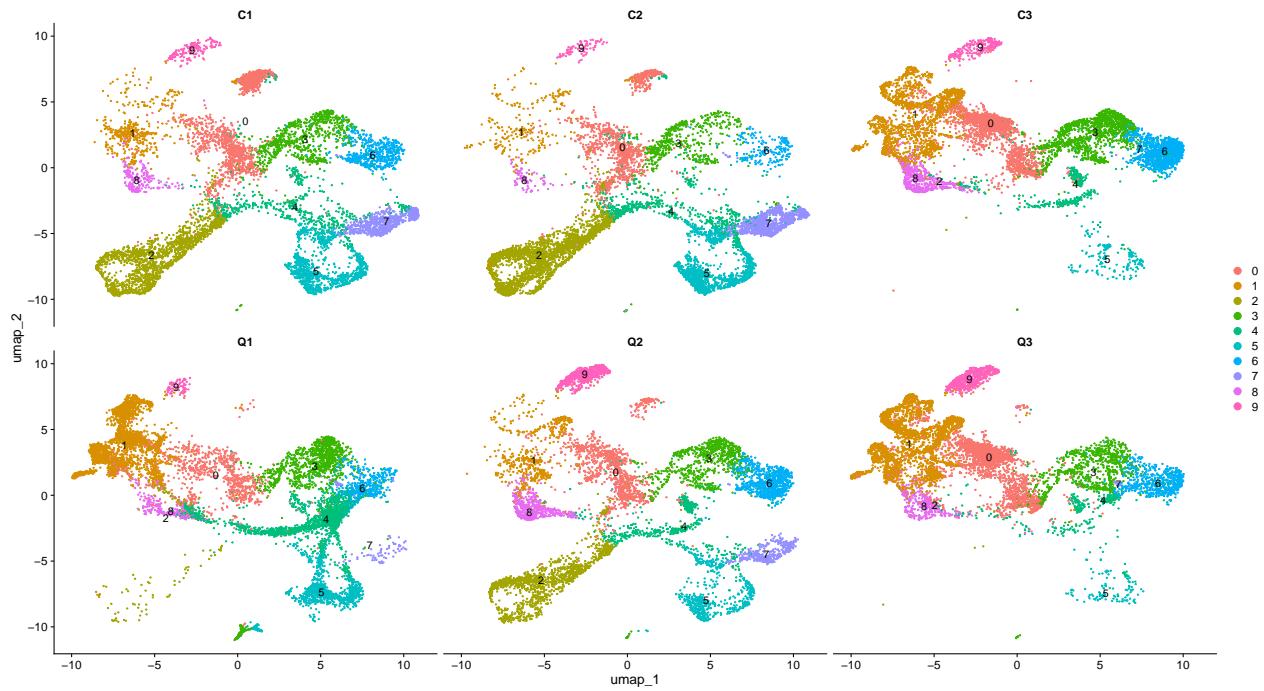
```
## [1] "UMAP for the source"
```

UMAP for the source



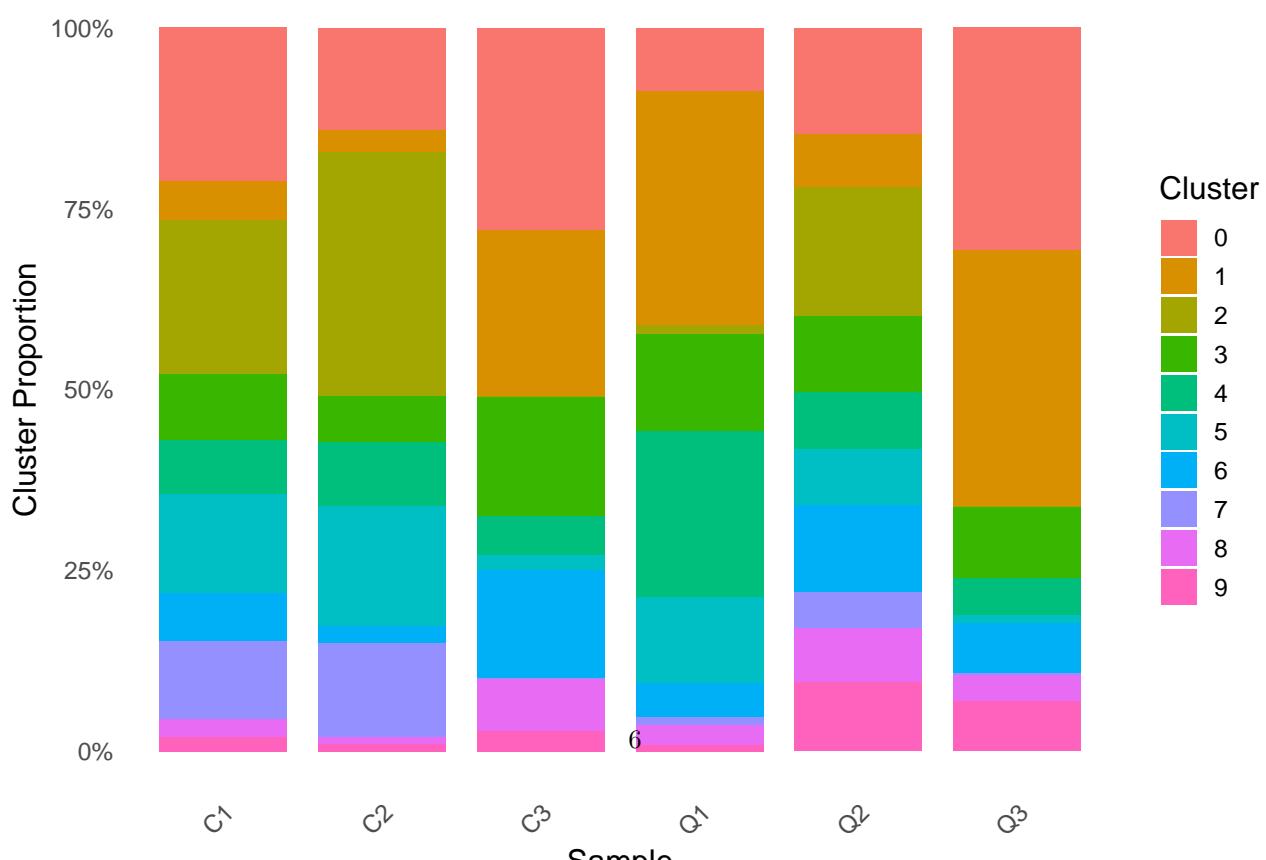
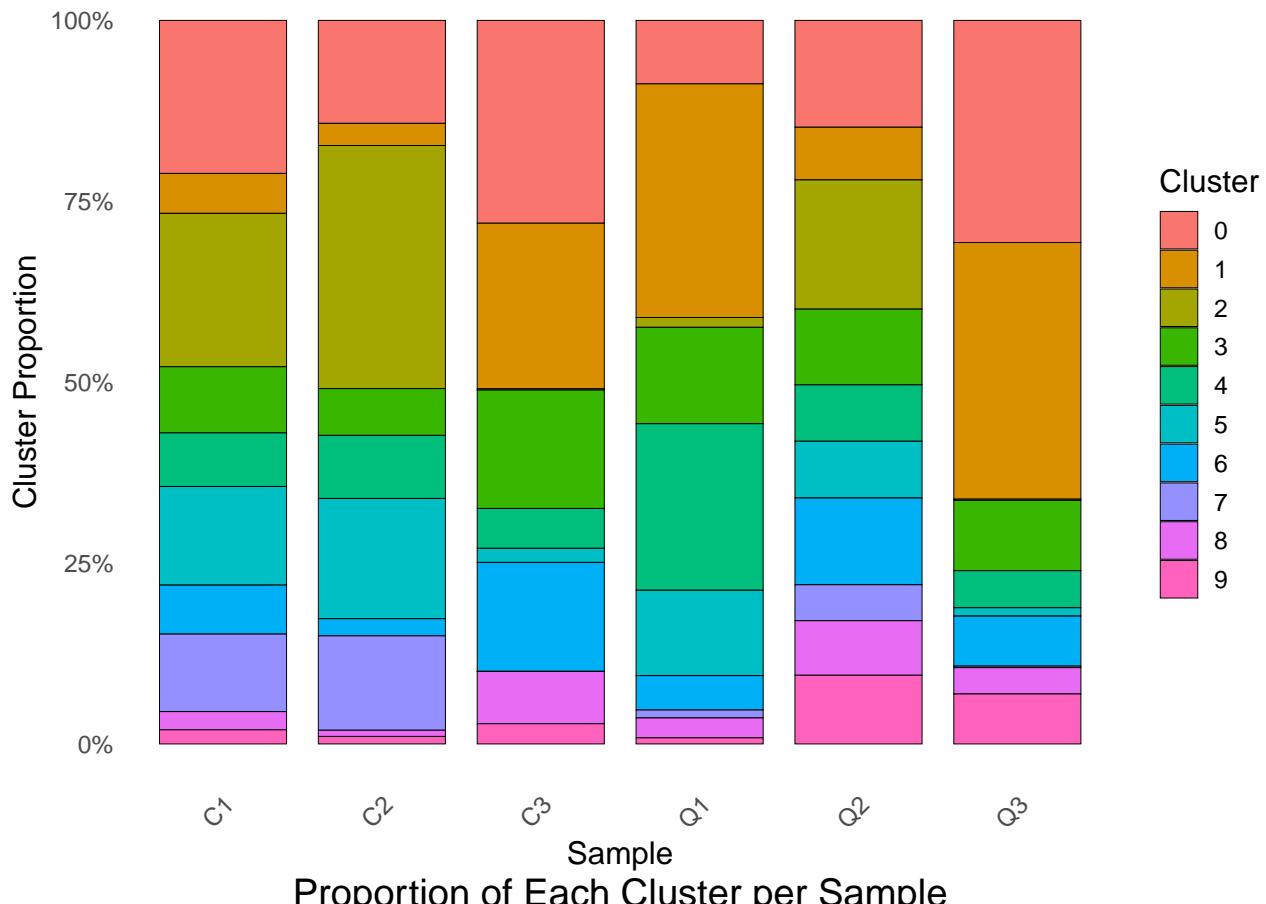
Plot the UMAP with source and Group



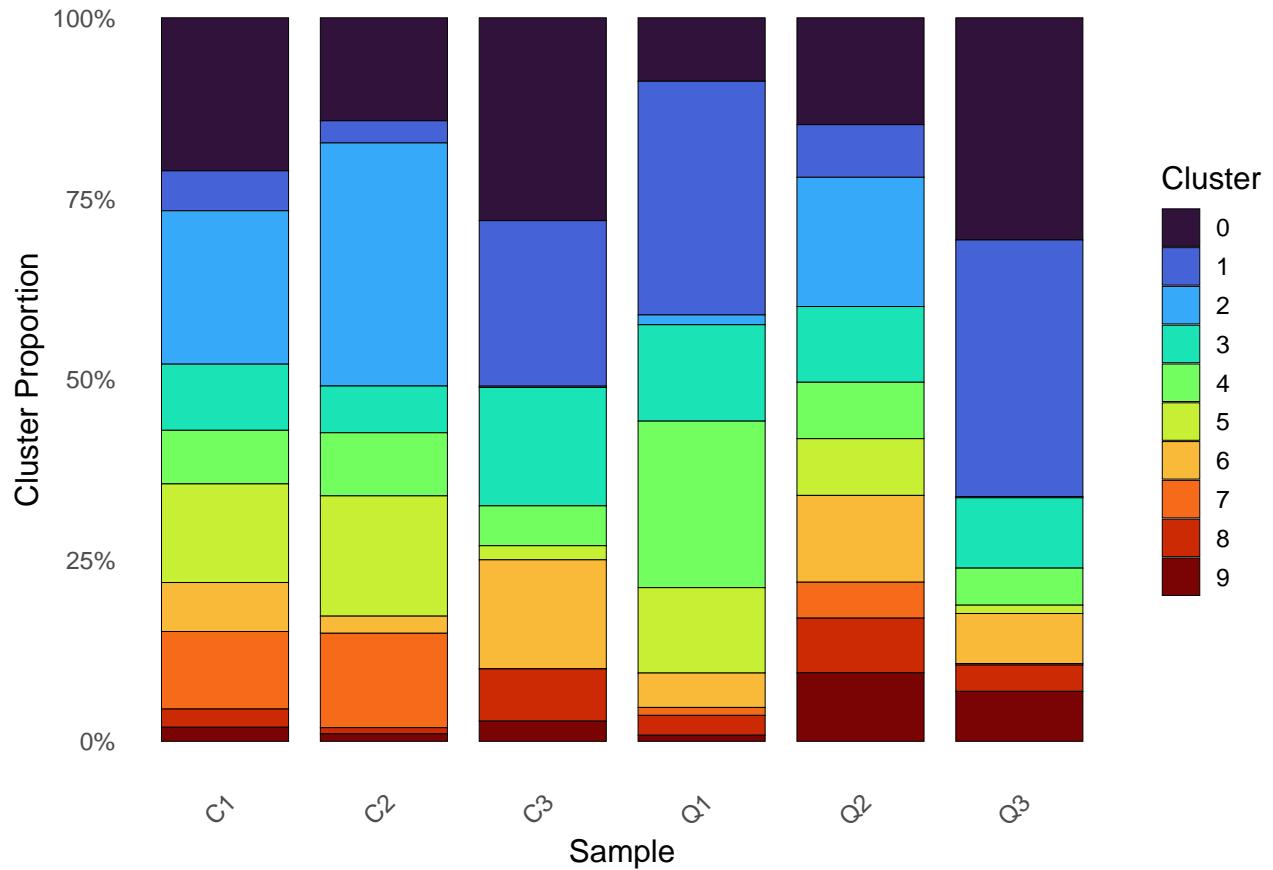


Plot the sample proportions of clusters

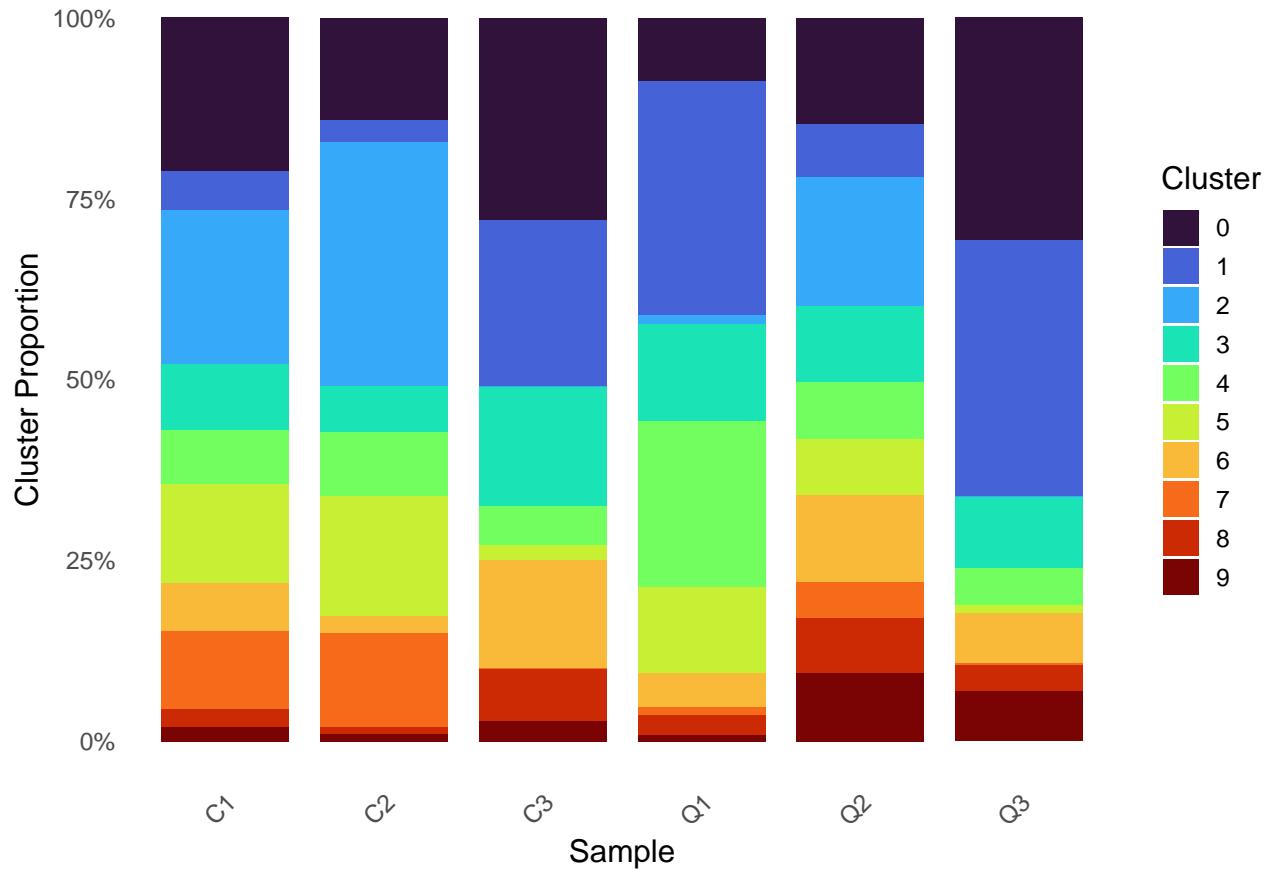
Proportion of Each Cluster per Sample



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 |
| 2503 | 2043 | 16 | 1461 | 492 | 174 | 1344 | 2 | 645 | 249 | C3 |
| 865 | 3185 | 134 | 1314 | 2270 | 1164 | 469 | 108 | 271 | 83 | Q1 |
| 1136 | 560 | 1374 | 805 | 600 | 603 | 923 | 382 | 580 | 730 | Q2 |
| 2935 | 3391 | 16 | 929 | 490 | 110 | 661 | 20 | 348 | 660 | Q3 |
| 0 | → | ∞ | ω | ▲ | ¤ | ¤ | ∞ | ~ | ∞ | ¤ |

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 |
| C3 | 2503 | 2043 | 16 | 1461 | 492 | 174 | 1344 | 2 | 645 | 249 |
| Q1 | 865 | 3185 | 134 | 1314 | 2270 | 1164 | 469 | 108 | 271 | 83 |
| Q2 | 1136 | 560 | 1374 | 805 | 600 | 603 | 923 | 382 | 580 | 730 |
| Q3 | 2935 | 3391 | 16 | 929 | 490 | 110 | 661 | 20 | 348 | 660 |

2. Find Marker Genes

Table 2: Cell Type Marker Count

| cell_name | total |
|---|-------|
| Astrocyte | 367 |
| B cell | 5 |
| Beta cell(cell) | 2 |
| Border-associated macrophage | 1 |
| CD4+ T cell | 29 |
| CD8+ T cell | 9 |
| Cajal-Retzius neuron | 1 |
| Cholinergic neuron | 1 |
| Cytotoxic CD8 T cell | 4 |
| Cytotoxic T cell | 6 |
| Dendritic cell | 1 |
| Disease-associated microglial cell | 1 |
| Dopaminergic neuron | 4 |
| Early-born neuron | 2 |
| Effector memory CD4+ T cell | 20 |
| Endothelial cell | 25 |
| Ependymal cell | 4 |
| Epithelial cell | 1 |
| Excitatory neuron | 16 |
| Extratelencephalic(ET) cell | 3 |
| Fibroblast | 10 |
| Glial cell | 4 |
| Glutamatergic neuron | 3 |
| Gonadotroph cell | 4 |
| Hematopoietic cell | 3 |
| Hematopoietic stem cell | 4 |
| Immune cell | 1 |
| Inhibitory neuron | 11 |
| Intermediate progenitor cell | 4 |
| Interneuron | 11 |
| Lactotroph cell | 4 |
| Late neuronal progenitor cell | 2 |
| Leptomeningeal cell | 2 |
| Lymphocyte | 7 |
| Macrophage | 29 |
| Mature astrocyte | 1 |
| Mature dendritic cell | 2 |
| Mature neuron | 1 |
| Mesenchymal cell | 2 |
| Mesoderm cell | 2 |
| Microglial cell | 496 |
| Microglial cell | 2 |
| Midbrain dopaminergic neuron | 3 |
| Monocyte | 10 |
| Motor neuron | 8 |
| Mucosa-associated invariant T (MAIT) cell | 1 |
| Mural cell | 6 |
| Myeloid cell | 13 |

| cell_name | total |
|---------------------------------------|-------|
| Natural killer T(NKT) cell | 13 |
| Natural killer cell | 8 |
| Neural crest cell | 4 |
| Neural crest stem cell | 4 |
| Neural progenitor cell | 10 |
| Neural stem cell | 11 |
| Neuron | 129 |
| Neuronal intermediate progenitor cell | 3 |
| Neuronal progenitor cell | 3 |
| Non-neuron | 6 |
| Oligodendrocyte | 30 |
| Oligodendrocyte precursor cell | 9 |
| Oligodendrocyte progenitor cell | 15 |
| Outer radial glia | 2 |
| Pan-neuronal cell | 4 |
| Pericyte | 23 |
| Pituitary stem cell | 3 |
| Plasma cell | 4 |
| Postmitotic neuron | 1 |
| Progenitor cell | 12 |
| Radial glial cell | 14 |
| Red blood cell (erythrocyte) | 4 |
| Sensory neuron | 6 |
| Smooth muscle cell | 3 |
| Somatotroph cell | 3 |
| Stem cell | 8 |
| Subplate cell | 2 |
| Subplate neuron | 2 |
| T cell | 34 |
| Truncated radial glial cell | 3 |
| Vascular smooth muscle cell(VSMC) | 1 |
| Ventricular radial glial cell | 2 |
| Young neuron | 6 |
| von Economo neuron(VEN) | 5 |

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
```

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## [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                ica_1.0-3
## [61] glue_1.8.0                 gridExtra_2.3
## [63] SparseArray_1.4.8          here_1.0.1
## [65] xfun_0.52                 MatrixGenerics_1.16.0
## [67] withr_3.0.2               BiocManager_1.30.25
## [69] fastmap_1.2.0              digest_0.6.37
## [71] timechange_0.3.0          R6_2.6.1
## [73] mime_0.13                  textshaping_1.0.1
## [75] colorspace_2.1-1          scattermore_1.2
## [77] tensor_1.5                 spatstat.data_3.1-6
## [79] dichromat_2.0-0.1          RSQLite_2.3.11
## [81] generics_0.1.4              httr_1.4.7
## [83] htmlwidgets_1.6.4           S4Arrays_1.4.1
## [85] uwot_0.2.3                 pkgconfig_2.0.3
## [87] gtable_0.3.6               blob_1.2.4
## [89] lmtest_0.9-40              XVector_0.44.0
## [91] htmltools_0.5.8.1          dotCall164_1.2
## [93] ProtGenerics_1.36.0         png_0.1-8
## [95] spatstat.univar_3.1-3      rstudioapi_0.17.1
## [97] tzdb_0.5.0                 reshape2_1.4.4
## [99] rjson_0.2.23              nlme_3.1-168
## [101] curl_6.2.2                cachem_1.1.0
## [103] zoo_1.8-14                BiocVersion_3.19.1
## [105] KernSmooth_2.23-26        parallel_4.4.0
## [107] miniUI_0.1.2              restfulr_0.0.15
## [109] pillar_1.10.2              grid_4.4.0
## [111] vctrs_0.6.5                RANN_2.6.2
## [113] promises_1.3.2             xtable_1.8-4
## [115] cluster_2.1.8.1           evaluate_1.0.3
## [117] tinytex_0.57               cli_3.6.5
## [119] compiler_4.4.0             Rsamtools_2.20.0
## [121] rlang_1.1.6                crayon_1.5.3
## [123] future.apply_1.11.3        labeling_0.4.3
## [125] plyr_1.8.9                 stringi_1.8.7

```

```
## [127] deldir_2.0-4           BiocParallel_1.38.0
## [129] Biostrings_2.72.1        lazyeval_0.2.2
## [131] spatstat.geom_3.3-6       Matrix_1.7-3
## [133] RcppHNSW_0.6.0          hms_1.1.3
## [135] bit64_4.6.0-1           future_1.49.0
## [137] KEGGREST_1.44.1         shiny_1.10.0
## [139] SummarizedExperiment_1.34.0 ROCR_1.0-11
## [141] igraph_2.1.4             memoise_2.0.1
## [143] fastmatch_1.1-6          bit_4.6.0
```