

# Cell Type Anotation

Cluster Marker

Ximing Ran

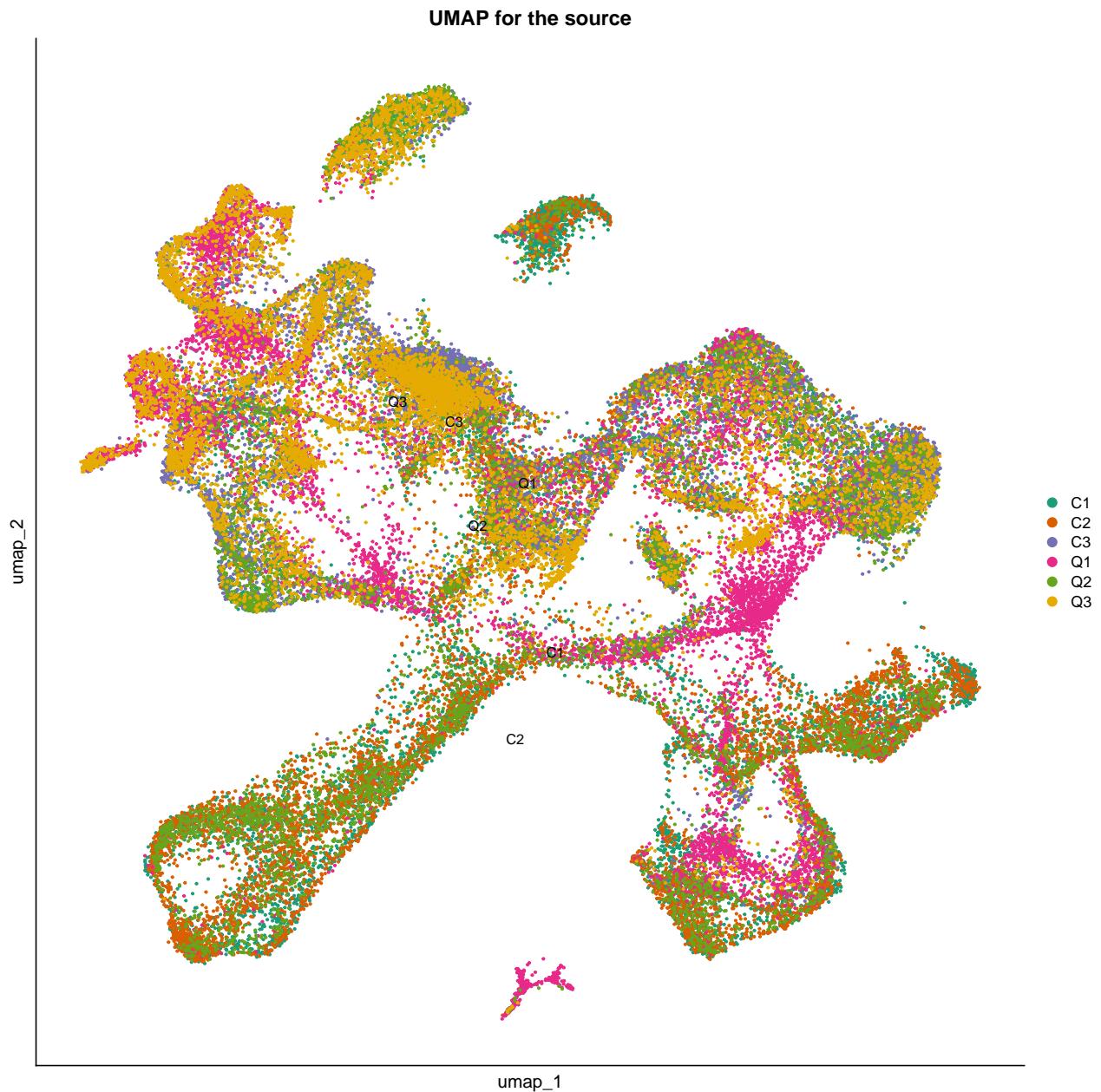
2025-05-15

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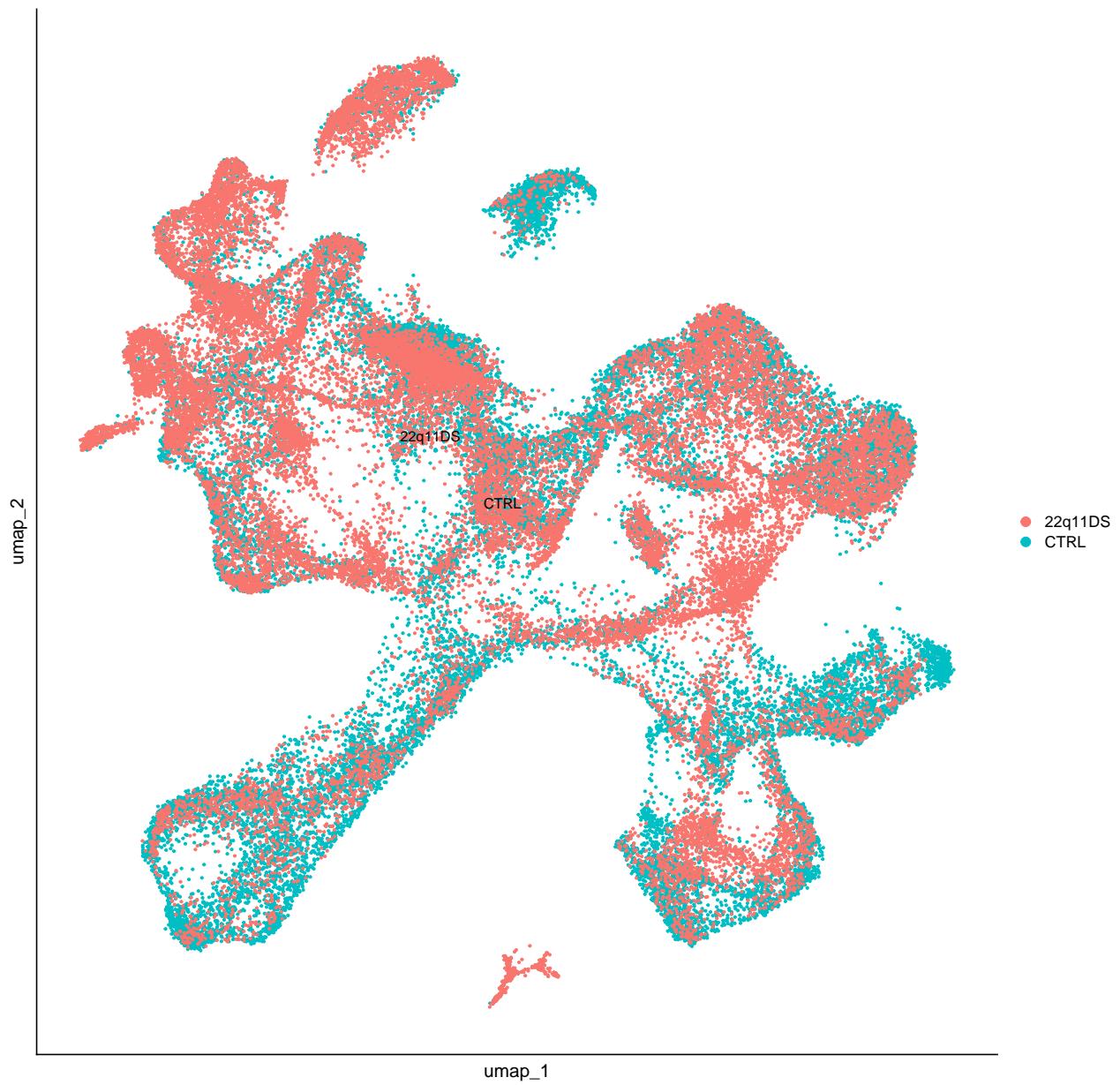
## 1. Read the merged Data

Plot the UMAP with source and Group

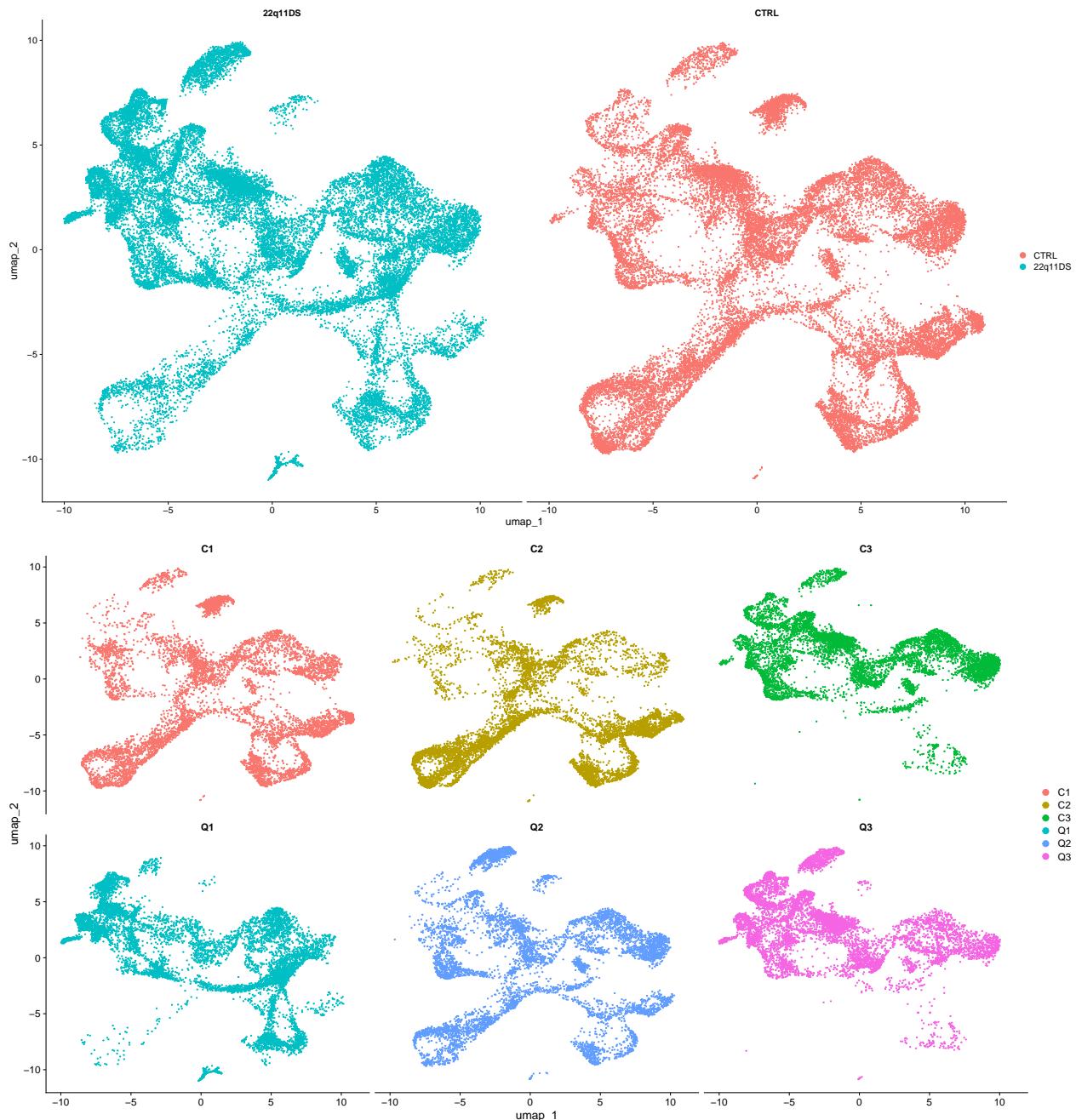


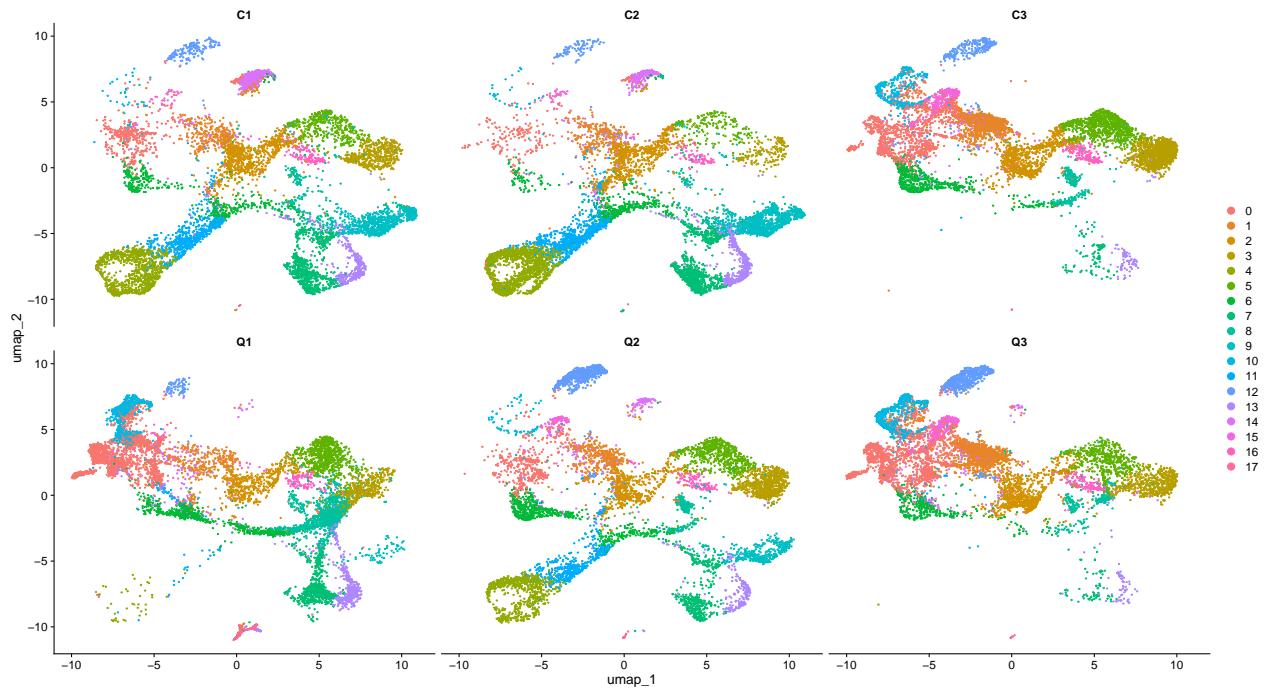
```
## [1] "UMAP for the source"
```

UMAP for the source

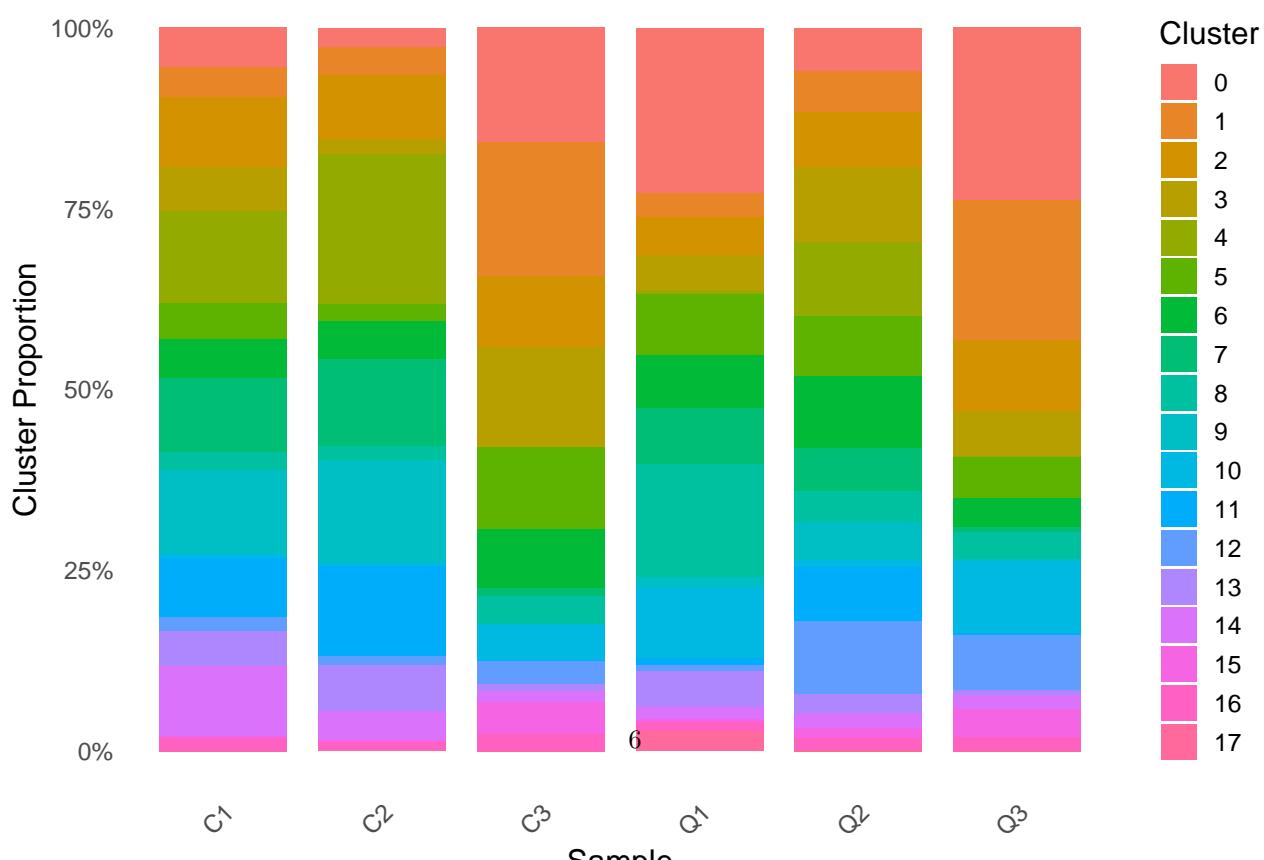
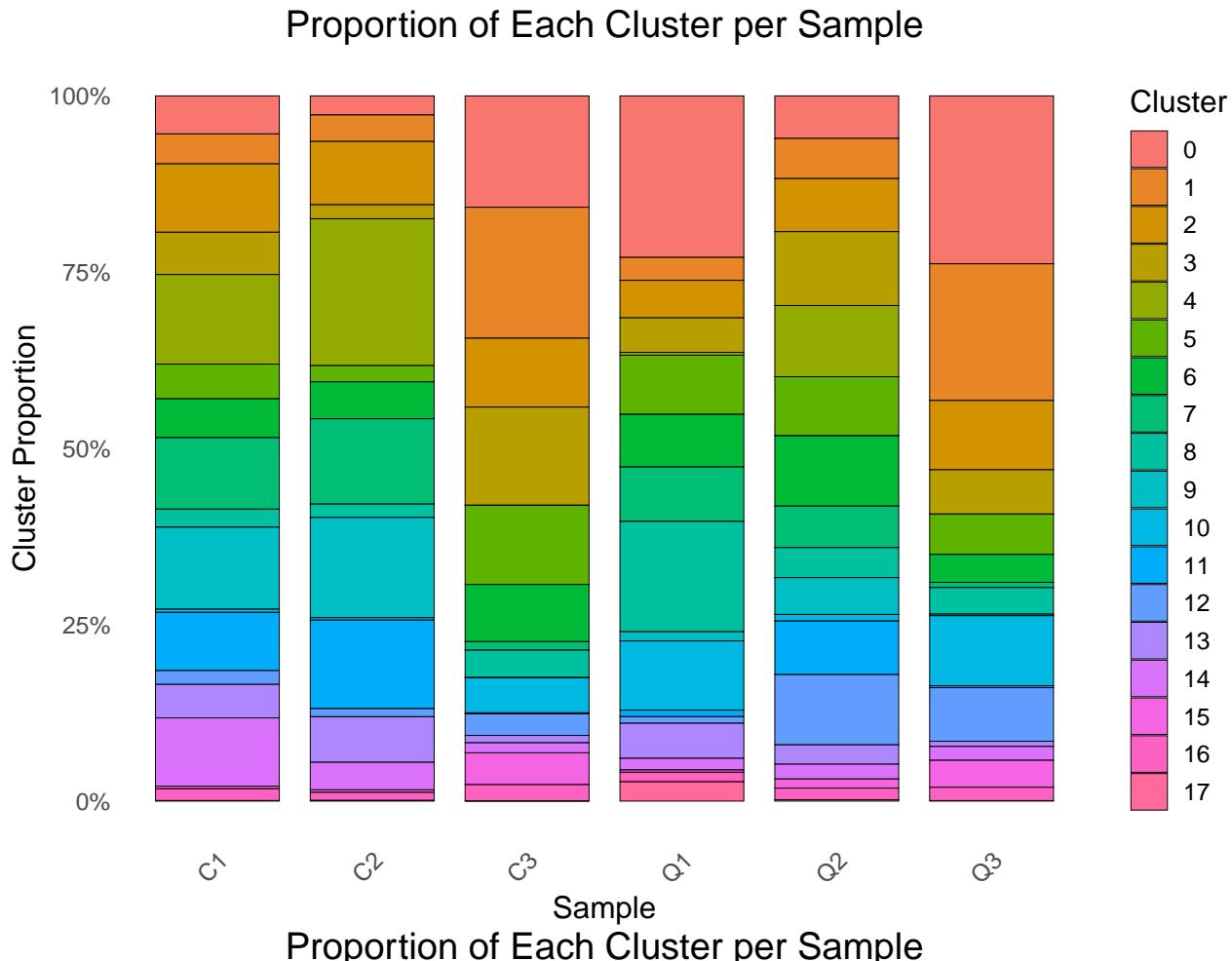


## Plot the UMAP with source and Group

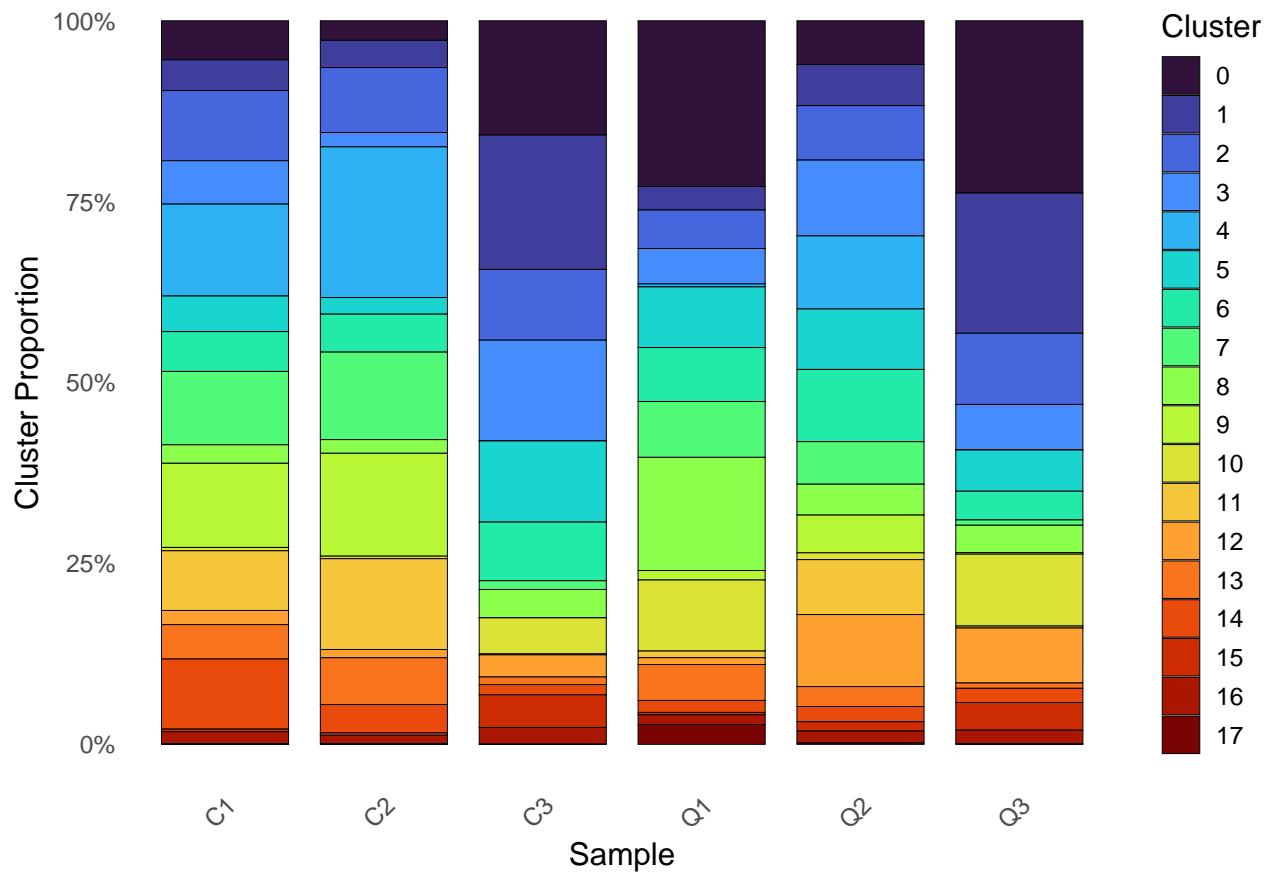




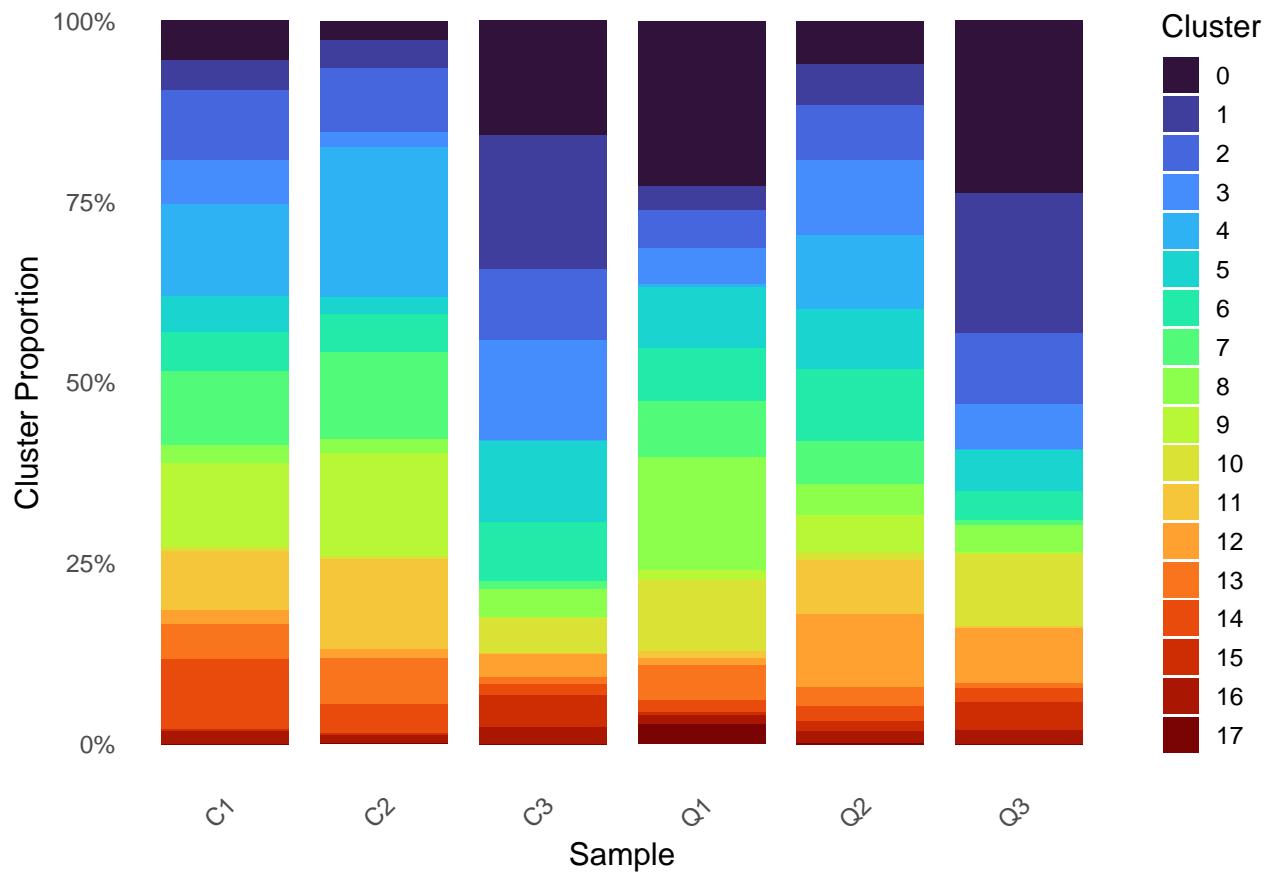
Plot the sample proportions of clusters



## Proportion of Each Cluster per Sample



## Proportion of Each Cluster per Sample



Heatmap of the cell type number in each sample

**Cell Type Number in Each Sample**

466	367	838	518	1098	425	476	876	221	1005	40	713	169	411	837	31	145	6	C1
230	321	765	169	1775	196	447	1031	161	1212	30	1070	97	551	333	31	97	8	C2
1410	1658	873	1241	3	1001	724	108	347	3	444	13	273	93	127	403	206	2	C3
2259	321	524	483	40	827	736	761	1543	129	968	91	93	490	163	32	133	270	Q1
464	438	579	806	777	643	768	452	328	402	72	584	766	212	161	100	126	15	Q2
2276	1853	940	599	3	545	379	70	361	21	950	26	726	71	187	366	181	6	Q3
0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	

Table 1: Cell Type Number in Each Sample

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
C1	466	367	838	518	1098	425	476	876	221	1005	40	713	169	411	837	31	145	6
C2	230	321	765	169	1775	196	447	1031	161	1212	30	1070	97	551	333	31	97	8
C3	1410	1658	873	1241	3	1001	724	108	347	3	444	13	273	93	127	403	206	2
Q1	2259	321	524	483	40	827	736	761	1543	129	968	91	93	490	163	32	133	270
Q2	464	438	579	806	777	643	768	452	328	402	72	584	766	212	161	100	126	15
Q3	2276	1853	940	599	3	545	379	70	361	21	950	26	726	71	187	366	181	6

## **2. Find Maker Genes**

```

## [1] "cluster marker genes loaded"
## [1] 0

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 2

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 3

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 4

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 5

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 6

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 7

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] "cluster marker genes loaded"
## [1] 0

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 1

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 2

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 3

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 4

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 5

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 6

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 7

## [1] "adding marker gene logfc...."

```

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## [1] "adding marker gene expr...."
## [1] 8

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 9

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] "cluster marker genes loaded"
## [1] 0

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 1

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 2

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 3

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 4

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 5

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 6

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 7

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
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## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 9

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 10

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 11

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 12

## [1] "adding marker gene logfc...."

```

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## [1] "adding marker gene expr...."
## [1] "cluster marker genes loaded"
## [1] 0

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 1

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 2

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 3

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 4

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
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## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 6

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
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## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
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## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 9

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 10

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 11

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 12

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 13

## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 14

## [1] "adding marker gene logfc...."

```

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## [1] "adding marker gene expr...."
## [1] 16
## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] "cluster marker genes loaded"
## [1] 0
## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 1
## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 2
## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 3
## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 4
## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
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## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 6
## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 7
## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 8
## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 9
## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 10
## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 11
## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 12
## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 13
## [1] "adding marker gene logfc...."
```

```
## [1] "adding marker gene expr...."
## [1] 14
## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 15
## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 16
## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
## [1] 17
## [1] "adding marker gene logfc...."
## [1] "adding marker gene expr...."
```

## 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                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
```