Analysis mutil Group

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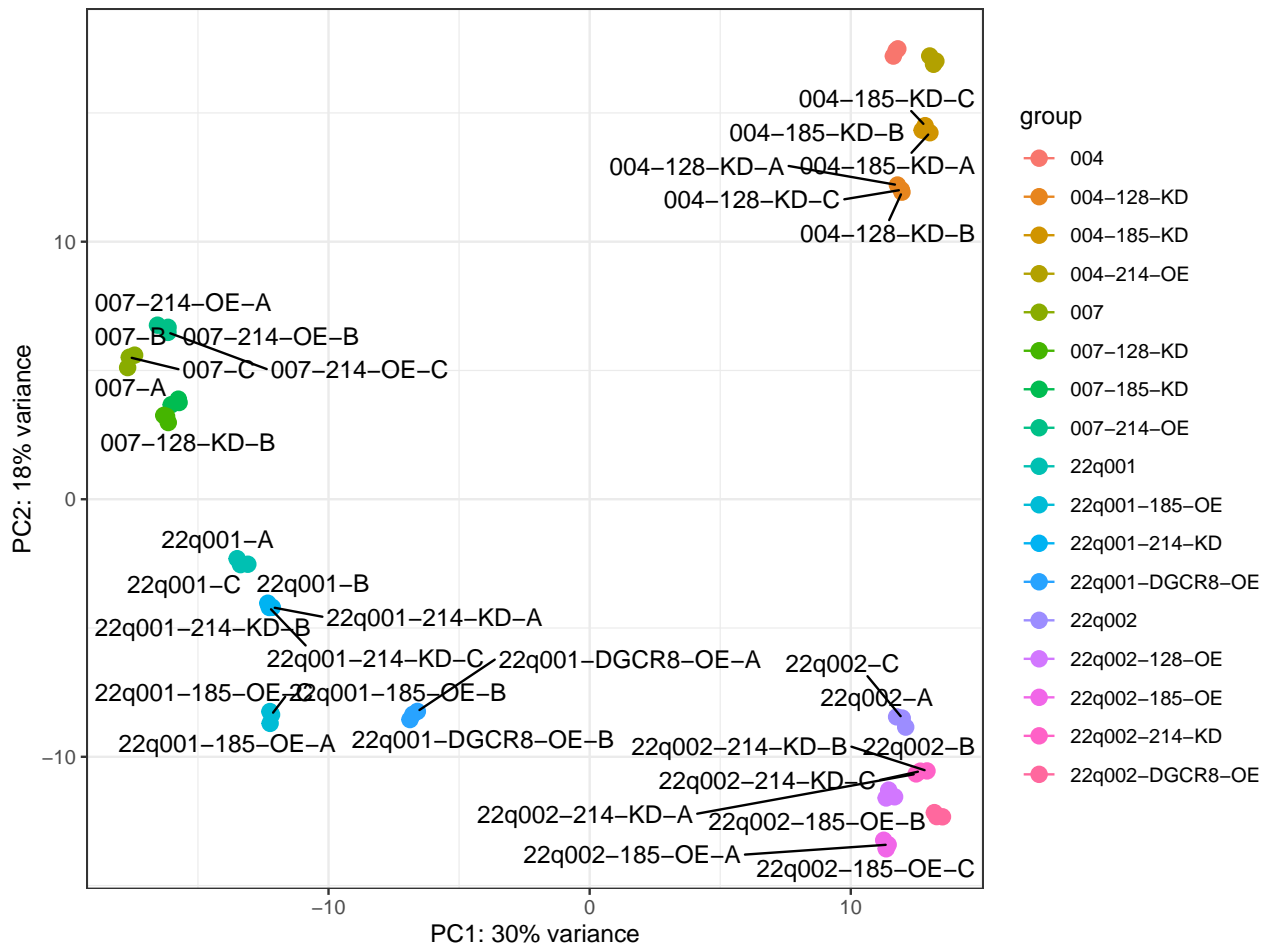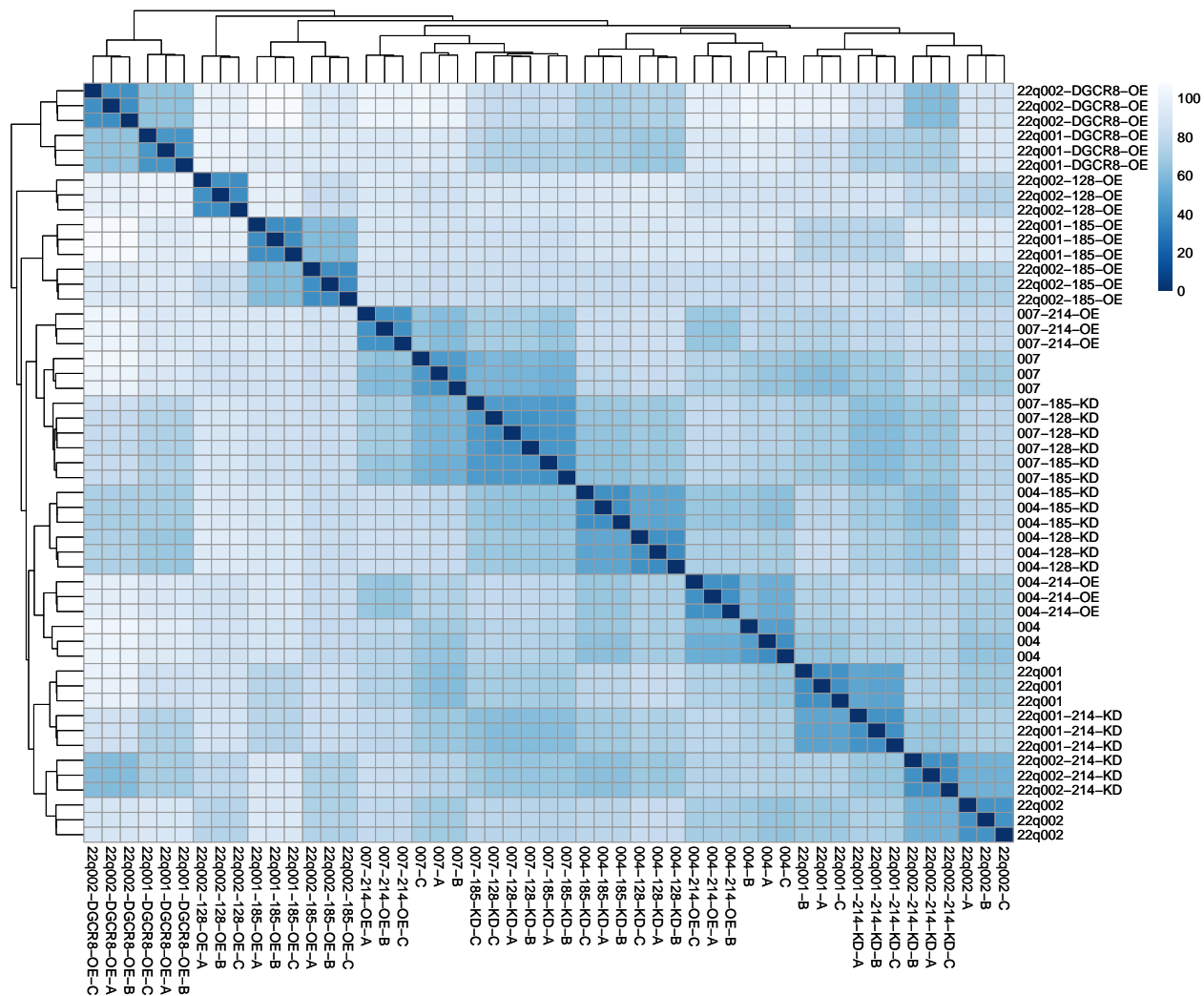# Contents

1. Read the count data

In this section, we will read the clean count data from the synaptosomes_bulkRNA folder. We will read the data and merge them into a single table.

2. Visualization for reuslt

(1) Sample information - PCA plot

(2) Sample information - Distance heatmap

miRNA 128

```
## pdf
##   2
```

```
## pdf
##   2
```

Sample 004

miRNA 185

Sample 004

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] parallel  stats4    stats     graphics  grDevices utils     datasets
## [8] methods   base
##
## other attached packages:
##  [1] ggsci_3.2.0              here_1.0.1
##  [3] GSEABase_1.66.0          graph_1.82.0
##  [5] annotate_1.82.0          XML_3.99-0.18
##  [7] extrafont_0.19           ggsignif_0.6.4
##  [9] patchwork_1.3.0          decoupleR_2.10.0
## [11] GSVA_1.52.3              BiocParallel_1.38.0
## [13] edgeR_4.2.2              limma_3.60.6
## [15] GenomicFeatures_1.56.0   biomaRt_2.60.1
## [17] gprofiler2_0.2.3         data.table_1.17.4
## [19] org.Hs.eg.db_3.19.1      AnnotationDbi_1.66.0
## [21] clusterProfiler_4.12.6   ggfortify_0.4.17
## [23] EnhancedVolcano_1.22.0   ggrepel_0.9.6
## [25] apeglm_1.26.1            DESeq2_1.44.0
## [27] SummarizedExperiment_1.34.0 Biobase_2.64.0
## [29] MatrixGenerics_1.16.0    matrixStats_1.5.0
## [31] reshape2_1.4.4           Matrix_1.7-3
## [33] Signac_1.14.0            Seurat_5.3.0
## [35] SeuratObject_5.1.0       sp_2.2-0
## [37] RColorBrewer_1.1-3       pheatmap_1.0.12
## [39] rtracklayer_1.64.0       GenomicRanges_1.56.2
## [41] GenomeInfoDb_1.40.1      IRanges_2.38.1
## [43] S4Vectors_0.42.1         BiocGenerics_0.50.0
## [45] knitr_1.50               lubridate_1.9.4
## [47] forcats_1.0.0            stringr_1.5.1
## [49] dplyr_1.1.4              purrr_1.0.4
## [51] readr_2.1.5              tidyr_1.3.1
## [53] tibble_3.2.1             ggplot2_3.5.2
## [55] tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
##   [1] SpatialExperiment_1.14.0  R.methodsS3_1.8.2
##   [3] dichromat_2.0-0.1         progress_1.2.3
##   [5] goftest_1.2-3             HDF5Array_1.32.1
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##   [7] Biostrings_2.72.1        vctrs_0.6.5
##   [9] spatstat.random_3.4-1    digest_0.6.37
##  [11] png_0.1-8                deldir_2.0-4
##  [13] parallelly_1.44.0        magick_2.8.6
##  [15] MASS_7.3-65              httpuv_1.6.16
##  [17] qvalue_2.36.0            withr_3.0.2
##  [19] xfun_0.52                ggfun_0.1.8
##  [21] survival_3.8-3           memoise_2.0.1
##  [23] gson_0.1.0               tidytree_0.4.6
##  [25] zoo_1.8-14               pbapply_1.7-2
##  [27] R.oo_1.27.1              prettyunits_1.2.0
##  [29] KEGGREST_1.44.1          promises_1.3.3
##  [31] httr_1.4.7               restfulr_0.0.15
##  [33] rhdf5filters_1.16.0      globals_0.18.0
##  [35] fitdistrplus_1.2-2       rhdf5_2.48.0
##  [37] rstudioapi_0.17.1        UCSC.utils_1.0.0
##  [39] miniUI_0.1.2             generics_0.1.4
##  [41] DOSE_3.30.5              curl_6.2.3
##  [43] zlibbioc_1.50.0          ScaledMatrix_1.12.0
##  [45] ggraph_2.2.1             polyclip_1.10-7
##  [47] GenomeInfoDbData_1.2.12  SparseArray_1.4.8
##  [49] xtable_1.8-4             evaluate_1.0.3
##  [51] S4Arrays_1.4.1           BiocFileCache_2.12.0
##  [53] hms_1.1.3                irlba_2.3.5.1
##  [55] colorspace_2.1-1         filelock_1.0.3
##  [57] ROCR_1.0-11              reticulate_1.42.0
##  [59] spatstat.data_3.1-6      magrittr_2.0.3
##  [61] lmtest_0.9-40            later_1.4.2
##  [63] viridis_0.6.5            ggtree_3.12.0
##  [65] lattice_0.22-7           spatstat.geom_3.4-1
##  [67] future.apply_1.11.3      scattermore_1.2
##  [69] shadowtext_0.1.4         cowplot_1.1.3
##  [71] RcppAnnoy_0.0.22         pillar_1.10.2
##  [73] nlme_3.1-168             compiler_4.4.0
##  [75] beachmat_2.20.0          RSpectra_0.16-2
##  [77] stringi_1.8.7            tensor_1.5
##  [79] GenomicAlignments_1.40.0 plyr_1.8.9
##  [81] crayon_1.5.3             abind_1.4-8
##  [83] BiocIO_1.14.0            gridGraphics_0.5-1
##  [85] emdbook_1.3.13           locfit_1.5-9.12
##  [87] graphlayouts_1.2.2       bit_4.6.0
##  [89] fastmatch_1.1-6          codetools_0.2-20
##  [91] BiocSingular_1.20.0      plotly_4.10.4
##  [93] mime_0.13                splines_4.4.0
##  [95] Rcpp_1.0.14              fastDummies_1.7.5
##  [97] sparseMatrixStats_1.16.0 dbplyr_2.5.0
##  [99] Rttf2pt1_1.3.12          blob_1.2.4
## [101] fs_1.6.6                 listenv_0.9.1
## [103] ggplotify_0.1.2          statmod_1.5.0
## [105] tzdb_0.5.0               tweenr_2.0.3
## [107] pkgconfig_2.0.3          tools_4.4.0
## [109] cachem_1.1.0             RSQLite_2.3.11
## [111] viridisLite_0.4.2        DBI_1.2.3
## [113] numDeriv_2016.8-1.1      fastmap_1.2.0
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## [115] rmarkdown_2.29              scales_1.4.0
## [117] grid_4.4.0                  ica_1.0-3
## [119] Rsamtools_2.20.0            coda_0.19-4.1
## [121] dotCall64_1.2               RANN_2.6.2
## [123] farver_2.1.2                tidygraph_1.3.1
## [125] scatterpie_0.2.4            yaml_2.3.10
## [127] cli_3.6.5                   lifecycle_1.0.4
## [129] uwot_0.2.3                  mvtnorm_1.3-3
## [131] timechange_0.3.0            gtable_0.3.6
## [133] rjson_0.2.23                ggridges_0.5.6
## [135] progressr_0.15.1            ape_5.8-1
## [137] jsonlite_2.0.0              RcppHNSW_0.6.0
## [139] bitops_1.0-9                bit64_4.6.0-1
## [141] Rtsne_0.17                  yulab.utils_0.2.0
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## [145] GOSemSim_2.30.2             spatstat.univar_3.1-3
## [147] R.utils_2.13.0              lazyeval_0.2.2
## [149] shiny_1.10.0                htmltools_0.5.8.1
## [151] enrichplot_1.24.4           GO.db_3.19.1
## [153] sctransform_0.4.2           rappdirs_0.3.3
## [155] tinytex_0.57                glue_1.8.0
## [157] spam_2.11-1                 httr2_1.1.2
## [159] XVector_0.44.0              RCurl_1.98-1.17
## [161] rprojroot_2.0.4             treeio_1.28.0
## [163] gridExtra_2.3               extrafontdb_1.0
## [165] igraph_2.1.4                R6_2.6.1
## [167] SingleCellExperiment_1.26.0 labeling_0.4.3
## [169] RcppRoll_0.3.1              cluster_2.1.8.1
## [171] bbmle_1.0.25.1              Rhdf5lib_1.26.0
## [173] aplot_0.2.5                 DelayedArray_0.30.1
## [175] tidyselect_1.2.1            ggforce_0.4.2
## [177] xml2_1.3.8                  future_1.49.0
## [179] rsvd_1.0.5                  KernSmooth_2.23-26
## [181] htmlwidgets_1.6.4           fgsea_1.30.0
## [183] rlang_1.1.6                 spatstat.sparse_3.1-0
## [185] spatstat.explore_3.4-3
```