Analysis mutil Group

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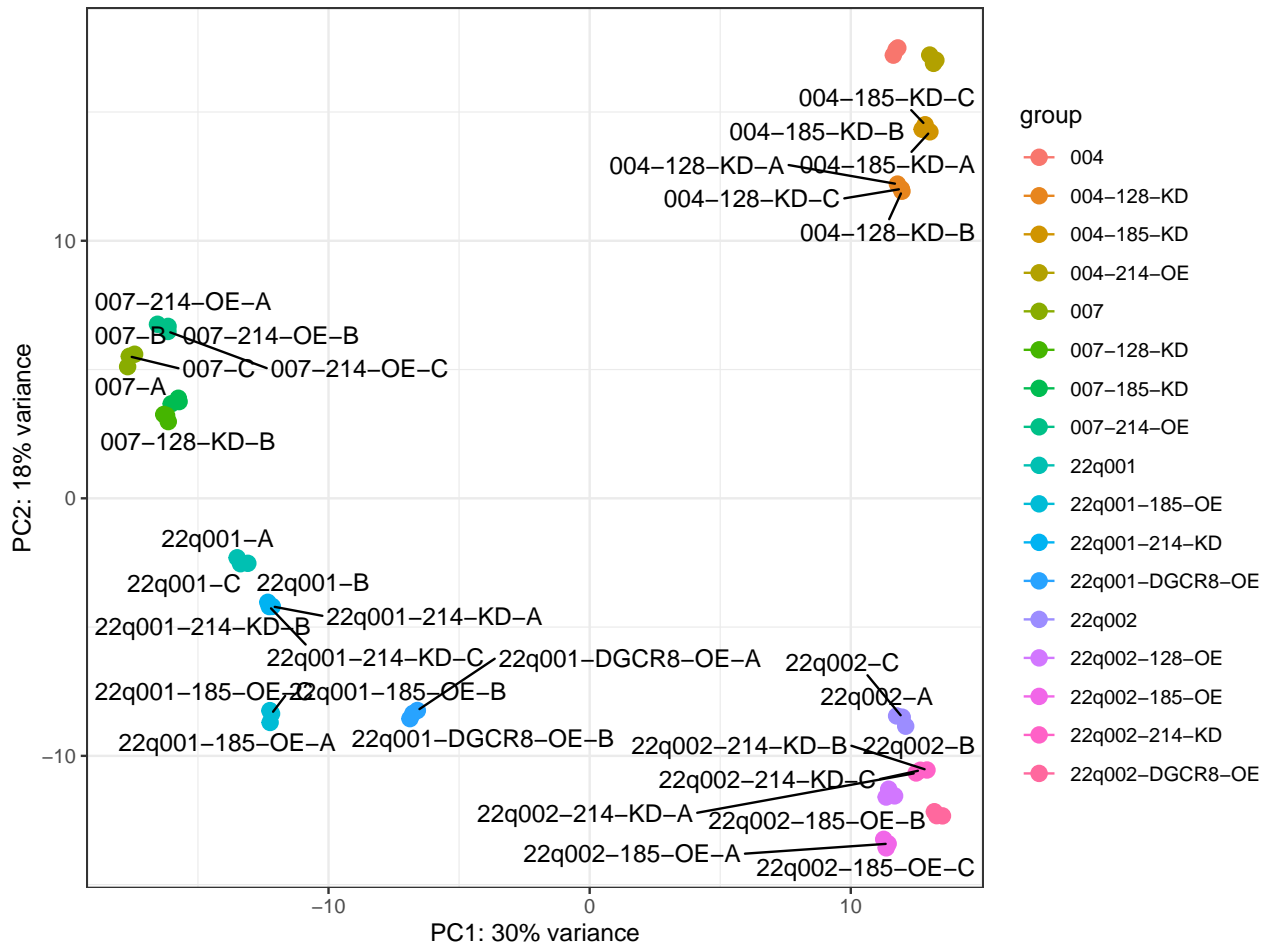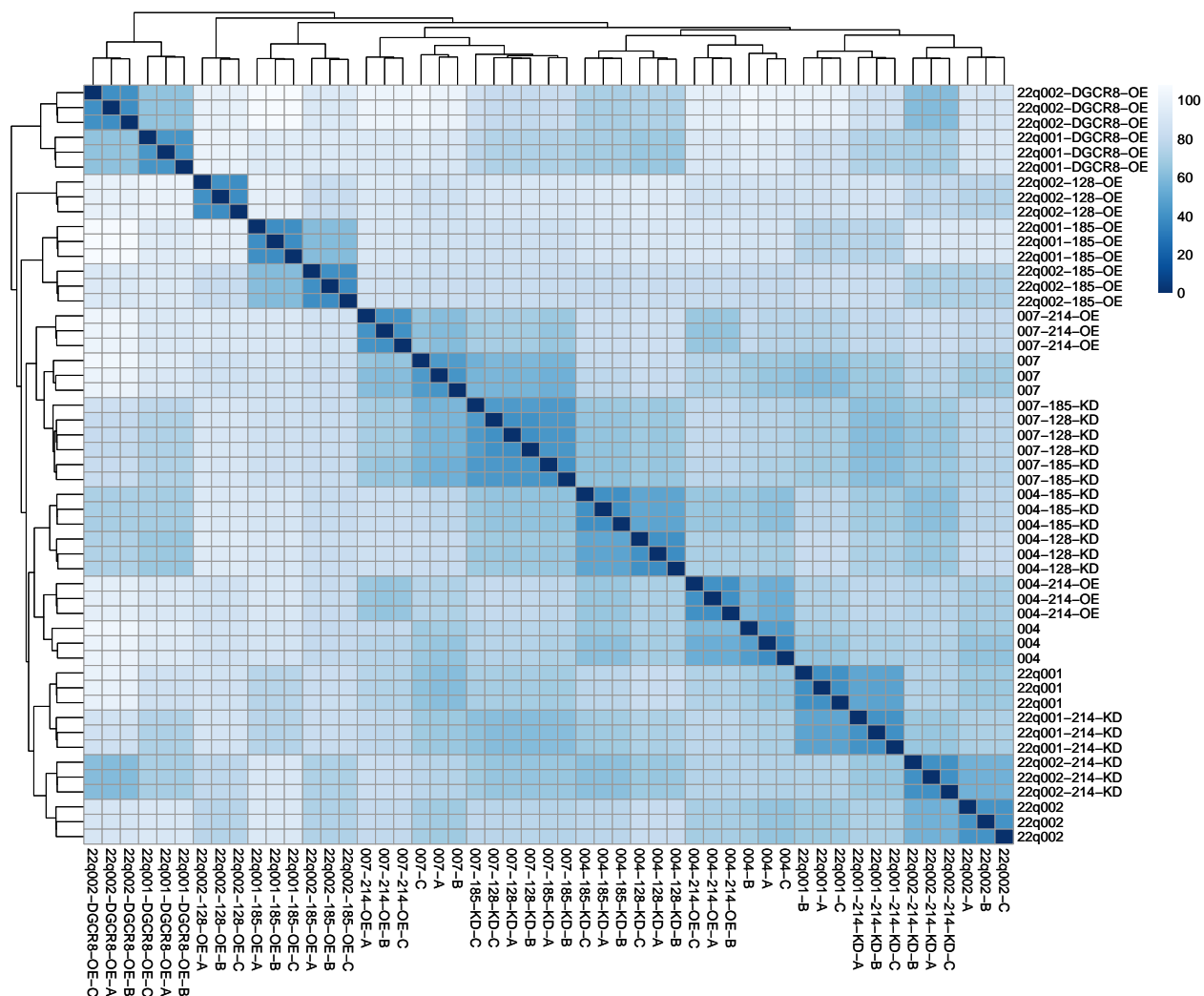# Contents

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
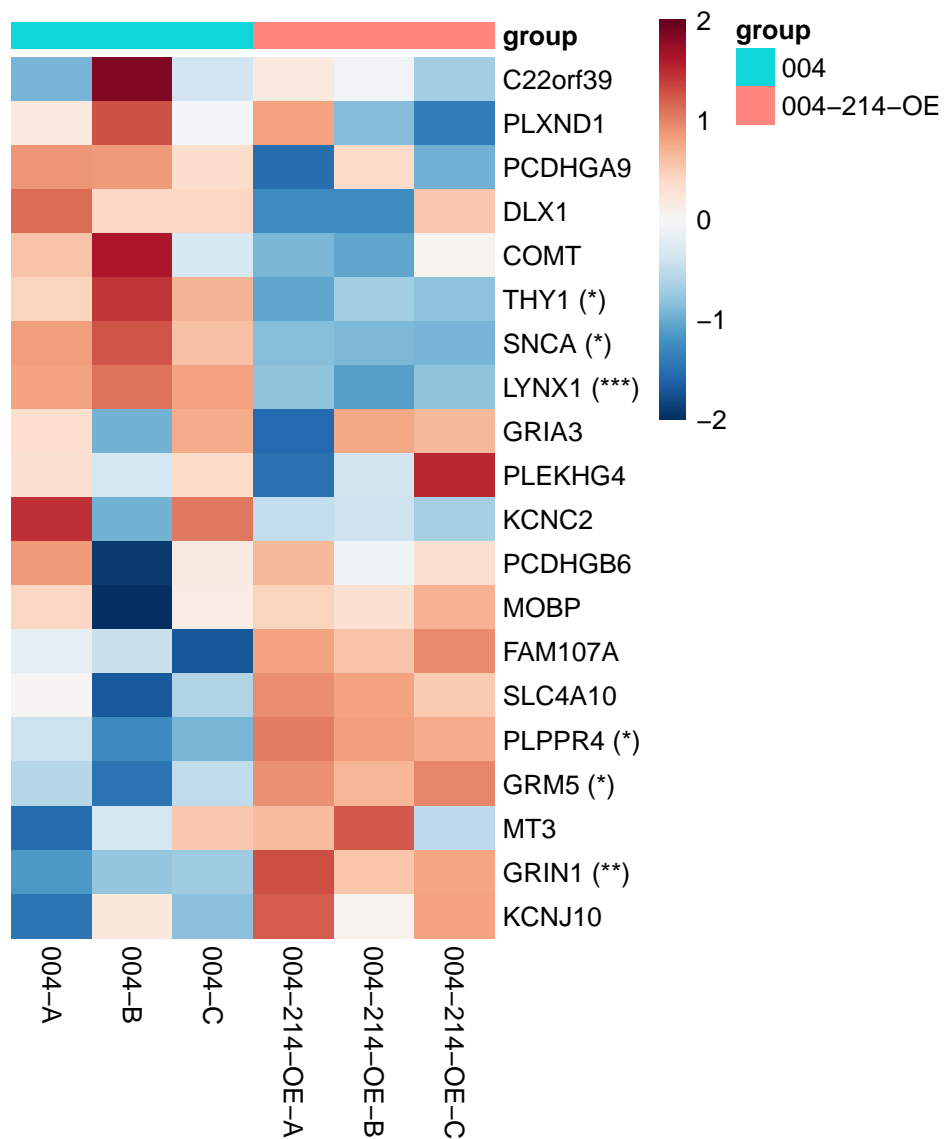
(1) Sample information - PCA plot

(2) Sample information - Distance heatmap


```
## Processing: 004-214-OE_vs_004
## Processing: 004-214-OE_vs_004
```
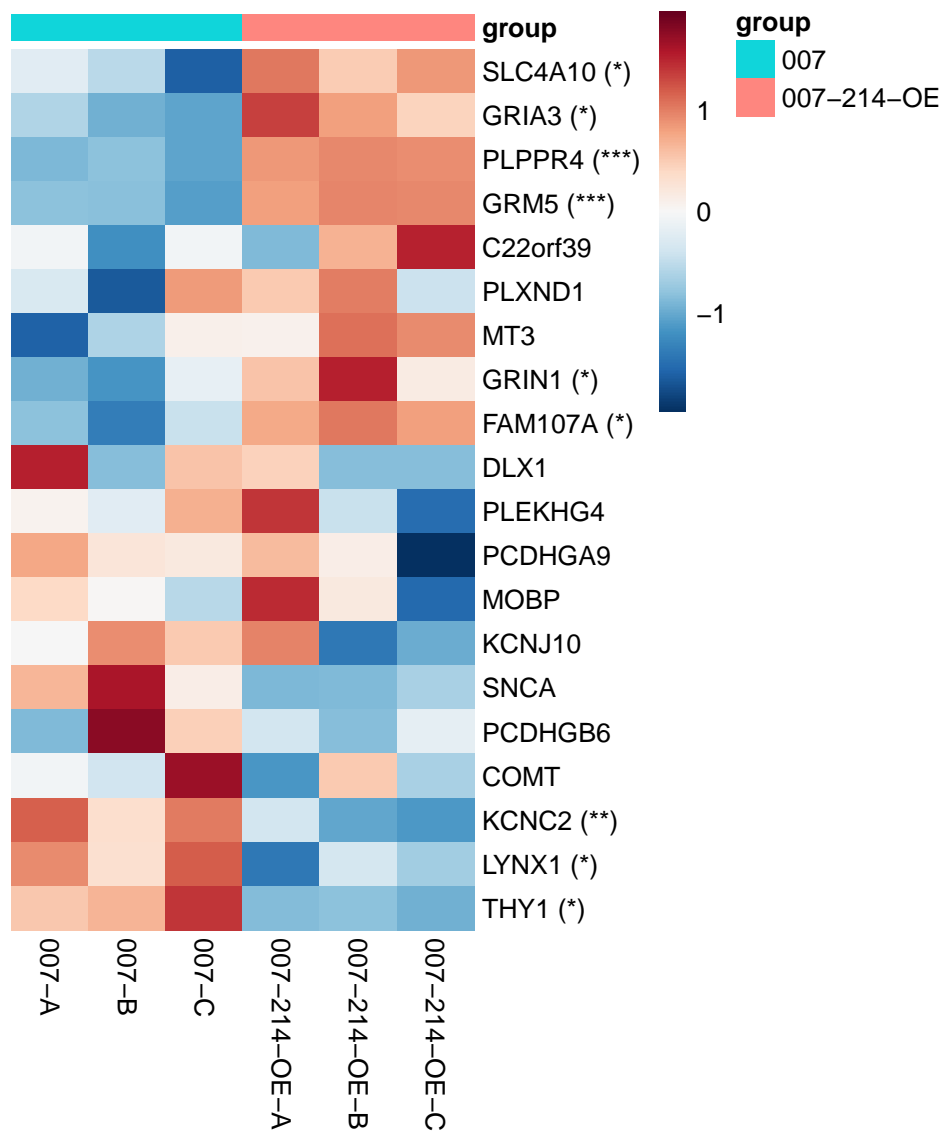
```
## Finished: 004-214-OE_vs_004
##
## Processing: 007-214-OE_vs_007
## Processing: 007-214-OE_vs_007
```

```
## Finished: 007-214-OE_vs_007
##
## Processing: 22q001-214-KD_vs_22q001
## Processing: 22q001-214-KD_vs_22q001
```

Finished: 22q002-214-KD_vs_22q002

```
## Processing: 22q002-128-OE_vs_22q002
## Processing: 22q002-128-OE_vs_22q002
```
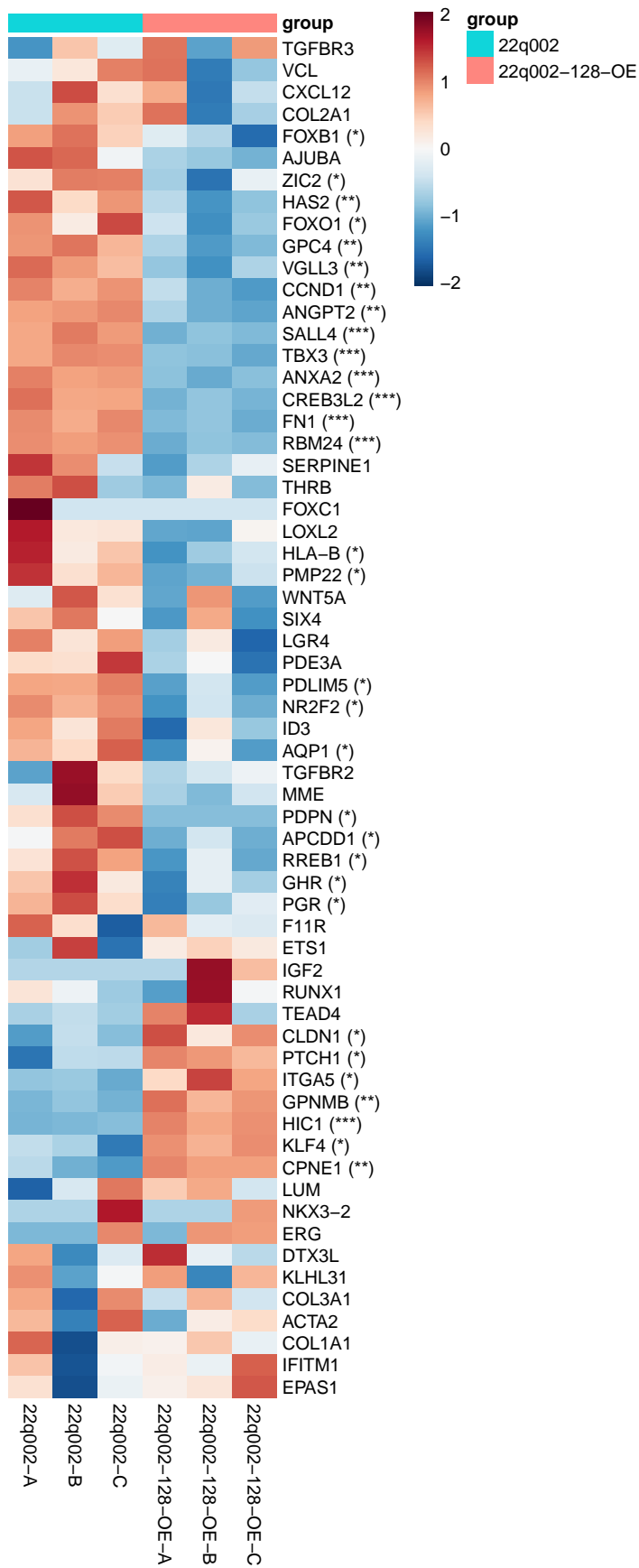
```
## Finished: 22q002-128-OE_vs_22q002
##
## Processing: 004-128-KD_vs_004
## Processing: 004-128-KD_vs_004
```
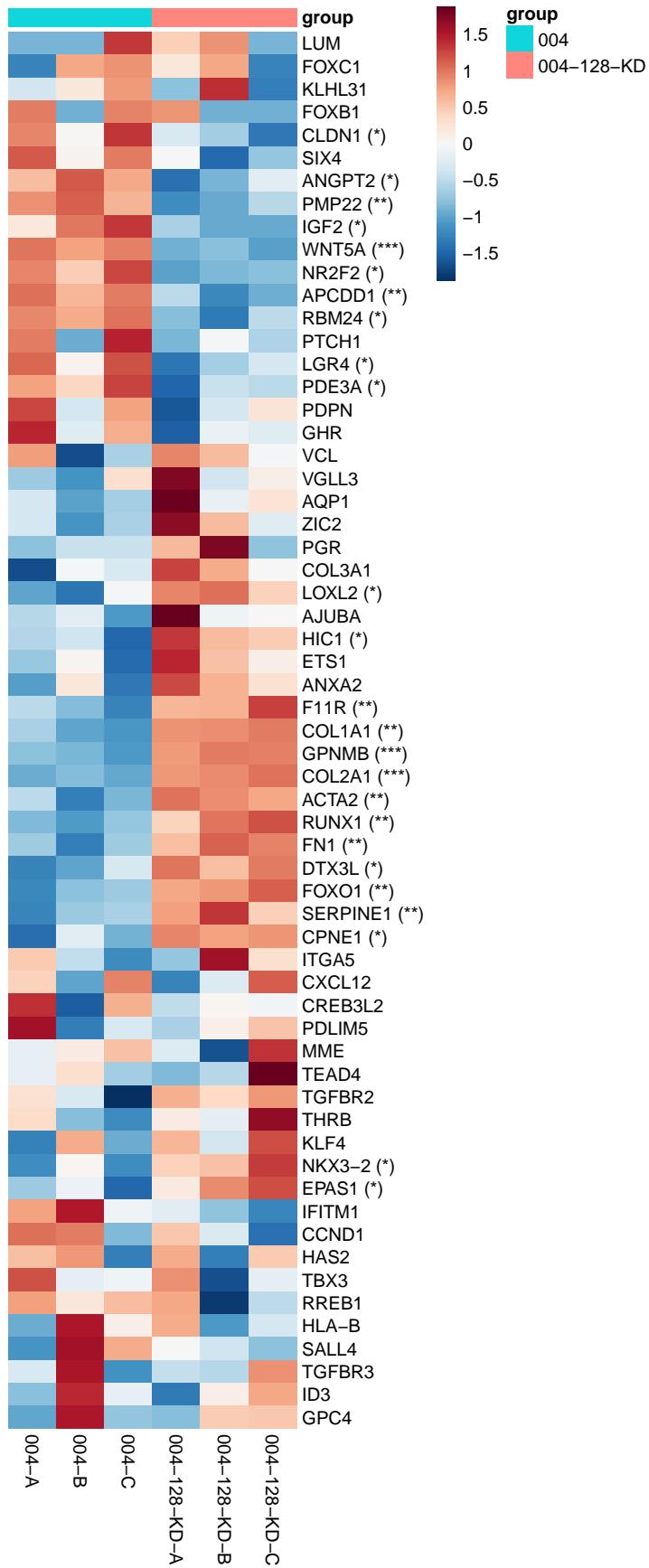
```
## Finished: 004-128-KD_vs_004
##
## Processing: 007-128-KD_vs_007
## Processing: 007-128-KD_vs_007
```

Finished: 007-128-KD_vs_007

```
## Processing: 22q001-185-OE_vs_22q001
## Processing: 22q001-185-OE_vs_22q001
```

```
## Finished: 22q001-185-OE_vs_22q001
##
## Processing: 22q002-185-OE_vs_22q002
## Processing: 22q002-185-OE_vs_22q002
```

```
## Finished: 22q002-185-OE_vs_22q002
##
## Processing: 004-185-KD_vs_004
## Processing: 004-185-KD_vs_004
```

```
## Finished: 004-185-KD_vs_004
##
## Processing: 007-185-KD_vs_007
## Processing: 007-185-KD_vs_007
```
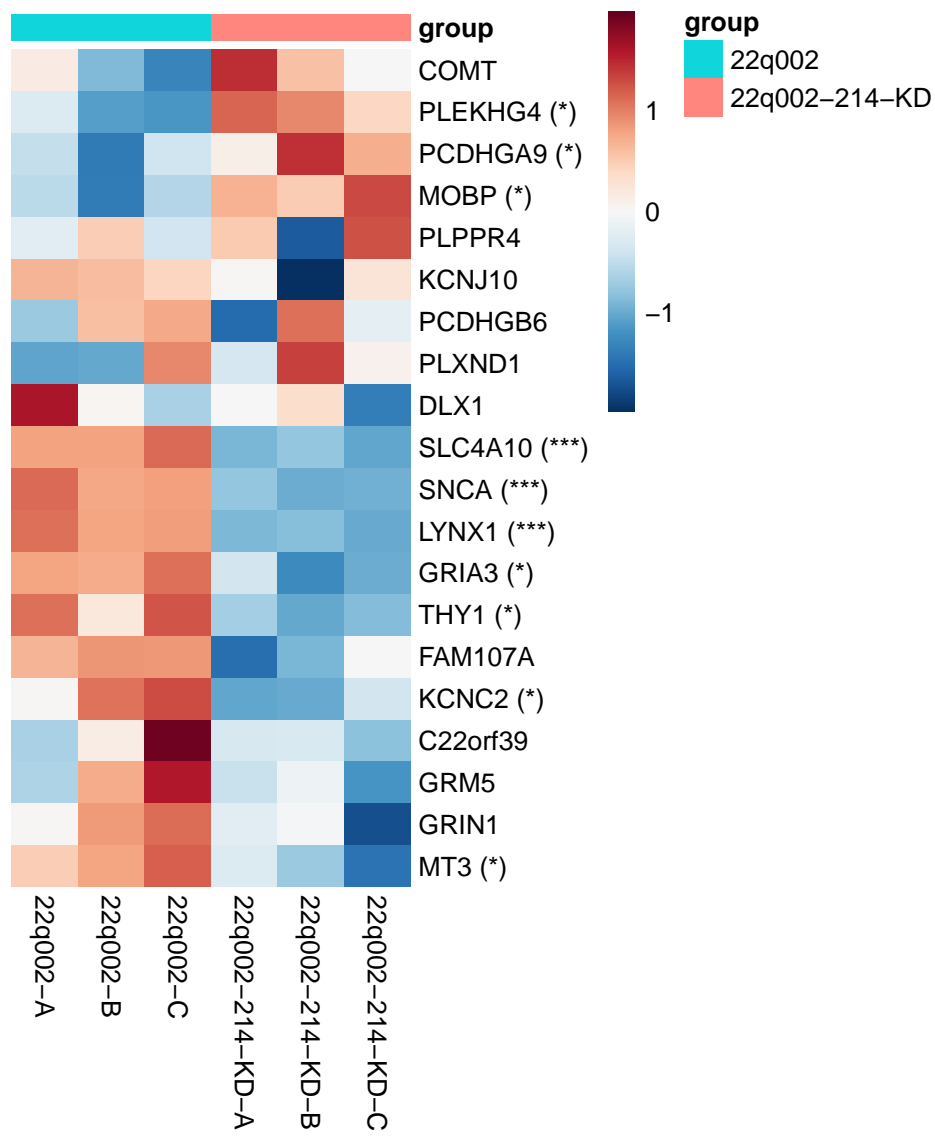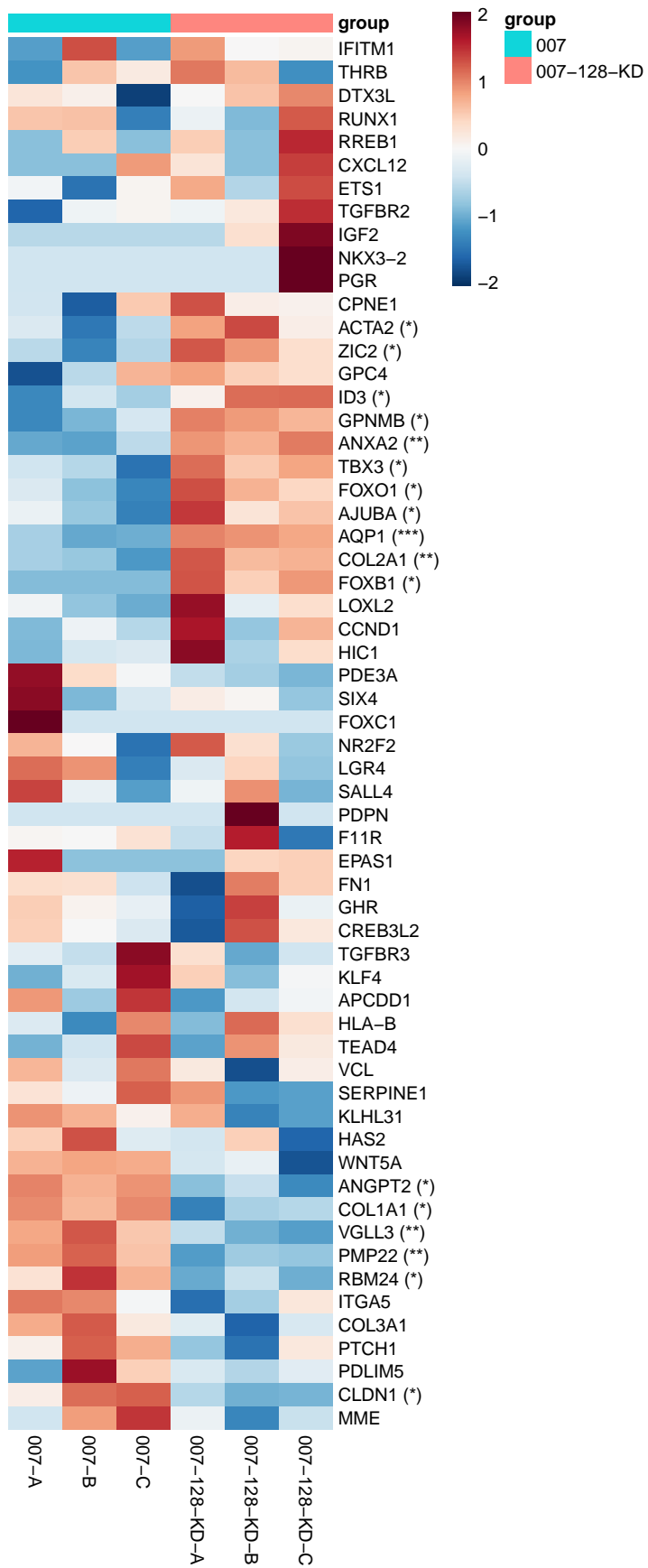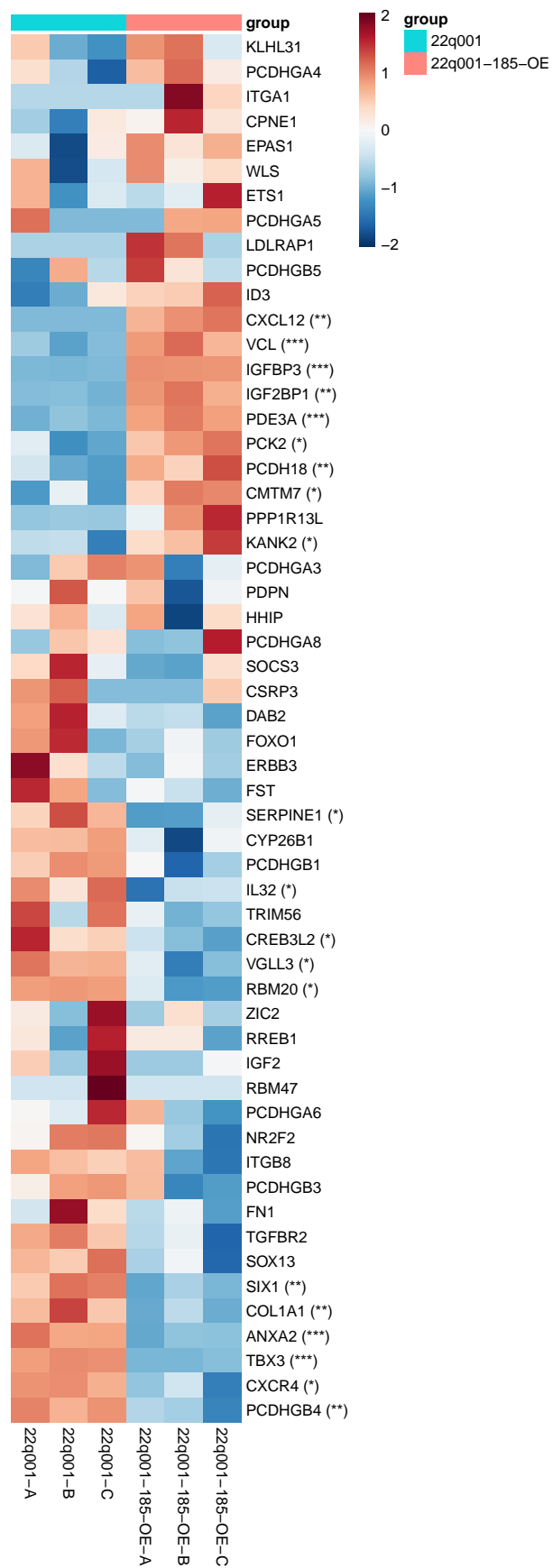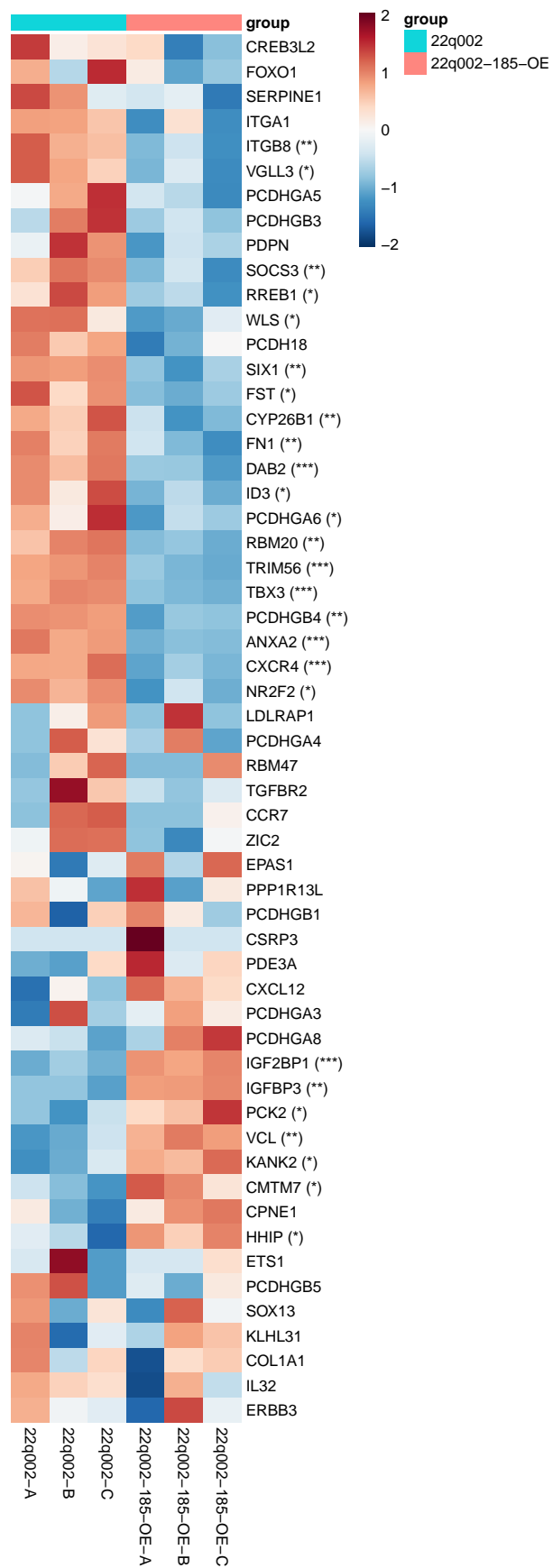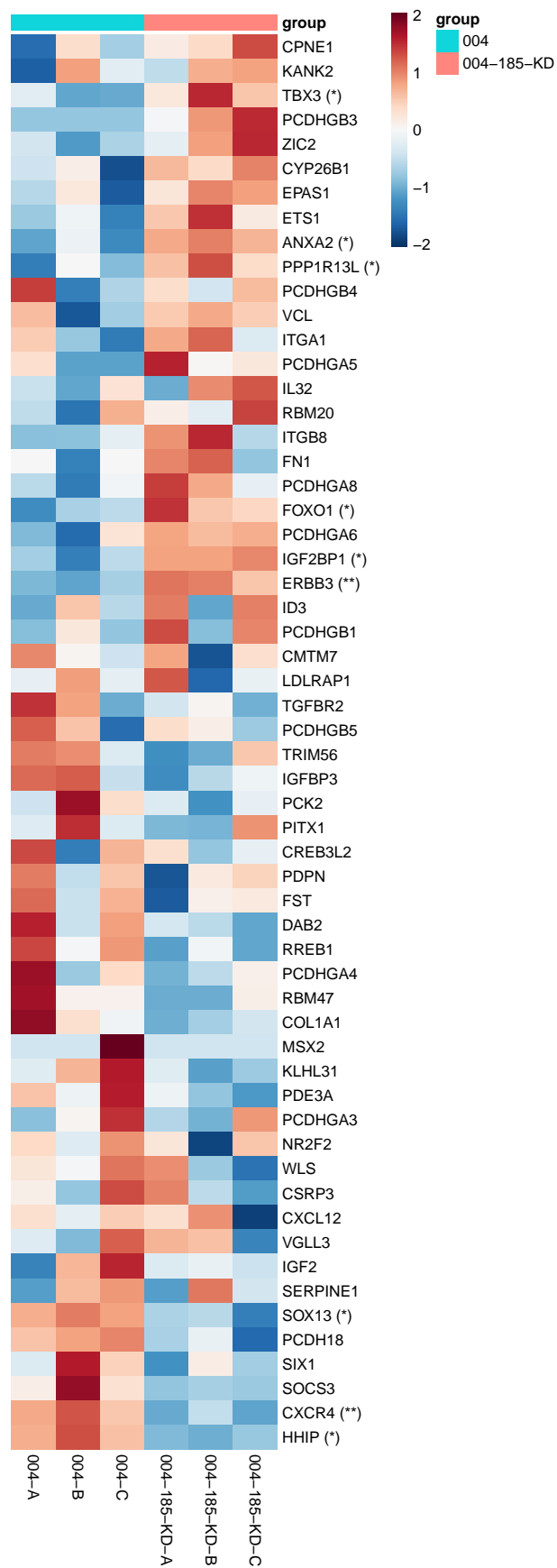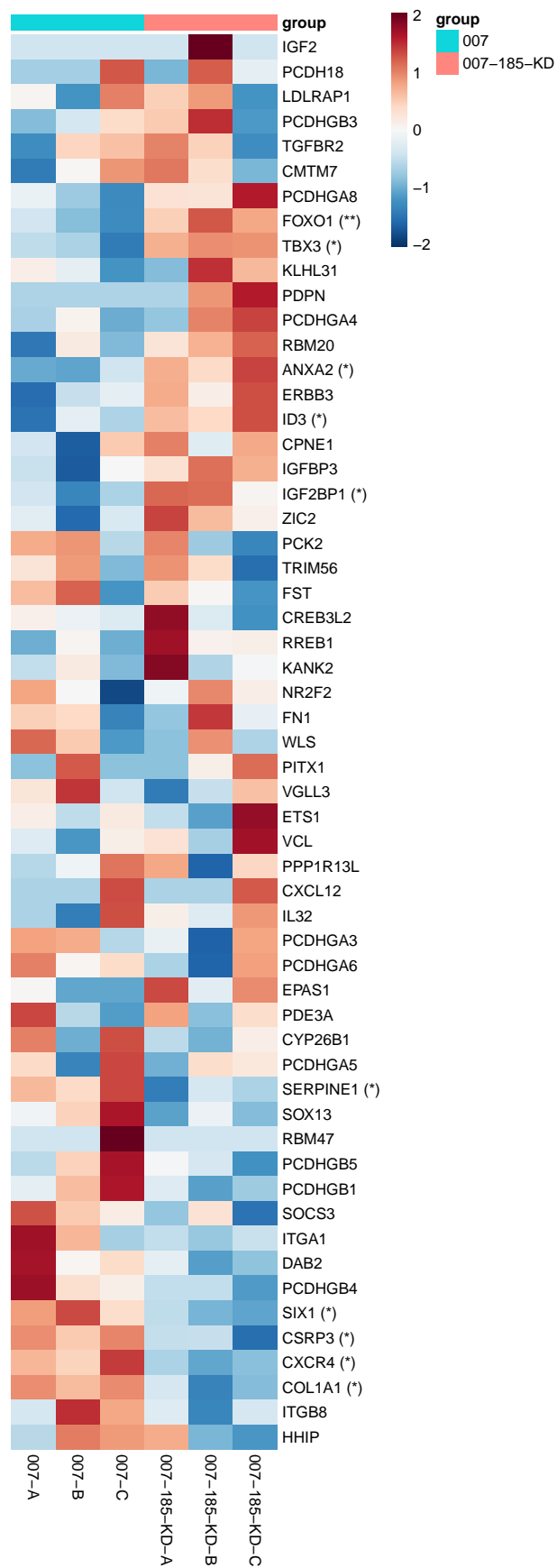
```
## Finished: 007-185-KD_vs_007
```

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 ve
##
## 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] GSEABase_1.66.0          graph_1.82.0
##  [3] annotate_1.82.0          XML_3.99-0.18
##  [5] extrafont_0.19           ggsignif_0.6.4
##  [7] patchwork_1.3.0          decoupleR_2.10.0
##  [9] GSVA_1.52.3              BiocParallel_1.38.0
## [11] edgeR_4.2.2              limma_3.60.6
## [13] GenomicFeatures_1.56.0   biomaRt_2.60.1
## [15] gprofiler2_0.2.3         RColorBrewer_1.1-3
## [17] data.table_1.17.4        org.Hs.eg.db_3.19.1
## [19] AnnotationDbi_1.66.0     clusterProfiler_4.12.6
## [21] ggfortify_0.4.17         pheatmap_1.0.12
## [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] rtracklayer_1.64.0       GenomicRanges_1.56.2
## [39] GenomeInfoDb_1.40.1      IRanges_2.38.1
## [41] S4Vectors_0.42.1         BiocGenerics_0.50.0
## [43] knitr_1.50               lubridate_1.9.4
## [45] forcats_1.0.0            stringr_1.5.1
## [47] dplyr_1.1.4              purrr_1.0.4
## [49] readr_2.1.5              tidyr_1.3.1
## [51] tibble_3.2.1             ggplot2_3.5.2
## [53] 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
##    [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                systemfonts_1.2.3
##   [25] ragg_1.4.0                tidytree_0.4.6
##   [27] zoo_1.8-14                pbapply_1.7-2
##   [29] R.oo_1.27.1               prettyunits_1.2.0
##   [31] KEGGREST_1.44.1            promises_1.3.3
##   [33] httr_1.4.7                restfulr_0.0.15
##   [35] rhdf5filters_1.16.0        globals_0.18.0
##   [37] fitdistrplus_1.2-2         rhdf5_2.48.0
##   [39] rstudioapi_0.17.1          UCSC.utils_1.0.0
##   [41] miniUI_0.1.2               generics_0.1.4
##   [43] DOSE_3.30.5               curl_6.2.3
##   [45] zlibbioc_1.50.0            ScaledMatrix_1.12.0
##   [47] ggraph_2.2.1               polyclip_1.10-7
##   [49] GenomeInfoDbData_1.2.12    SparseArray_1.4.8
##   [51] xtable_1.8-4              evaluate_1.0.3
##   [53] S4Arrays_1.4.1            BiocFileCache_2.12.0
##   [55] hms_1.1.3                 irlba_2.3.5.1
##   [57] colorspace_2.1-1          filelock_1.0.3
##   [59] ROCR_1.0-11               reticulate_1.42.0
##   [61] spatstat.data_3.1-6        magrittr_2.0.3
##   [63] lmtest_0.9-40             later_1.4.2
##   [65] viridis_0.6.5             ggtree_3.12.0
##   [67] lattice_0.22-7            spatstat.geom_3.4-1
##   [69] future.apply_1.11.3        scattermore_1.2
##   [71] shadowtext_0.1.4          cowplot_1.1.3
##   [73] RcppAnnoy_0.0.22          pillar_1.10.2
##   [75] nlme_3.1-168              compiler_4.4.0
##   [77] beachmat_2.20.0           RSpectra_0.16-2
##   [79] stringi_1.8.7             tensor_1.5
##   [81] GenomicAlignments_1.40.0   plyr_1.8.9
##   [83] crayon_1.5.3              abind_1.4-8
##   [85] BiocIO_1.14.0             gridGraphics_0.5-1
##   [87] emdbook_1.3.13            locfit_1.5-9.12
##   [89] graphlayouts_1.2.2        bit_4.6.0
##   [91] fastmatch_1.1-6           textshaping_1.0.1
##   [93] codetools_0.2-20          BiocSingular_1.20.0
##   [95] plotly_4.10.4             mime_0.13
##   [97] splines_4.4.0             Rcpp_1.0.14
##   [99] fastDummies_1.7.5         sparseMatrixStats_1.16.0
##  [101] dbplyr_2.5.0              Rttf2pt1_1.3.12
##  [103] blob_1.2.4                here_1.0.1
##  [105] fs_1.6.6                  listenv_0.9.1
##  [107] ggplotify_0.1.2           statmod_1.5.0
##  [109] tzdb_0.5.0                tweenr_2.0.3
```

```
## [111] pkgconfig_2.0.3          tools_4.4.0
## [113] cachem_1.1.0            RSQLite_2.3.11
## [115] viridisLite_0.4.2       DBI_1.2.3
## [117] numDeriv_2016.8-1.1     fastmap_1.2.0
## [119] rmarkdown_2.29          scales_1.4.0
## [121] grid_4.4.0              ica_1.0-3
## [123] Rsamtools_2.20.0        coda_0.19-4.1
## [125] dotCall64_1.2           RANN_2.6.2
## [127] farver_2.1.2            tidygraph_1.3.1
## [129] scatterpie_0.2.4        yaml_2.3.10
## [131] cli_3.6.5               lifecycle_1.0.4
## [133] uwot_0.2.3              mvtnorm_1.3-3
## [135] timechange_0.3.0        gtable_0.3.6
## [137] rjson_0.2.23            ggridges_0.5.6
## [139] progressr_0.15.1        ape_5.8-1
## [141] jsonlite_2.0.0          RcppHNSW_0.6.0
## [143] bitops_1.0-9            bit64_4.6.0-1
## [145] Rtsne_0.17              yulab.utils_0.2.0
## [147] spatstat.utils_3.1-4    bdsmatrix_1.3-7
## [149] GOSemSim_2.30.2         spatstat.univar_3.1-3
## [151] R.utils_2.13.0          lazyeval_0.2.2
## [153] shiny_1.10.0            htmltools_0.5.8.1
## [155] enrichplot_1.24.4       GO.db_3.19.1
## [157] sctransform_0.4.2       rappdirs_0.3.3
## [159] tinytex_0.57            glue_1.8.0
## [161] spam_2.11-1             httr2_1.1.2
## [163] XVector_0.44.0          RCurl_1.98-1.17
## [165] rprojroot_2.0.4         treeio_1.28.0
## [167] gridExtra_2.3           extrafontdb_1.0
## [169] igraph_2.1.4            R6_2.6.1
## [171] SingleCellExperiment_1.26.0 labeling_0.4.3
## [173] RcppRoll_0.3.1          cluster_2.1.8.1
## [175] bbmle_1.0.25.1          Rhdf5lib_1.26.0
## [177] aplot_0.2.5             DelayedArray_0.30.1
## [179] tidyselect_1.2.1        ggforce_0.4.2
## [181] xml2_1.3.8              future_1.49.0
## [183] rsvd_1.0.5              KernSmooth_2.23-26
## [185] htmlwidgets_1.6.4       fgsea_1.30.0
## [187] rlang_1.1.6             spatstat.sparse_3.1-0
## [189] spatstat.explore_3.4-3
```