

Boxplot for miRNA

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Contents

1. Read the count data	2
2. Normalization and DESeq2 analysis	2
3. Visualization for result	3
(1) Sample information Heatmap	3
(2) Sample information PCA plot	4
Session information	11

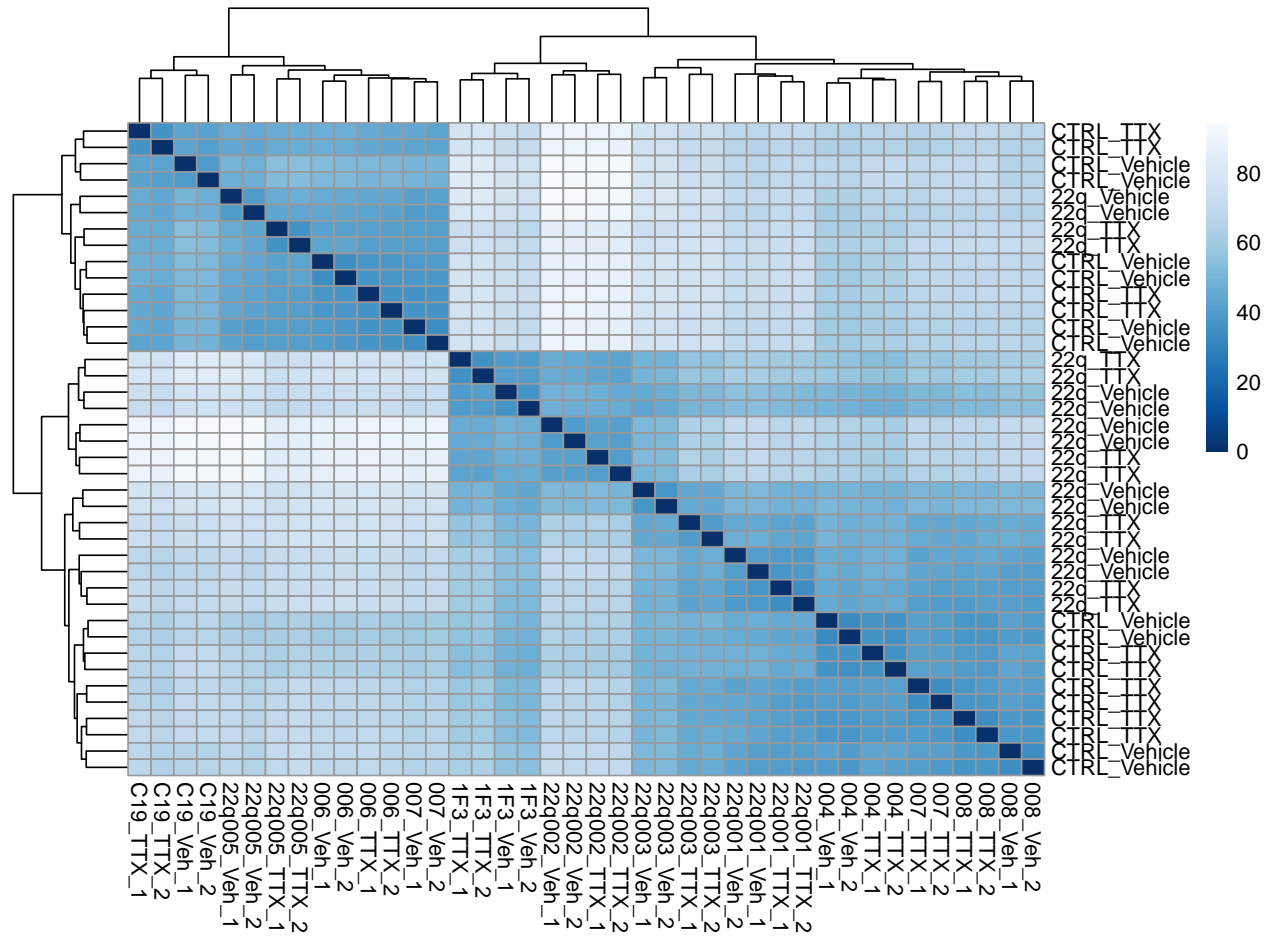
1. Read the count data

In this section, we will read the clean count data from the `synaptosomes_miRNARNA` folder. The data is stored in the format of `.csv`. We will read the data and filter the columns based on the condition list. The final table will be stored in `results/02-DEG-Vehicle/DESeq2_results.csv`.

2. Normalization and DESeq2 analysis

3. Visualization for reuslt

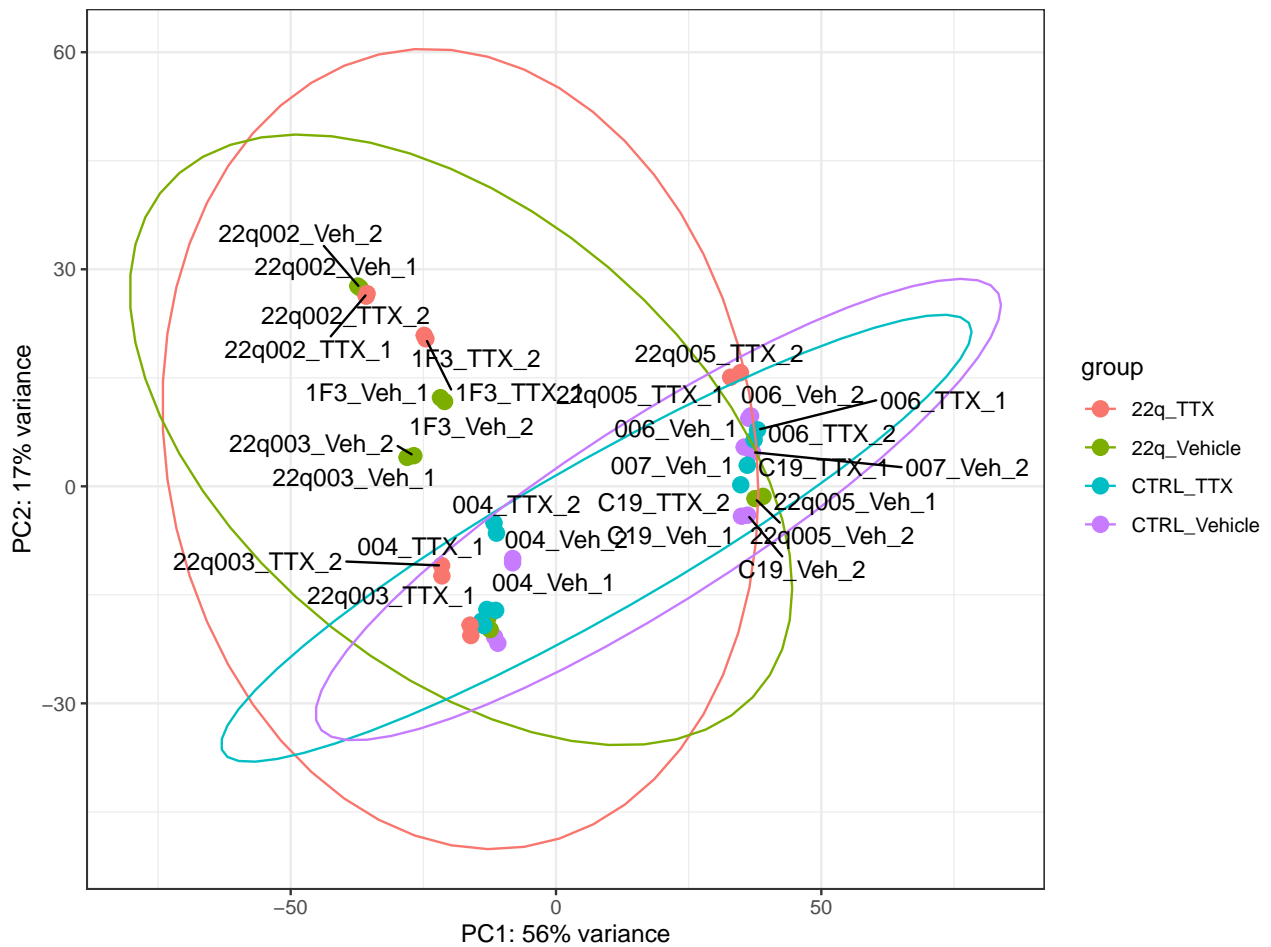
(1) Sample information Heatmap



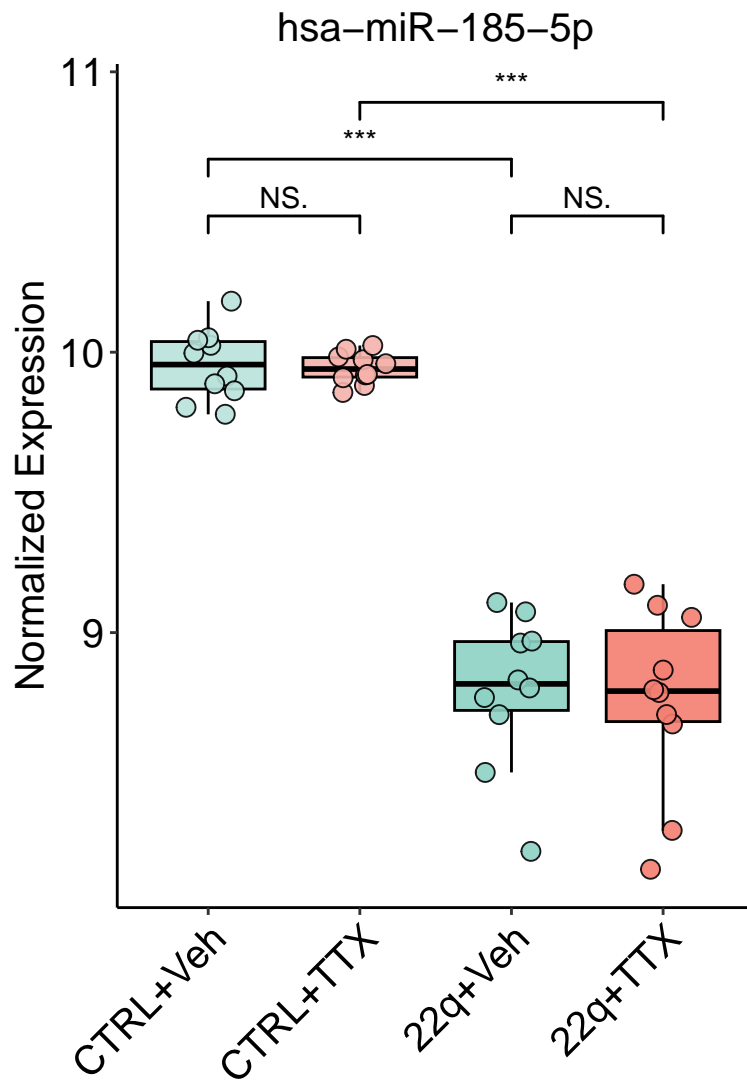
```
## [1] "Sample distance heatmap is done"
```

(2) Sample information PCA plot

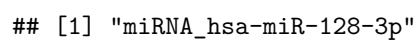
```
## [1] "PCA plot is done"
```

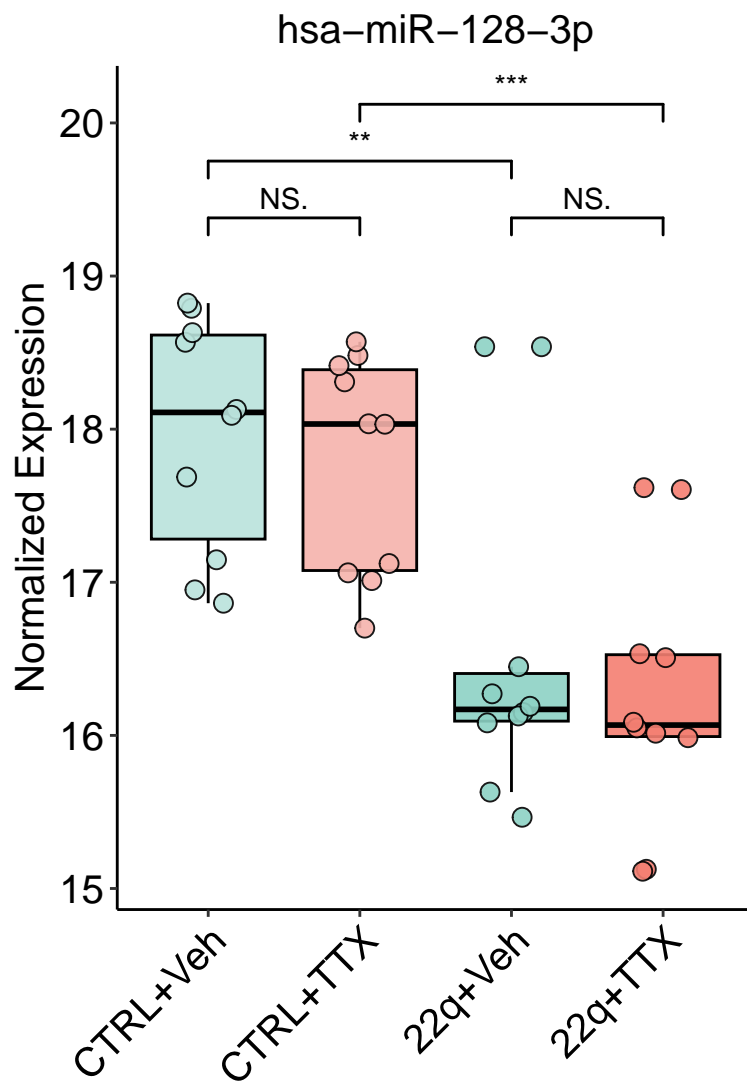


[1] "miRNA_hsa-miR-185-5p"

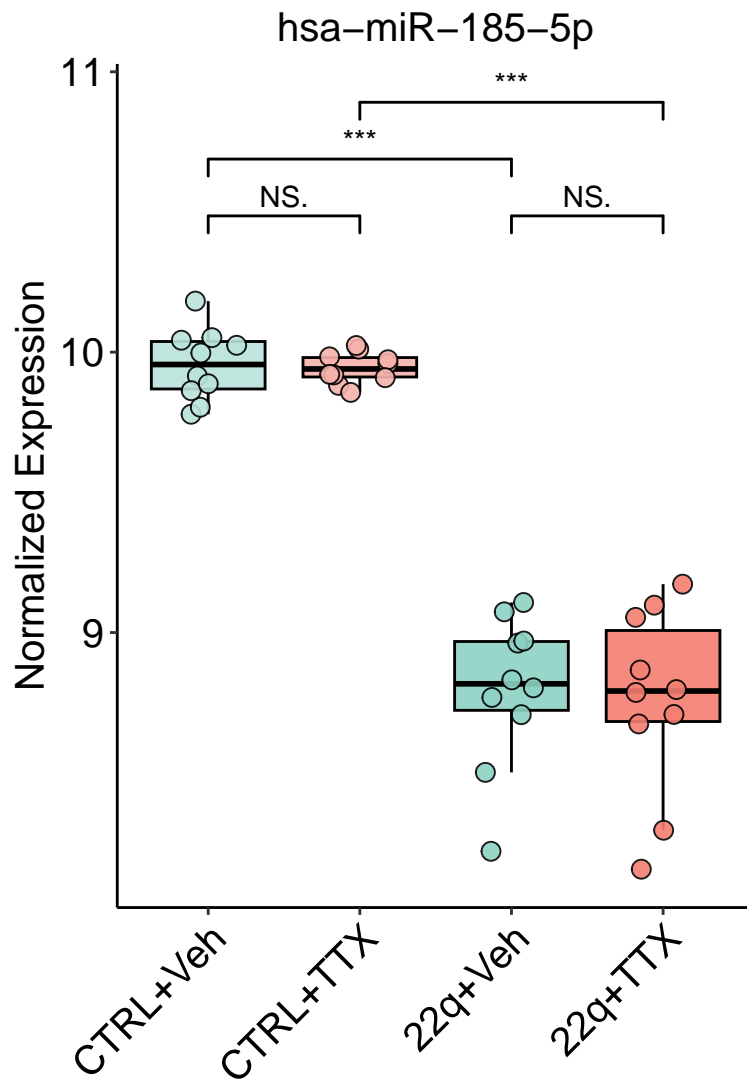


[1] "miRNA_hsa-miR-214-3p"

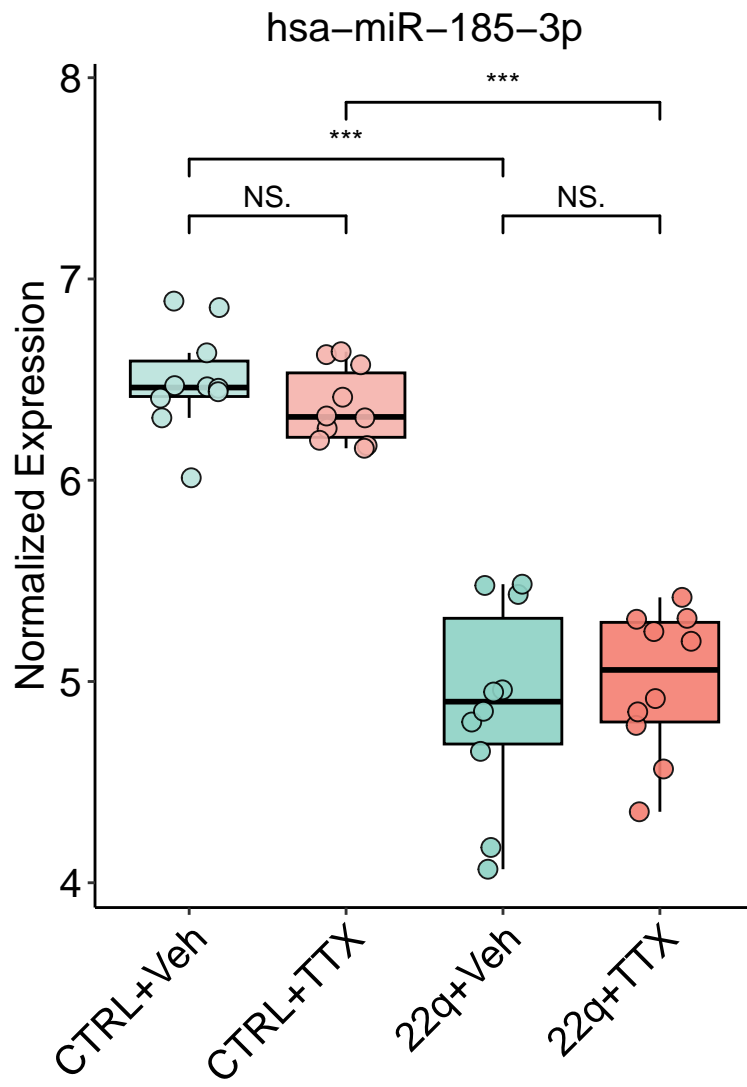




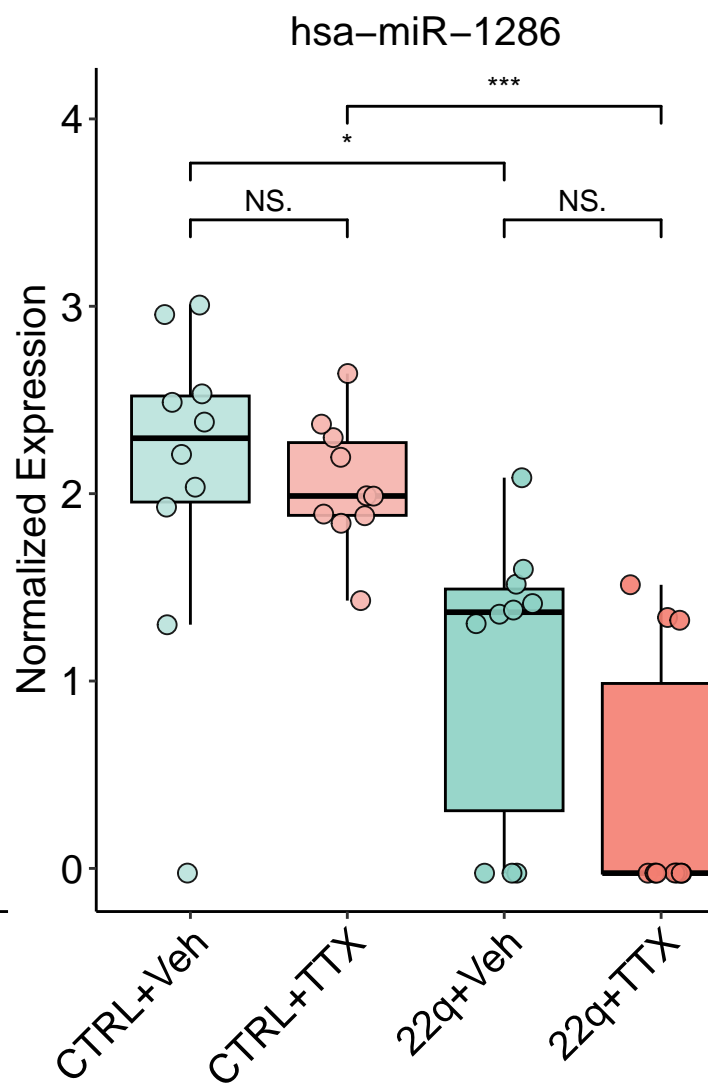
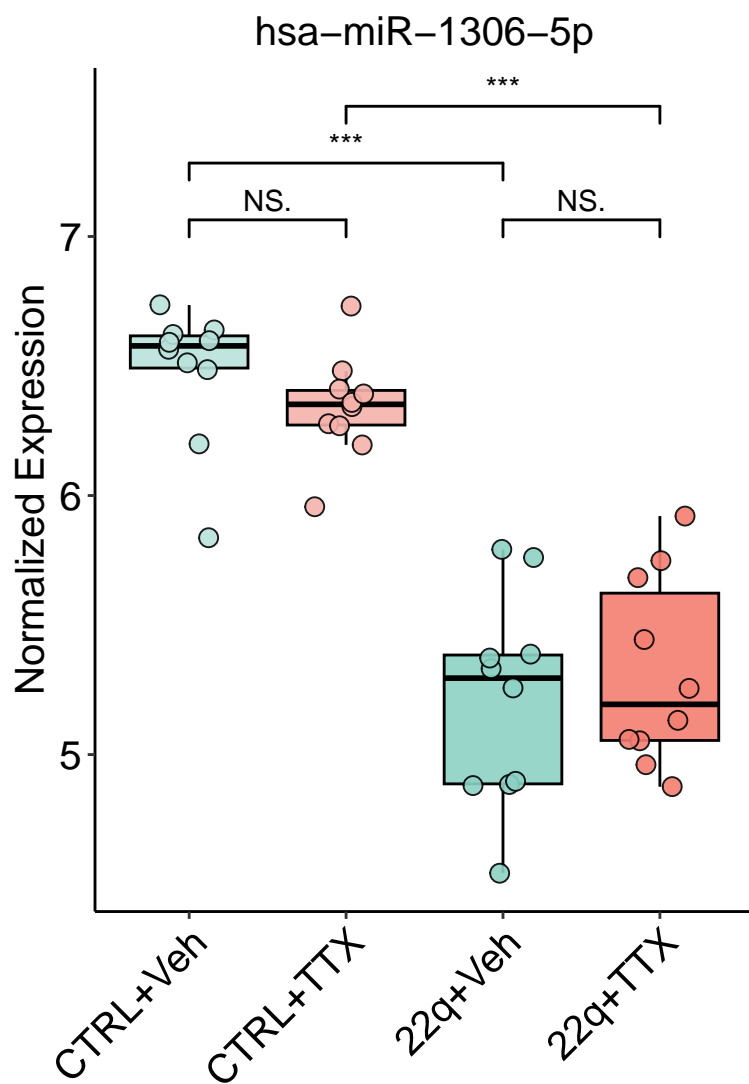
[1] "miRNA_hsa-miR-185-5p"



[1] "miRNA_hsa-miR-185-3p"



[1] "miRNA_hsa-miR-1306-5p"



[1] "miRNA_hsa-miR-1286"

Session information

```
## R version 4.4.0 (2024-04-24)
## Platform: aarch64-apple-darwin20
## Running under: macOS Sonoma 14.3.1
##
## 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] 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_1.16.4 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_1.7-2
## [33] Signac_1.14.0 Seurat_5.2.1
## [35] SeuratObject_5.0.2 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_1.49 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_3.5.1
## [53] tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
## [1] SpatialExperiment_1.14.0 R.methodsS3_1.8.2
## [3] progress_1.2.3 goftest_1.2-3
## [5] HDF5Array_1.32.1 Biostrings_2.72.1
## [7] vctrs_0.6.5 spatstat.random_3.3-2
```

## [9] digest_0.6.37	png_0.1-8
## [11] deldir_2.0-4	parallelly_1.42.0
## [13] magick_2.8.5	MASS_7.3-64
## [15] httpuv_1.6.15	qvalue_2.36.0
## [17] withr_3.0.2	xfun_0.51
## [19] ggfun_0.1.8	survival_3.8-3
## [21] memoise_2.0.1	gson_0.1.0
## [23] systemfonts_1.2.1	ragg_1.3.3
## [25] tidytree_0.4.6	zoo_1.8-12
## [27] pbapply_1.7-2	R.oo_1.27.0
## [29] prettyunits_1.2.0	KEGGREST_1.44.1
## [31] promises_1.3.2	httr_1.4.7
## [33] restfulr_0.0.15	rhdf5filters_1.16.0
## [35] globals_0.16.3	fitdistrplus_1.2-2
## [37] rhdf5_2.48.0	rstudioapi_0.17.1
## [39] UCSC.utils_1.0.0	miniUI_0.1.1.1
## [41] generics_0.1.3	DOSE_3.30.5
## [43] curl_6.2.1	zlibbioc_1.50.0
## [45] ScaledMatrix_1.12.0	ggraph_2.2.1
## [47] polyclip_1.10-7	GenomeInfoDbData_1.2.12
## [49] SparseArray_1.4.8	xtable_1.8-4
## [51] evaluate_1.0.3	S4Arrays_1.4.1
## [53] BiocFileCache_2.12.0	hms_1.1.3
## [55] irlba_2.3.5.1	colorspace_2.1-1
## [57] filelock_1.0.3	ROCR_1.0-11
## [59] reticulate_1.40.0	spatstat.data_3.1-4
## [61] magrittr_2.0.3	lmtest_0.9-40
## [63] later_1.4.1	viridis_0.6.5
## [65] ggtree_3.12.0	lattice_0.22-6
## [67] spatstat.geom_3.3-5	future.apply_1.11.3
## [69] scattermore_1.2	shadowtext_0.1.4
## [71] cowplot_1.1.3	RcppAnnoy_0.0.22
## [73] pillar_1.10.1	nlme_3.1-167
## [75] compiler_4.4.0	beachmat_2.20.0
## [77] RSpectra_0.16-2	stringi_1.8.4
## [79] tensor_1.5	GenomicAlignments_1.40.0
## [81] plyr_1.8.9	crayon_1.5.3
## [83] abind_1.4-8	BiocIO_1.14.0
## [85] gridGraphics_0.5-1	emdbbook_1.3.13
## [87] locfit_1.5-9.11	graphlayouts_1.2.2
## [89] bit_4.5.0.1	fastmatch_1.1-6
## [91] textshaping_1.0.0	codetools_0.2-20
## [93] BiocSingular_1.20.0	plotly_4.10.4
## [95] mime_0.12	splines_4.4.0
## [97] Rcpp_1.0.14	fastDummies_1.7.5
## [99] sparseMatrixStats_1.16.0	dbplyr_2.5.0
## [101] Rttf2pt1_1.3.12	blob_1.2.4
## [103] here_1.0.1	fs_1.6.5
## [105] listenv_0.9.1	ggplotify_0.1.2
## [107] statmod_1.5.0	tzdb_0.4.0
## [109] tweenr_2.0.3	pkgconfig_2.0.3
## [111] tools_4.4.0	cachem_1.1.0
## [113] RSQLite_2.3.9	viridisLite_0.4.2
## [115] DBI_1.2.3	numDeriv_2016.8-1.1

## [117] fastmap_1.2.0	rmarkdown_2.29
## [119] scales_1.3.0	grid_4.4.0
## [121] ica_1.0-3	Rsamtools_2.20.0
## [123] coda_0.19-4.1	dotCall64_1.2
## [125] RANN_2.6.2	farver_2.1.2
## [127] tidygraph_1.3.1	scatterpie_0.2.4
## [129] yaml_2.3.10	cli_3.6.4
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## [137] gggridges_0.5.6	progressr_0.15.1
## [139] ape_5.8-1	jsonlite_1.9.0
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## [151] lazyeval_0.2.2	shiny_1.10.0
## [153] htmltools_0.5.8.1	enrichplot_1.24.4
## [155] GO.db_3.19.1	sctransform_0.4.1
## [157] rappdirs_0.3.3	tinytex_0.55
## [159] glue_1.8.0	spam_2.11-1
## [161] httr2_1.1.0	XVector_0.44.0
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## [165] treeio_1.28.0	gridExtra_2.3
## [167] extrafontdb_1.0	igraph_2.1.4
## [169] R6_2.6.1	SingleCellExperiment_1.26.0
## [171] labeling_0.4.3	RcppRoll_0.3.1
## [173] cluster_2.1.8	bbmle_1.0.25.1
## [175] Rhdf5lib_1.26.0	aplot_0.2.4
## [177] DelayedArray_0.30.1	tidyselect_1.2.1
## [179] ggforce_0.4.2	xml2_1.3.6
## [181] future_1.34.0	rsvd_1.0.5
## [183] munsell_0.5.1	KernSmooth_2.23-26
## [185] htmlwidgets_1.6.4	fgsea_1.30.0
## [187] rlang_1.1.5	spatstat.sparse_3.1-0
## [189] spatstat.explore_3.3-4	