

GSVA analysis for mutil Group

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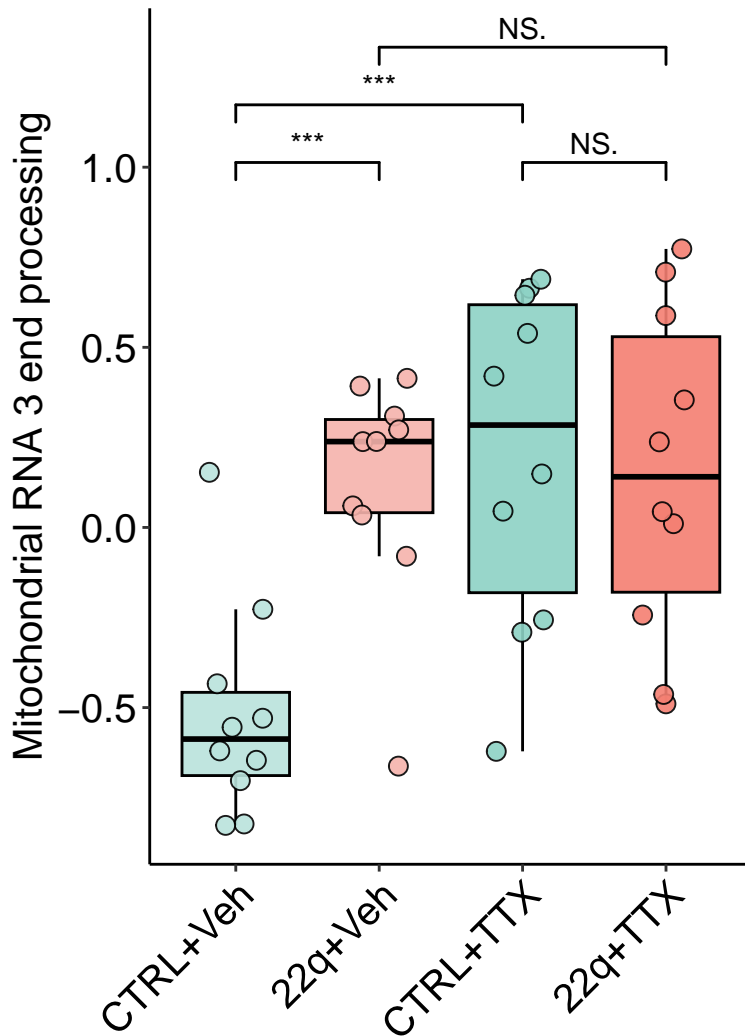
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1. Read the count data

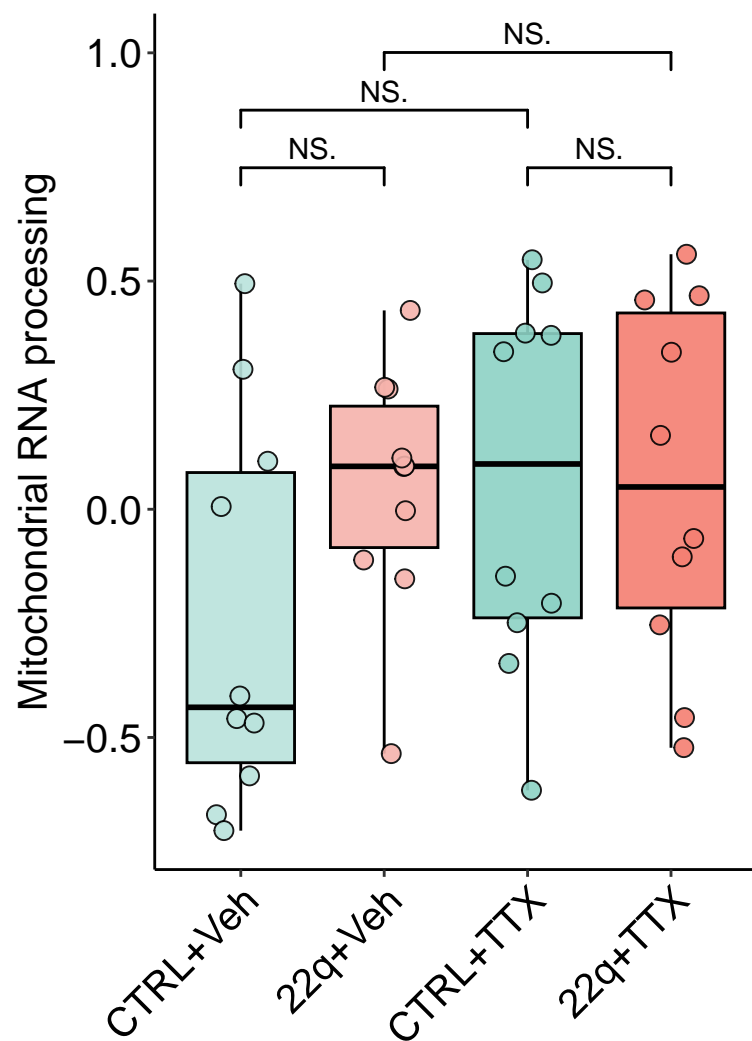
In this section, we will read the clean count data from the `synaptosomes_bulkRNA` folder. We will read the data and merge them into a single table. The final table will be stored in `results/02-DEG-Vehicle/synaptosomes_bulkRNA_counts`.

2. GSVA analysis

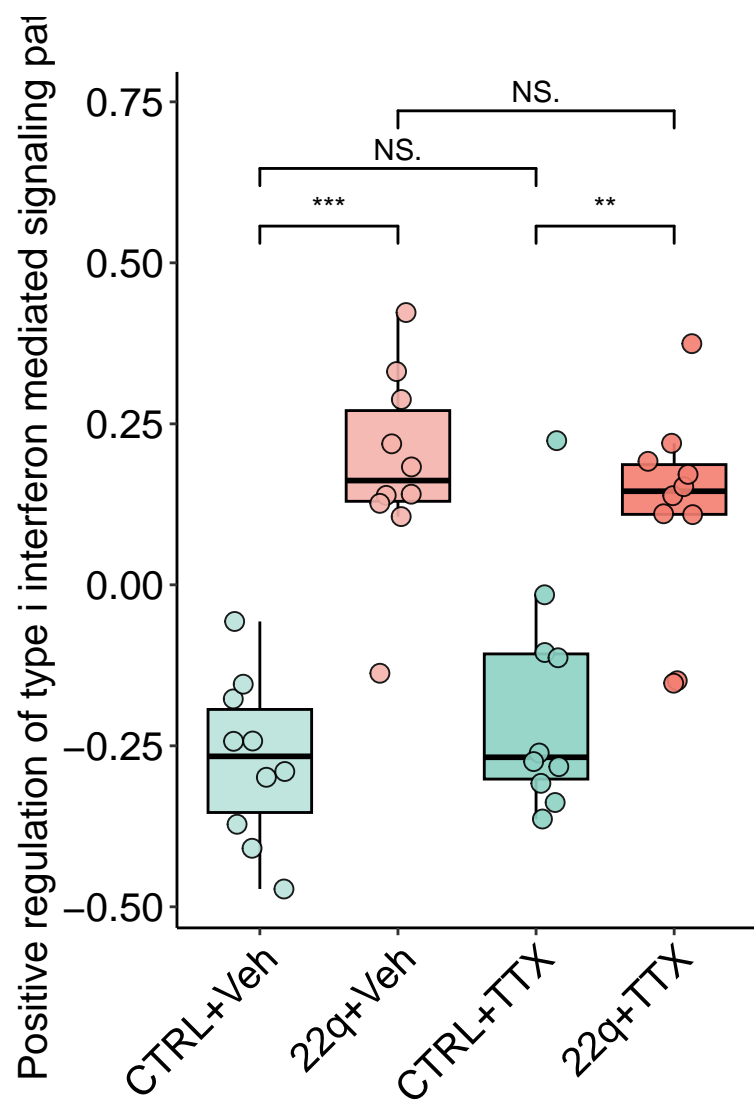
```
## [1] "GOBP_MITOCHONDRIAL_RNA_3_END_PROCESSING"
```



```
## [1] "GOBP_MITOCHONDRIAL_RNA_PROCESSING"
```



[1] "GOBP_POSITIVE_REGULATION_OF_TYPE_I_INTERFERON_MEDIATED_SIGNALING_PATHWAY"



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] tidytree_0.4.6	zoo_1.8-12
## [25] pbapply_1.7-2	R.oo_1.27.0
## [27] prettyunits_1.2.0	KEGGREST_1.44.1
## [29] promises_1.3.2	httr_1.4.7
## [31] restfulr_0.0.15	rhdf5filters_1.16.0
## [33] globals_0.16.3	fitdistrplus_1.2-2
## [35] rhdf5_2.48.0	rstudioapi_0.17.1
## [37] UCSC.utils_1.0.0	miniUI_0.1.1.1
## [39] generics_0.1.3	DOSE_3.30.5
## [41] curl_6.2.1	zlibbioc_1.50.0
## [43] ScaledMatrix_1.12.0	ggraph_2.2.1
## [45] polyclip_1.10-7	GenomeInfoDbData_1.2.12
## [47] SparseArray_1.4.8	xtable_1.8-4
## [49] evaluate_1.0.3	S4Arrays_1.4.1
## [51] BiocFileCache_2.12.0	hms_1.1.3
## [53] irlba_2.3.5.1	colorspace_2.1-1
## [55] filelock_1.0.3	ROCR_1.0-11
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## [63] ggtree_3.12.0	lattice_0.22-6
## [65] spatstat.geom_3.3-5	future.apply_1.11.3
## [67] scattermore_1.2	shadowtext_0.1.4
## [69] cowplot_1.1.3	RcppAnnoy_0.0.22
## [71] pillar_1.10.1	nlme_3.1-167
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## [81] abind_1.4-8	BiocIO_1.14.0
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## [85] locfit_1.5-9.11	graphlayouts_1.2.2
## [87] bit_4.5.0.1	fastmatch_1.1-6
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## [99] blob_1.2.4	here_1.0.1
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