GSVA for mutil Group

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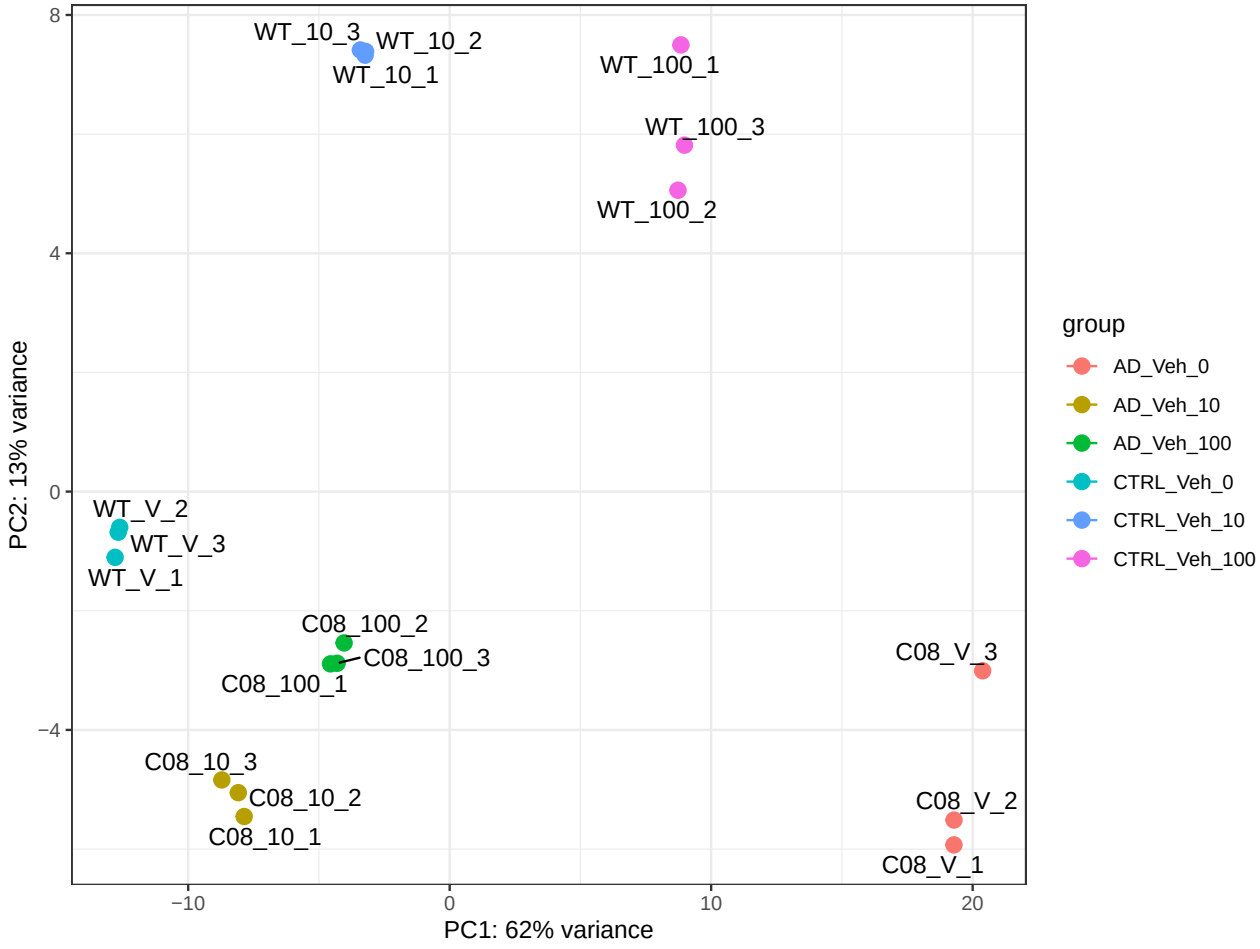
Contents

1. Read the count data

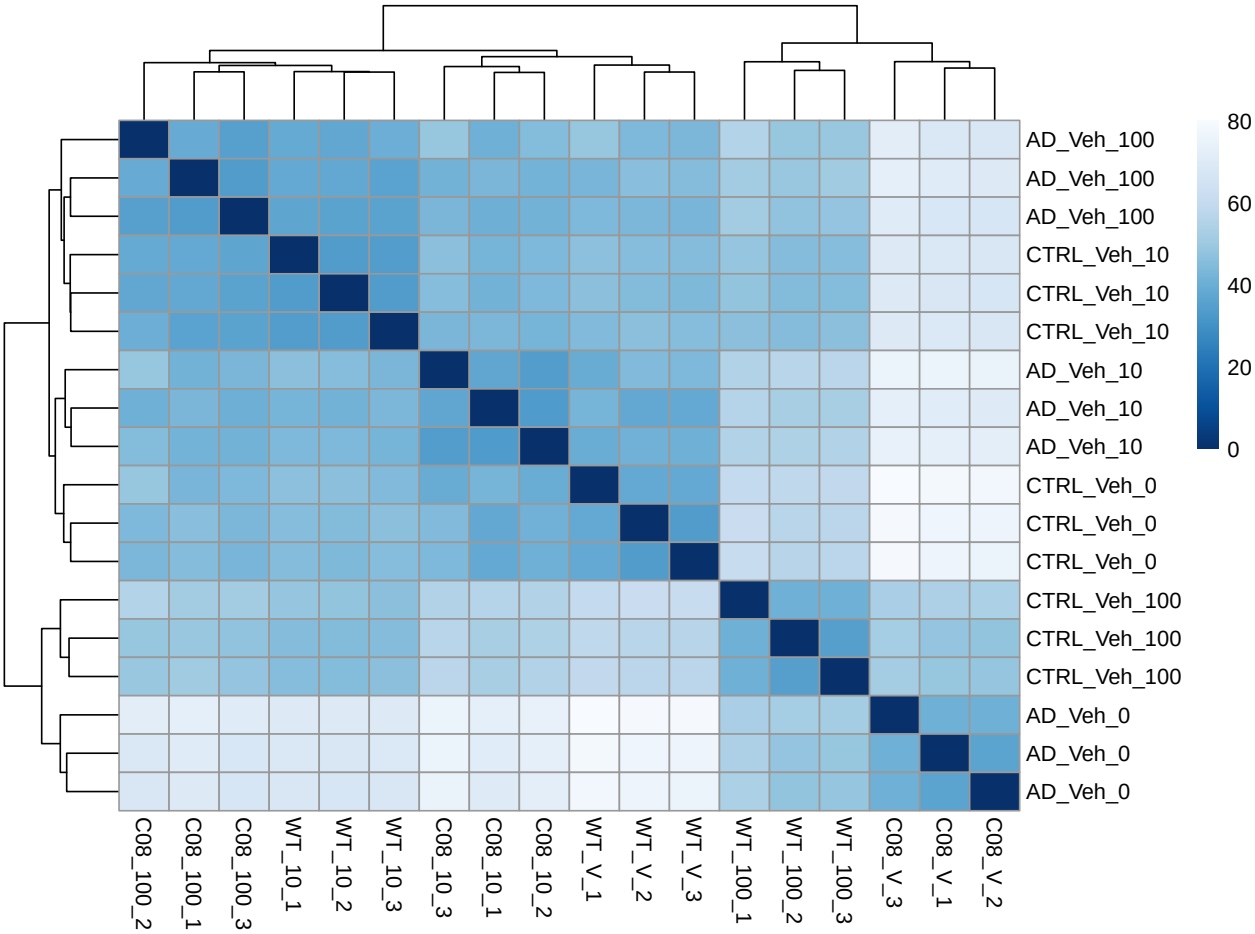
In this section, we will read the clean count data from the synaptosomes_bulkRNA folder. We will read the data and merge them into a single table.

2. Visualization for reuslt

(1) Sample information - PCA plot



(2) Sample information - Distance heatmap



3. GSVA analysis

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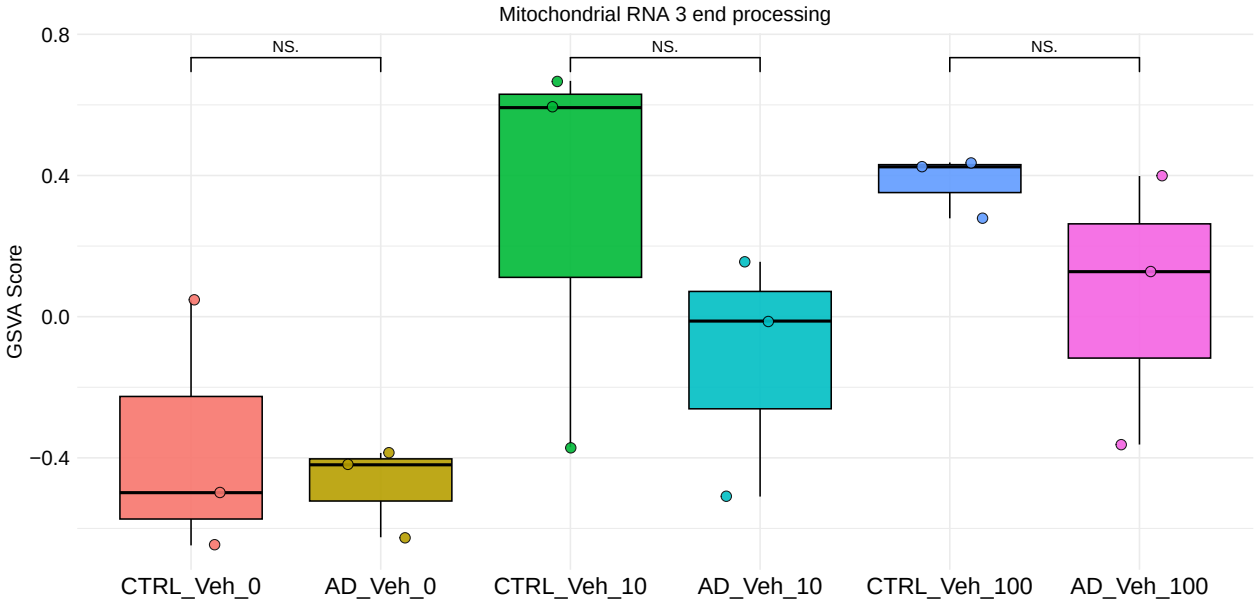
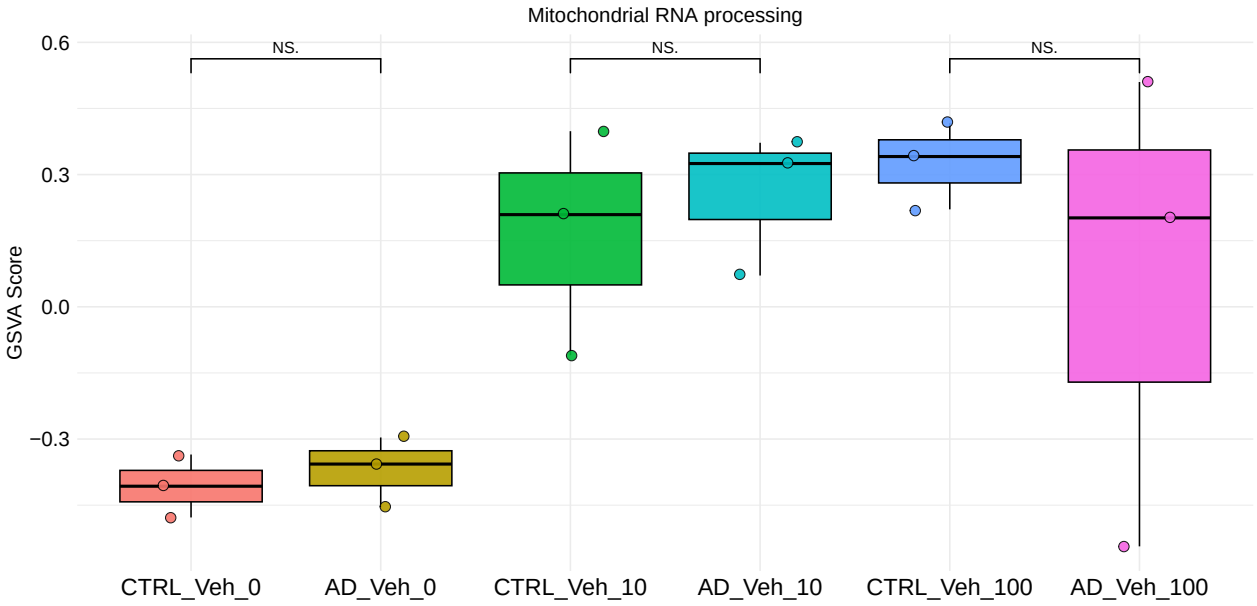
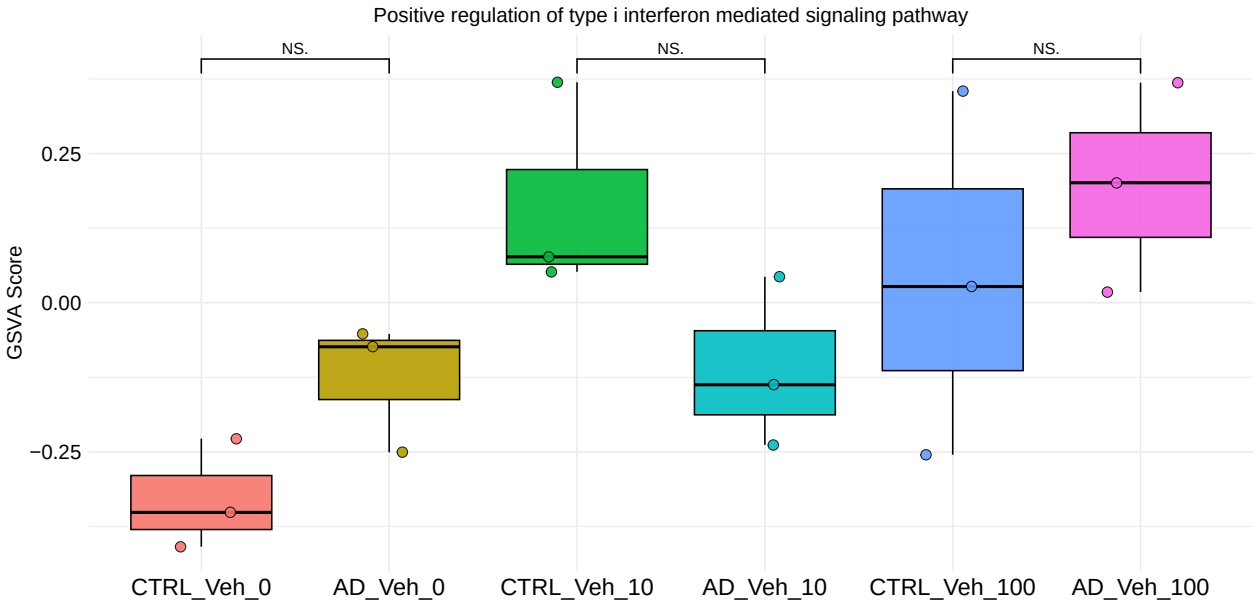



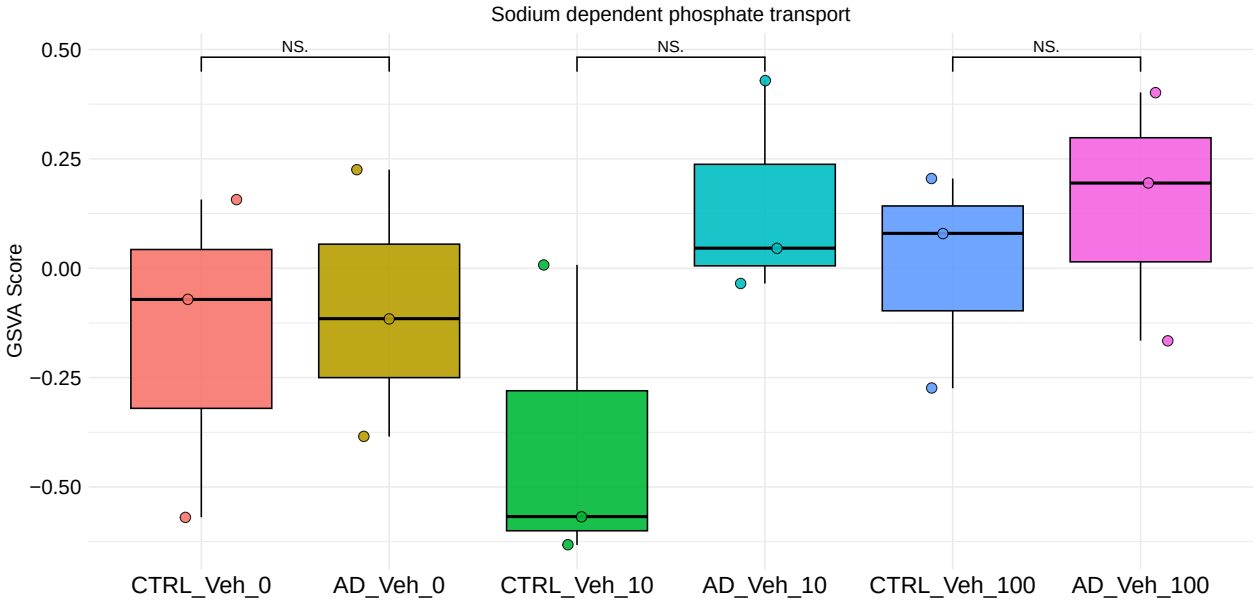

```
## [1] "GOBP_POSITIVE_REGULATION_OF_TYPE_I_INTERFERON_MEDIATED_SIGNALING_PATHWAY"
```



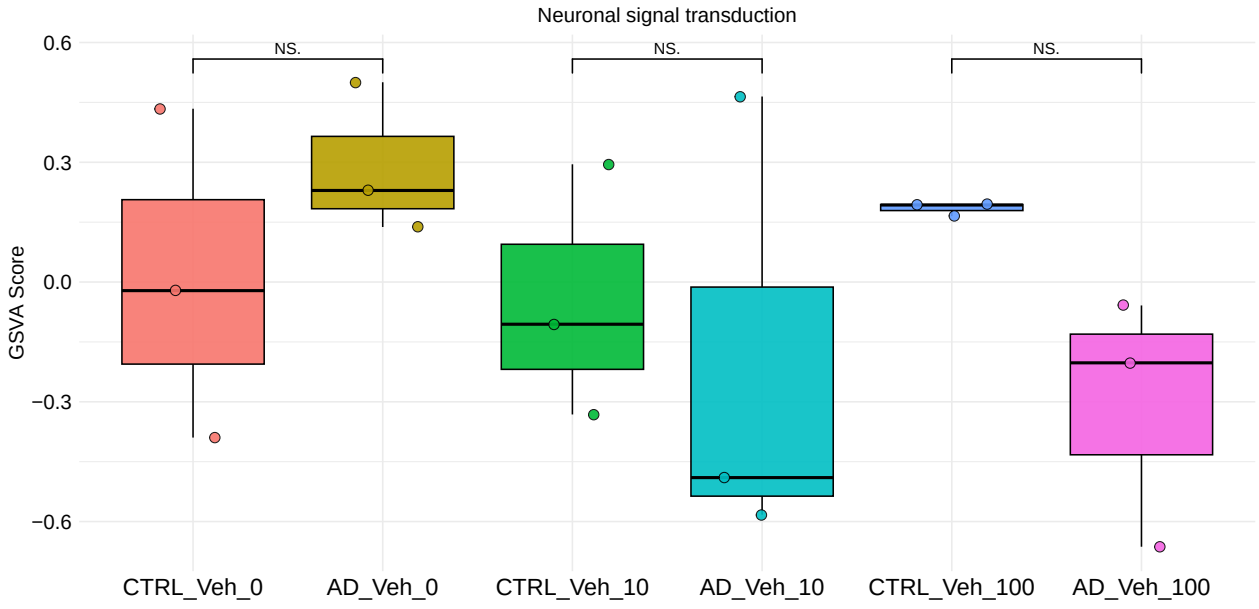

```
## [1] "GOBP_SODIUM_DEPENDENT_PHOSPHATE_TRANSPORT"
```



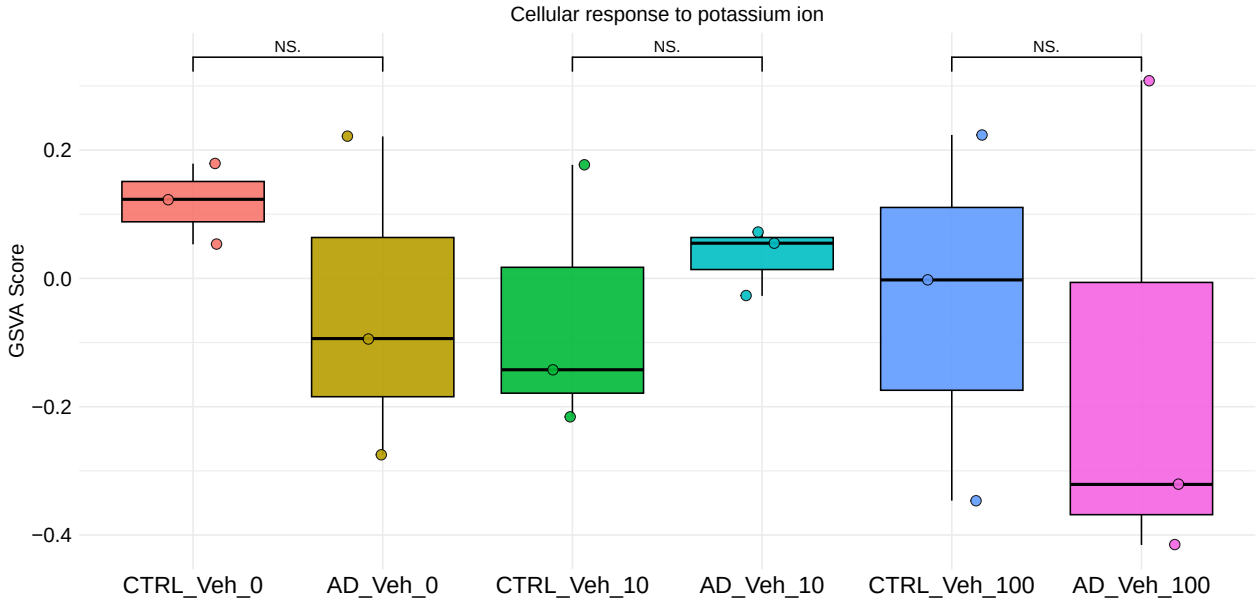

```
## [1] "GOBP_NEURONAL_SIGNAL_TRANSDUCTION"
```



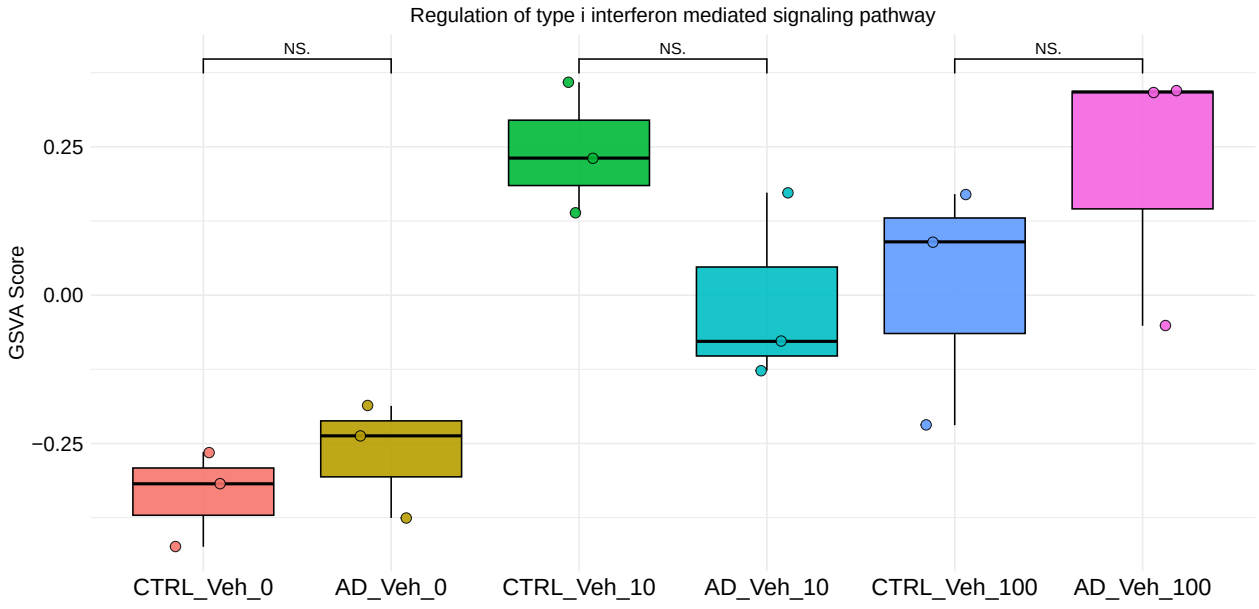

```
## [1] "GOBP_CELLULAR_RESPONSE_TO_POTASSIUM_ION"
```



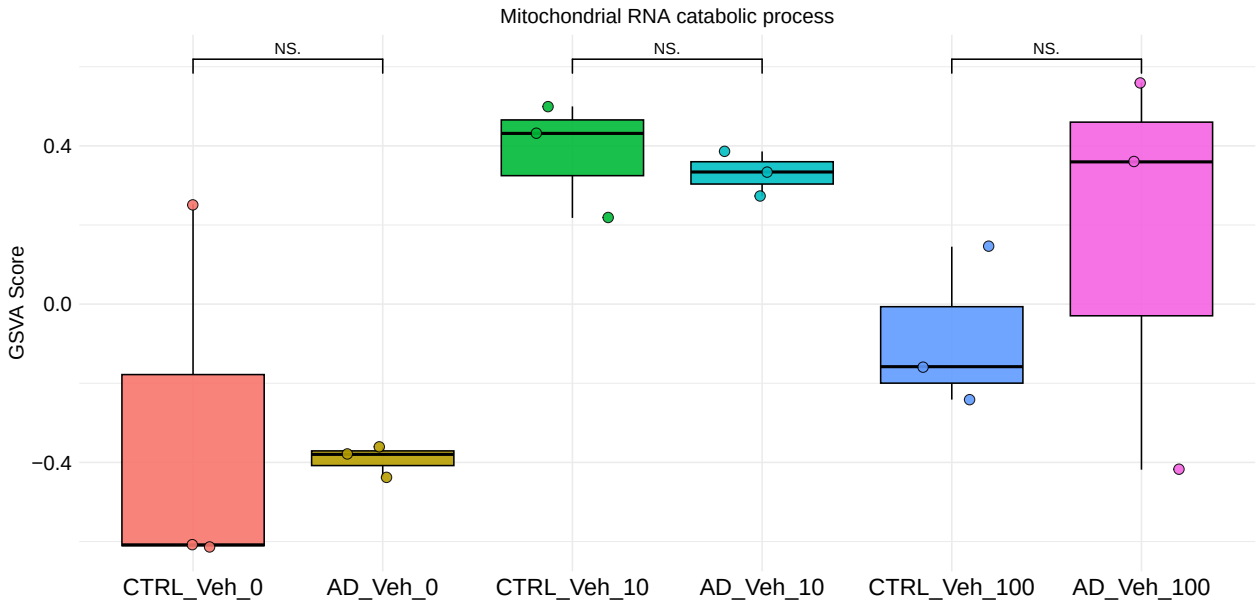

```
## [1] "GOBP_REGULATION_OF_TYPE_I_INTERFERON_MEDIATED_SIGNALING_PATHWAY"
```



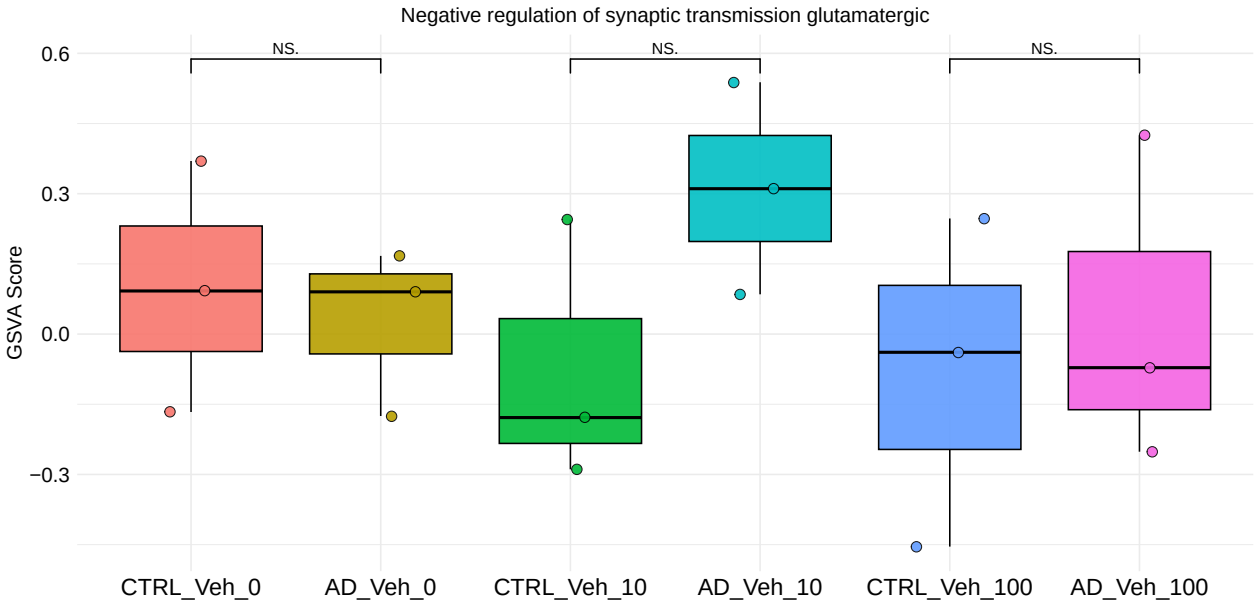

```
## [1] "GOBP_MITOCHONDRIAL_RNA_CATABOLIC_PROCESS"
```



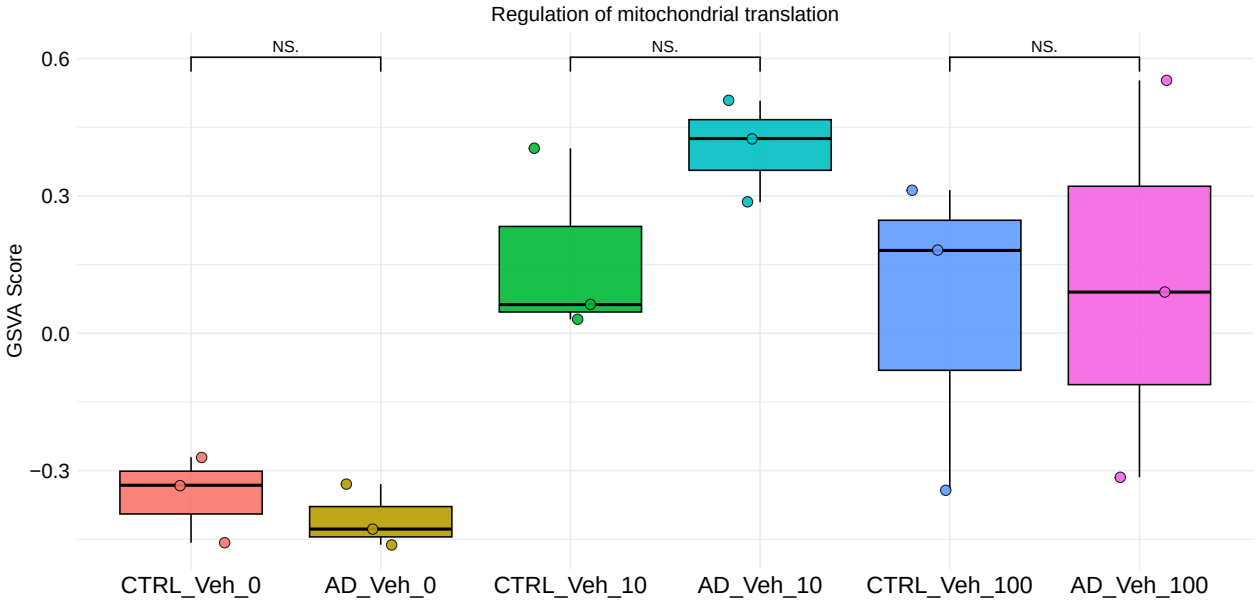

```
## [1] "GOBP_NEGATIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC"
```




```
## [1] "GOBP_REGULATION_OF_MITOCHONDRIAL_TRANSLATION"
```




```
## [1] "GOBP_NEGATIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION"
```

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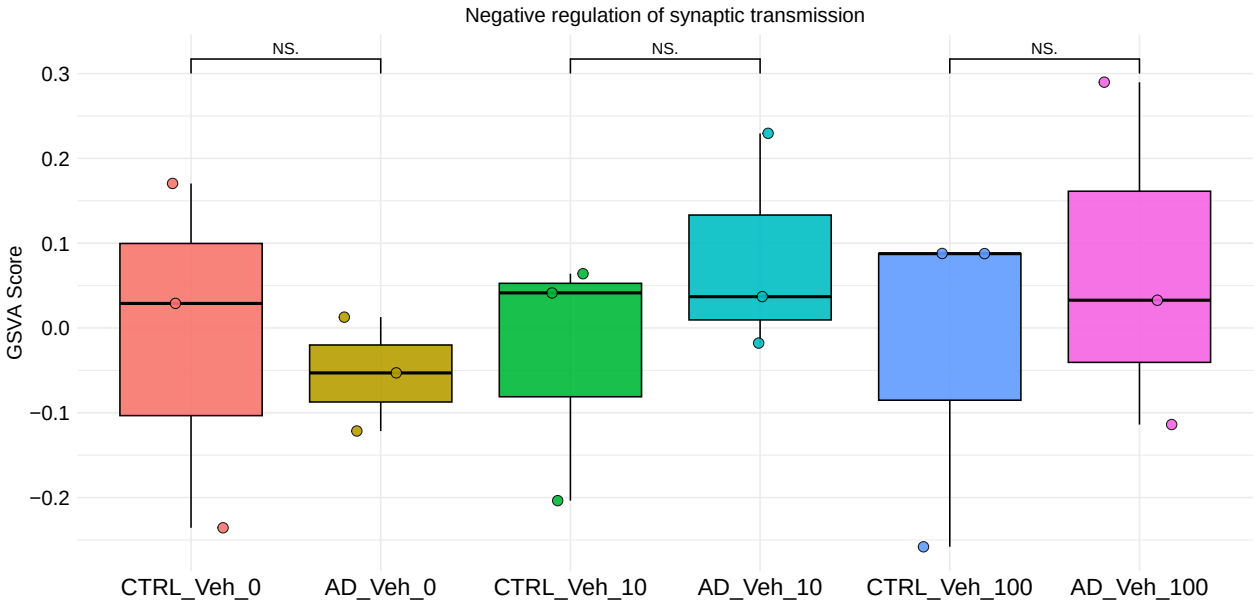
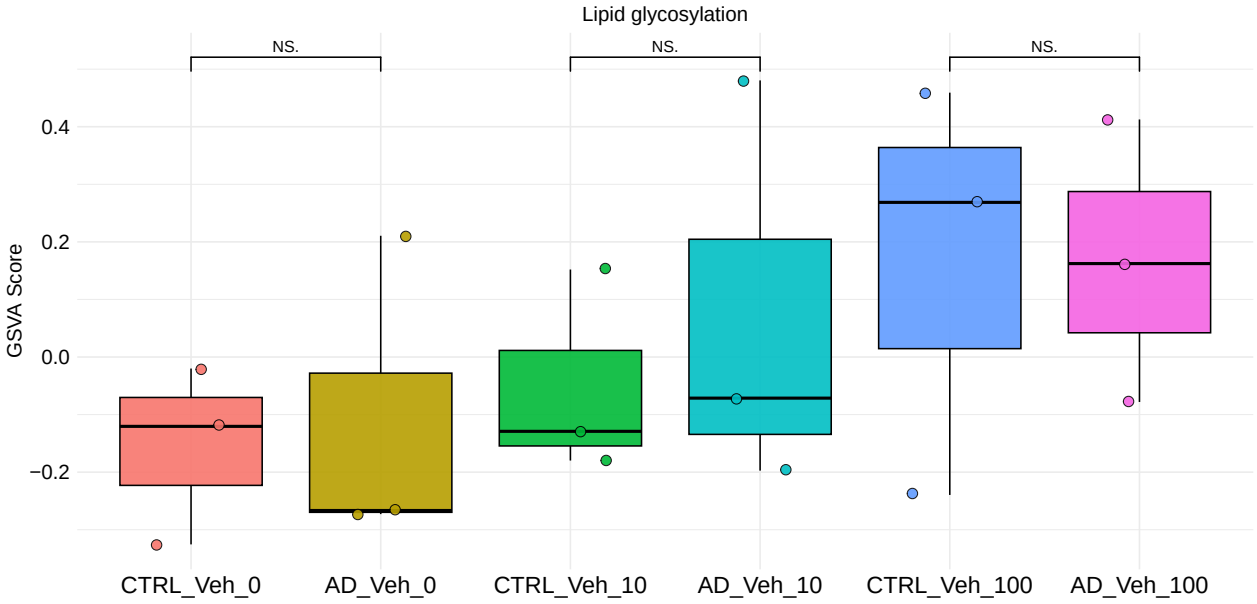
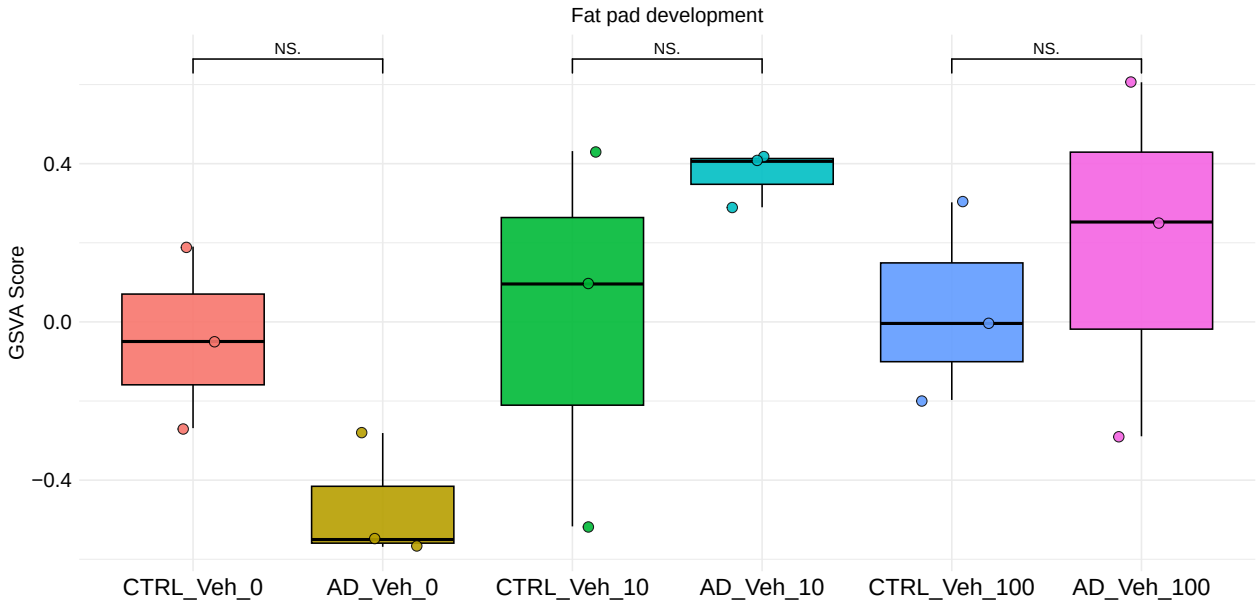
## [1] "GOBP_LIPID_GLYCOSYLATION"
```



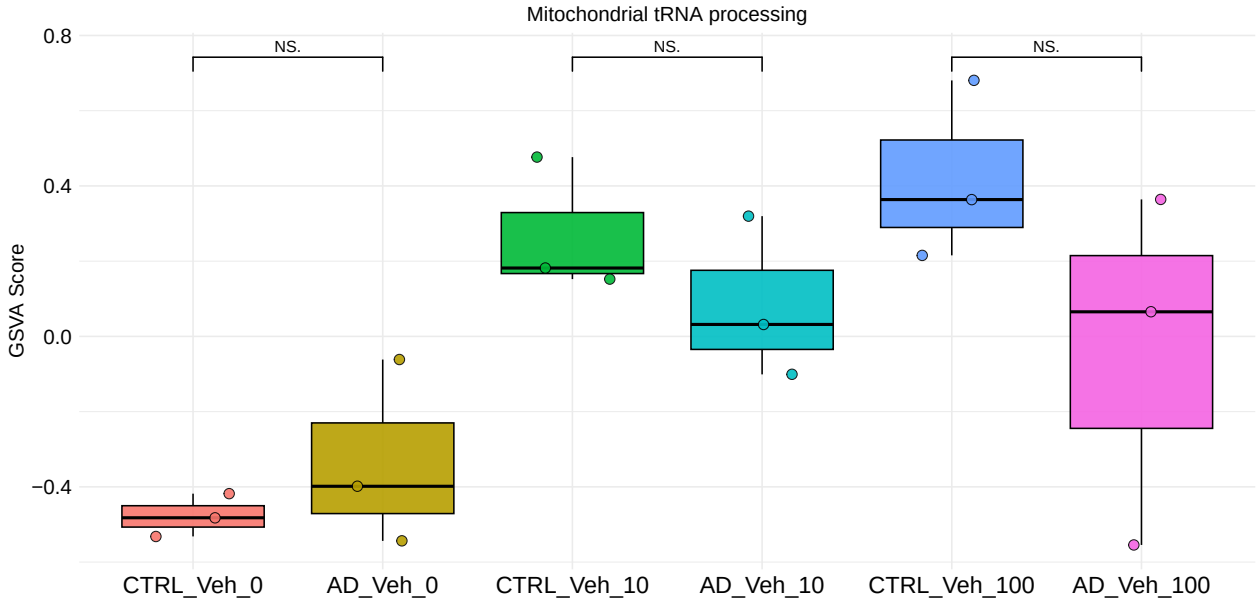

```
## [1] "GOBP_FAT_PAD_DEVELOPMENT"
```



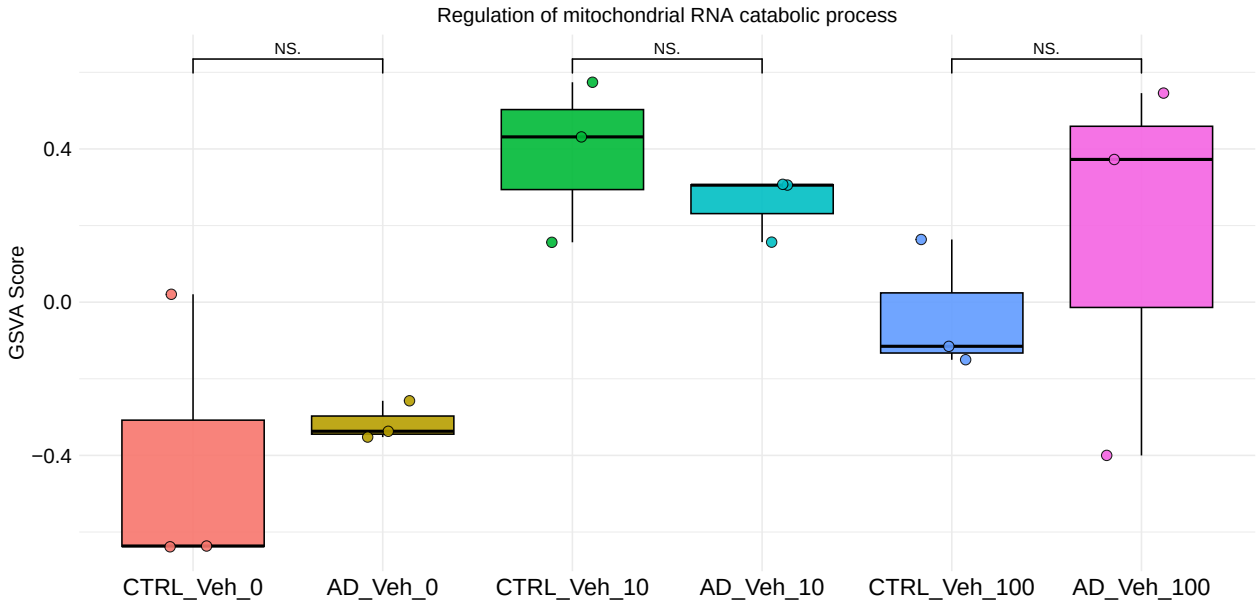

```
## [1] "GOBP_MITOCHONDRIAL_TRNA_PROCESSING"
```



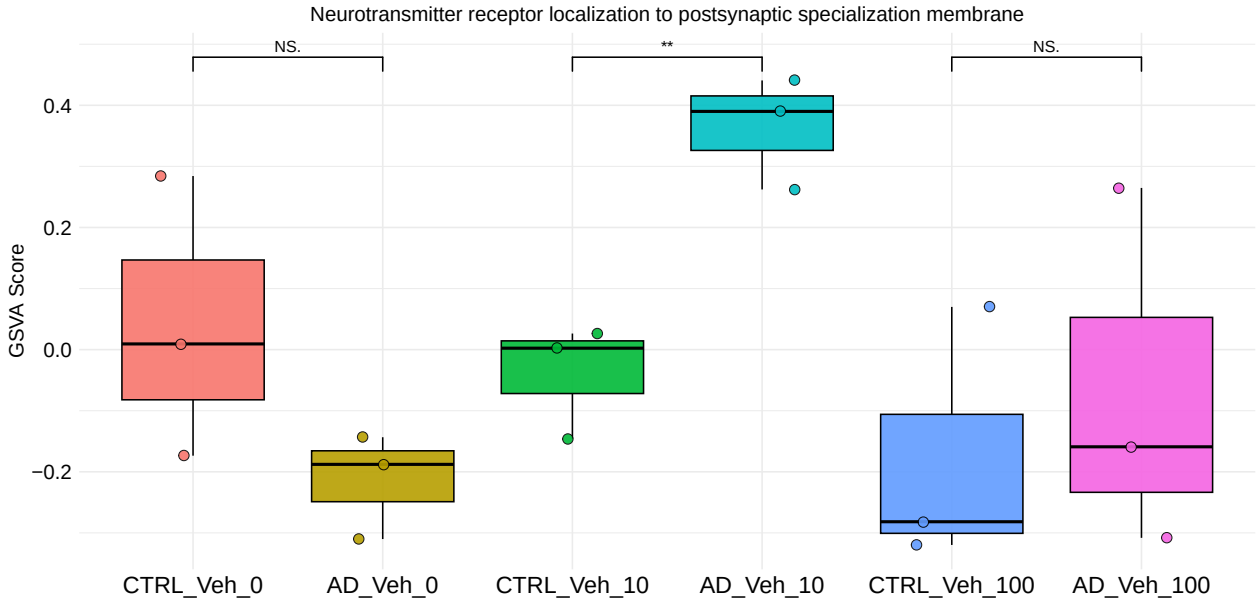

```
## [1] "GOBP_REGULATION_OF_MITOCHONDRIAL_RNA_CATABOLIC_PROCESS"
```



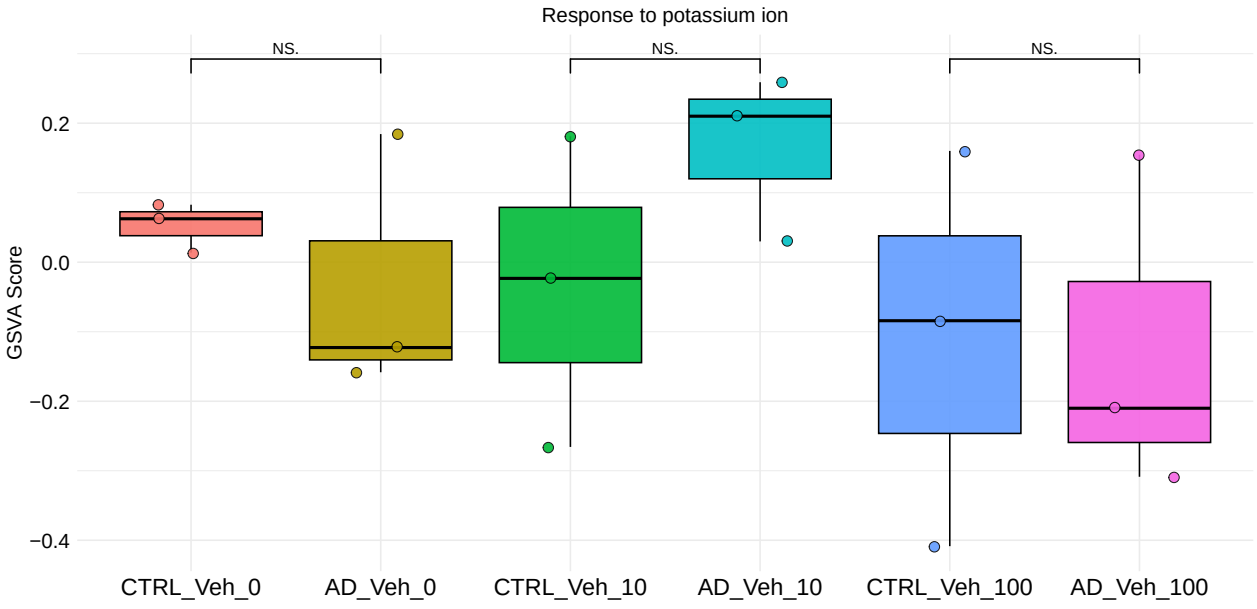

```
## [1] "GOBP_NEUROTRANSMITTER_RECEPTOR_LOCALIZATION_TO_POSTSYNAPTIC_SPECIALIZATION_MEMBRANE"
```




```
## [1] "GOBP_RESPONSE_TO_POTASSIUM_ION"
```




```
## [1] "GOBP_POSITIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC"
```




```
## [1] "GOBP_NEUROTRANSMITTER_LOADING_INTO_SYNAPTIC_VESICLE"
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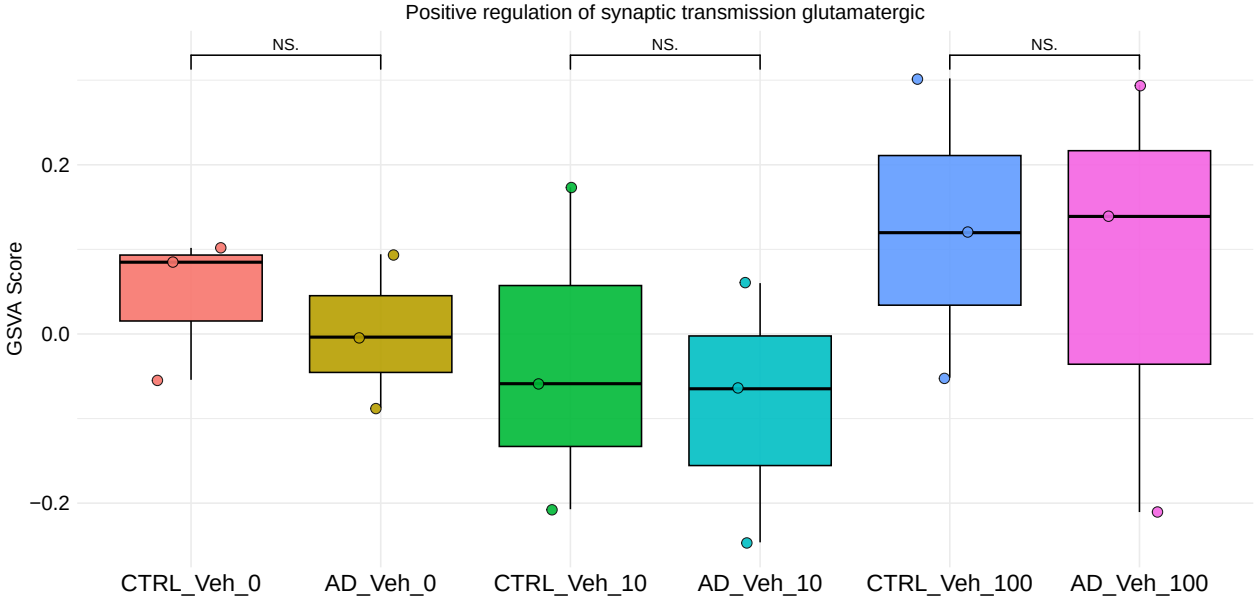
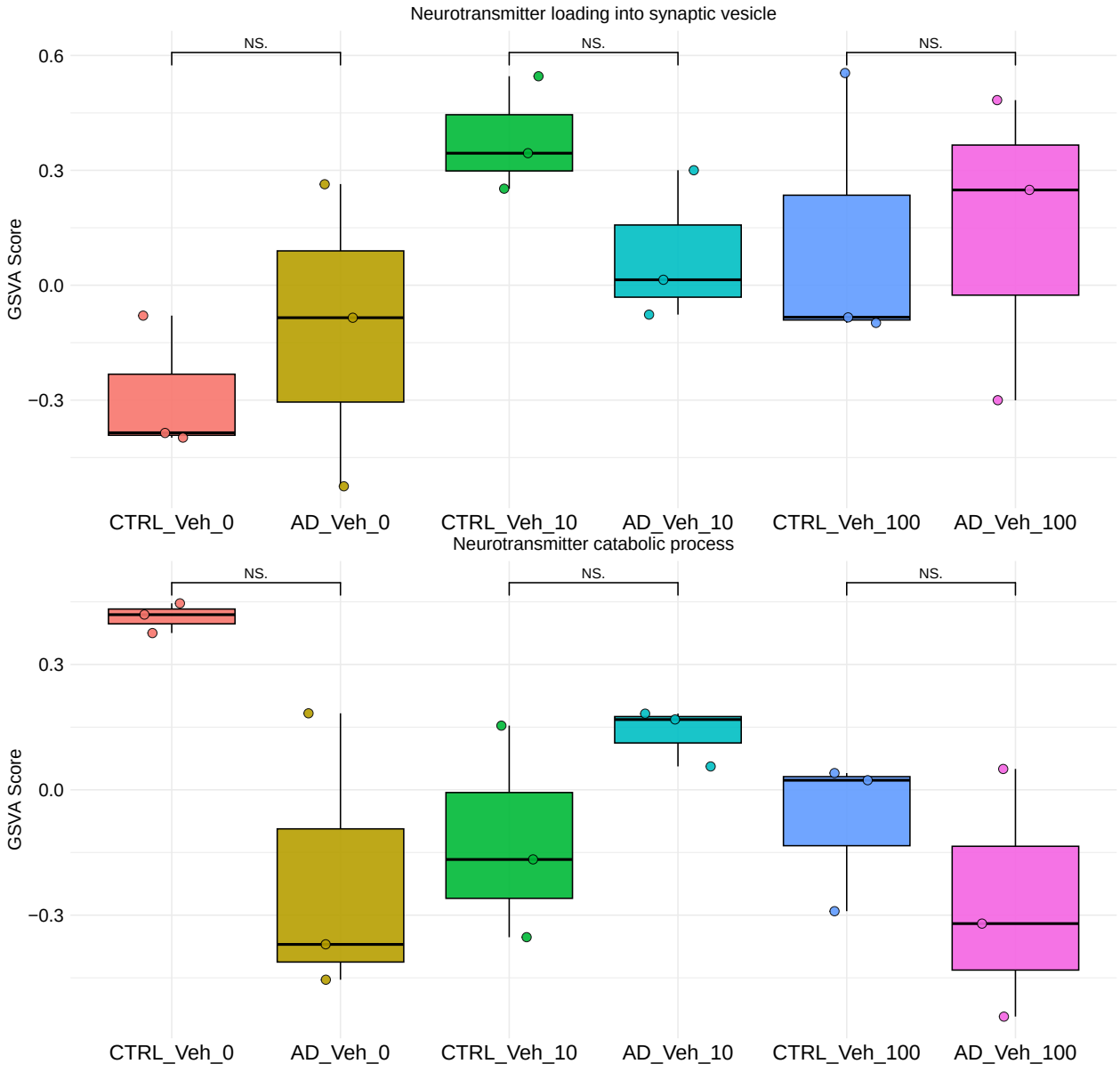



```
## [1] "GOBP_NEUROTRANSMITTER_CATABOLIC_PROCESS"
```



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
```

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##  [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         emdbook_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
## [131] lifecycle_1.0.4            uwot_0.2.2
## [133] mvtnorm_1.3-3              timechange_0.3.0
## [135] gtable_0.3.6               rjson_0.2.23
## [137] ggridges_0.5.6             progressr_0.15.1
## [139] ape_5.8-1                  jsonlite_1.9.0
## [141] RcppHNSW_0.6.0             bitops_1.0-9
## [143] bit64_4.6.0-1              Rtsne_0.17
## [145] yulab.utils_0.2.0          spatstat.utils_3.1-2
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## [147] bdsmatrix_1.3-7            GOSemSim_2.30.2
## [149] spatstat.univar_3.1-1      R.utils_2.12.3
## [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
## [163] RCurl_1.98-1.16            rprojroot_2.0.4
## [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
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