

BioDomain analysis for AD and CTRL

Ximing Ran

2025-04-25

Contents

1. BioDomain analysis	2
Load the GSVA analysis	2
2.result for C03 vs A33	2
(1) Ridge plot for GSVA score	3
(3) Rug and density plot for GSVA score	5
3.result for C09 vs A33	6
(1) Ridge plot for GSVA score	7
(3) Rug and density plot for GSVA score	9
Session information	10

1. BioDomain analysis

Load the GSVA analysis

2.result for C03 vs A33

```
## [1] FALSE

## [1] 15598      9

##   gs_exact_source gs_cat gs_subcat
## 1      GO:0000002     C5    GO:BP
## 2      GO:0000003     C5    GO:BP
## 3      GO:0000012     C5    GO:BP
## 4      GO:0000014     C5    GO:MF
## 5      GO:0000018     C5    GO:BP
## 6      GO:0000019     C5    GO:BP

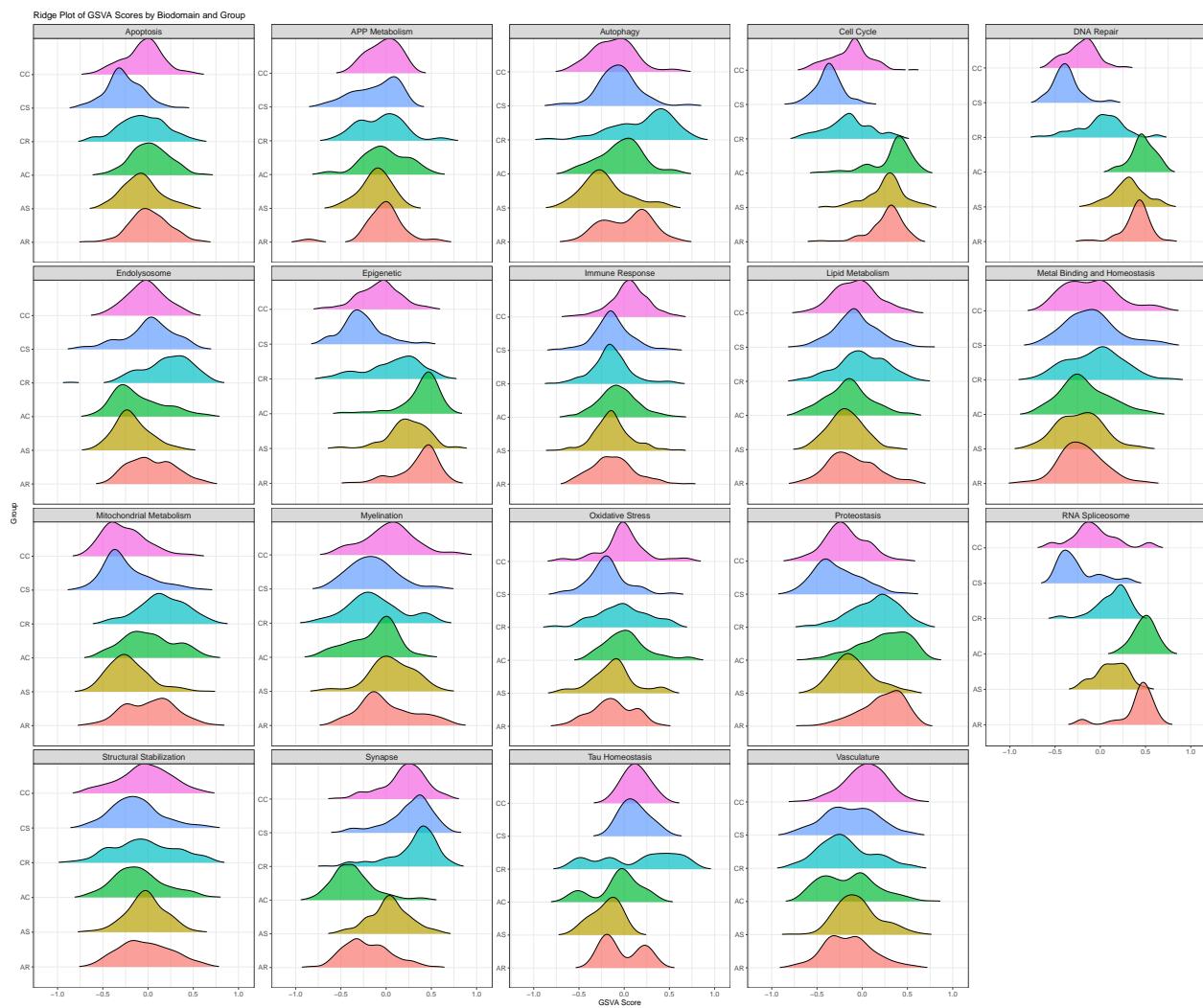
##                                     gs_name
## 1                      GOBP_MITOCHONDRIAL_GENOME_MAINTENANCE
## 2                      GOBP_REPRODUCTION
## 3          GOBP_SINGLE_STRAND_BREAK_REPAIR
## 4 GOMF_SINGLE_STRANDED_DNA_ENDODEOXYRIBONUCLEASE_ACTIVITY
## 5          GOBP_REGULATION_OF_DNA_RECOMBINATION
## 6          GOBP_REGULATION_OF_MITOTIC_RECOMBINATION

##                                     Bioboardian                               GOterm_Name
## 1 Mitochondrial Metabolism           mitochondrial genome maintenance
## 2                               <NA>                                <NA>
## 3          DNA Repair                  single strand break repair
## 4          DNA Repair single-stranded DNA endodeoxyribonuclease activity
## 5          Cell Cycle                 regulation of DNA recombination
## 6                               <NA>                                <NA>

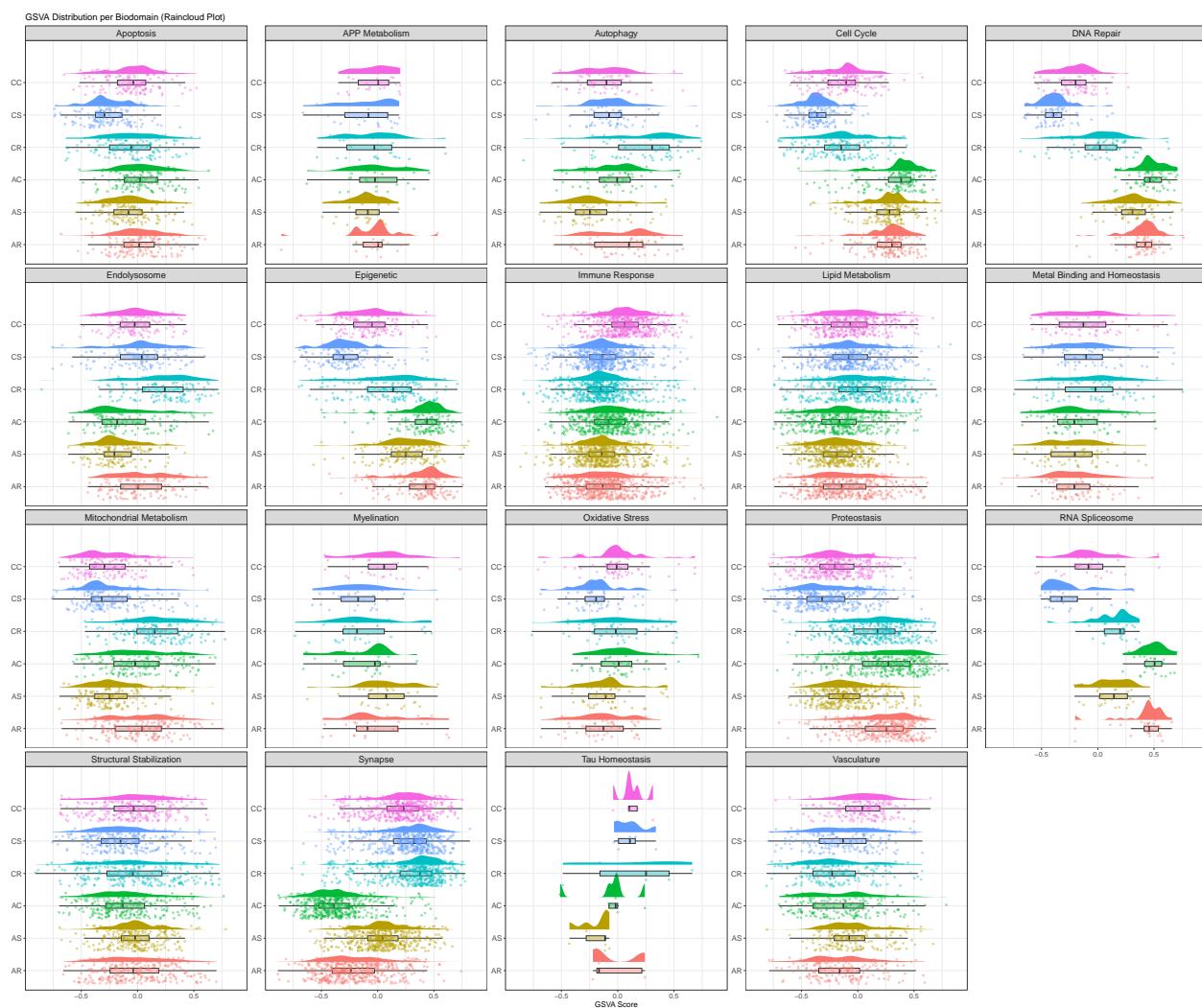
##   n_ensGene n_entrezGene n_hgncSymbol
## 1      12        11        11
## 2       NA        NA        NA
## 3      11        11        11
## 4       9         9         9
## 5       5         5         5
## 6       NA        NA        NA

## [1] 11979
```

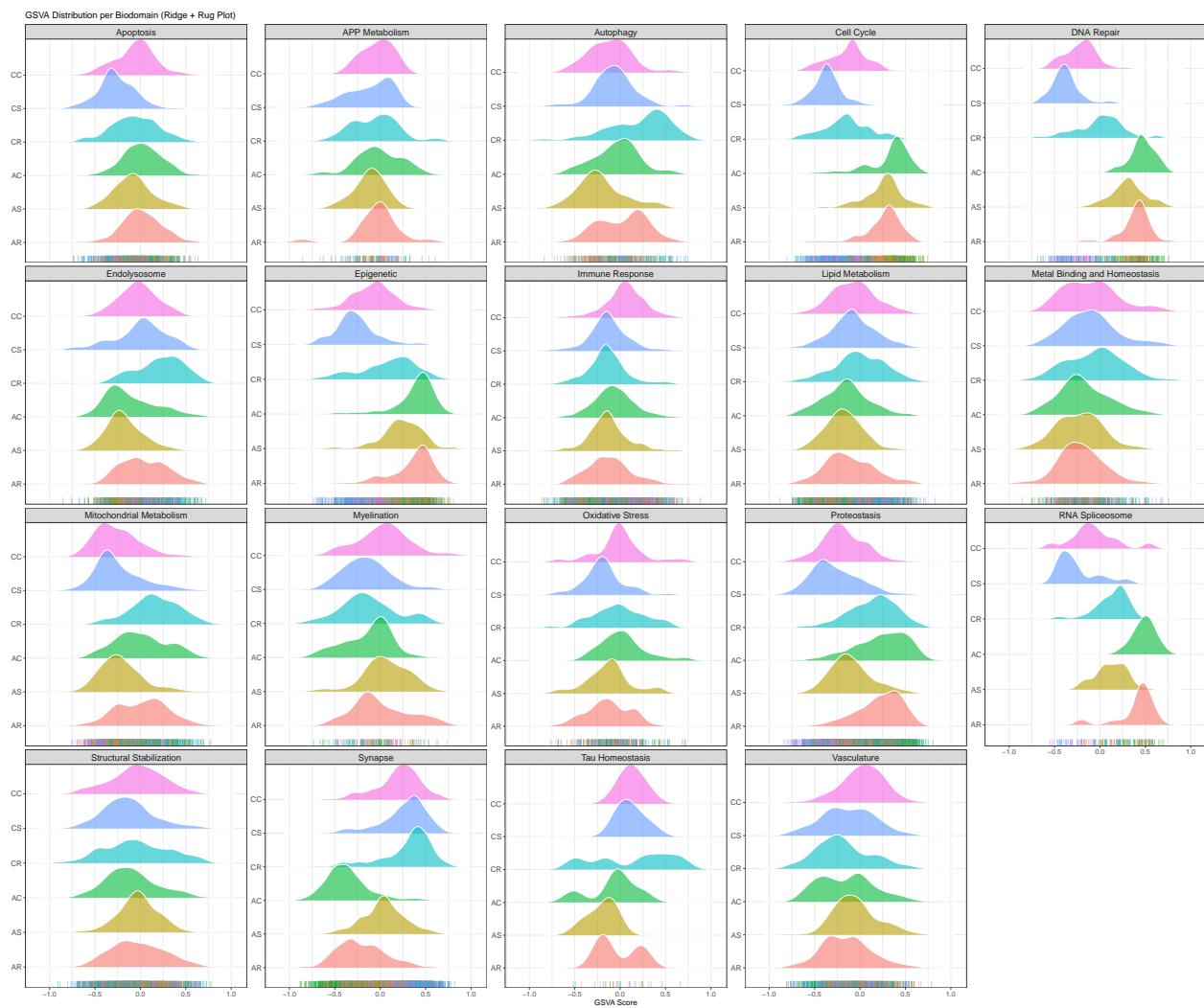
(1) Ridge plot for GSVA score



(2) Raincloud plot for GSVA score



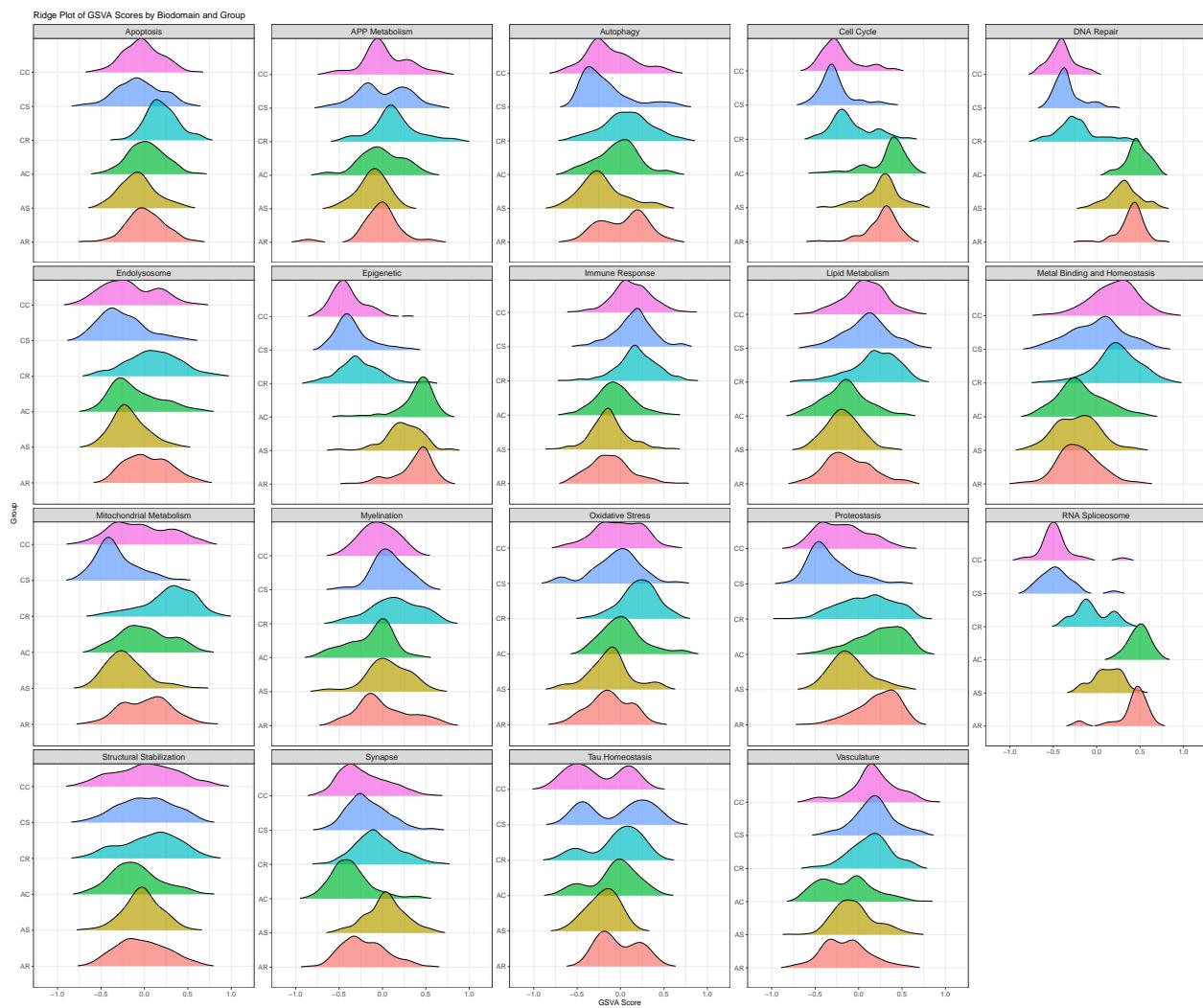
(3) Rug and density plot for GSVA score



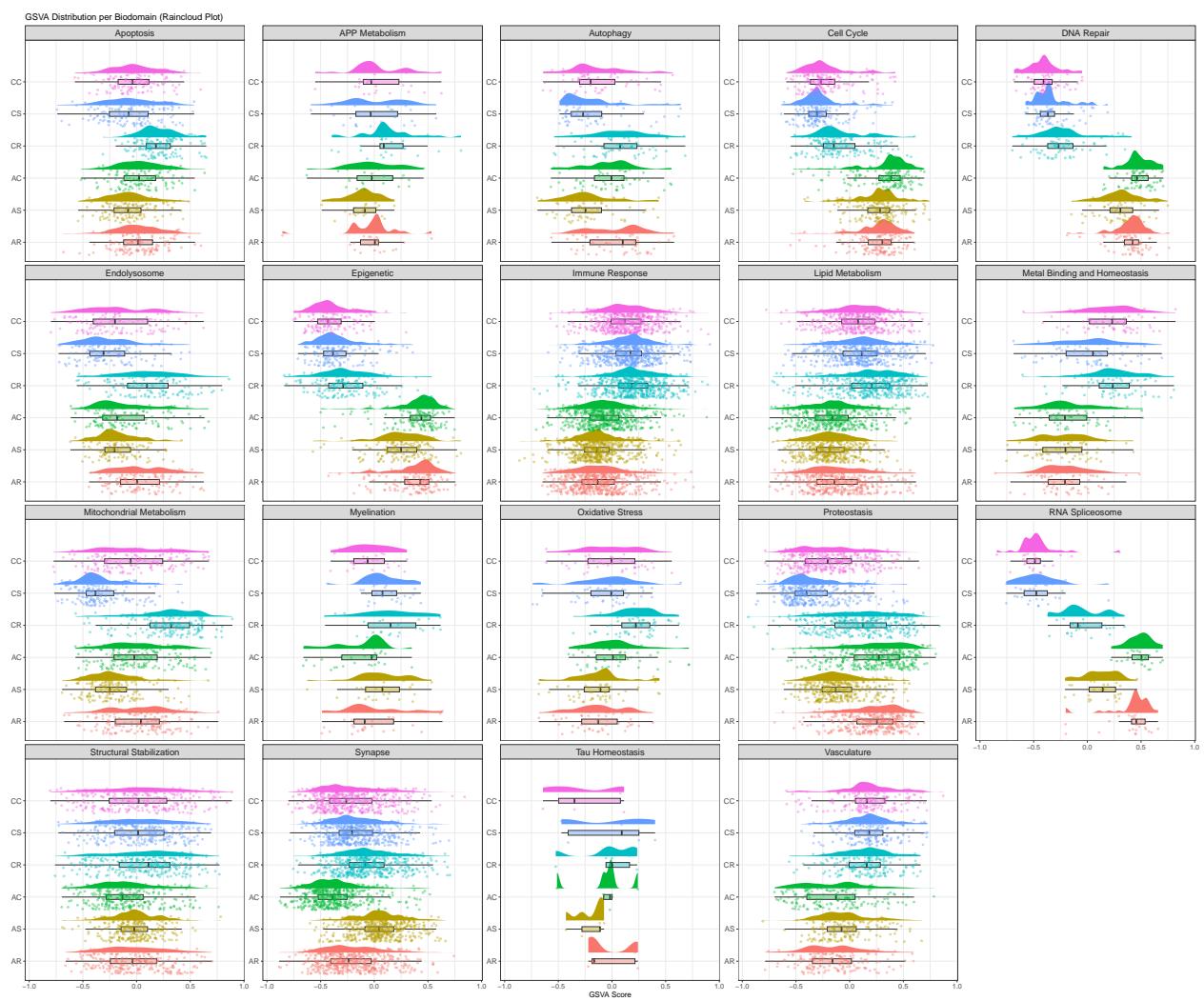
3.result for C09 vs A33

```
## [1] FALSE
## [1] 15598      9
##   gs_exact_source gs_cat gs_subcat
## 1      GO:0000002      C5      GO:BP
## 2      GO:0000003      C5      GO:BP
## 3      GO:0000012      C5      GO:BP
## 4      GO:0000014      C5      GO:MF
## 5      GO:0000018      C5      GO:BP
## 6      GO:0000019      C5      GO:BP
##                                     gs_name
## 1          GOBP_MITOCHONDRIAL_GENOME_MAINTENANCE
## 2          GOBP_REPRODUCTION
## 3          GOBP_SINGLE_STRAND_BREAK_REPAIR
## 4 GOMF_SINGLE_STRANDED_DNA_ENDODEOXYRIBONUCLEASE_ACTIVITY
## 5          GOBP_REGULATION_OF_DNA_RECOMBINATION
## 6          GOBP_REGULATION_OF_MITOTIC_RECOMBINATION
##           Biodomain                               GOterm_Name
## 1 Mitochondrial Metabolism                  mitochondrial genome maintenance
## 2                               <NA>                                <NA>
## 3          DNA Repair                         single strand break repair
## 4          DNA Repair single-stranded DNA endodeoxyribonuclease activity
## 5          Cell Cycle                        regulation of DNA recombination
## 6                               <NA>                                <NA>
##   n_ensGene n_entrezGene n_hgncSymbol
## 1      12        11       11
## 2       NA        NA       NA
## 3      11        11       11
## 4       9         9        9
## 5       5         5        5
## 6       NA        NA       NA
## [1] 11979
```

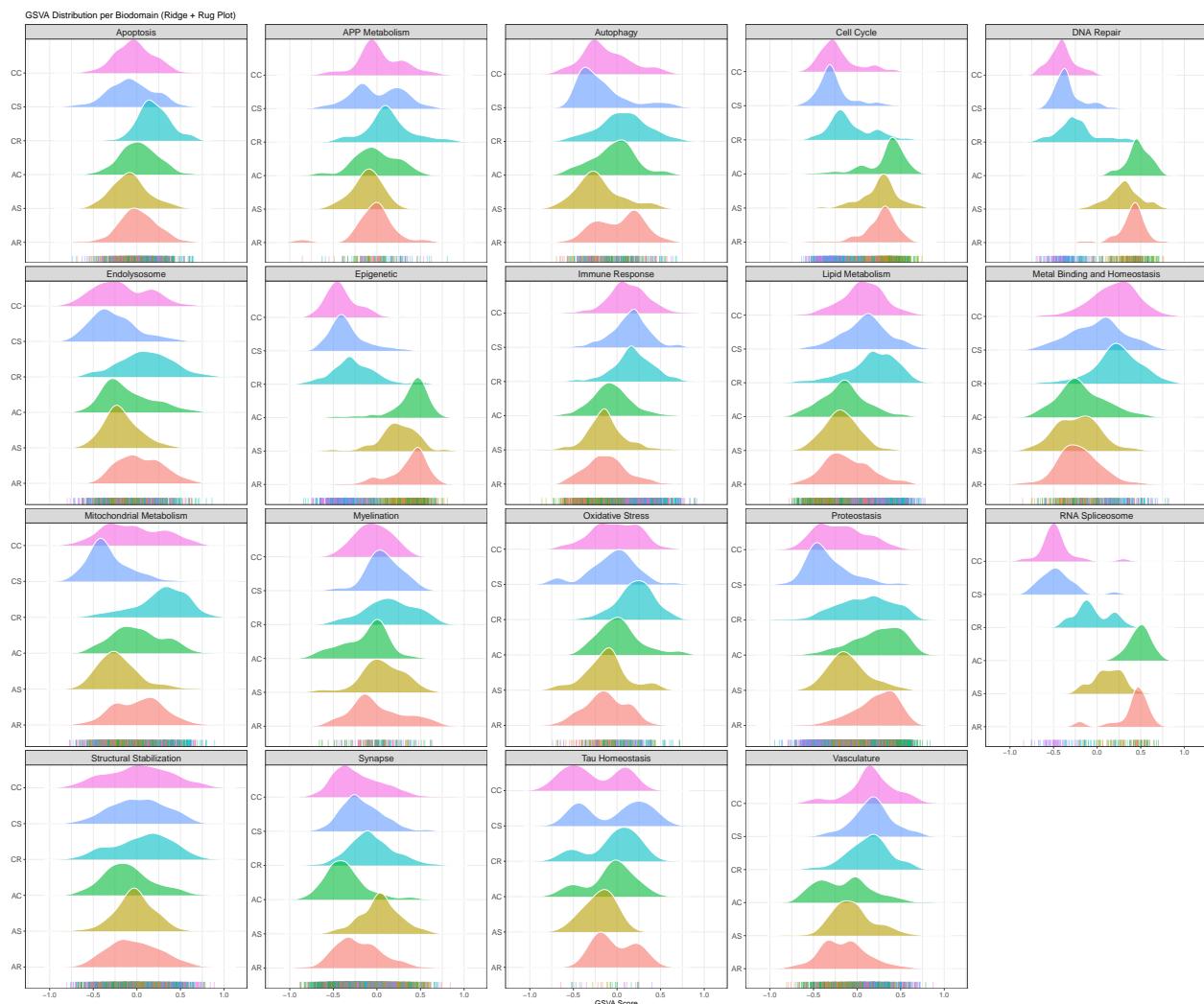
(1) Ridge plot for GSVA score



(2) Raincloud plot for GSVA score



(3) Rug and density plot for GSVA score



Session information

```
## R version 4.4.0 (2024-04-24)
## Platform: aarch64-apple-darwin20
## Running under: macOS 15.4
##
## 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] ggdist_3.3.2          ggridges_0.5.6
##  [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       RColorBrewer_1.1-3
## [19] data.table_1.17.0      org.Hs.eg.db_3.19.1
## [21] AnnotationDbi_1.66.0   clusterProfiler_4.12.6
## [23] ggrepify_0.4.17        pheatmap_1.0.12
## [25] EnhancedVolcano_1.22.0 ggrepel_0.9.6
## [27] apeglm_1.26.1          DESeq2_1.44.0
## [29] SummarizedExperiment_1.34.0 Biobase_2.64.0
## [31] MatrixGenerics_1.16.0  matrixStats_1.5.0
## [33] reshape2_1.4.4          Matrix_1.7-3
## [35] Signac_1.14.0          Seurat_5.2.1
## [37] SeuratObject_5.0.2     sp_2.2-0
## [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             tidyrr_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] progress_1.2.3              goftest_1.2-3
##  [5] HDF5Array_1.32.1           Biostrings_2.72.1
```

```

## [7] vctrs_0.6.5
## [9] digest_0.6.37
## [11] deldir_2.0-4
## [13] magick_2.8.6
## [15] httpuv_1.6.16
## [17] withr_3.0.2
## [19] ggfun_0.1.8
## [21] memoise_2.0.1
## [23] systemfonts_1.2.2
## [25] tidytree_0.4.6
## [27] pbapply_1.7-2
## [29] prettyunits_1.2.0
## [31] promises_1.3.2
## [33] restfulr_0.0.15
## [35] globals_0.17.0
## [37] rhdf5_2.48.0
## [39] UCSC.utils_1.0.0
## [41] generics_0.1.3
## [43] curl_6.2.2
## [45] ScaledMatrix_1.12.0
## [47] polyclip_1.10-7
## [49] SparseArray_1.4.8
## [51] evaluate_1.0.3
## [53] BiocFileCache_2.12.0
## [55] irlba_2.3.5.1
## [57] filelock_1.0.3
## [59] reticulate_1.42.0
## [61] magrittr_2.0.3
## [63] later_1.4.2
## [65] ggtree_3.12.0
## [67] spatstat.geom_3.3-6
## [69] scattermore_1.2
## [71] cowplot_1.1.3
## [73] pillar_1.10.2
## [75] compiler_4.4.0
## [77] RSpectra_0.16-2
## [79] tensor_1.5
## [81] plyr_1.8.9
## [83] abind_1.4-8
## [85] gridGraphics_0.5-1
## [87] locfit_1.5-9.12
## [89] bit_4.6.0
## [91] textshaping_1.0.0
## [93] BiocSingular_1.20.0
## [95] mime_0.13
## [97] Rcpp_1.0.14
## [99] sparseMatrixStats_1.16.0
## [101] Rttf2pt1_1.3.12
## [103] here_1.0.1
## [105] listenv_0.9.1
## [107] statmod_1.5.0
## [109] tweenr_2.0.3
## [111] tools_4.4.0
## [113] RSQLite_2.3.9
spatstat.random_3.3-3
png_0.1-8
parallelly_1.43.0
MASS_7.3-65
qvalue_2.36.0
xfun_0.52
survival_3.8-3
gson_0.1.0
ragg_1.4.0
zoo_1.8-14
R.oo_1.27.0
KEGGREST_1.44.1
httr_1.4.7
rhdf5filters_1.16.0
fitdistrplus_1.2-2
rstudioapi_0.17.1
miniUI_0.1.2
DOSE_3.30.5
zlibbioc_1.50.0
ggraph_2.2.1
GenomeInfoDbData_1.2.12
xtable_1.8-4
S4Arrays_1.4.1
hms_1.1.3
colorspace_2.1-1
ROCR_1.0-11
spatstat.data_3.1-6
lmtest_0.9-40
viridis_0.6.5
lattice_0.22-7
future.apply_1.11.3
shadowtext_0.1.4
RcppAnnoy_0.0.22
nlme_3.1-168
beachmat_2.20.0
stringi_1.8.7
GenomicAlignments_1.40.0
crayon_1.5.3
BiocIO_1.14.0
emdbook_1.3.13
graphlayouts_1.2.2
fastmatch_1.1-6
codetools_0.2-20
plotly_4.10.4
splines_4.4.0
fastDummies_1.7.5
dbplyr_2.5.0
blob_1.2.4
fs_1.6.6
ggplotify_0.1.2
tzdb_0.5.0
pkgconfig_2.0.3
cachem_1.1.0
viridisLite_0.4.2

```

```

## [115] DBI_1.2.3
## [117] fastmap_1.2.0
## [119] scales_1.3.0
## [121] ica_1.0-3
## [123] coda_0.19-4.1
## [125] RANN_2.6.2
## [127] tidygraph_1.3.1
## [129] yaml_2.3.10
## [131] lifecycle_1.0.4
## [133] mvtnorm_1.3-3
## [135] gtable_0.3.6
## [137] progressr_0.15.1
## [139] jsonlite_2.0.0
## [141] bitops_1.0-9
## [143] Rtsne_0.17
## [145] spatstat.utils_3.1-3
## [147] GOSemSim_2.30.2
## [149] spatstat.univar_3.1-2
## [151] lazyeval_0.2.2
## [153] htmltools_0.5.8.1
## [155] GO.db_3.19.1
## [157] rappdirs_0.3.3
## [159] glue_1.8.0
## [161] httr2_1.1.2
## [163] RCurl_1.98-1.17
## [165] treeio_1.28.0
## [167] extrafontdb_1.0
## [169] R6_2.6.1
## [171] labeling_0.4.3
## [173] cluster_2.1.8.1
## [175] Rhdf5lib_1.26.0
## [177] DelayedArray_0.30.1
## [179] ggforce_0.4.2
## [181] future_1.40.0
## [183] munsell_0.5.1
## [185] htmlwidgets_1.6.4
## [187] rlang_1.1.6
## [189] spatstat.explore_3.4-2
                                         numDeriv_2016.8-1.1
                                         rmarkdown_2.29
                                         grid_4.4.0
                                         Rsamtools_2.20.0
                                         dotCall64_1.2
                                         farver_2.1.2
                                         scatterpie_0.2.4
                                         cli_3.6.4
                                         uwot_0.2.3
                                         timechange_0.3.0
                                         rjson_0.2.23
                                         ape_5.8-1
                                         RcppHNSW_0.6.0
                                         bit64_4.6.0-1
                                         yulab.utils_0.2.0
                                         bdsmatrix_1.3-7
                                         distributional_0.5.0
                                         R.utils_2.13.0
                                         shiny_1.10.0
                                         enrichplot_1.24.4
                                         sctransform_0.4.1
                                         tinytex_0.57
                                         spam_2.11-1
                                         XVector_0.44.0
                                         rprojroot_2.0.0.4
                                         gridExtra_2.3
                                         igraph_2.1.4
                                         SingleCellExperiment_1.26.0
                                         RcppRoll_0.3.1
                                         bbmle_1.0.25.1
                                         aplot_0.2.5
                                         tidyselect_1.2.1
                                         xml2_1.3.8
                                         rsvd_1.0.5
                                         KernSmooth_2.23-26
                                         fgsea_1.30.0
                                         spatstat.sparse_3.1-0

```