BioDomain analysis for FXS and CTRL

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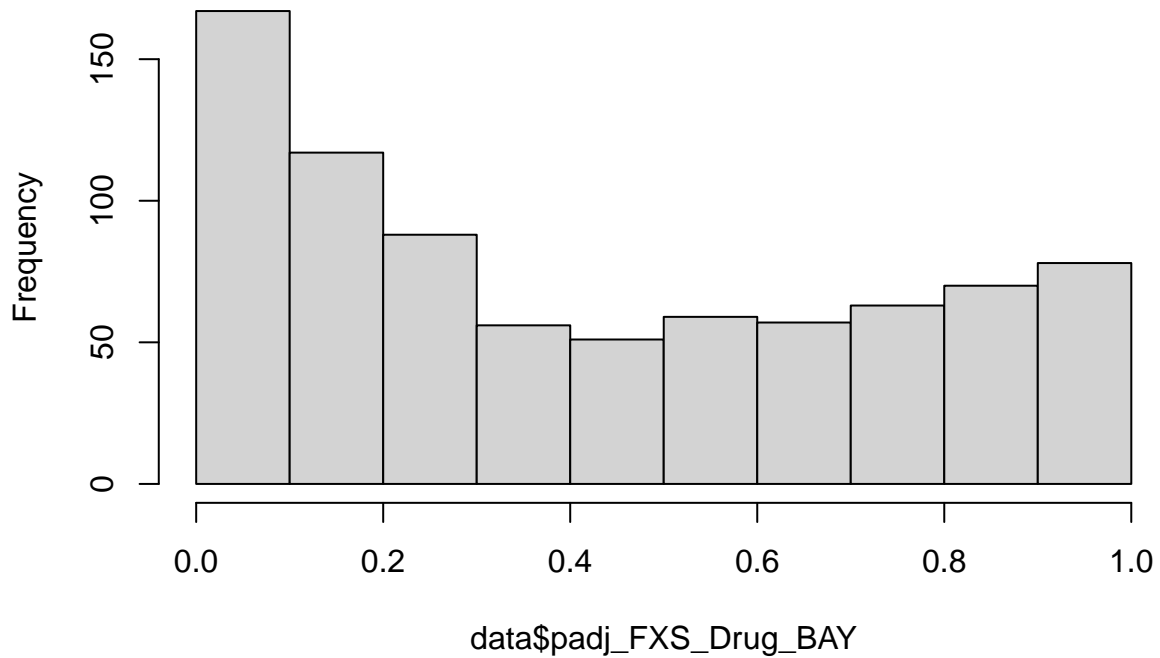# Contents

1. BioDomain analysis

Load the GSVA analysis

2.Load GSVA result

Histogram of data$padj_FXS_Drug_BAY

data$padj_FXS_Drug_BAY

```
## [1] "padj_FXS_Drug_BAY < 0.05"

##
## FALSE   TRUE
##   724     82
```

Histogram of data$p_FXS_Drug_BAY


```
## [1] "p_FXS_Drug_BAY < 0.05"

##
## FALSE   TRUE
##   485    321
```

Histogram of data$padj_FXS_Drug_BP
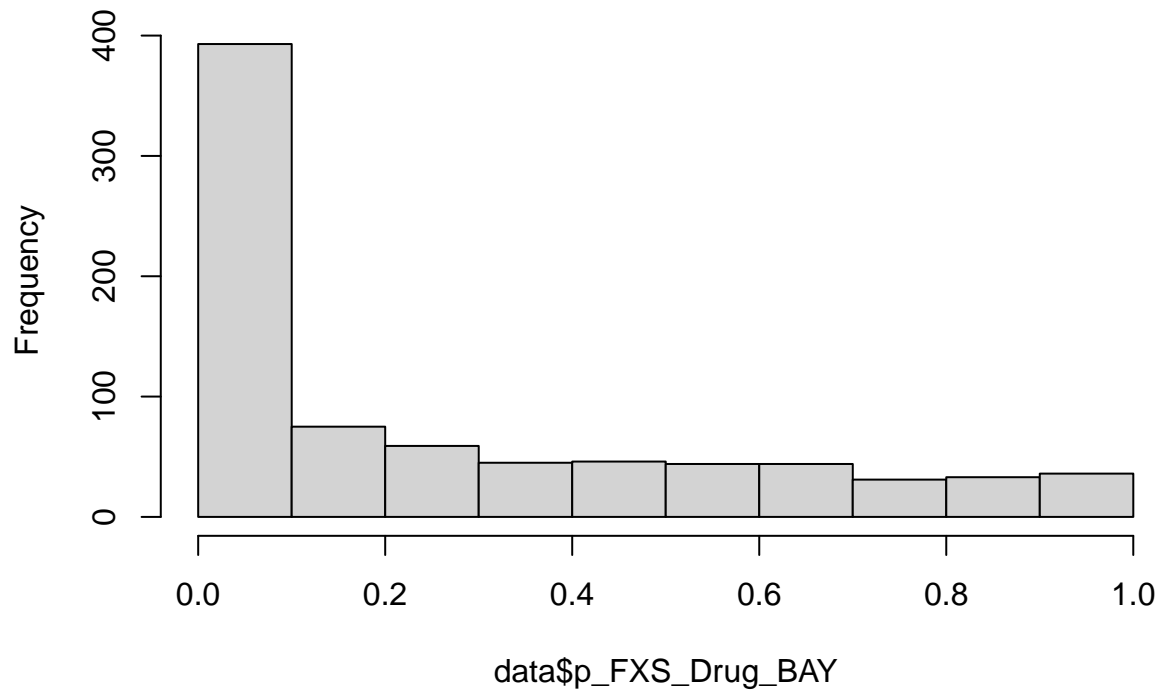
```
## [1] "padj_FXS_Drug_BP < 0.05"
```

```
##
## FALSE   TRUE
##   805      1
```

Histogram of data$p_FXS_Drug_BP
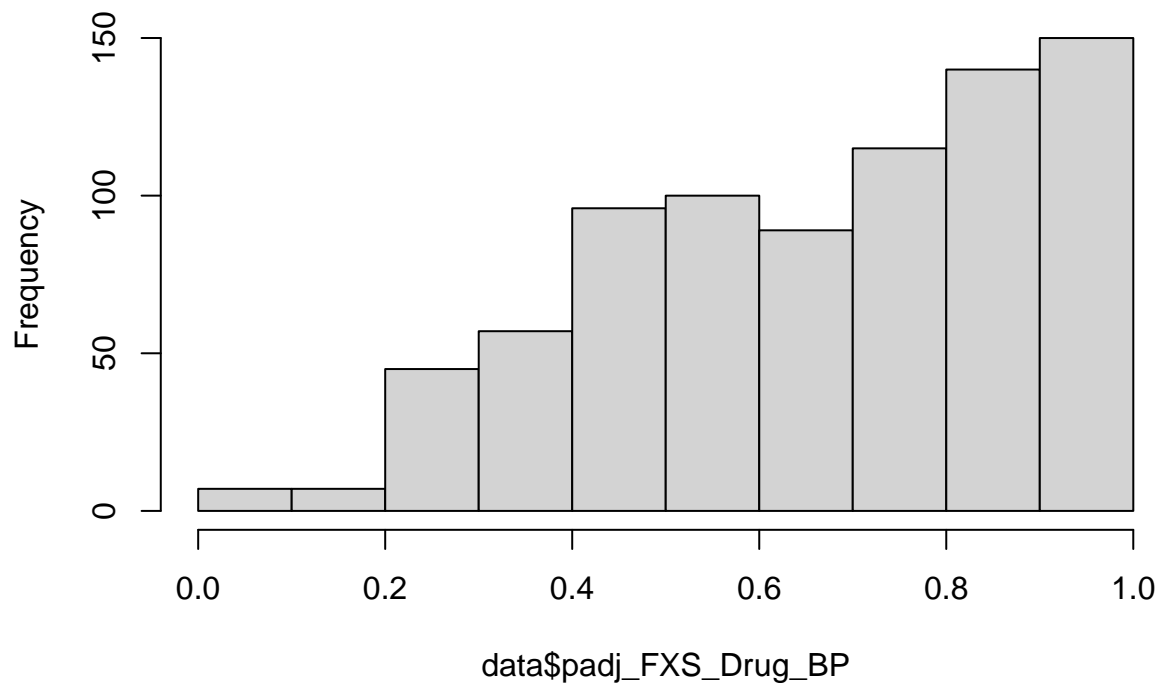


```
## [1] "p_FXS_Drug_BP < 0.05"
```

```
##
## FALSE   TRUE
##   649    157
```

Histogram of data$padj_FXS_Drug_BPN

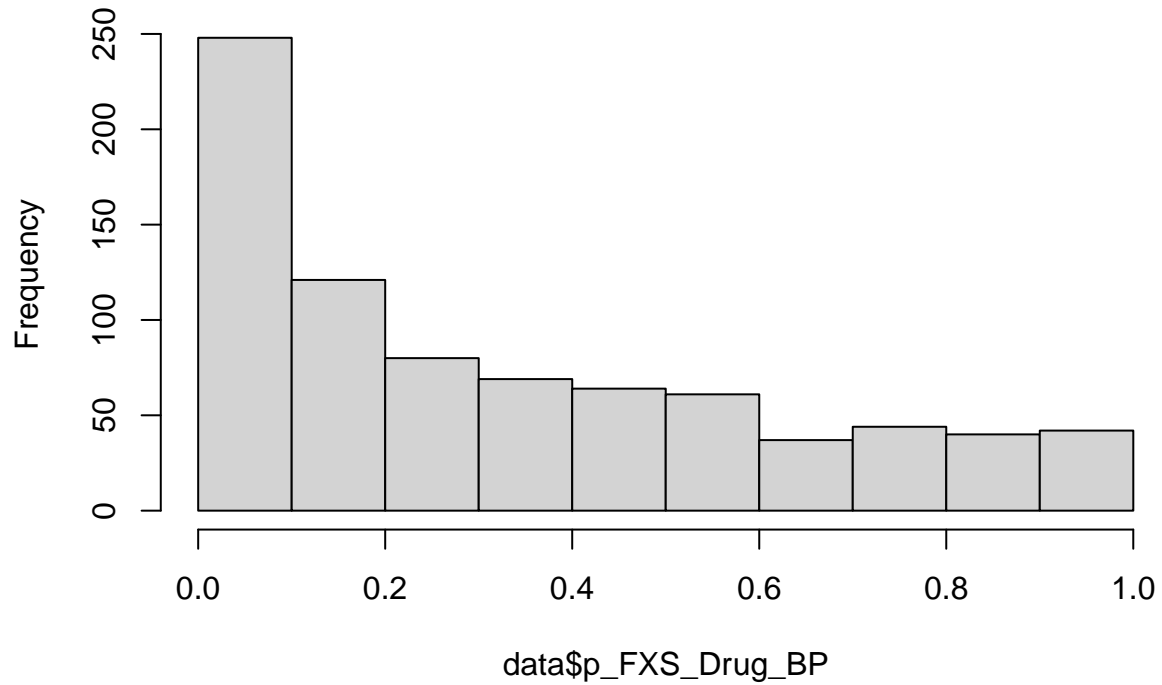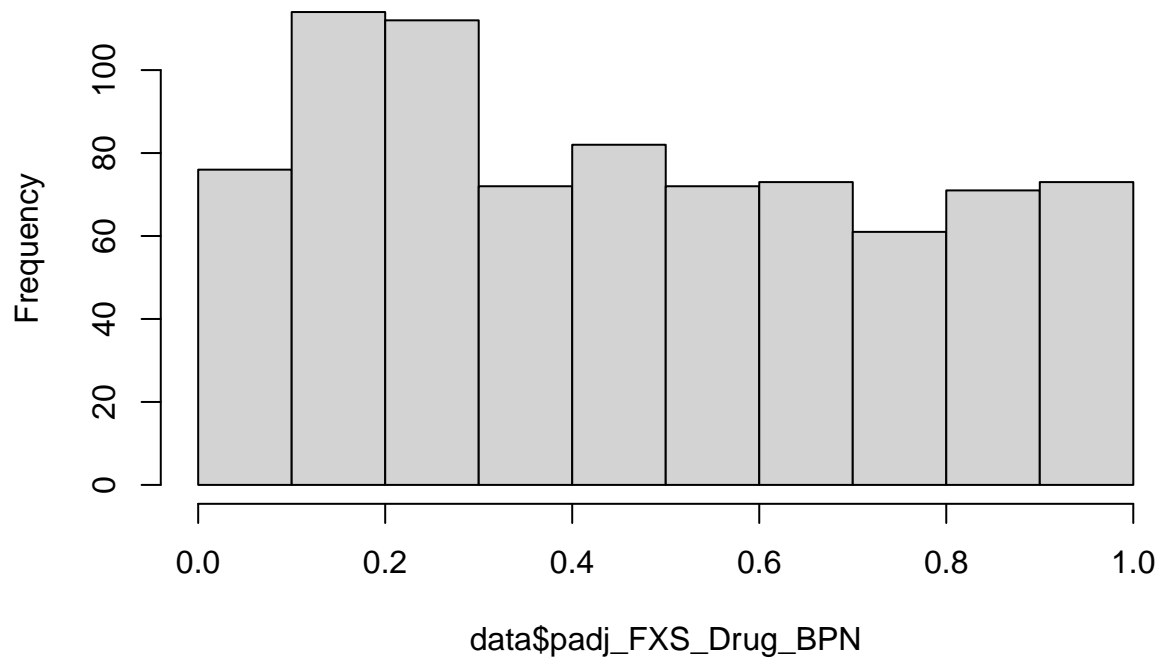```
[1] "padj_FXS_Drug_BPN < 0.05"

##
FALSE   TRUE
798   8
```

## Histogram of data$p_FXS_Drug_BPN
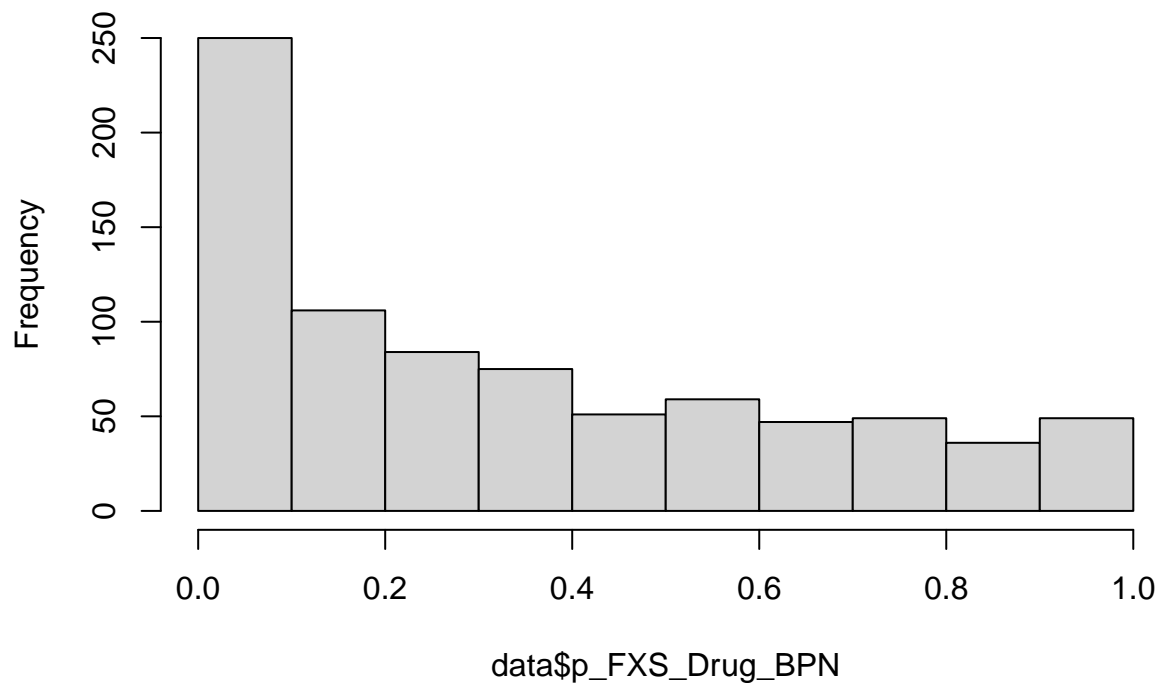
```
## [1] "p_FXS_Drug_BPN < 0.05"

##
## FALSE   TRUE
##   645    161
```

3. Define the fully rescue and partical rescue

```
## [1] "BAY"

##
## No Side Effect    Side Effect
##             657            149

##
##     Full Rescue       No Rescue Partial Rescue    Side Effect
##              67             458            132            149
## [1] "BP"

##
## No Side Effect    Side Effect
##             374            432

##
##     Full Rescue       No Rescue Partial Rescue    Side Effect
##              13             334             27            432
## [1] "BPN"

##
## No Side Effect    Side Effect
##             695            111

##
##     Full Rescue       No Rescue Partial Rescue    Side Effect
##              42             588             65            111
```

4. Bubble plot for the BioDomain

BioDomain Bubble Plot: FXS

[1] "FXS"

BioDomain Bubble Plot: FXS + BAY Rescue
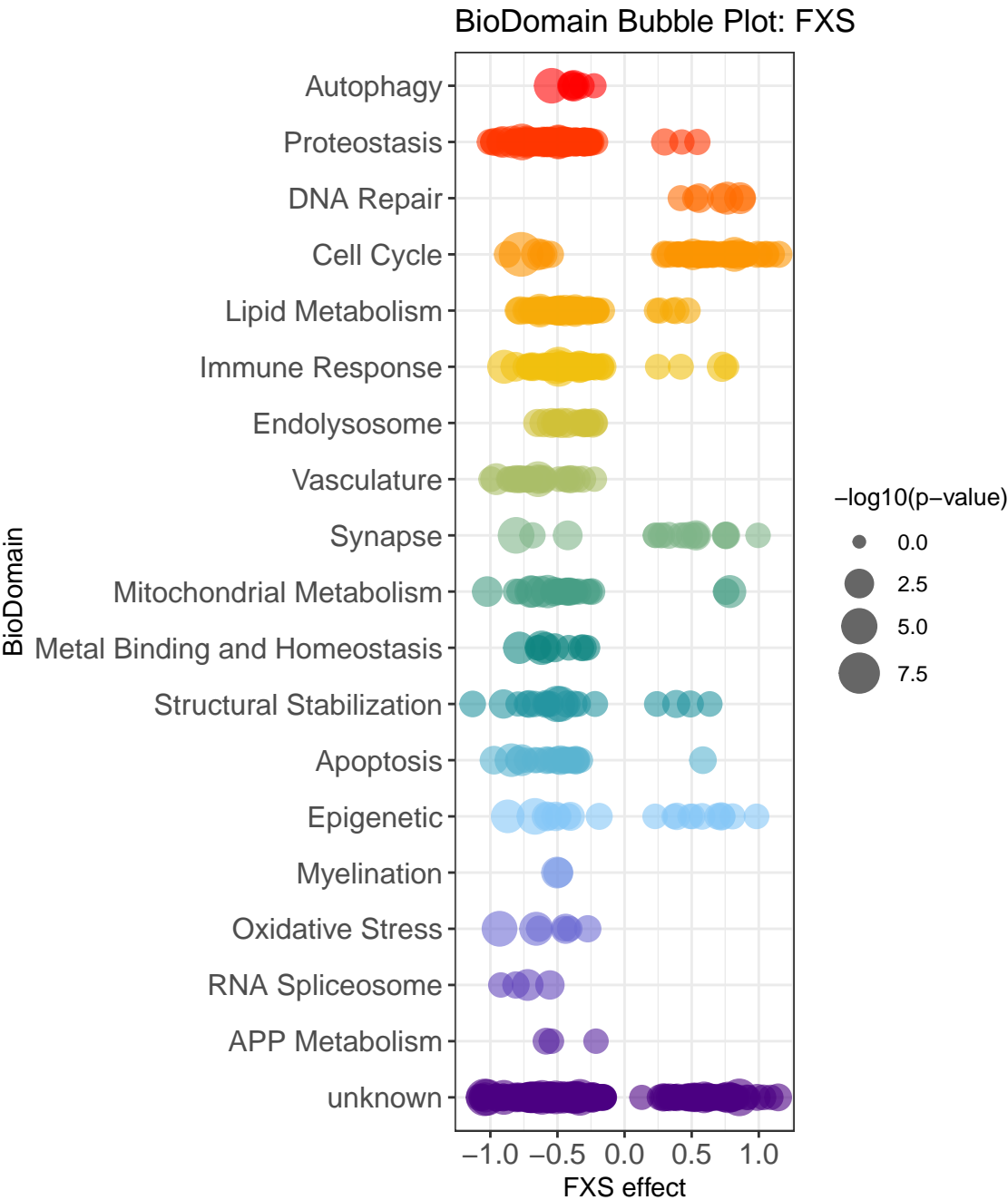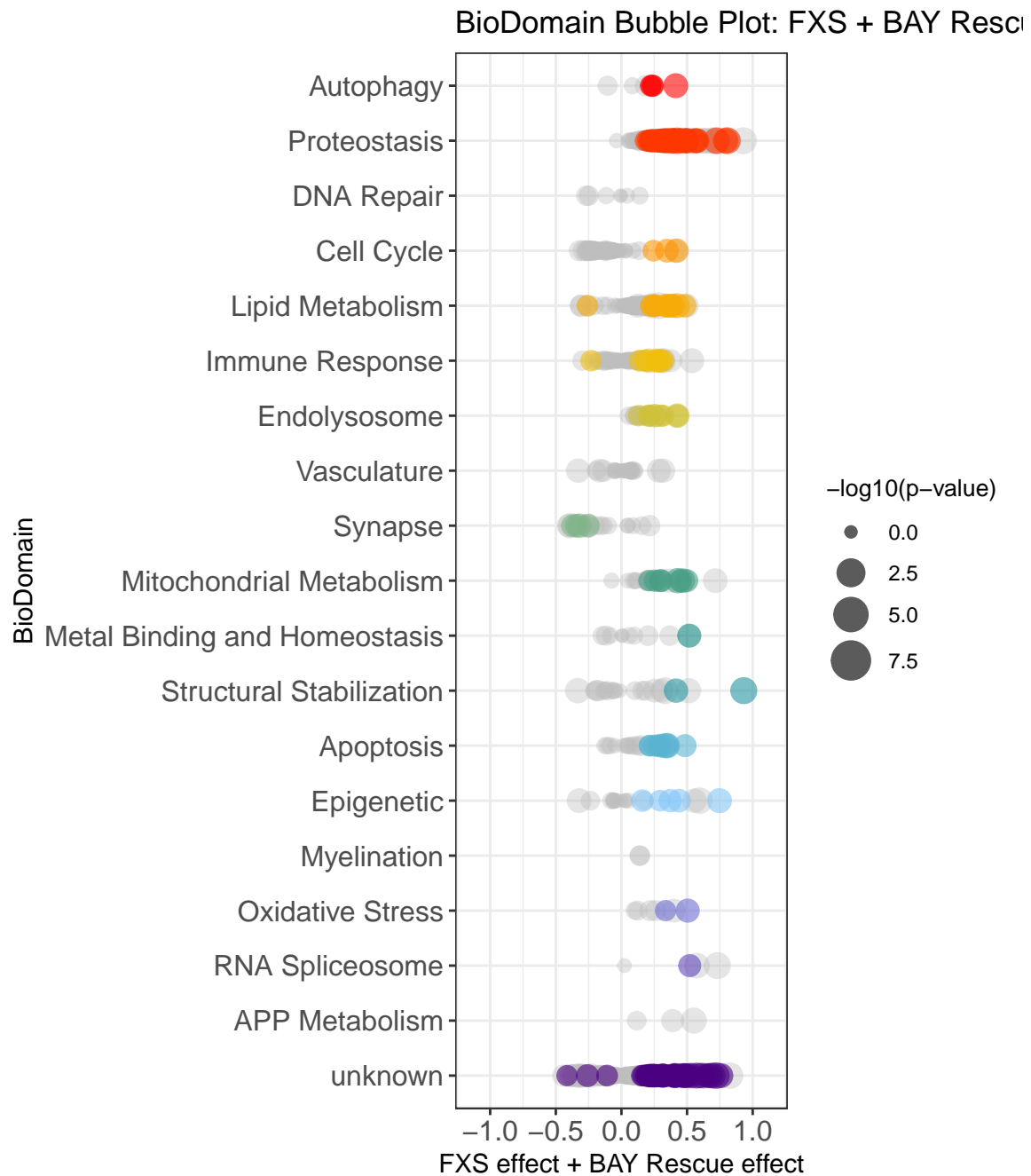
[1] "FXS_+_BAY_Rescue"

BioDomain Bubble Plot: FXS + BP Rescue
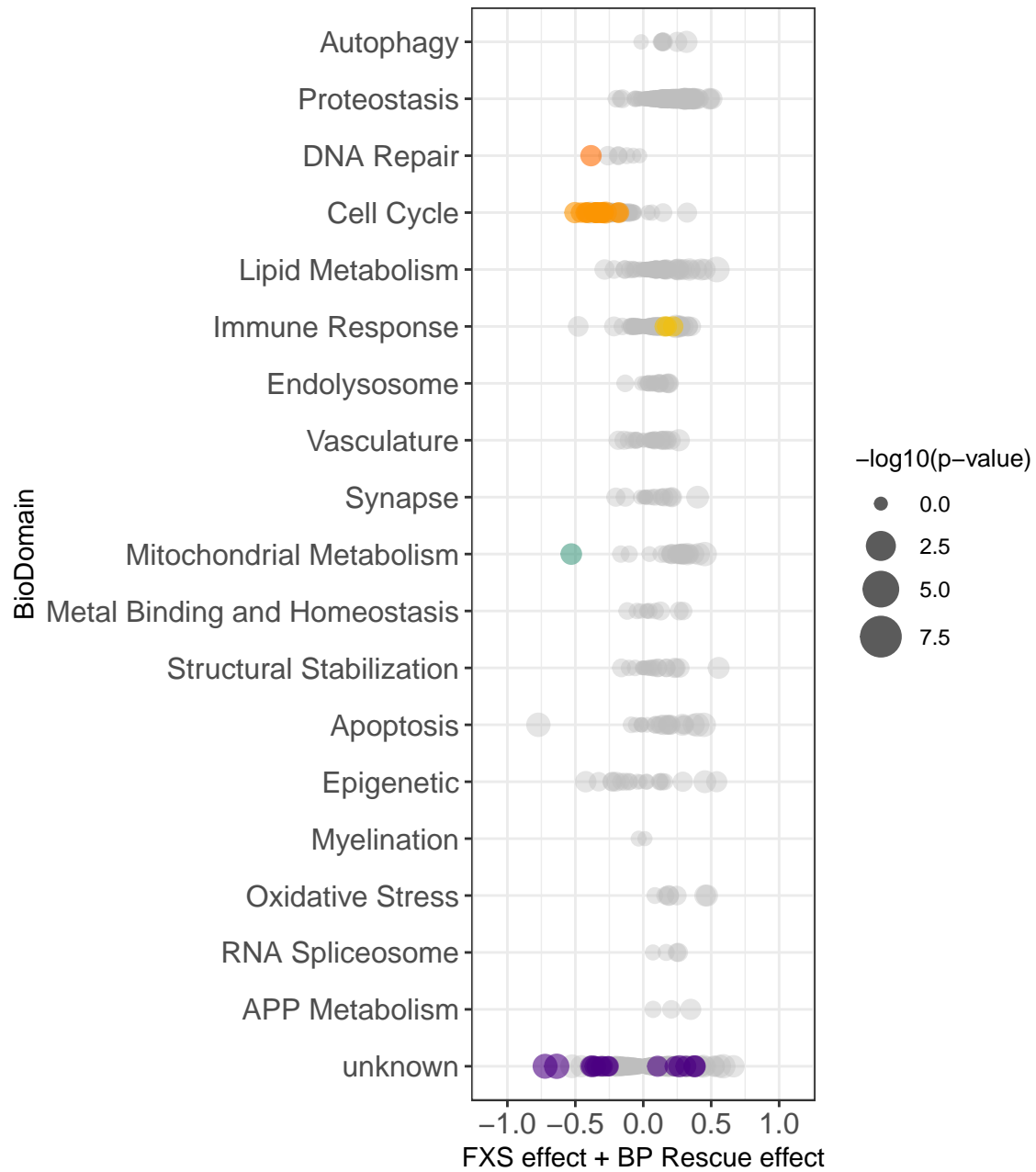
[1] "FXS_+_BP_Rescue"

BioDomain Bubble Plot: FXS + BPN Resc
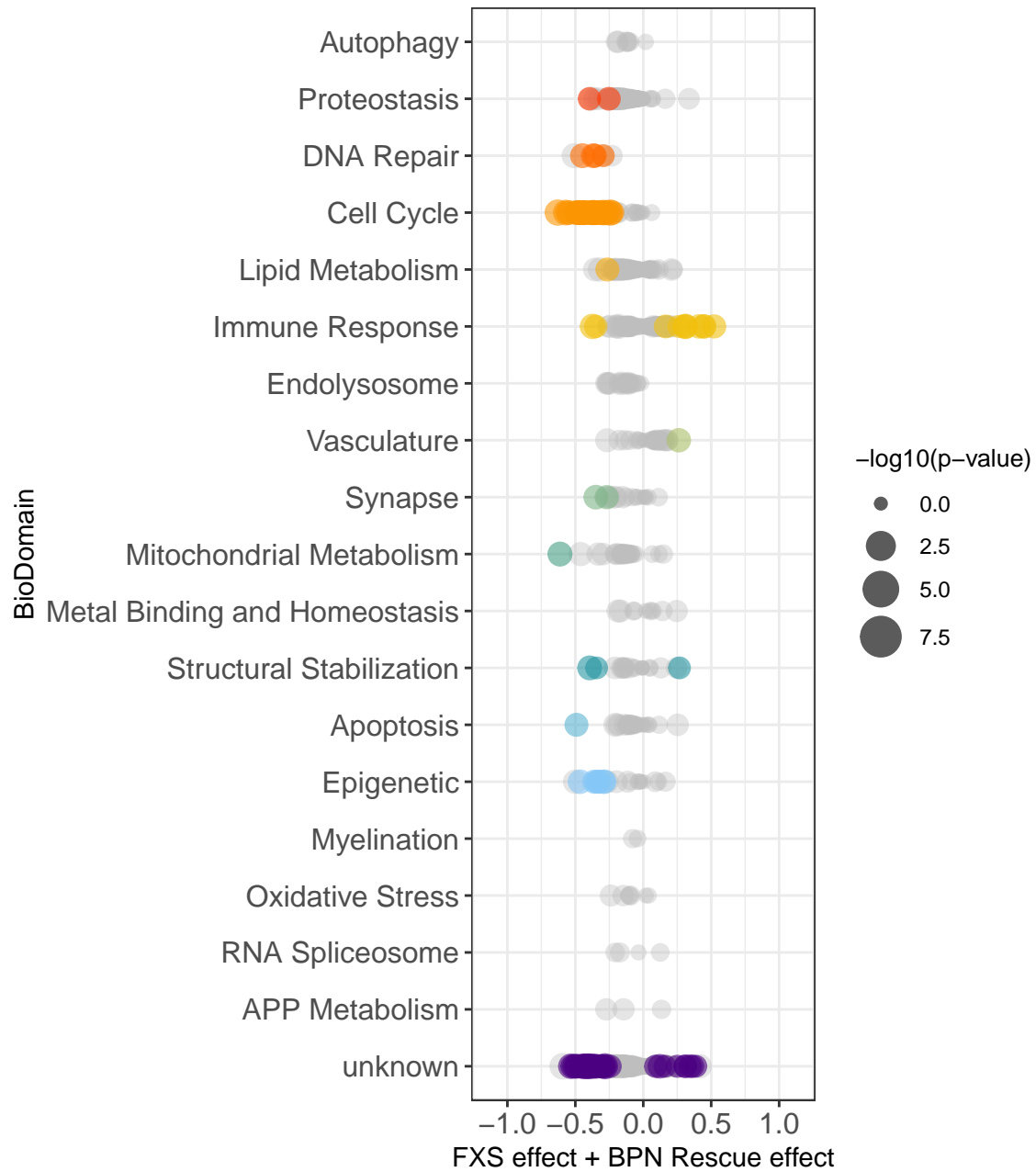
[1] "FXS_+_BPN_Rescue"

Plot the gene heatmap

```
## [1] "Durg : BAY, BioDomain : Apoptosis"
## [1] "Durg : BAY, BioDomain : Autophagy"
## [1] "Durg : BAY, BioDomain : Cell Cycle"
## [1] "Durg : BAY, BioDomain : Endolysosome"
## [1] "Durg : BAY, BioDomain : Epigenetic"
## [1] "Durg : BAY, BioDomain : Immune Response"
## [1] "Durg : BAY, BioDomain : Lipid Metabolism"
## [1] "Durg : BAY, BioDomain : Metal Binding and Homeostasis"
## [1] "Durg : BAY, BioDomain : Mitochondrial Metabolism"
## [1] "Durg : BAY, BioDomain : Oxidative Stress"
## [1] "Durg : BAY, BioDomain : Proteostasis"
## [1] "Durg : BAY, BioDomain : RNA Spliceosome"
## [1] "Durg : BAY, BioDomain : Structural Stabilization"
## [1] "Durg : BAY, BioDomain : Synapse"
## [1] "Durg : BP, BioDomain : Cell Cycle"
## [1] "Durg : BP, BioDomain : DNA Repair"
## [1] "Durg : BP, BioDomain : Immune Response"
## [1] "Durg : BP, BioDomain : Mitochondrial Metabolism"
## [1] "Durg : BPN, BioDomain : Apoptosis"
## [1] "Durg : BPN, BioDomain : Cell Cycle"
## [1] "Durg : BPN, BioDomain : DNA Repair"
## [1] "Durg : BPN, BioDomain : Epigenetic"
## [1] "Durg : BPN, BioDomain : Immune Response"
## [1] "Durg : BPN, BioDomain : Lipid Metabolism"
## [1] "Durg : BPN, BioDomain : Mitochondrial Metabolism"
## [1] "Durg : BPN, BioDomain : Proteostasis"
## [1] "Durg : BPN, BioDomain : Structural Stabilization"
## [1] "Durg : BPN, BioDomain : Synapse"
## [1] "Durg : BPN, BioDomain : Vasculature"
```

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] grid      parallel  stats4    stats     graphics  grDevices utils
##  [8] datasets  methods   base
##
## other attached packages:
##  [1] msigdbr_10.0.2          GSEABase_1.66.0
##  [3] graph_1.82.0            annotate_1.82.0
##  [5] XML_3.99-0.18           extrafont_0.19
##  [7] ggsignif_0.6.4          patchwork_1.3.0
##  [9] decoupleR_2.10.0        GSVA_1.52.3
## [11] BiocParallel_1.38.0     edgeR_4.2.2
## [13] limma_3.60.6            GenomicFeatures_1.56.0
## [15] biomaRt_2.60.1          gprofiler2_0.2.3
## [17] RColorBrewer_1.1-3      data.table_1.17.2
## [19] org.Hs.eg.db_3.19.1     AnnotationDbi_1.66.0
## [21] clusterProfiler_4.12.6  ggfortify_0.4.17
## [23] pheatmap_1.0.12         EnhancedVolcano_1.22.0
## [25] ggrepel_0.9.6           apeglm_1.26.1
## [27] DESeq2_1.44.0           SummarizedExperiment_1.34.0
## [29] Biobase_2.64.0          MatrixGenerics_1.16.0
## [31] matrixStats_1.5.0       reshape2_1.4.4
## [33] Matrix_1.7-3            Signac_1.14.0
## [35] Seurat_5.3.0            SeuratObject_5.1.0
## [37] sp_2.2-0                rtracklayer_1.64.0
## [39] GenomicRanges_1.56.2    GenomeInfoDb_1.40.1
## [41] IRanges_2.38.1          S4Vectors_0.42.1
## [43] BiocGenerics_0.50.0     knitr_1.50
## [45] lubridate_1.9.4         forcats_1.0.0
## [47] stringr_1.5.1           dplyr_1.1.4
## [49] purrr_1.0.4             readr_2.1.5
## [51] tidyr_1.3.1             tibble_3.2.1
## [53] ggplot2_3.5.2           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_3.3-3   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              tidytree_0.4.6
## [25] zoo_1.8-14              pbapply_1.7-2
## [27] R.oo_1.27.1             prettyunits_1.2.0
## [29] KEGGREST_1.44.1         promises_1.3.2
## [31] httr_1.4.7              restfulr_0.0.15
## [33] rhdf5filters_1.16.0     globals_0.18.0
## [35] fitdistrplus_1.2-2      rhdf5_2.48.0
## [37] rstudioapi_0.17.1       UCSC.utils_1.0.0
## [39] miniUI_0.1.2            generics_0.1.4
## [41] DOSE_3.30.5             babelgene_22.9
## [43] curl_6.2.2              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_1.42.0       spatstat.data_3.1-6
## [61] magrittr_2.0.3          lmtest_0.9-40
## [63] later_1.4.2             viridis_0.6.5
## [65] ggtree_3.12.0           lattice_0.22-7
## [67] spatstat.geom_3.3-6     future.apply_1.11.3
## [69] scattermore_1.2         shadowtext_0.1.4
## [71] cowplot_1.1.3           RcppAnnoy_0.0.22
## [73] pillar_1.10.2           nlme_3.1-168
## [75] compiler_4.4.0          beachmat_2.20.0
## [77] RSpectra_0.16-2         stringi_1.8.7
## [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_1.5-9.12         graphlayouts_1.2.2
## [89] bit_4.6.0               fastmatch_1.1-6
## [91] codetools_0.2-20        BiocSingular_1.20.0
## [93] plotly_4.10.4           mime_0.13
## [95] splines_4.4.0           Rcpp_1.0.14
## [97] fastDummies_1.7.5       sparseMatrixStats_1.16.0
## [99] dbplyr_2.5.0            Rttf2pt1_1.3.12
## [101] blob_1.2.4             here_1.0.1
## [103] fs_1.6.6               listenv_0.9.1
## [105] ggplotify_0.1.2        statmod_1.5.0
## [107] tzdb_0.5.0             tweenr_2.0.3
## [109] pkgconfig_2.0.3        tools_4.4.0
## [111] cachem_1.1.0           RSQLite_2.3.11
## [113] viridisLite_0.4.2      DBI_1.2.3
## [115] numDeriv_2016.8-1.1    fastmap_1.2.0
```

```
## [117] rmarkdown_2.29              scales_1.4.0
## [119] ica_1.0-3                   Rsamtools_2.20.0
## [121] coda_0.19-4.1               dotCall64_1.2
## [123] RANN_2.6.2                  farver_2.1.2
## [125] tidygraph_1.3.1             scatterpie_0.2.4
## [127] yaml_2.3.10                 msigdbdf_24.1.1
## [129] cli_3.6.5                   lifecycle_1.0.4
## [131] uwot_0.2.3                  mvtnorm_1.3-3
## [133] timechange_0.3.0            gtable_0.3.6
## [135] rjson_0.2.23                ggridges_0.5.6
## [137] progressr_0.15.1            ape_5.8-1
## [139] jsonlite_2.0.0              RcppHNSW_0.6.0
## [141] bitops_1.0-9                assertthat_0.2.1
## [143] bit64_4.6.0-1               Rtsne_0.17
## [145] yulab.utils_0.2.0           spatstat.utils_3.1-3
## [147] bdsmatrix_1.3-7             GOSemSim_2.30.2
## [149] spatstat.univar_3.1-3       R.utils_2.13.0
## [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_0.4.2
## [157] rappdirs_0.3.3              tinytex_0.57
## [159] glue_1.8.0                  spam_2.11-1
## [161] httr2_1.1.2                 XVector_0.44.0
## [163] RCurl_1.98-1.17             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_2.1.8.1             bbmle_1.0.25.1
## [175] Rhdf5lib_1.26.0             aplot_0.2.5
## [177] DelayedArray_0.30.1         tidyselect_1.2.1
## [179] ggforce_0.4.2               xml2_1.3.8
## [181] future_1.49.0               rsvd_1.0.5
## [183] KernSmooth_2.23-26          htmlwidgets_1.6.4
## [185] fgsea_1.30.0                rlang_1.1.6
## [187] spatstat.sparse_3.1-0       spatstat.explore_3.4-2
```