BioDomain analysis for FXS and CTRL

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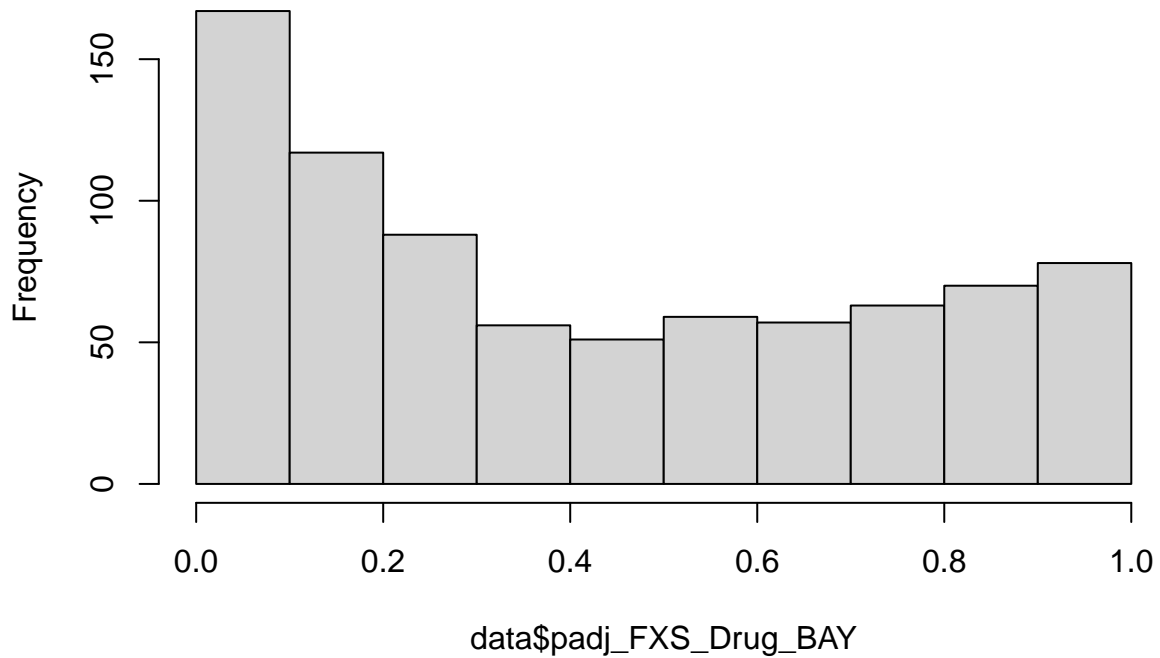
Contents

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
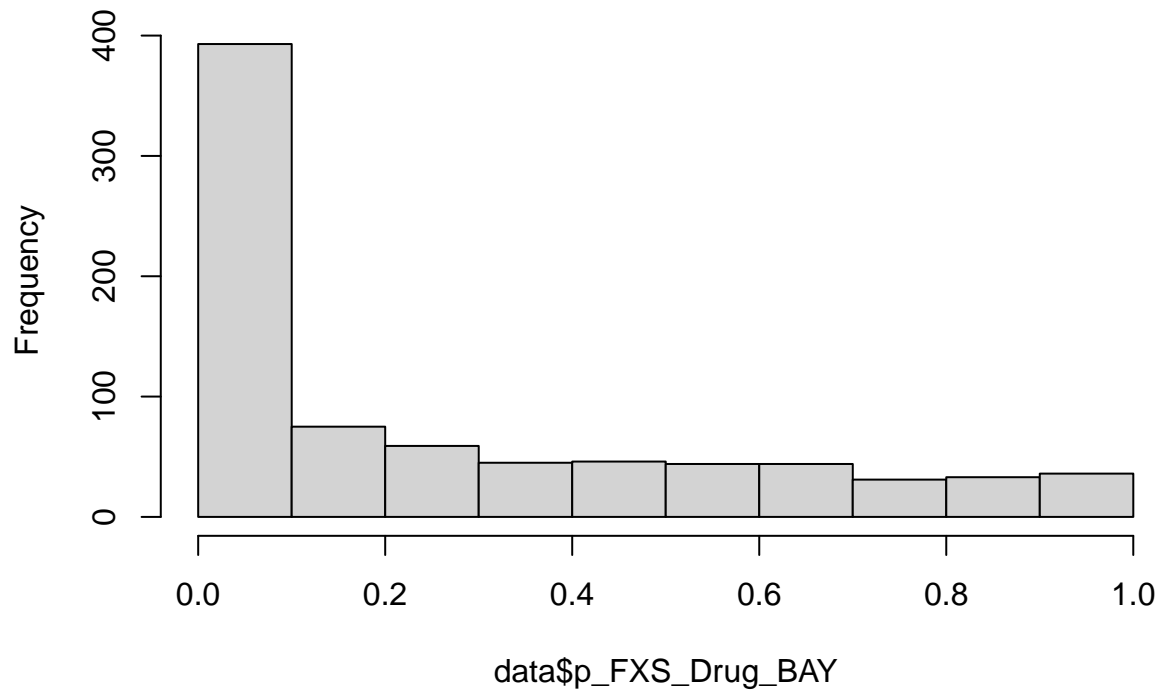

```
## [1] "p_FXS_Drug_BAY < 0.05"

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

Histogram of data$padj_FXS_Drug_BP

```
## [1] "padj_FXS_Drug_BP < 0.05"
##
## FALSE   TRUE
##   805      1
```
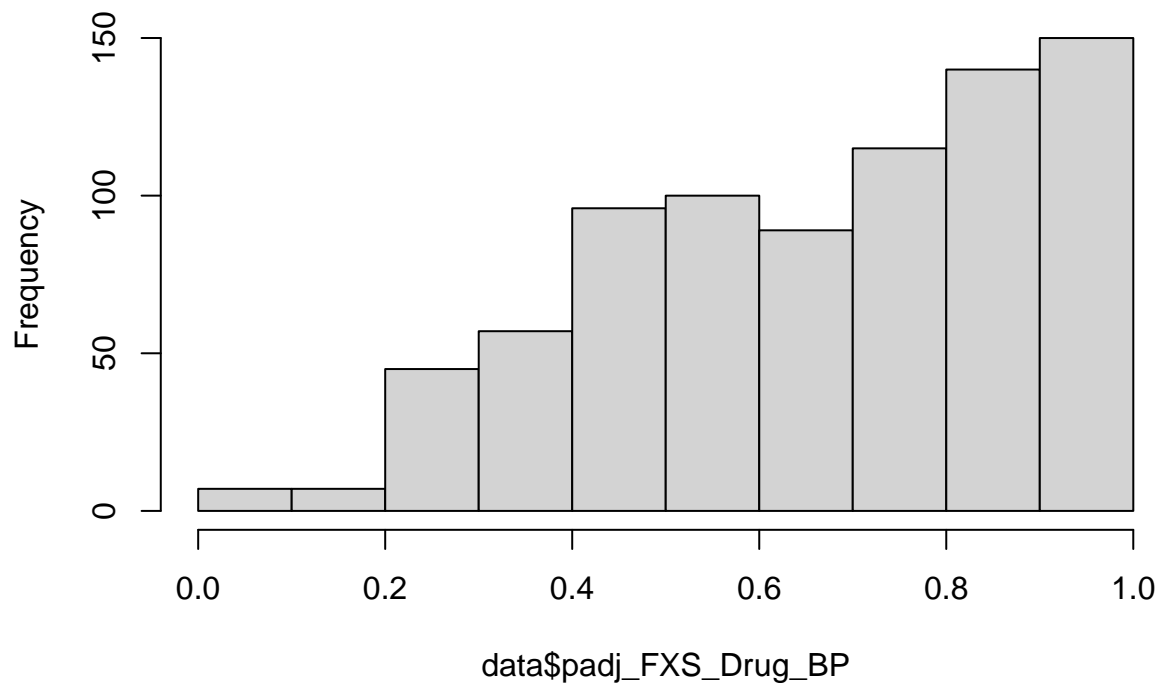
Histogram of data$p_FXS_Drug_BP


```
## [1] "p_FXS_Drug_BP < 0.05"
##
## FALSE   TRUE
##   649    157
```

Histogram of data$padj_FXS_Drug_BPN
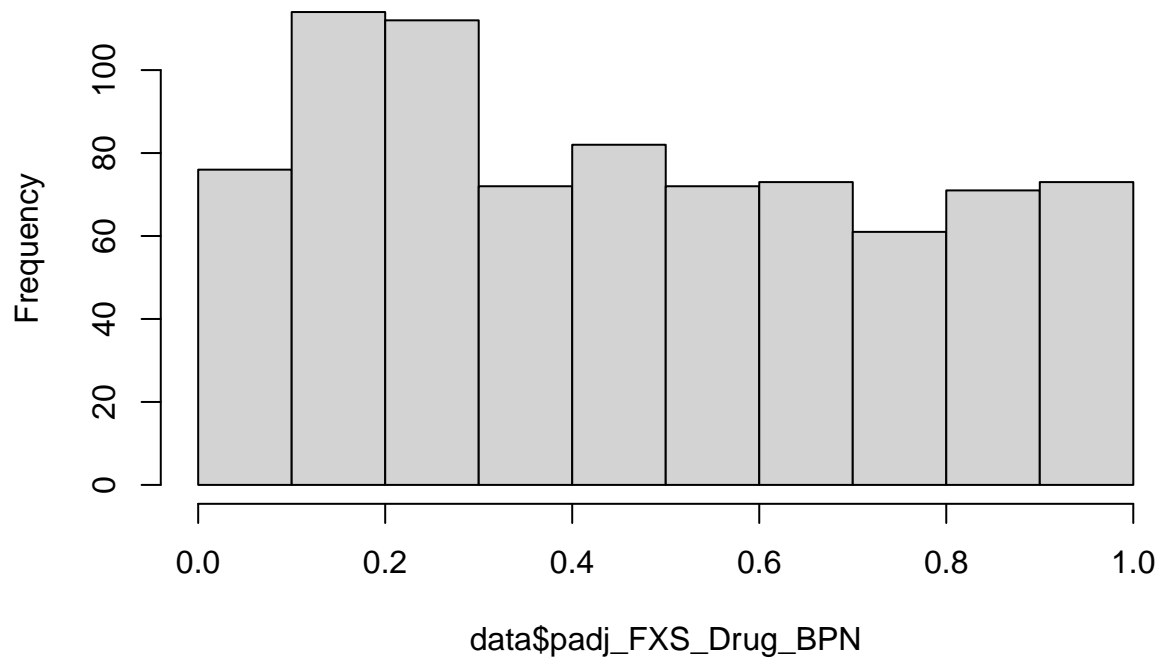

```
## [1] "padj_FXS_Drug_BPN < 0.05"

##
## FALSE   TRUE
##  798      8
```
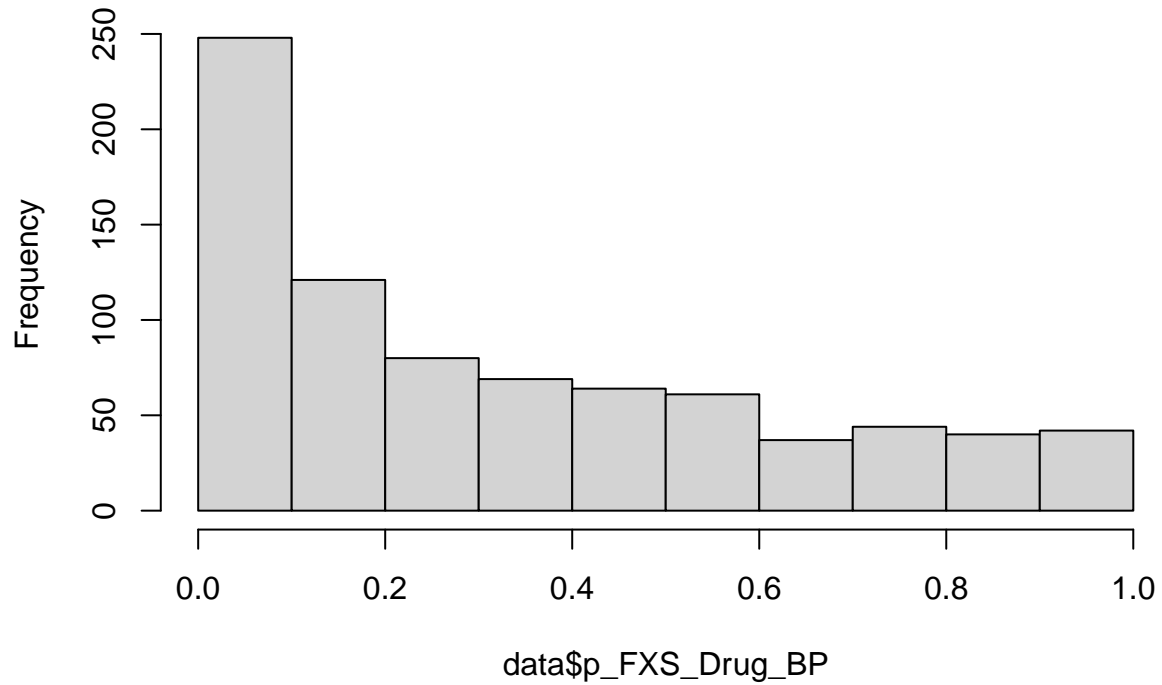
Histogram of data$p_FXS_Drug_BPN
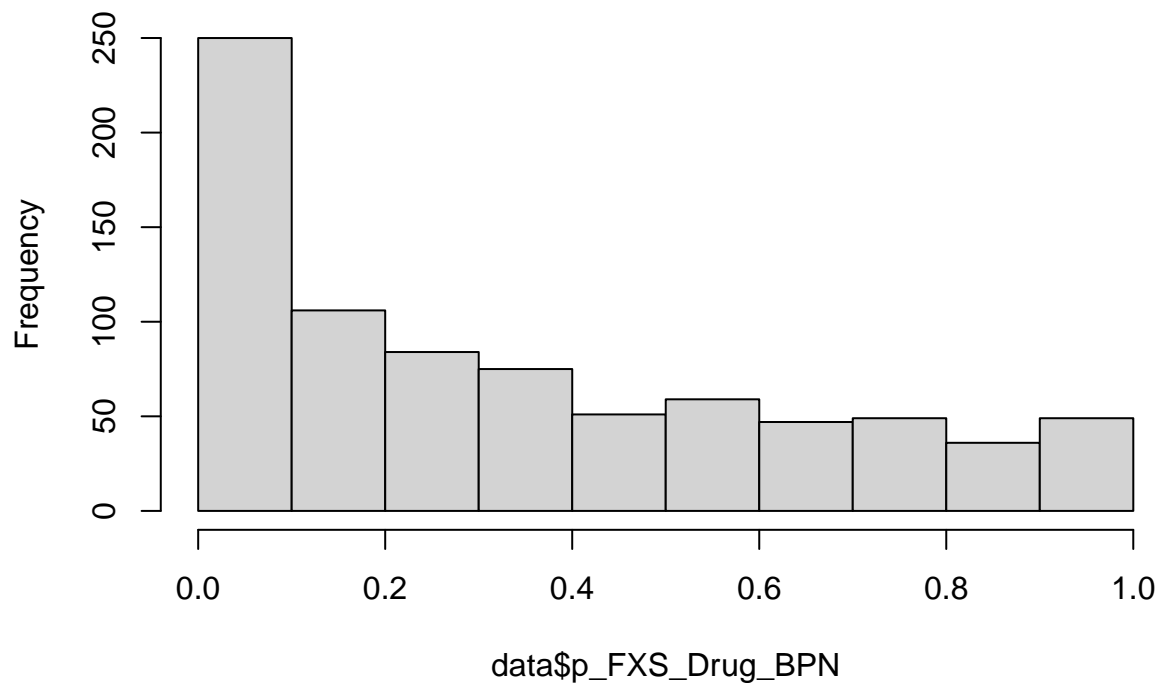
```
## [1] "p_FXS_Drug_BPN < 0.05"

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

3. Define the fully rescue and partical rescue

```
## [1] "BAY rescues:"
##
##     Full Rescue     Not Rescue Partial Rescue
##              88            498            220
## [1] "BP rescues:"
##
##     Full Rescue     Not Rescue Partial Rescue
##              15            652            139
## [1] "BPN rescues:"
##
##     Full Rescue     Not Rescue Partial Rescue
##              43            686             77
```

4. Bubble plot for the BioDomain

```
## [1] "FXS"
```


BioDomain Bubble Plot: FXS

```
## [1] "FXS + BAY Rescue"
```

BioDomain Bubble Plot: FXS + BAY Rescue

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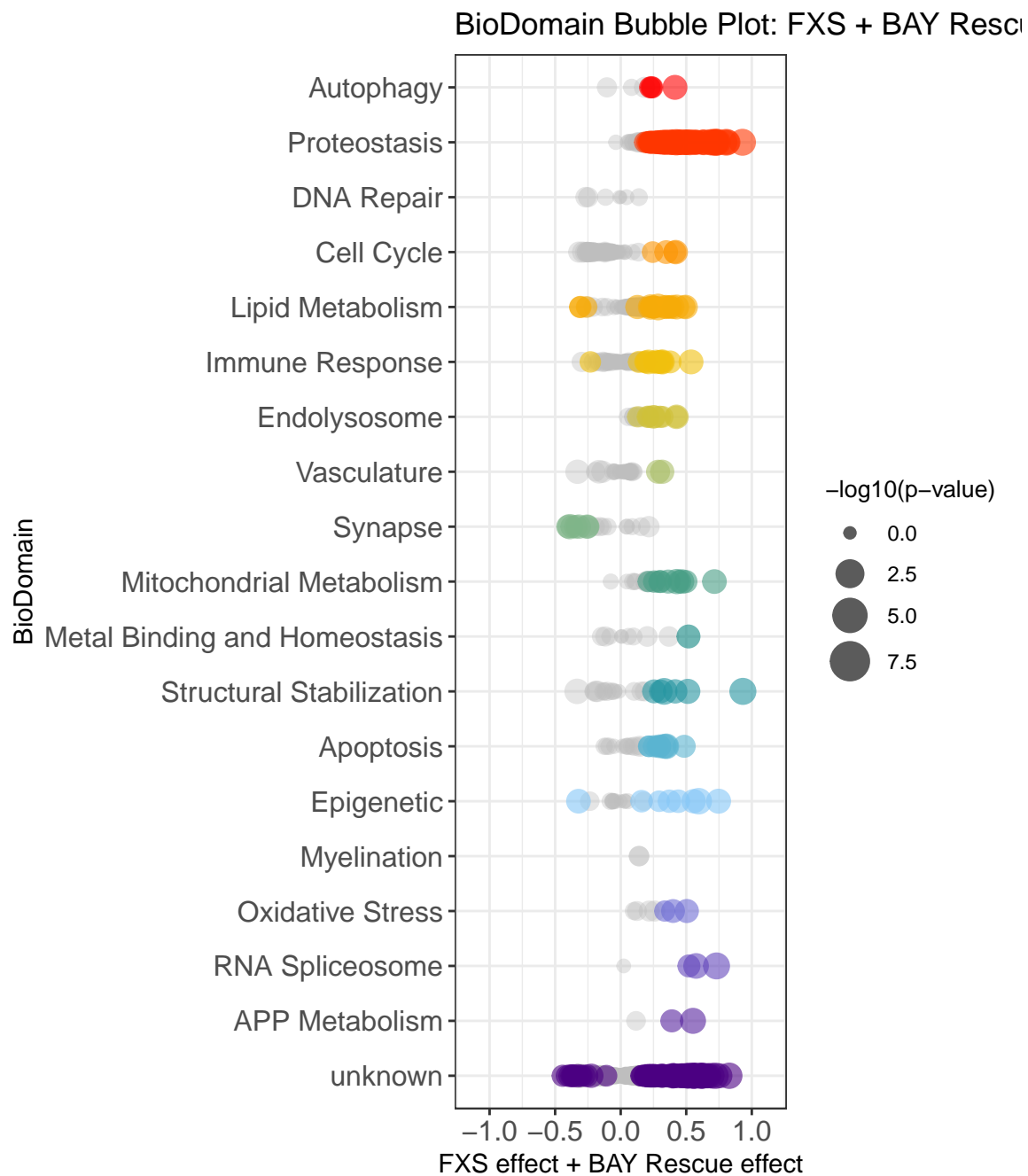
BioDomain Bubble Plot: FXS + BP Rescue
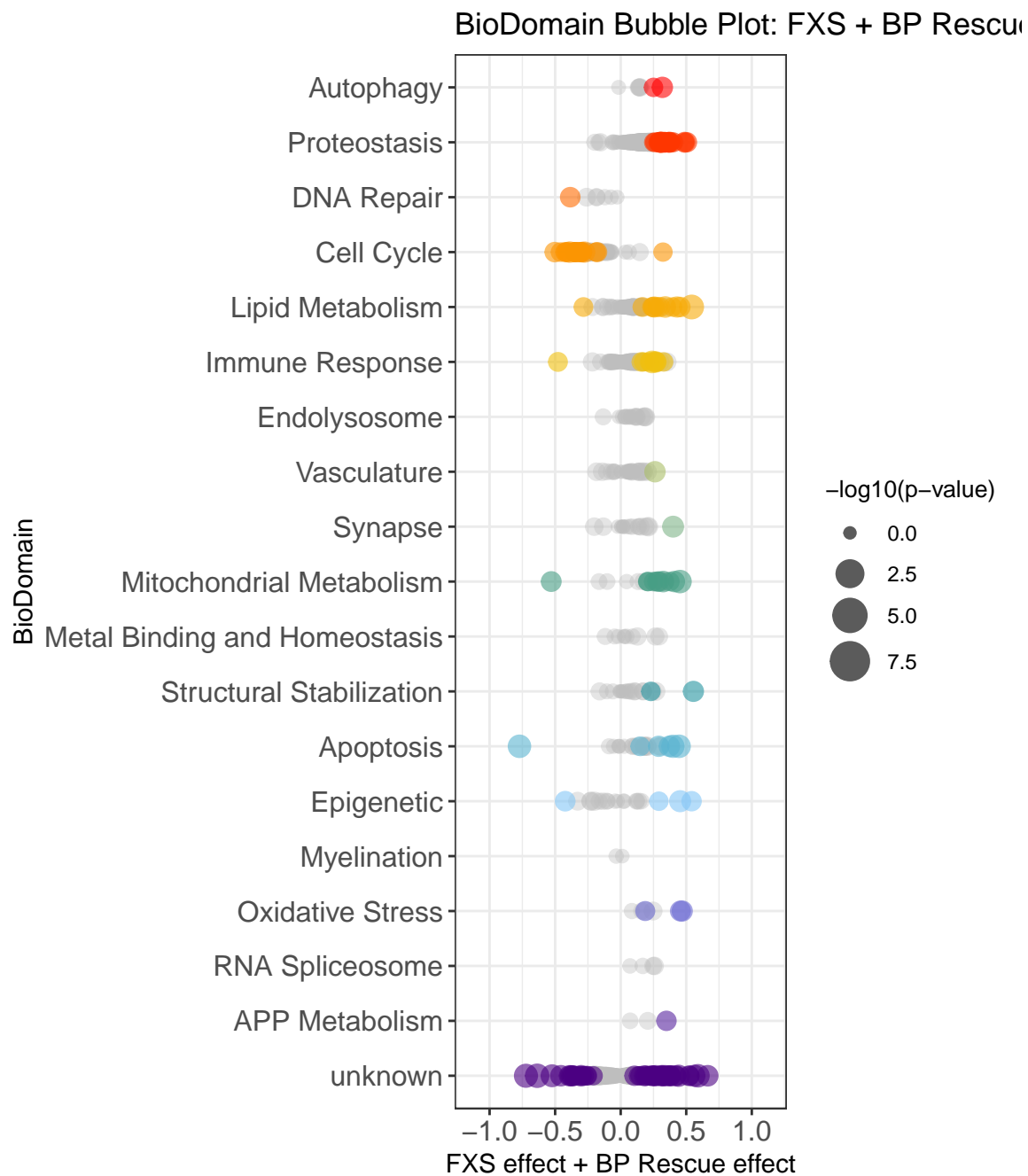
[1] "FXS + BPN Rescue"

BioDomain Bubble Plot: FXS + BPN Resc
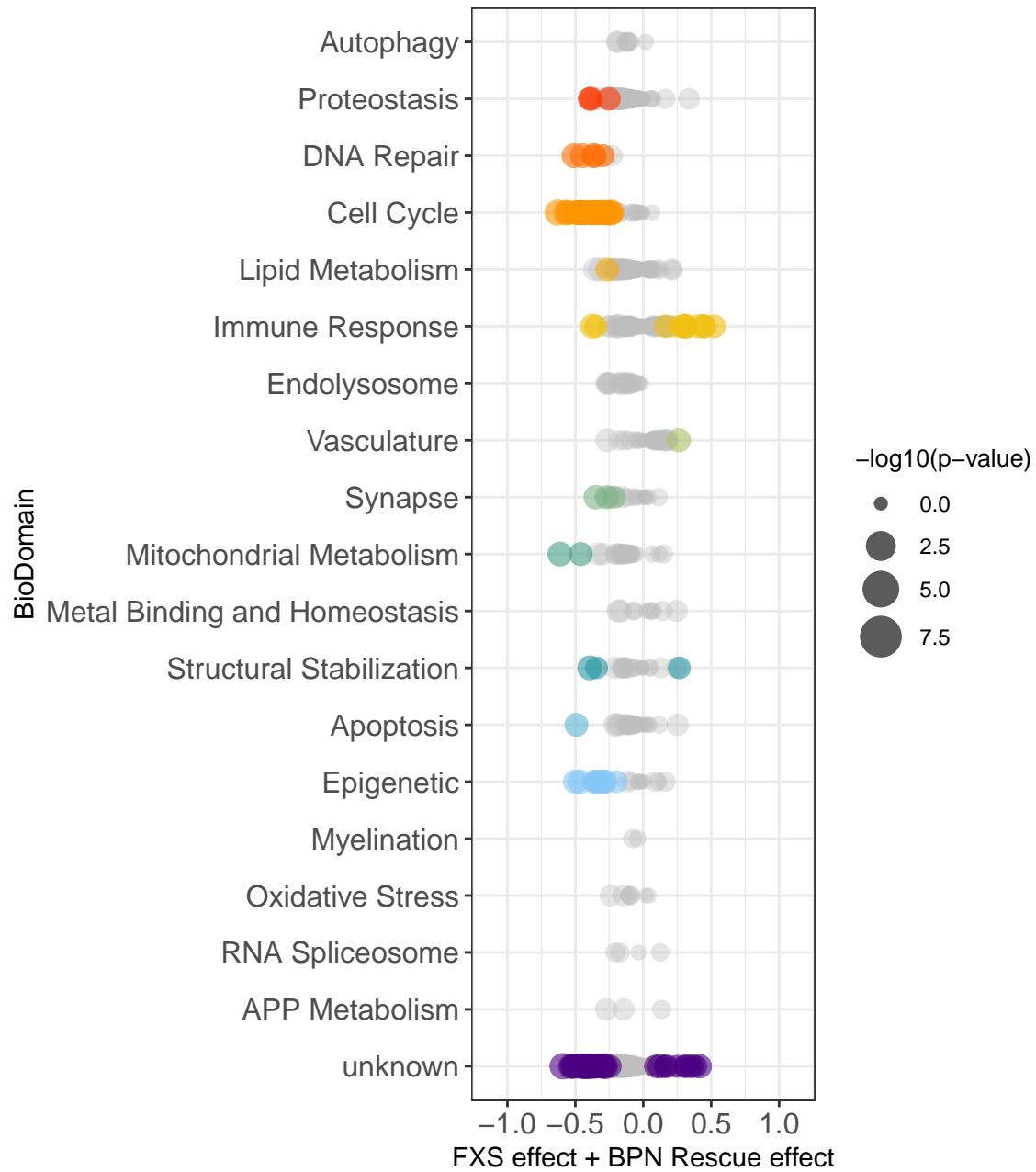
Session information

```
## 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 ve
##
## 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_1.17.0         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_1.7-3
## [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_1.50                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_3.5.2
## [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_3.3-3
```

```
##    [9] digest_0.6.37              png_0.1-8
##   [11] deldir_2.0-4               parallelly_1.43.0
##   [13] magick_2.8.6               MASS_7.3-65
##   [15] httpuv_1.6.16              qvalue_2.36.0
##   [17] withr_3.0.2                xfun_0.52
##   [19] ggfun_0.1.8                survival_3.8-3
##   [21] memoise_2.0.1              gson_0.1.0
##   [23] systemfonts_1.2.2          ragg_1.4.0
##   [25] tidytree_0.4.6             zoo_1.8-14
##   [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_0.17.0             fitdistrplus_1.2-2
##   [37] rhdf5_2.48.0               rstudioapi_0.17.1
##   [39] UCSC.utils_1.0.0           miniUI_0.1.2
##   [41] generics_0.1.3             DOSE_3.30.5
##   [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] textshaping_1.0.0          codetools_0.2-20
##   [93] BiocSingular_1.20.0        plotly_4.10.4
##   [95] mime_0.13                  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_1.6.6
##  [105] listenv_0.9.1              ggplotify_0.1.2
##  [107] statmod_1.5.0              tzdb_0.5.0
##  [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_0.2.3
## [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_2.0.0
## [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_3.1-3
## [147] bdsmatrix_1.3-7             GOSemSim_2.30.2
## [149] spatstat.univar_3.1-2       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_0.4.1
## [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_1.40.0               rsvd_1.0.5
## [183] munsell_0.5.1               KernSmooth_2.23-26
## [185] htmlwidgets_1.6.4           fgsea_1.30.0
## [187] rlang_1.1.6                 spatstat.sparse_3.1-0
## [189] spatstat.explore_3.4-2
```