

BioDomain analysis for FXS and CTRL

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Contents

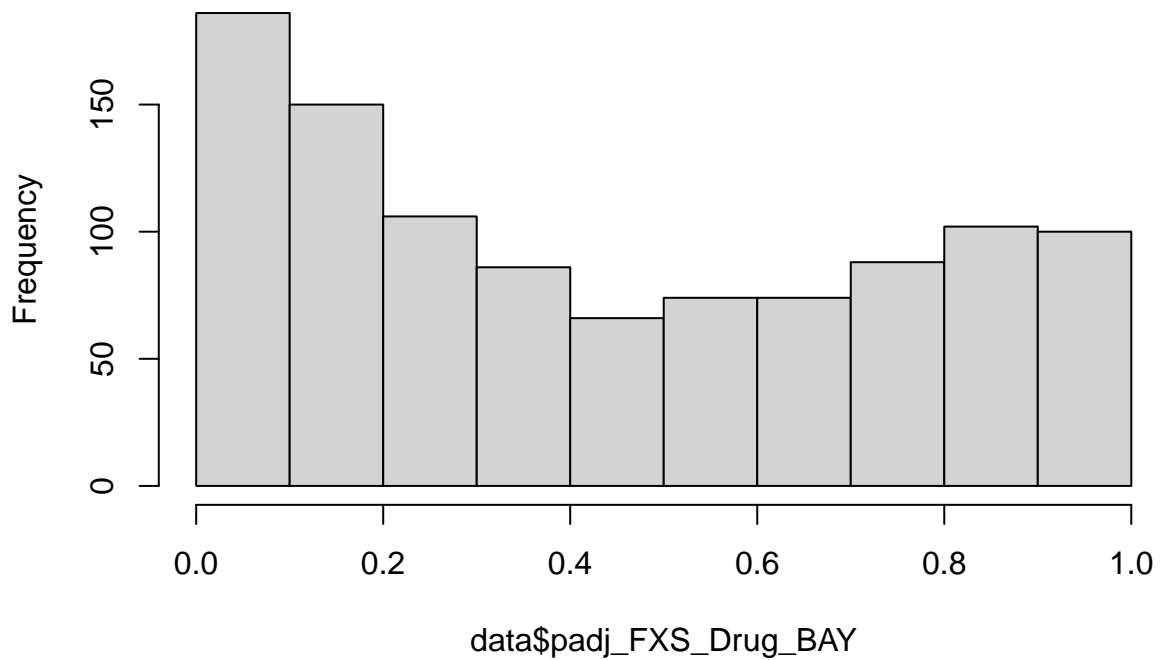
1. BioDomain analysis	2
Load the GSVA analysis	2
2. Load GSVA result	2
3. Define the fully rescue and partical rescue	7
4. Bubble plot for the BioDomain	8
Session information	12

1. BioDomain analysis

Load the GSVA analysis

2. Load GSVA result

Histogram of data\$padj_FXS_Drug_BAY



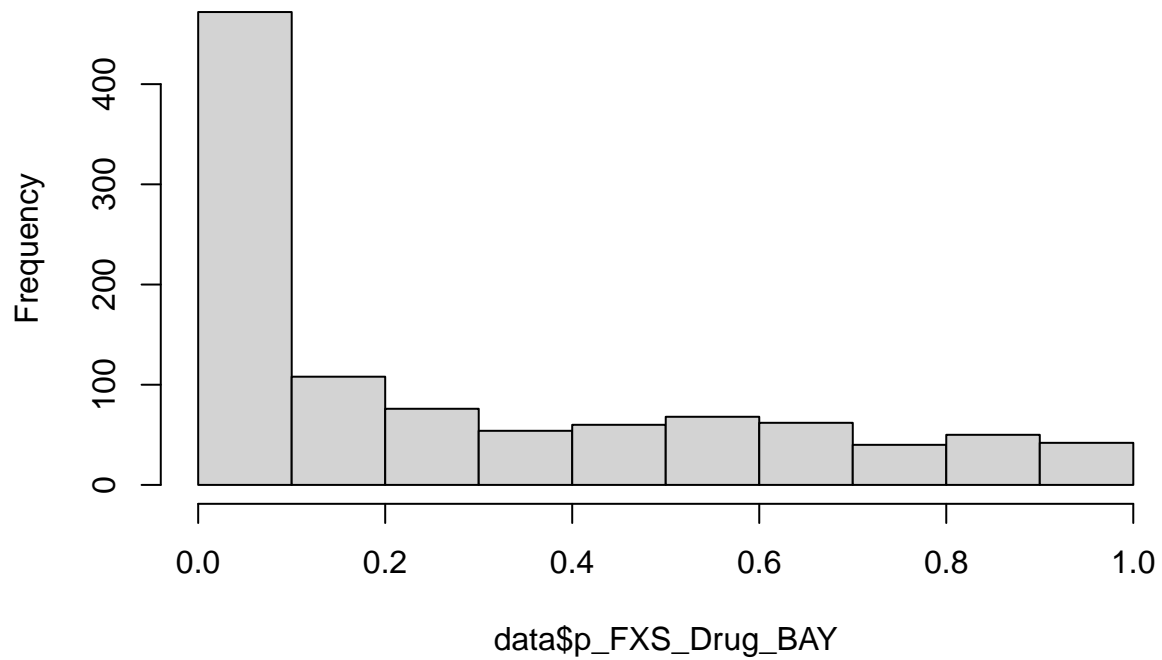
```
## [1] "padj_FXS_Drug_BAY < 0.05"
```

```
##
```

```
## FALSE TRUE
```

```
## 954 78
```

Histogram of data\$p_FXS_Drug_BAY



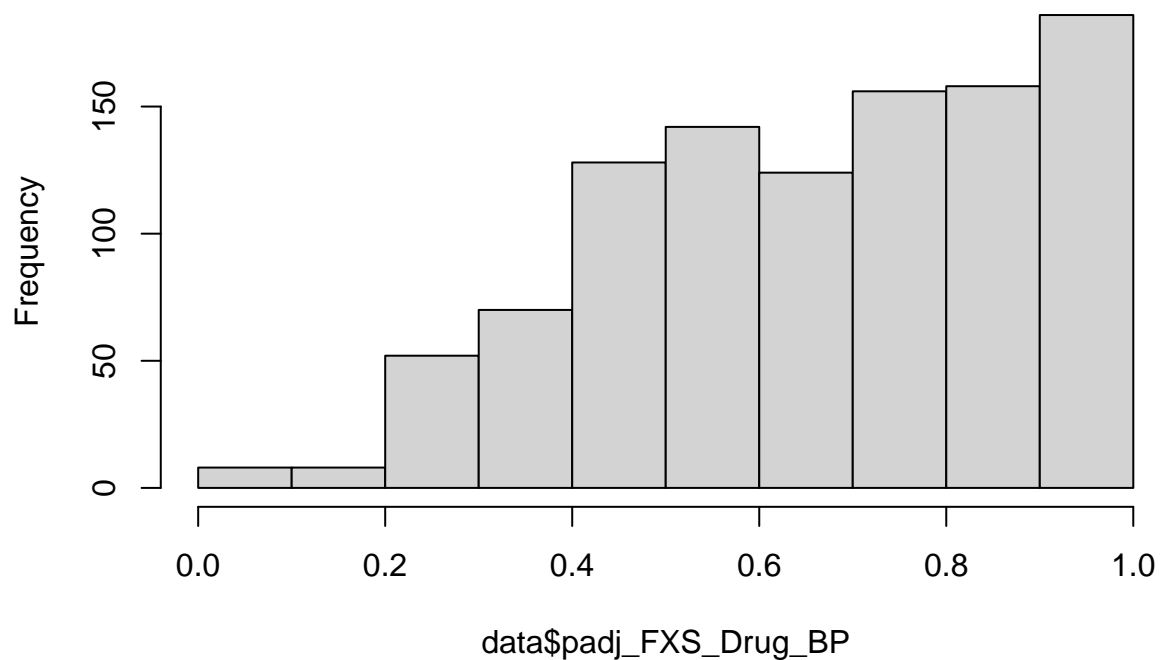
```
## [1] "p_FXS_Drug_BAY < 0.05"
```

```
##
```

```
## FALSE TRUE
```

```
## 648 384
```

Histogram of data\$padj_FXS_Drug_BP



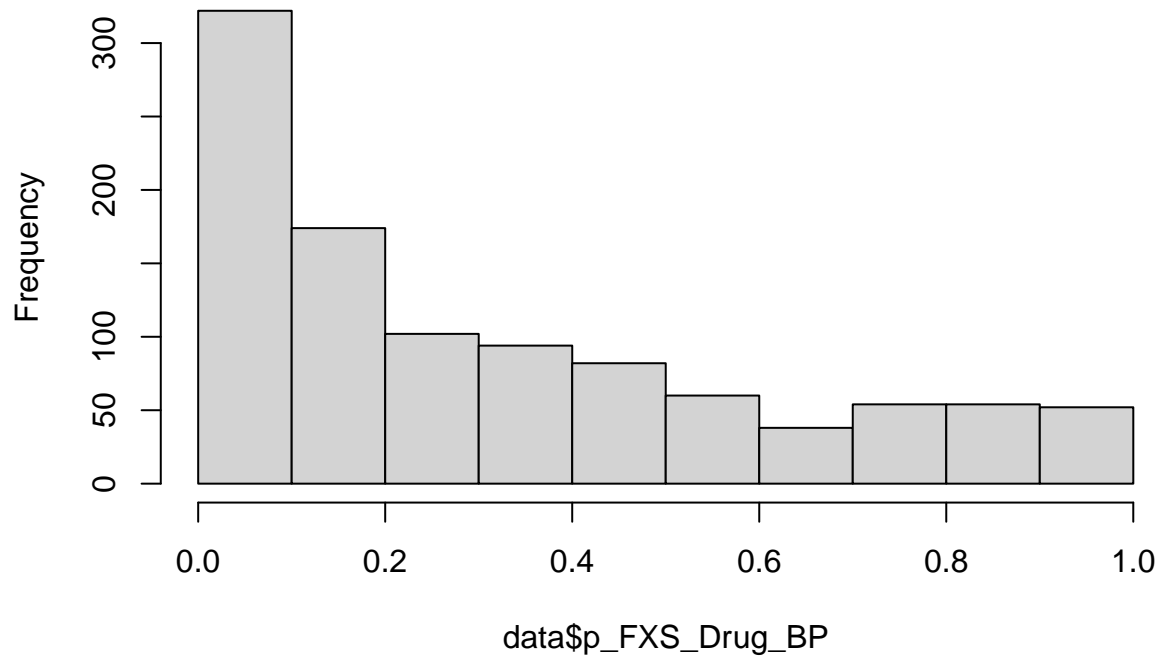
```
## [1] "p_adj_FXS_Drug_BP < 0.05"
```

```
##
```

```
## FALSE TRUE
```

```
## 1030 2
```

Histogram of data\$p_FXS_Drug_BP



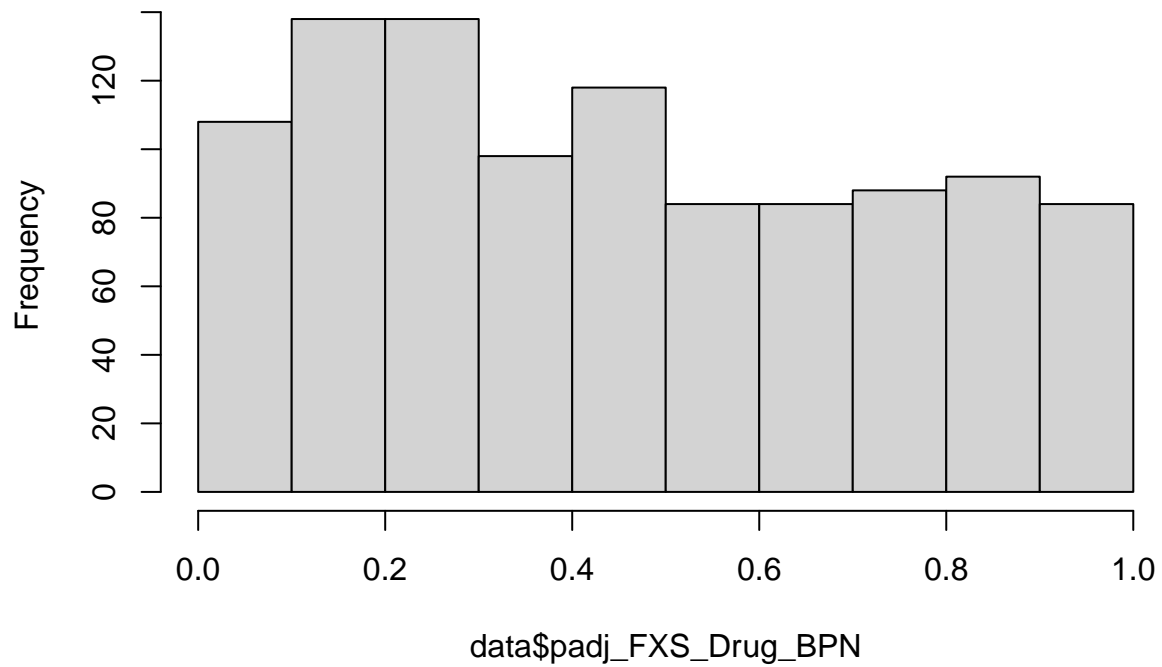
```
## [1] "p_FXS_Drug_BP < 0.05"
```

```
##
```

```
## FALSE TRUE
```

```
## 846 186
```

Histogram of data\$padj_FXS_Drug_BPN



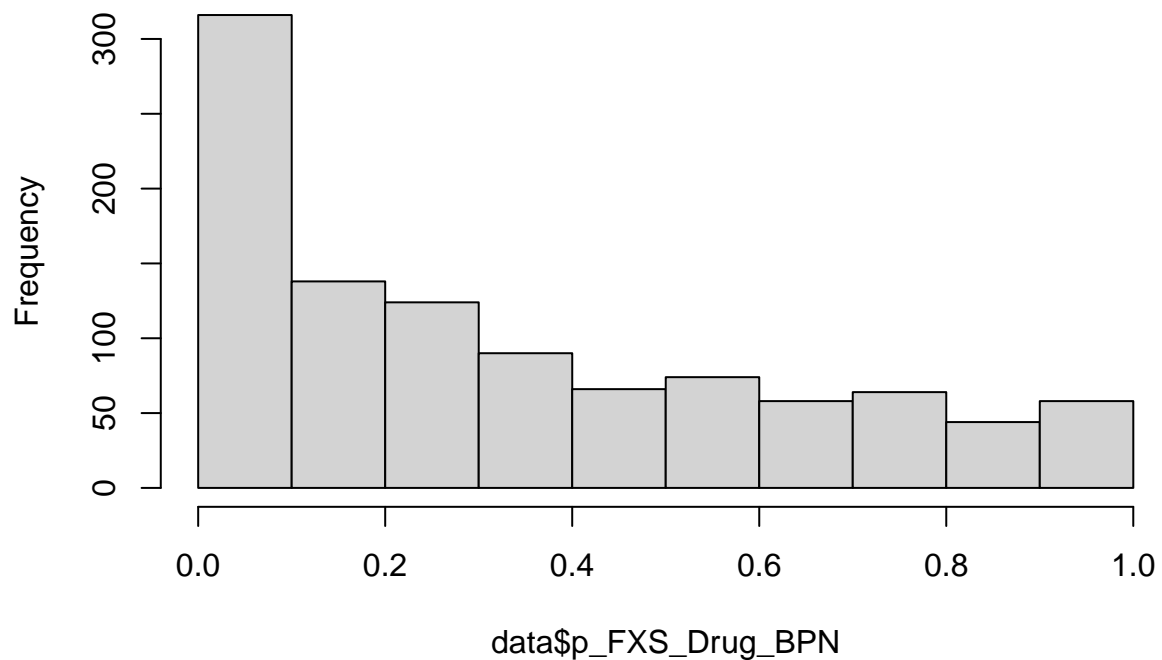
```
## [1] "padj_FXS_Drug_BPN < 0.05"
```

```
##
```

```
## FALSE TRUE
```

```
## 1026 6
```

Histogram of data\$p_FXS_Drug_BPN



```
## [1] "p_FXS_Drug_BPN < 0.05"  
##  
## FALSE TRUE  
## 824 208
```

3. Define the fully rescue and partical rescue

```
## [1] "BAY"
```

```
##
```

```
## No Side Effect    Side Effect
##           878           154
```

```
##
```

```
##    Full Rescue    No Rescue Partial Rescue    Side Effect
##           80           614           184           154
```

```
## [1] "BP"
```

```
##
```

```
## No Side Effect    Side Effect
##           506           526
```

```
##
```

```
##    Full Rescue    No Rescue Partial Rescue    Side Effect
##           16           454           36           526
```

```
## [1] "BPN"
```

```
##
```

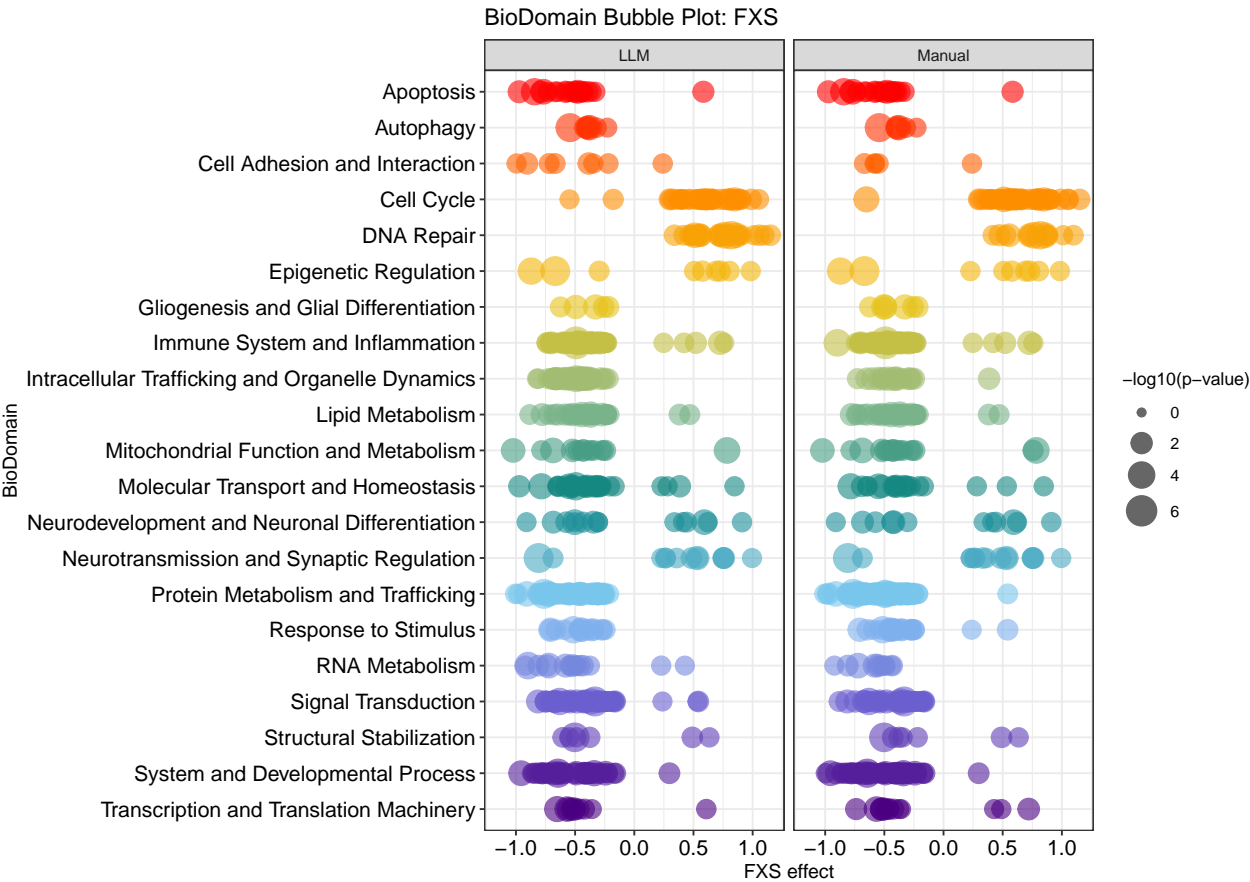
```
## No Side Effect    Side Effect
##           904           128
```

```
##
```

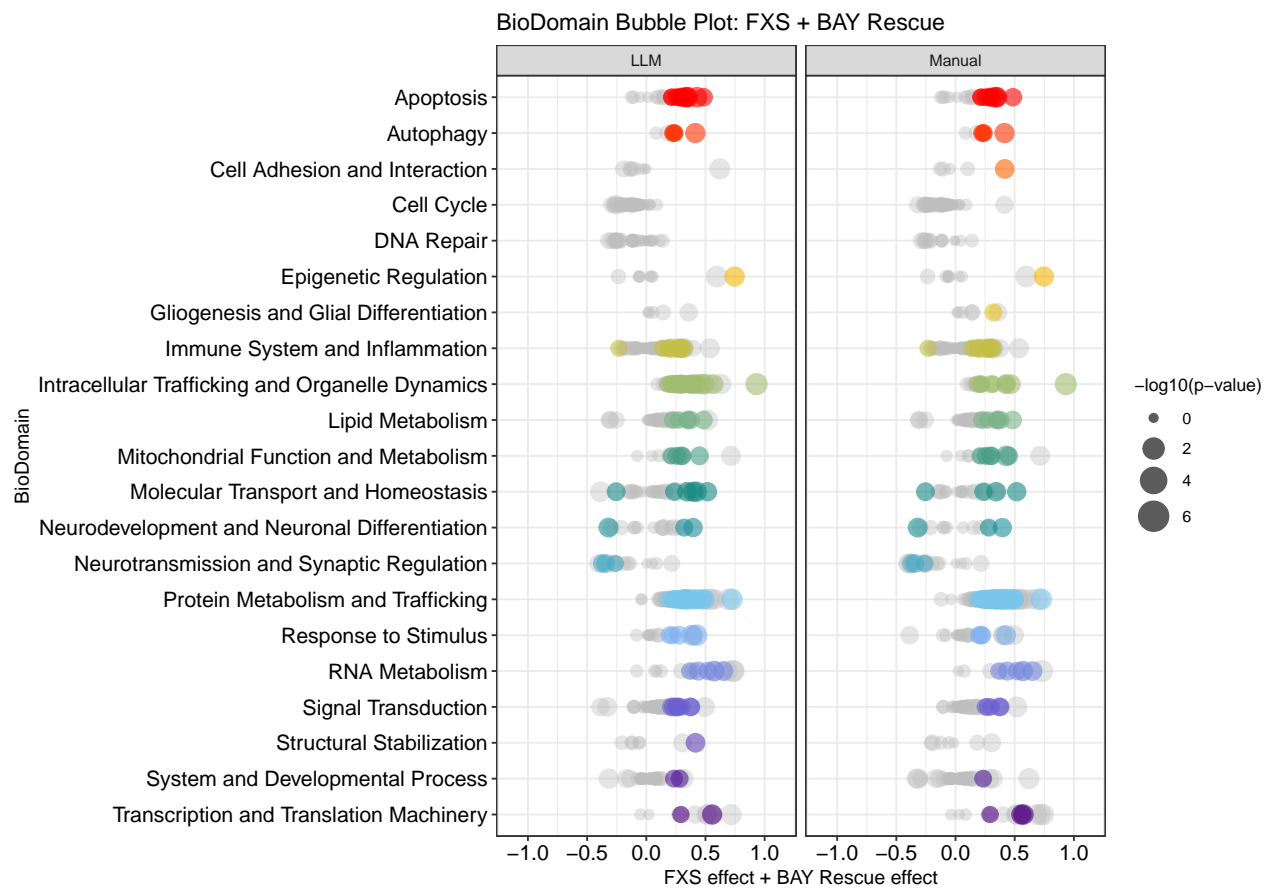
```
##    Full Rescue    No Rescue Partial Rescue    Side Effect
##           56           756           92           128
```

4. Bubble plot for the BioDomain

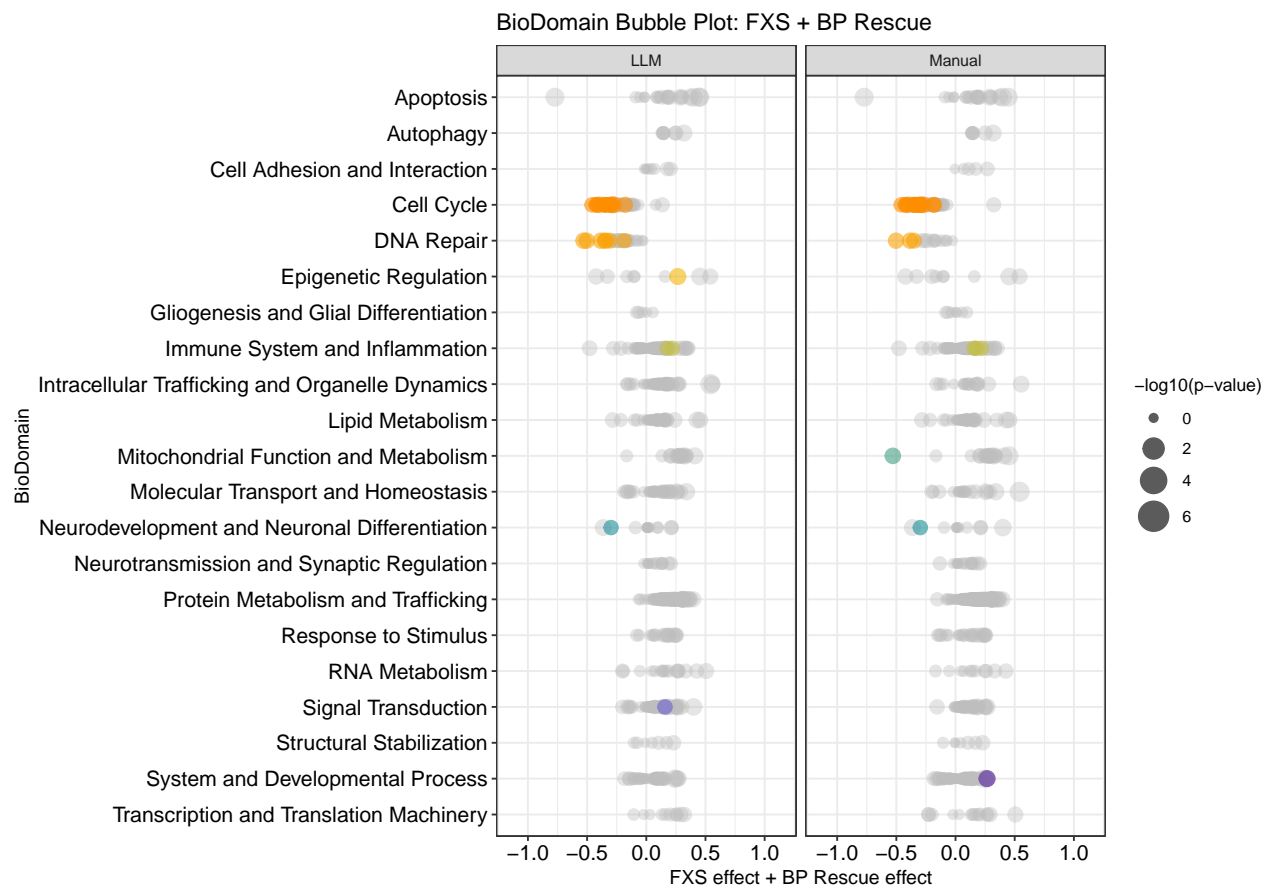
[1] "FXS"



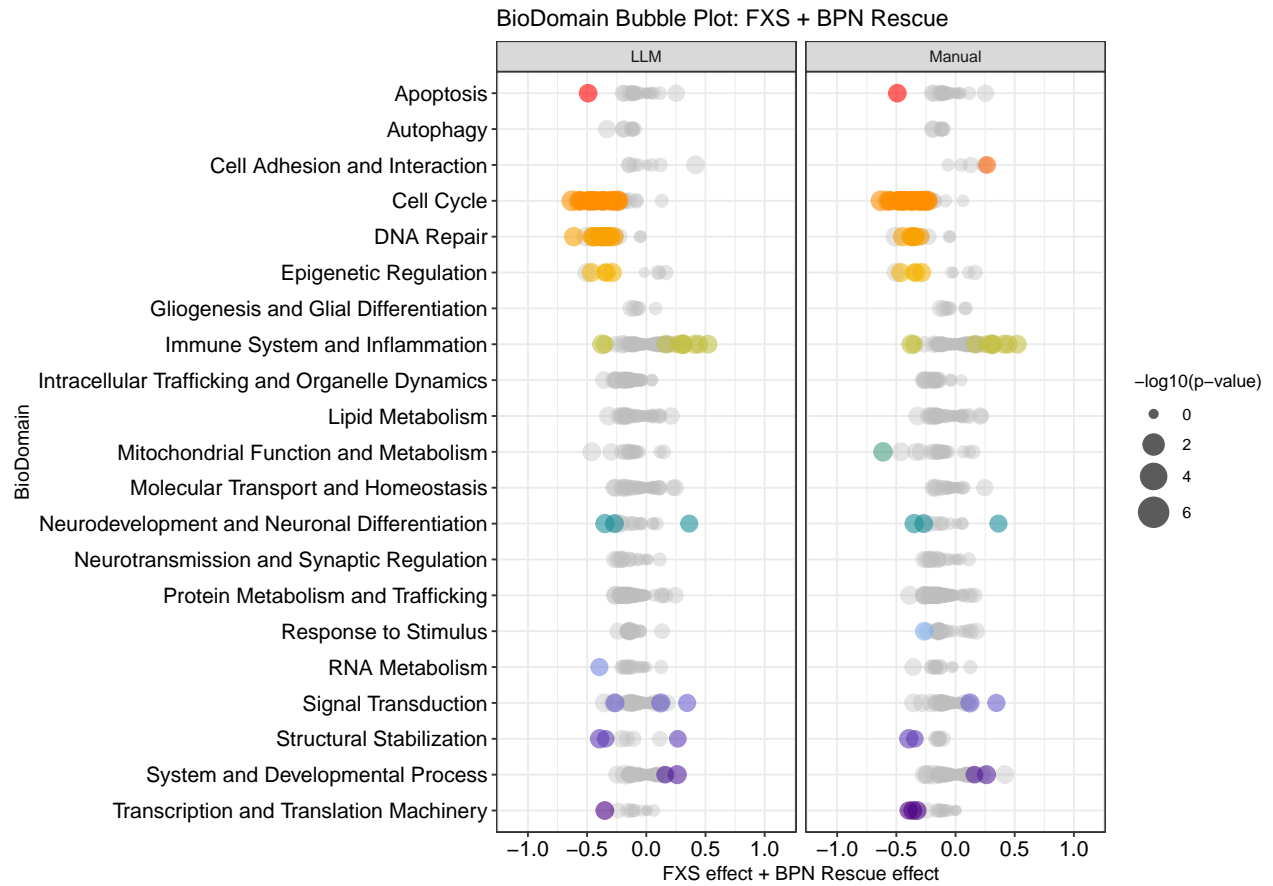
[1] "FXS_+_BAY_Rescue"



```
## [1] "FXS_+_BP_Rescue"
```



```
## [1] "FXS+_BPN_Rescue"
```



Session information

```
## R version 4.4.0 (2024-04-24)
## Platform: aarch64-apple-darwin20
## Running under: macOS 15.5
##
## 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_1.17.4 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_1.7-3
## [33] Signac_1.14.0 Seurat_5.3.0
## [35] SeuratObject_5.1.0 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] 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_3.4-1	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	systemfonts_1.2.3
## [25] ragg_1.4.0	tidytree_0.4.6
## [27] zoo_1.8-14	pbapply_1.7-2
## [29] R.oo_1.27.1	prettyunits_1.2.0
## [31] KEGGREST_1.44.1	promises_1.3.3
## [33] httr_1.4.7	restfulr_0.0.15
## [35] rhdf5filters_1.16.0	globals_0.18.0
## [37] fitdistrplus_1.2-2	rhdf5_2.48.0
## [39] rstudioapi_0.17.1	UCSC.utils_1.0.0
## [41] miniUI_0.1.2	generics_0.1.4
## [43] DOSE_3.30.5	curl_6.2.3
## [45] zlibbioc_1.50.0	ScaledMatrix_1.12.0
## [47] ggraph_2.2.1	polyclip_1.10-7
## [49] GenomeInfoDbData_1.2.12	SparseArray_1.4.8
## [51] xtable_1.8-4	evaluate_1.0.3
## [53] S4Arrays_1.4.1	BiocFileCache_2.12.0
## [55] hms_1.1.3	irlba_2.3.5.1
## [57] colorspace_2.1-1	filelock_1.0.3
## [59] ROCR_1.0-11	reticulate_1.42.0
## [61] spatstat.data_3.1-6	magrittr_2.0.3
## [63] lmtest_0.9-40	later_1.4.2
## [65] viridis_0.6.5	ggtree_3.12.0
## [67] lattice_0.22-7	spatstat.geom_3.4-1
## [69] future.apply_1.11.3	scattermore_1.2
## [71] shadowtext_0.1.4	cowplot_1.1.3
## [73] RcppAnnoy_0.0.22	pillar_1.10.2
## [75] nlme_3.1-168	compiler_4.4.0
## [77] beachmat_2.20.0	RSpectra_0.16-2
## [79] stringi_1.8.7	tensor_1.5
## [81] GenomicAlignments_1.40.0	plyr_1.8.9
## [83] crayon_1.5.3	abind_1.4-8
## [85] BiocIO_1.14.0	gridGraphics_0.5-1
## [87] emdbook_1.3.13	locfit_1.5-9.12
## [89] graphlayouts_1.2.2	bit_4.6.0
## [91] fastmatch_1.1-6	textshaping_1.0.1
## [93] codetools_0.2-20	BiocSingular_1.20.0
## [95] plotly_4.10.4	mime_0.13
## [97] splines_4.4.0	Rcpp_1.0.14
## [99] fastDummies_1.7.5	sparseMatrixStats_1.16.0
## [101] dbplyr_2.5.0	Rttf2pt1_1.3.12
## [103] blob_1.2.4	here_1.0.1
## [105] fs_1.6.6	listenv_0.9.1
## [107] ggplotify_0.1.2	statmod_1.5.0
## [109] tzdb_0.5.0	tweenr_2.0.3
## [111] pkgconfig_2.0.3	tools_4.4.0
## [113] cachem_1.1.0	RSQLite_2.3.11
## [115] viridisLite_0.4.2	DBI_1.2.3

## [117] numDeriv_2016.8-1.1	fastmap_1.2.0
## [119] rmarkdown_2.29	scales_1.4.0
## [121] grid_4.4.0	ica_1.0-3
## [123] Rsamtools_2.20.0	coda_0.19-4.1
## [125] dotCall64_1.2	RANN_2.6.2
## [127] farver_2.1.2	tidygraph_1.3.1
## [129] scatterpie_0.2.4	yaml_2.3.10
## [131] cli_3.6.5	lifecycle_1.0.4
## [133] uwot_0.2.3	mvtnorm_1.3-3
## [135] timechange_0.3.0	gtable_0.3.6
## [137] rjson_0.2.23	ggridges_0.5.6
## [139] progressr_0.15.1	ape_5.8-1
## [141] jsonlite_2.0.0	RcppHNSW_0.6.0
## [143] bitops_1.0-9	bit64_4.6.0-1
## [145] Rtsne_0.17	yulab.utils_0.2.0
## [147] spatstat.utils_3.1-4	bdsmatrix_1.3-7
## [149] GOSemSim_2.30.2	spatstat.univar_3.1-3
## [151] R.utils_2.13.0	lazyeval_0.2.2
## [153] shiny_1.10.0	htmltools_0.5.8.1
## [155] enrichplot_1.24.4	GO.db_3.19.1
## [157] sctransform_0.4.2	rappdirs_0.3.3
## [159] tinytex_0.57	glue_1.8.0
## [161] spam_2.11-1	httr2_1.1.2
## [163] XVector_0.44.0	RCurl_1.98-1.17
## [165] rprojroot_2.0.4	treeio_1.28.0
## [167] gridExtra_2.3	extrafontdb_1.0
## [169] igraph_2.1.4	R6_2.6.1
## [171] SingleCellExperiment_1.26.0	labeling_0.4.3
## [173] RcppRoll_0.3.1	cluster_2.1.8.1
## [175] bbmle_1.0.25.1	Rhdf5lib_1.26.0
## [177] aplot_0.2.5	DelayedArray_0.30.1
## [179] tidyselect_1.2.1	ggforce_0.4.2
## [181] xml2_1.3.8	future_1.49.0
## [183] rsvd_1.0.5	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_3.4-3	