

BioDomain analysis for FXS and CTRL

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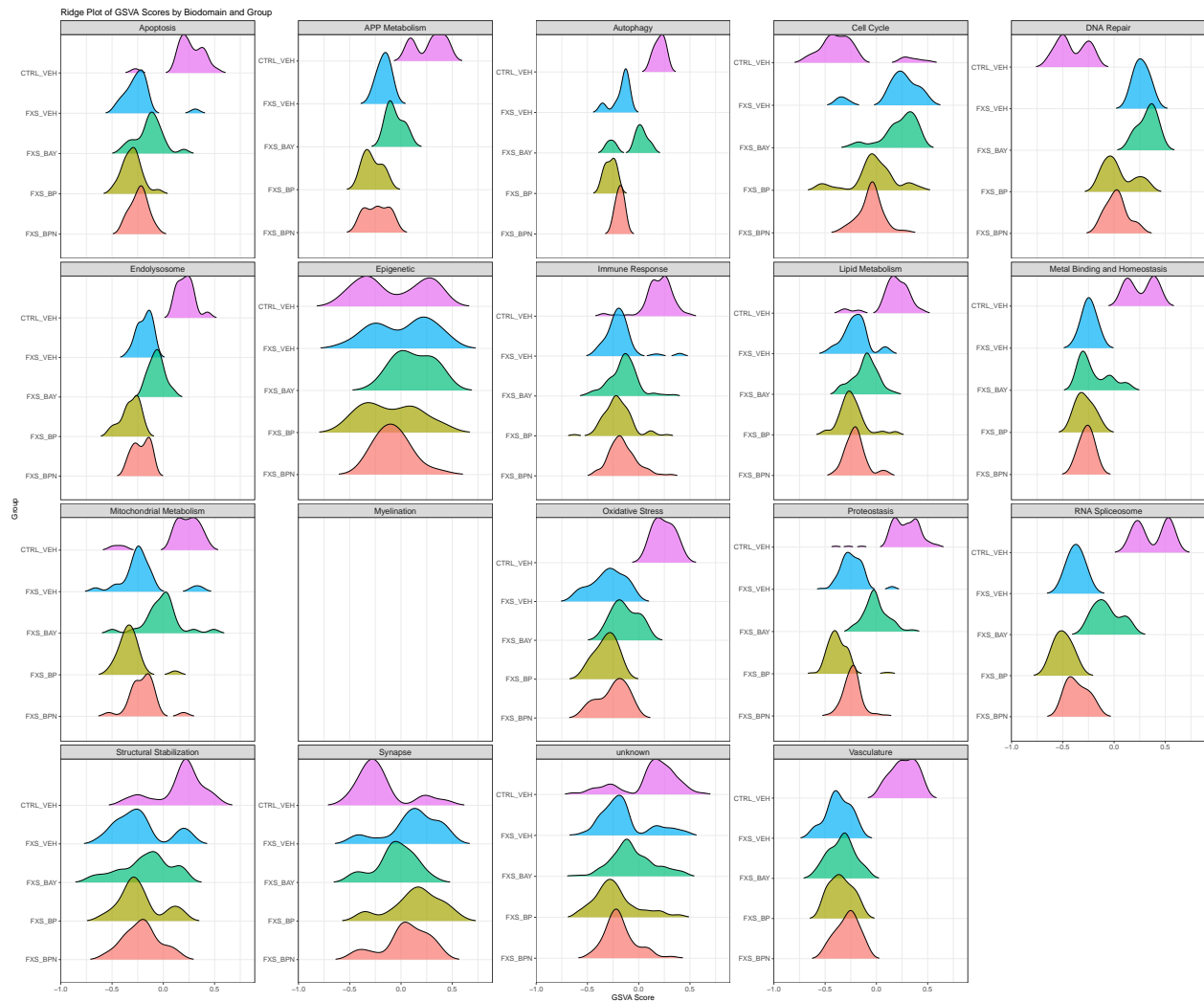
1. BioDomain analysis

Load the GSVA analysis

2.result for C03 vs A33

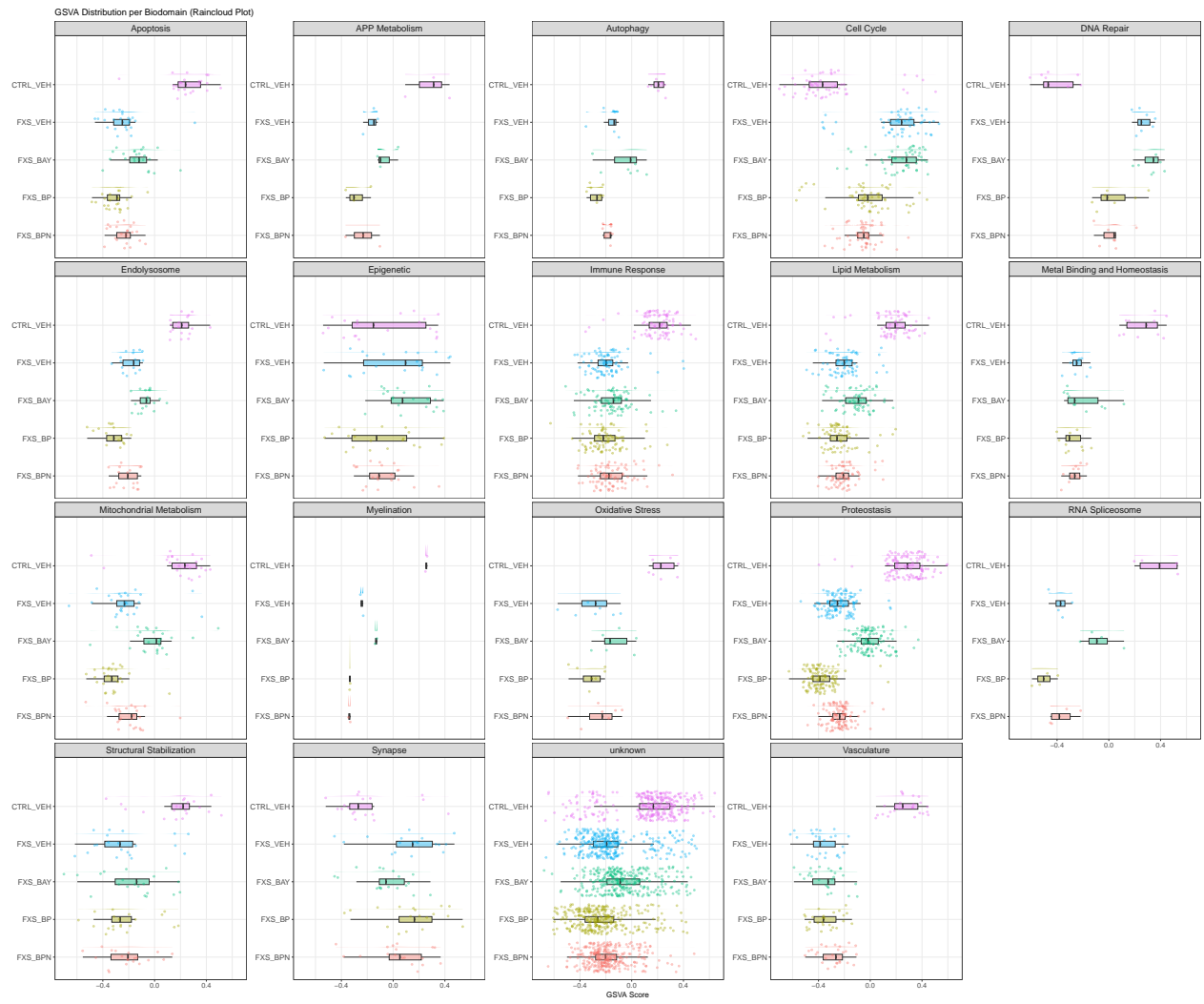
```
## [1] 806 2
```

(1) Ridge plot for GSVA score

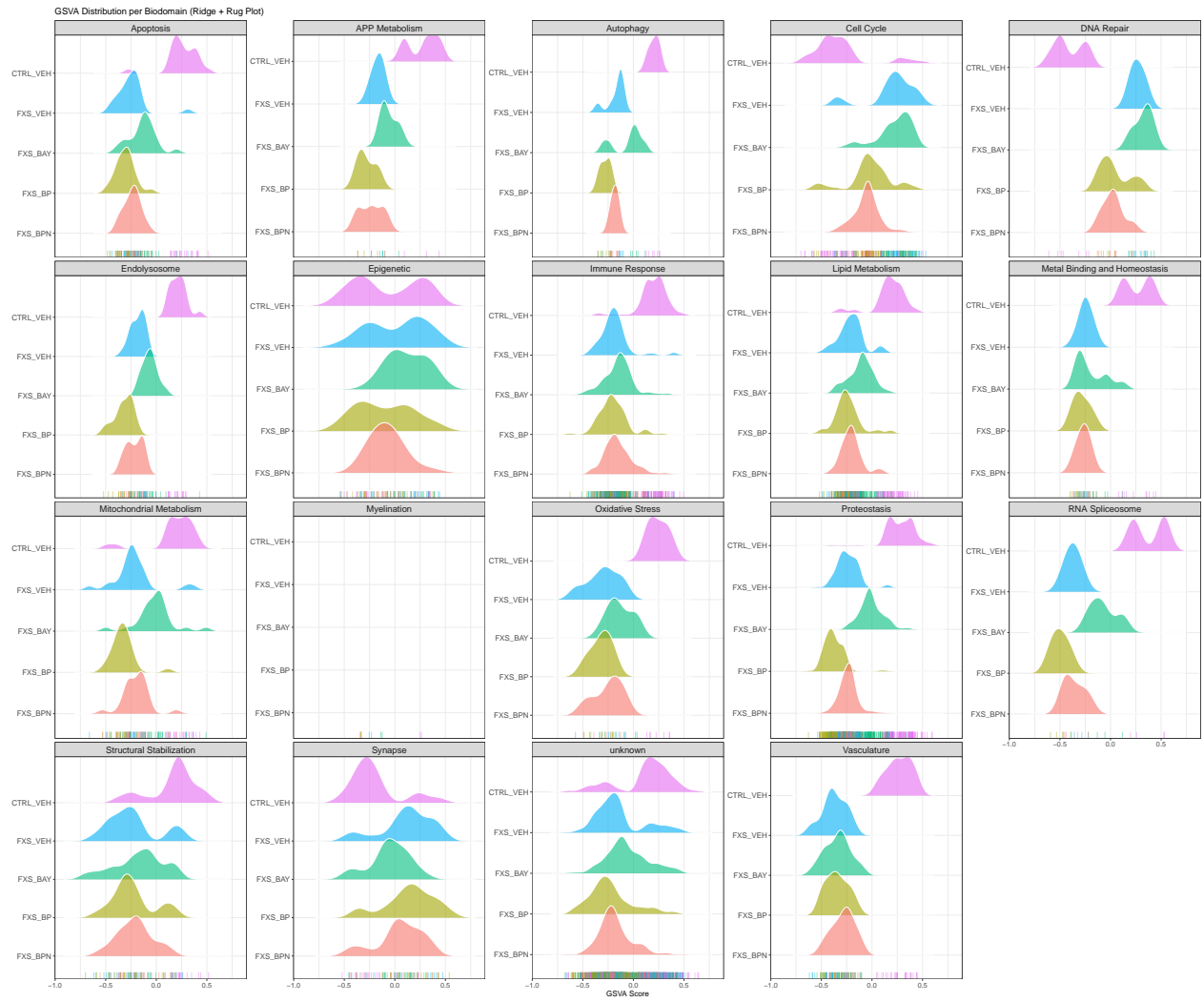


(2) Raincloud plot for GSEA score

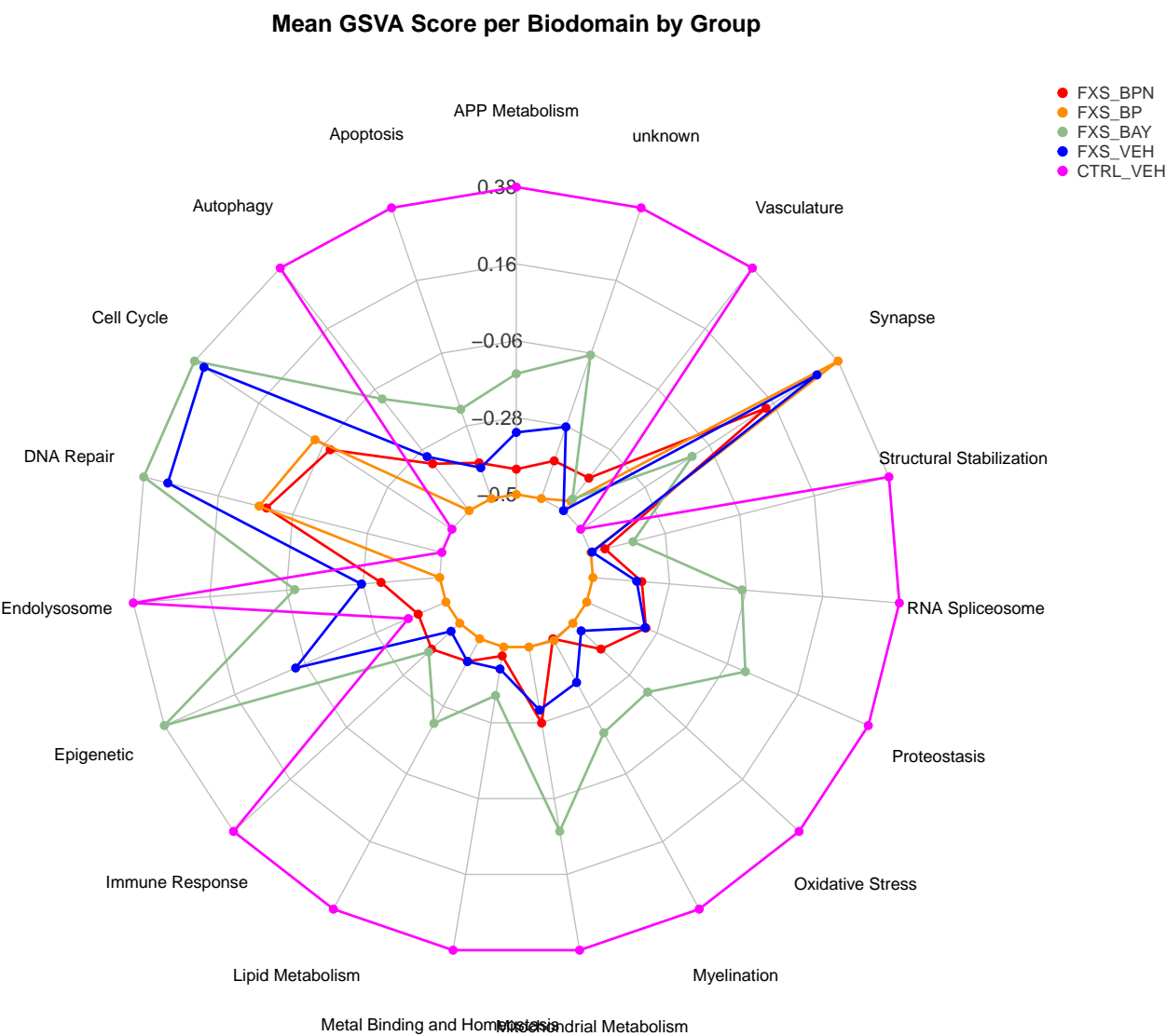




(3) Rug and density plot for GSVA score



3. Spider plot for GSVA score



pdf
2
pdf
2

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] fmsb_0.7.6 ggdist_3.3.2
## [3] ggridges_0.5.6 GSEABase_1.66.0
## [5] graph_1.82.0 annotate_1.82.0
## [7] XML_3.99-0.18 extrafont_0.19
## [9] ggsignif_0.6.4 patchwork_1.3.0
## [11] decoupleR_2.10.0 GSVA_1.52.3
## [13] BiocParallel_1.38.0 edgeR_4.2.2
## [15] limma_3.60.6 GenomicFeatures_1.56.0
## [17] biomaRt_2.60.1 gprofiler2_0.2.3
## [19] RColorBrewer_1.1-3 data.table_1.17.0
## [21] org.Hs.eg.db_3.19.1 AnnotationDbi_1.66.0
## [23] clusterProfiler_4.12.6 ggfortify_0.4.17
## [25] pheatmap_1.0.12 EnhancedVolcano_1.22.0
## [27] ggrepel_0.9.6 apeglm_1.26.1
## [29] DESeq2_1.44.0 SummarizedExperiment_1.34.0
## [31] Biobase_2.64.0 MatrixGenerics_1.16.0
## [33] matrixStats_1.5.0 reshape2_1.4.4
## [35] Matrix_1.7-3 Signac_1.14.0
## [37] Seurat_5.2.1 SeuratObject_5.0.2
## [39] sp_2.2-0 rtracklayer_1.64.0
## [41] GenomicRanges_1.56.2 GenomeInfoDb_1.40.1
## [43] IRanges_2.38.1 S4Vectors_0.42.1
## [45] BiocGenerics_0.50.0 knitr_1.50
## [47] lubridate_1.9.4 forcats_1.0.0
## [49] stringr_1.5.1 dplyr_1.1.4
## [51] purrr_1.0.4 readr_2.1.5
## [53] tidyr_1.3.1 tibble_3.2.1
## [55] 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] progress_1.2.3 goftest_1.2-3
## [5] HDF5Array_1.32.1 Biostrings_2.72.1
```

##	[7]	vctr_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] progressr_0.15.1	ape_5.8-1
## [139] jsonlite_2.0.0	RcppHNSW_0.6.0
## [141] bitops_1.0-9	bit64_4.6.0-1
## [143] Rtsne_0.17	yulab.utils_0.2.0
## [145] spatstat.utils_3.1-3	bdsmatrix_1.3-7
## [147] GOSemSim_2.30.2	distributional_0.5.0
## [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	