

Analysis mutil Group

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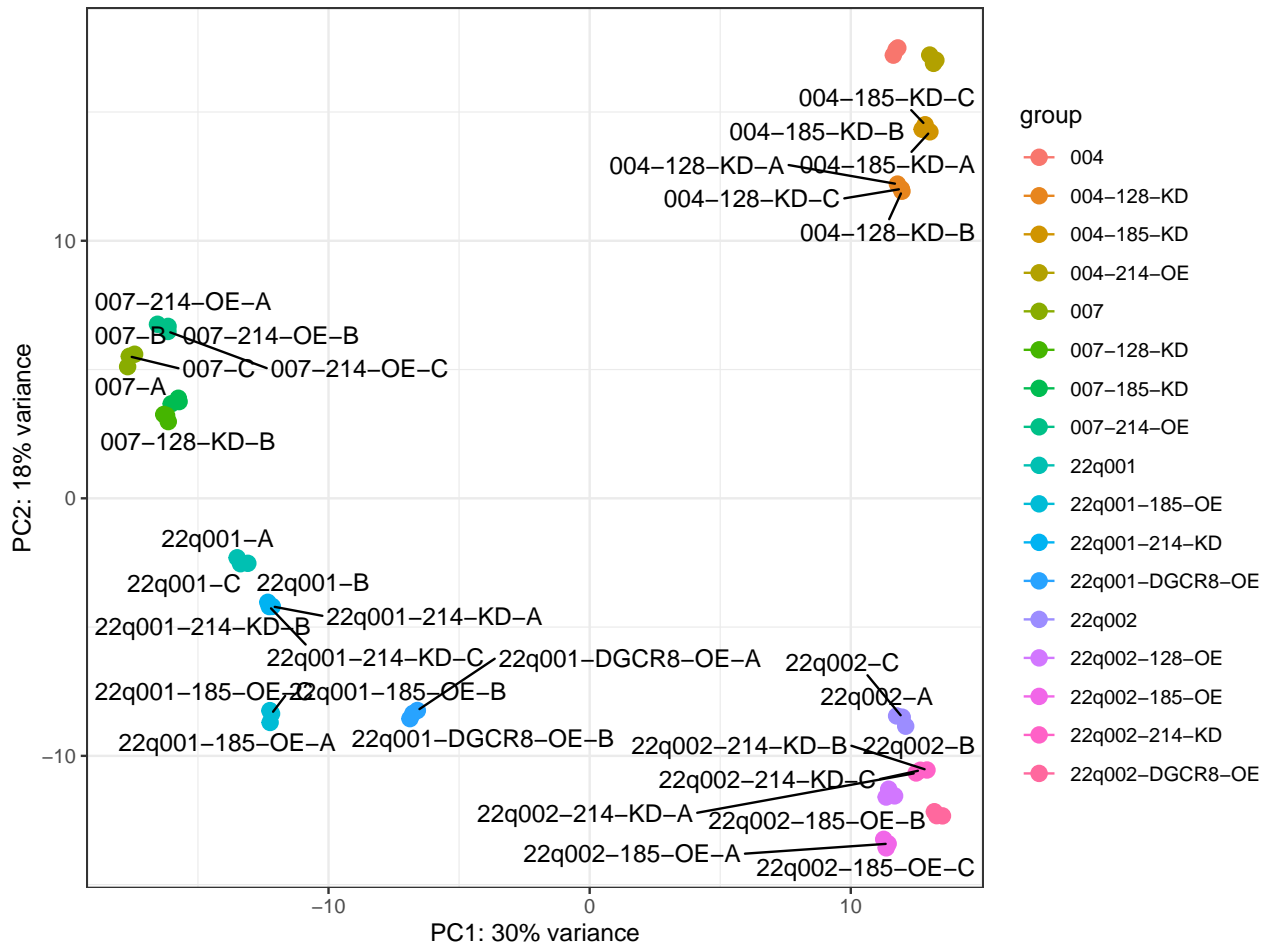
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1. Read the count data

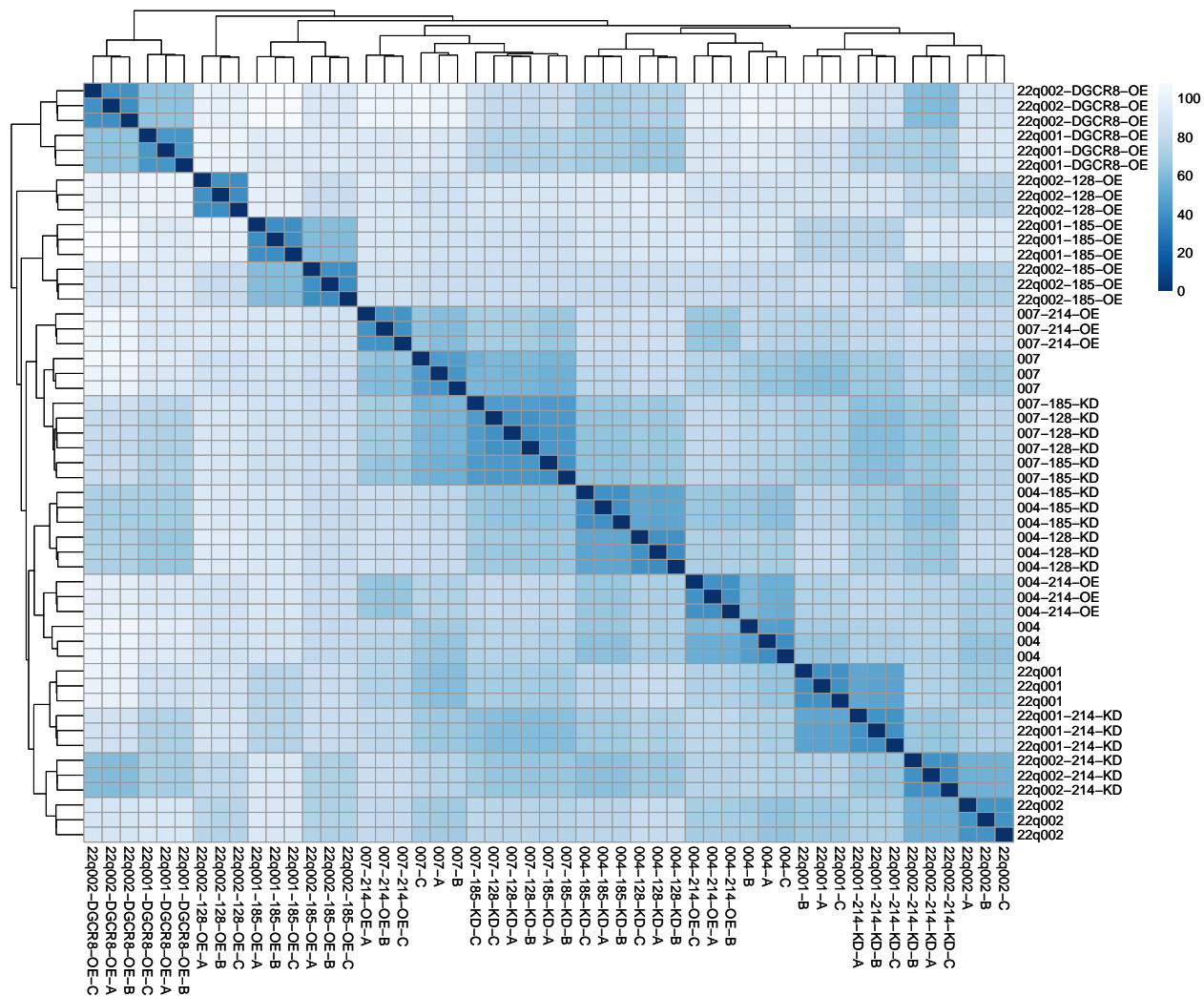
In this section, we will read the clean count data from the `synaptosomes_bulkRNA` folder. We will read the data and merge them into a single table.

2. Visualization for reuslt

(1) Sample information - PCA plot

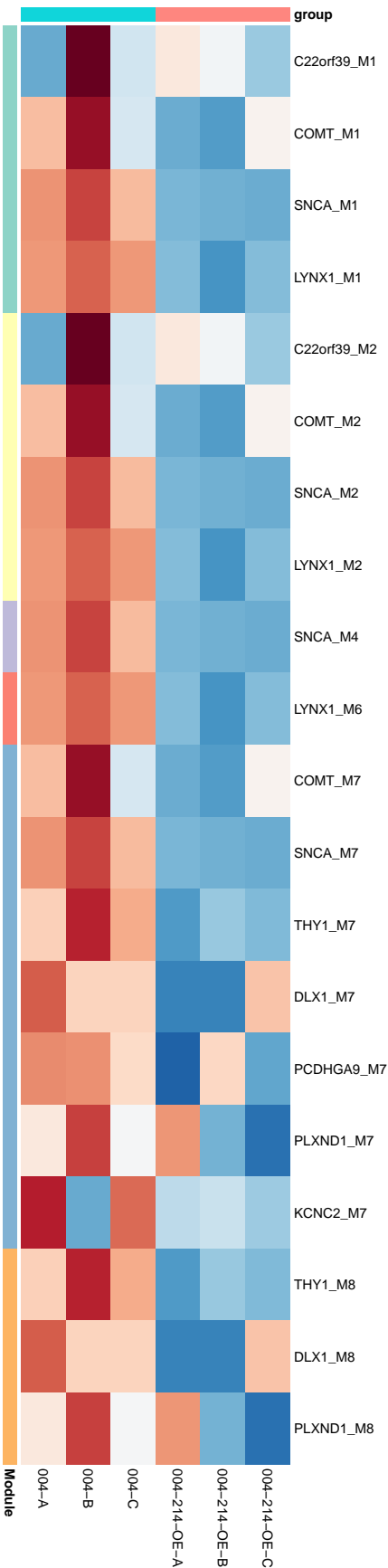


(2) Sample information - Distance heatmap

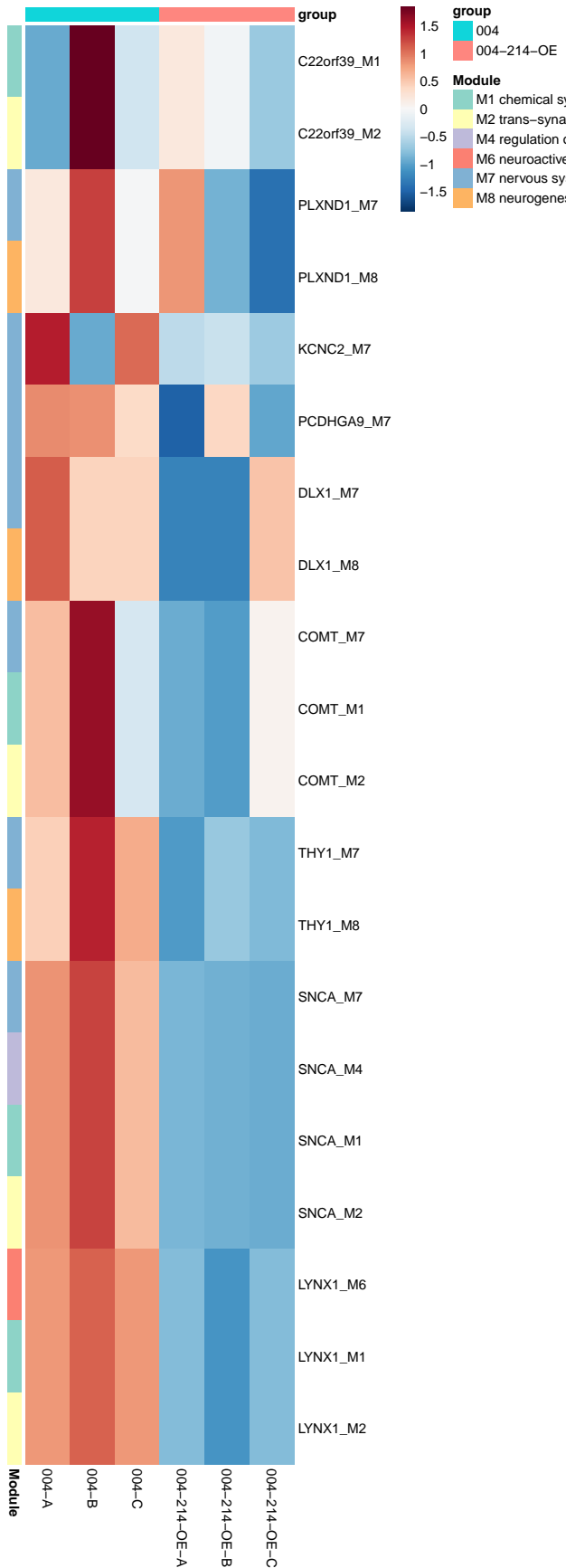


miRNA 214

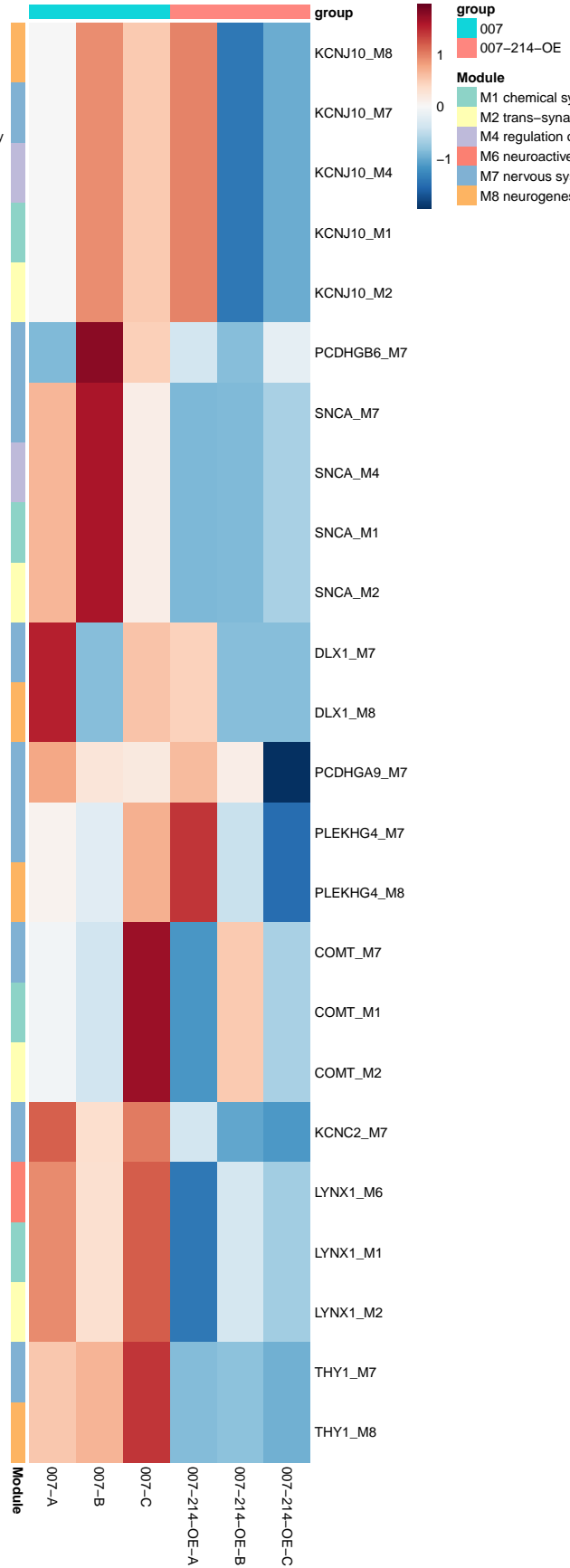
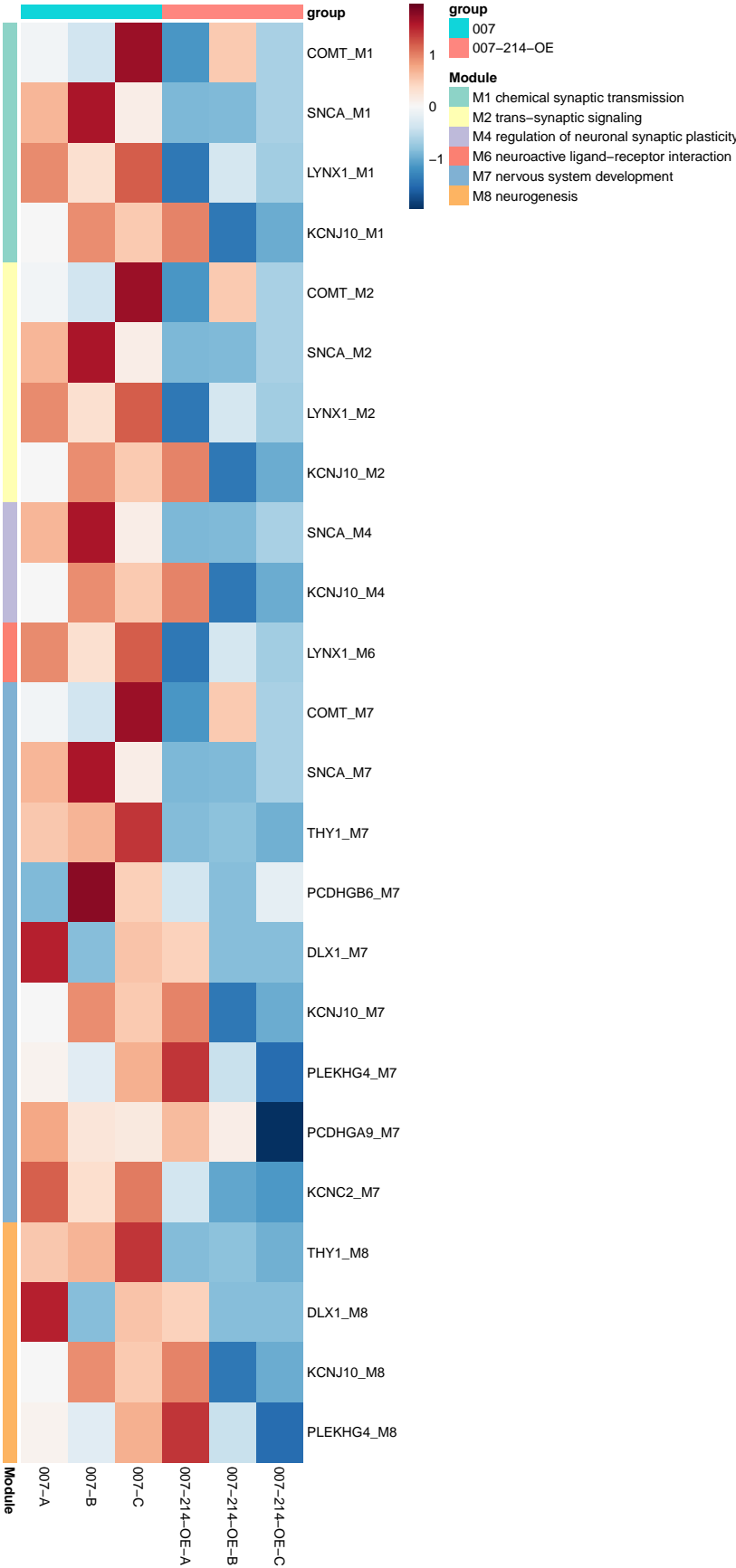
Sample 004



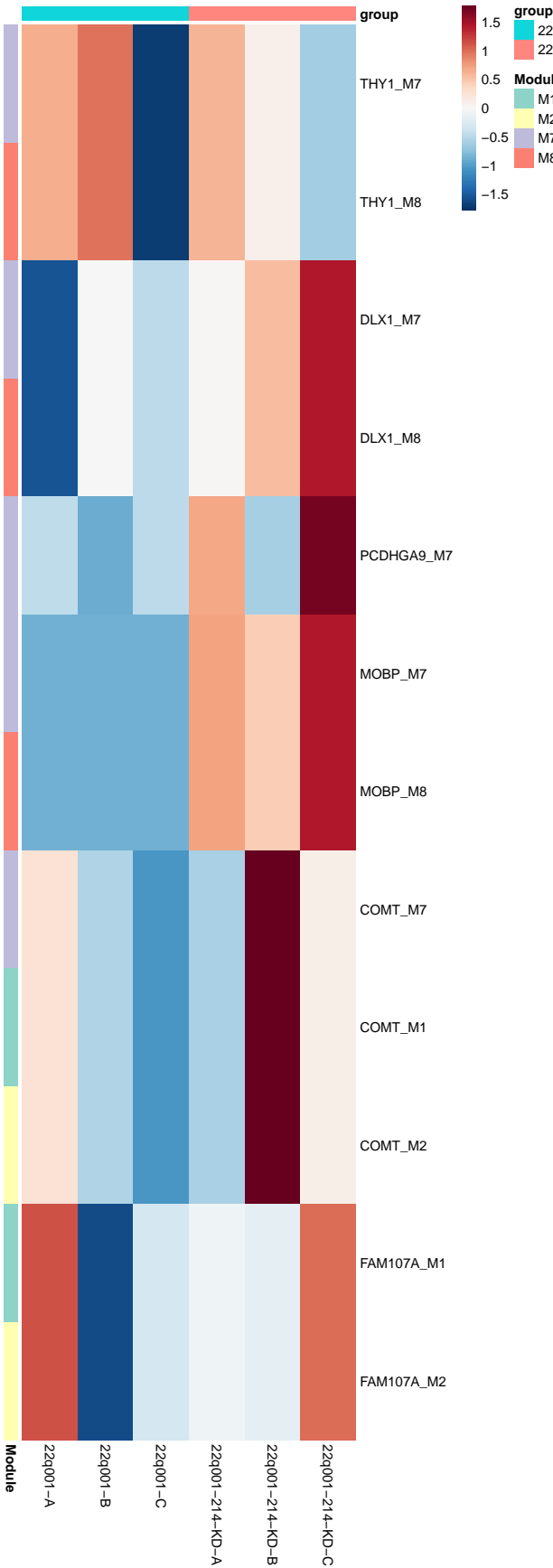
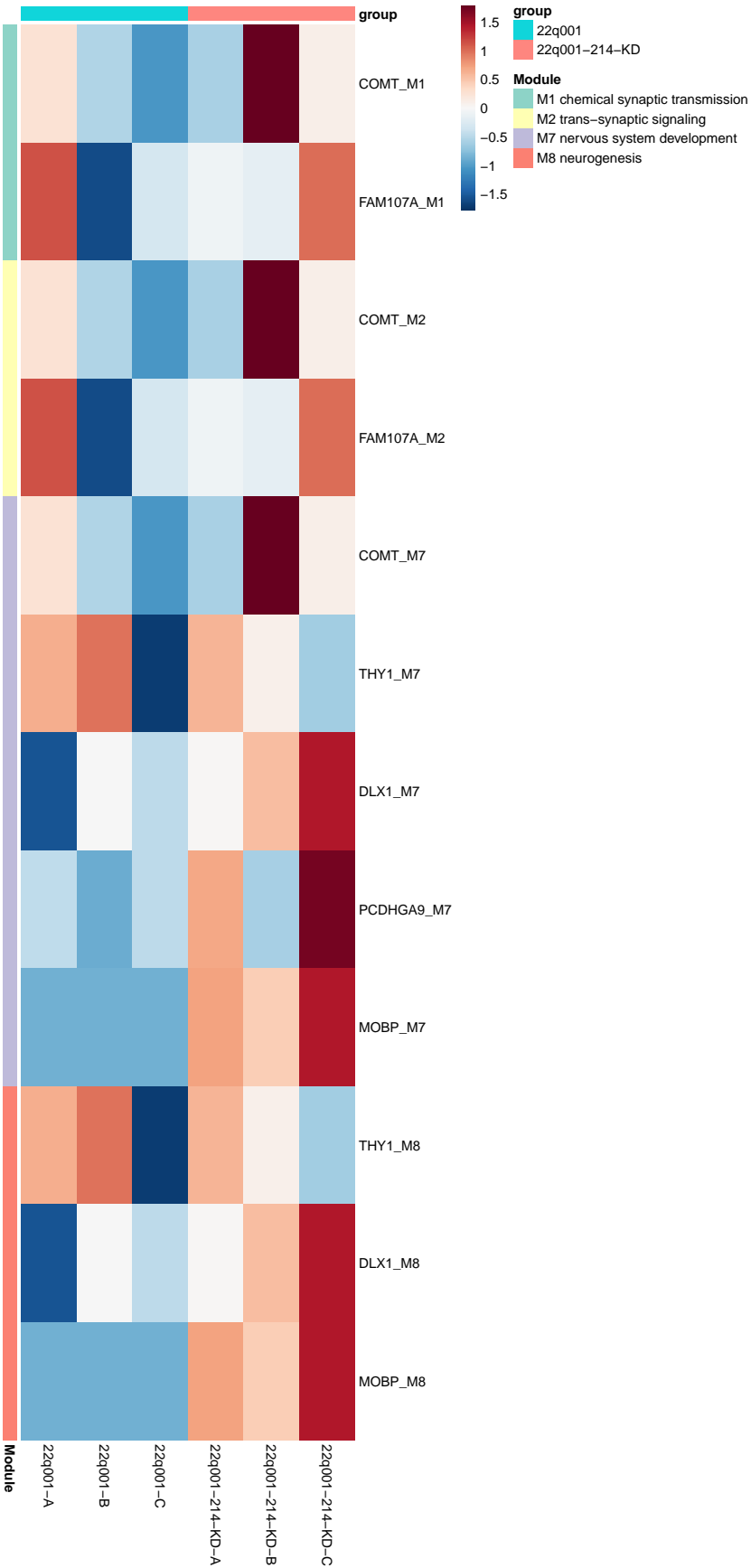
5



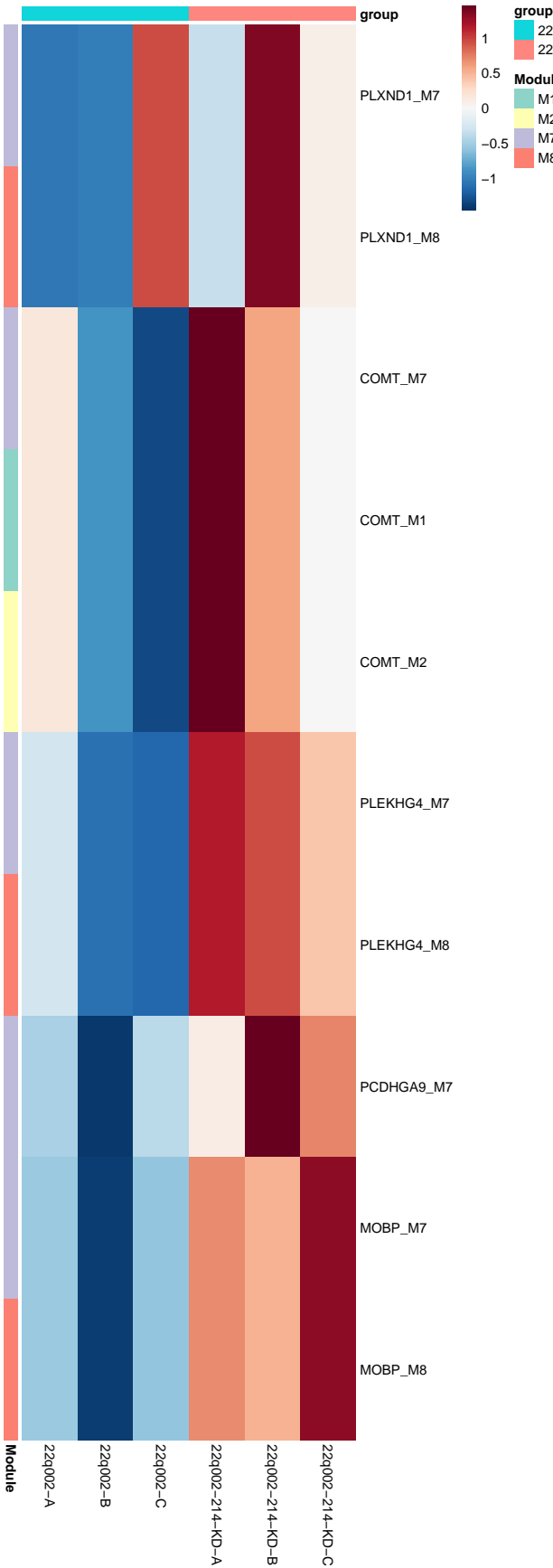
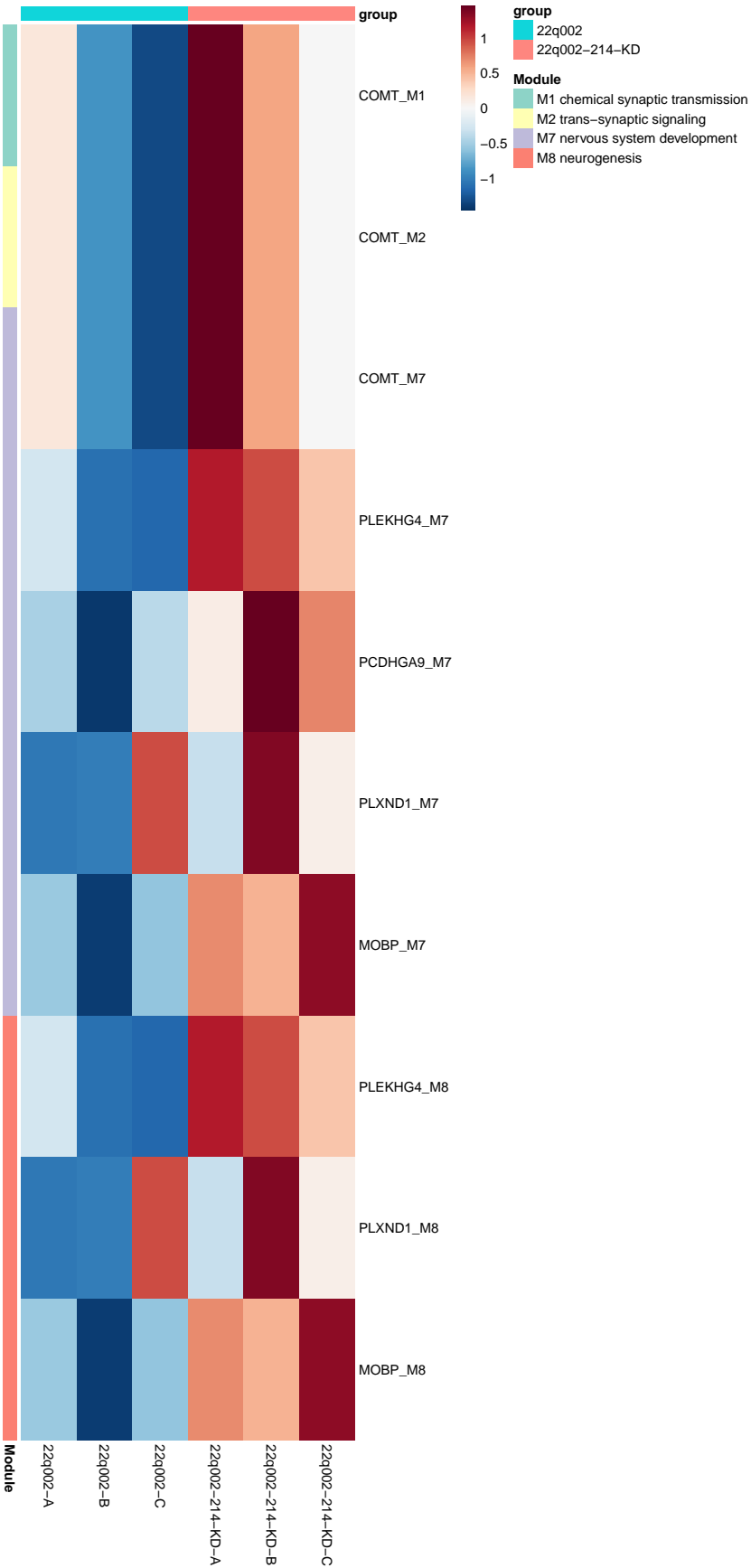
Sample 007



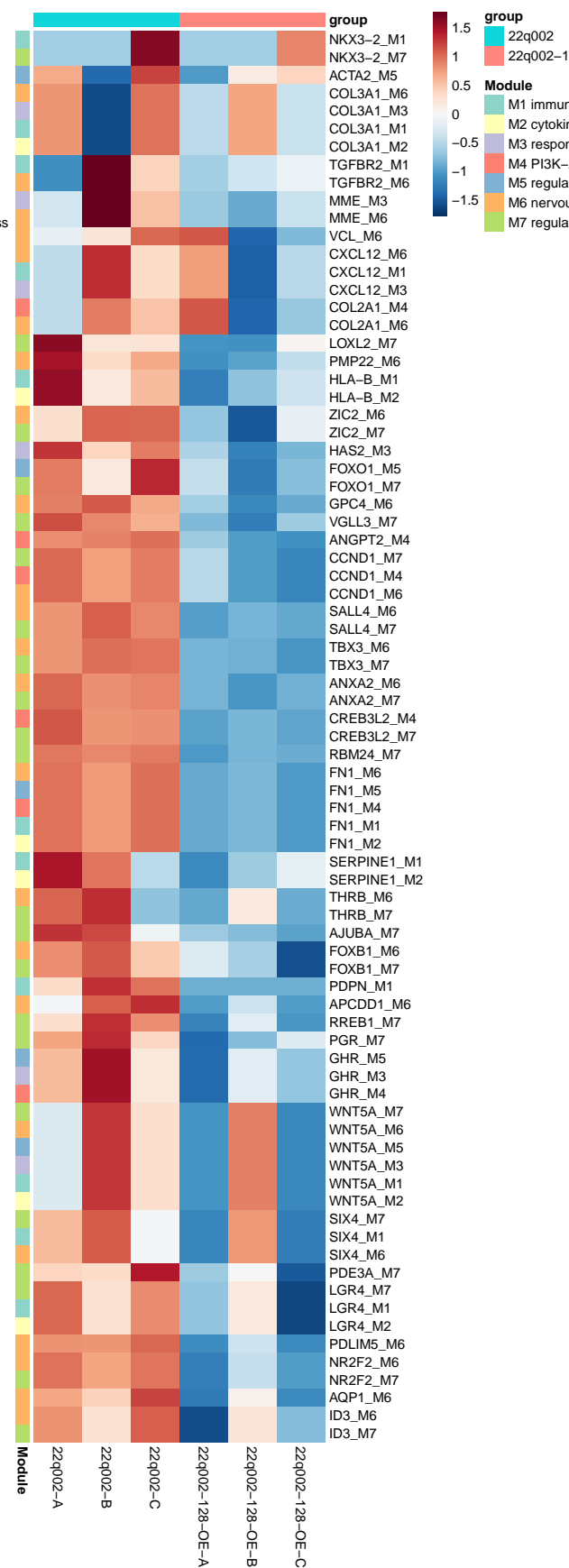
Sample 001



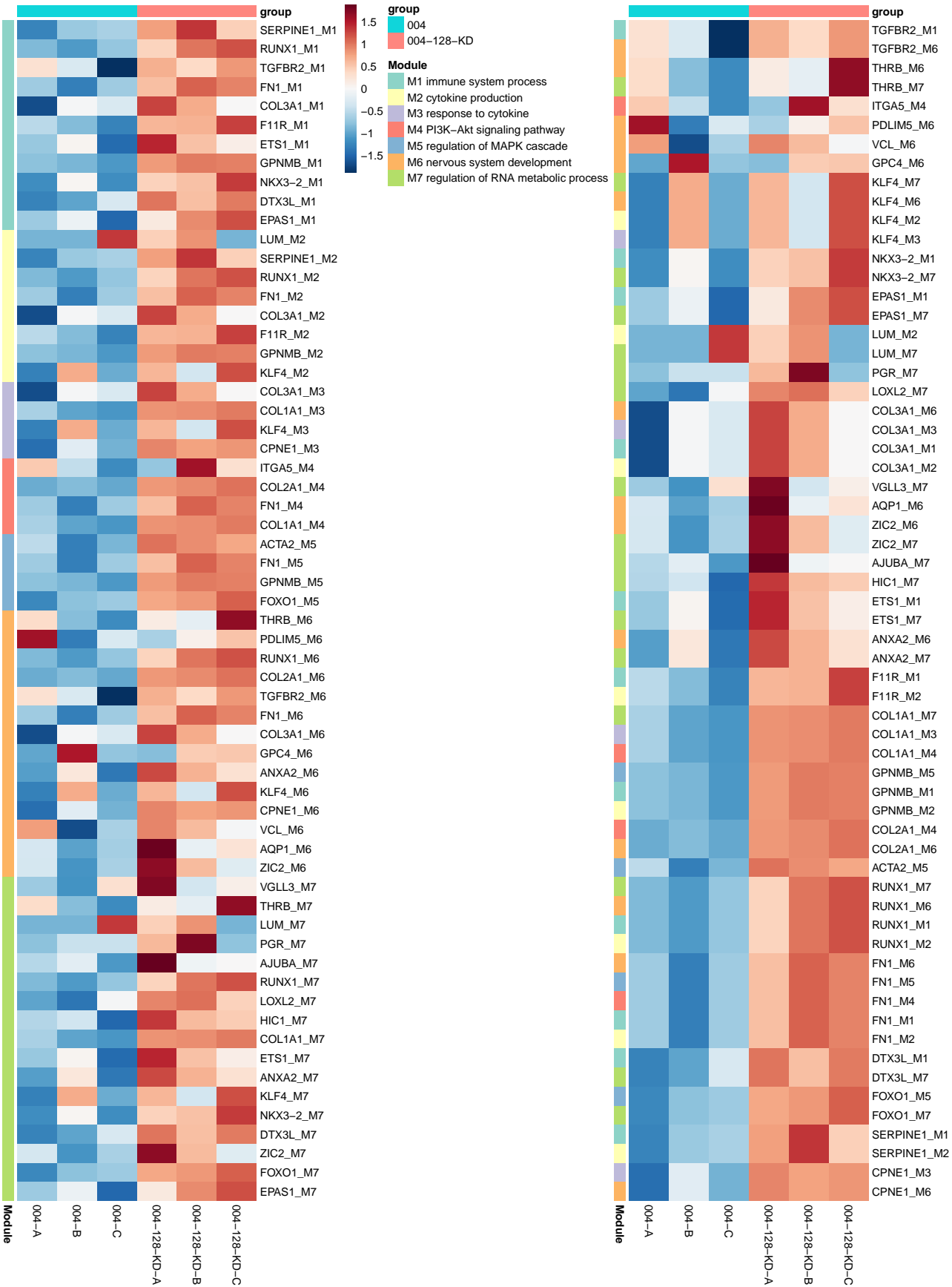
Sample 002



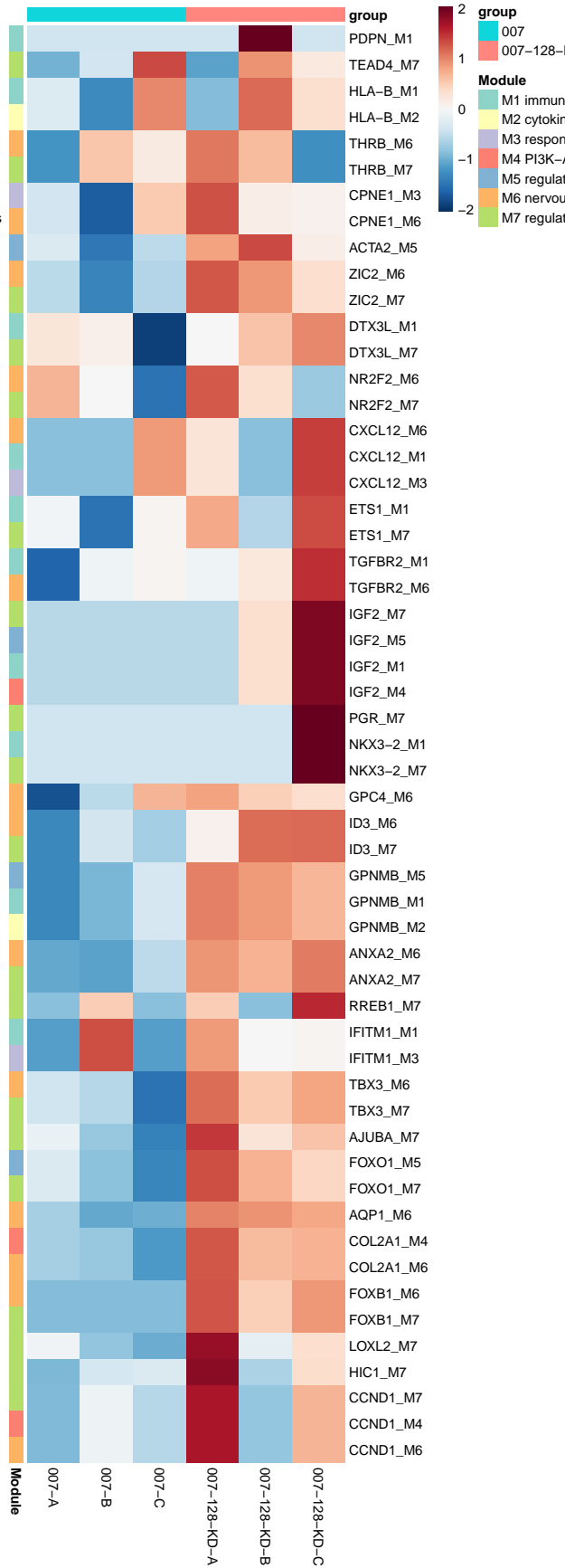
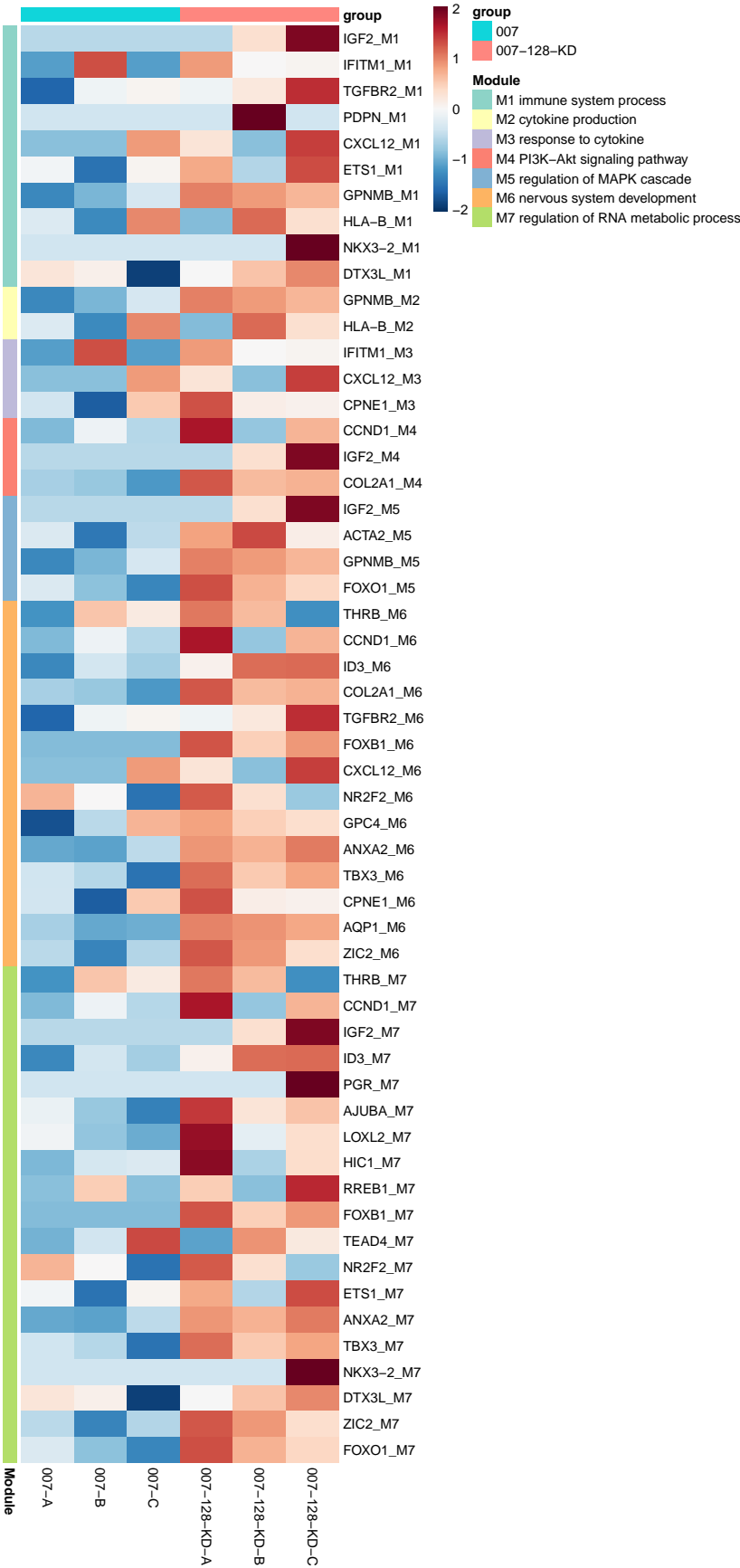
Sample 002



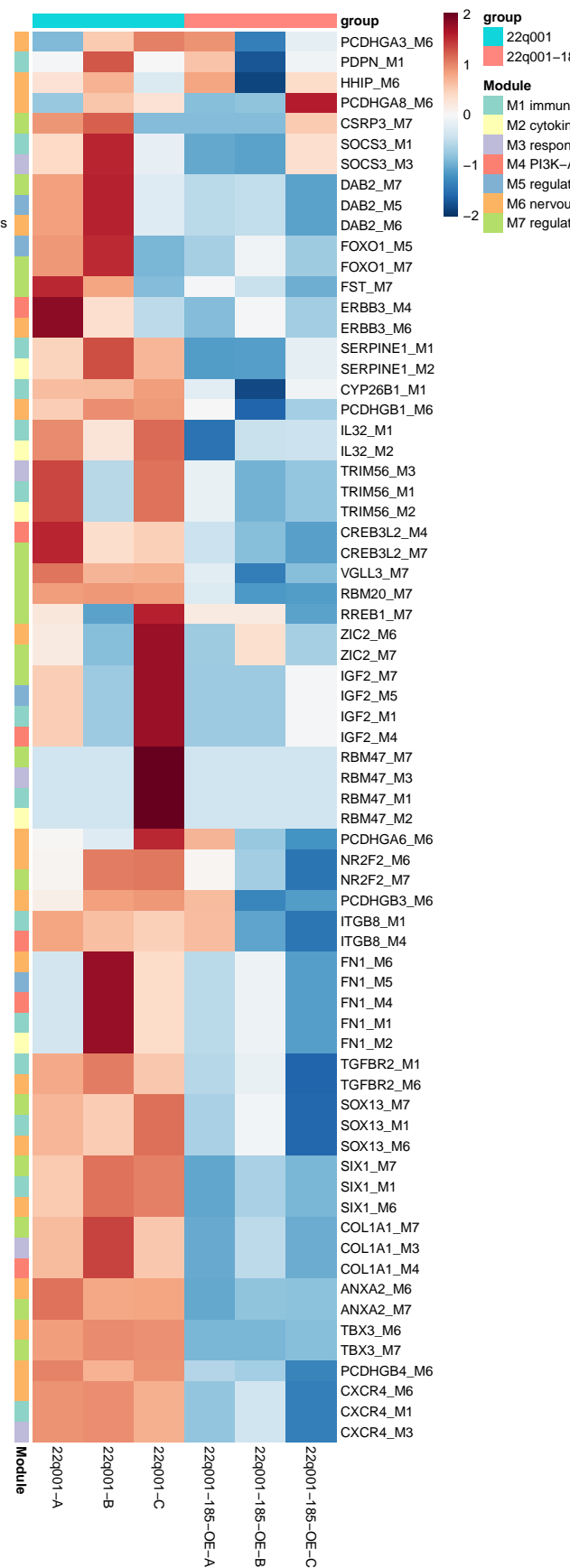
Sample 004



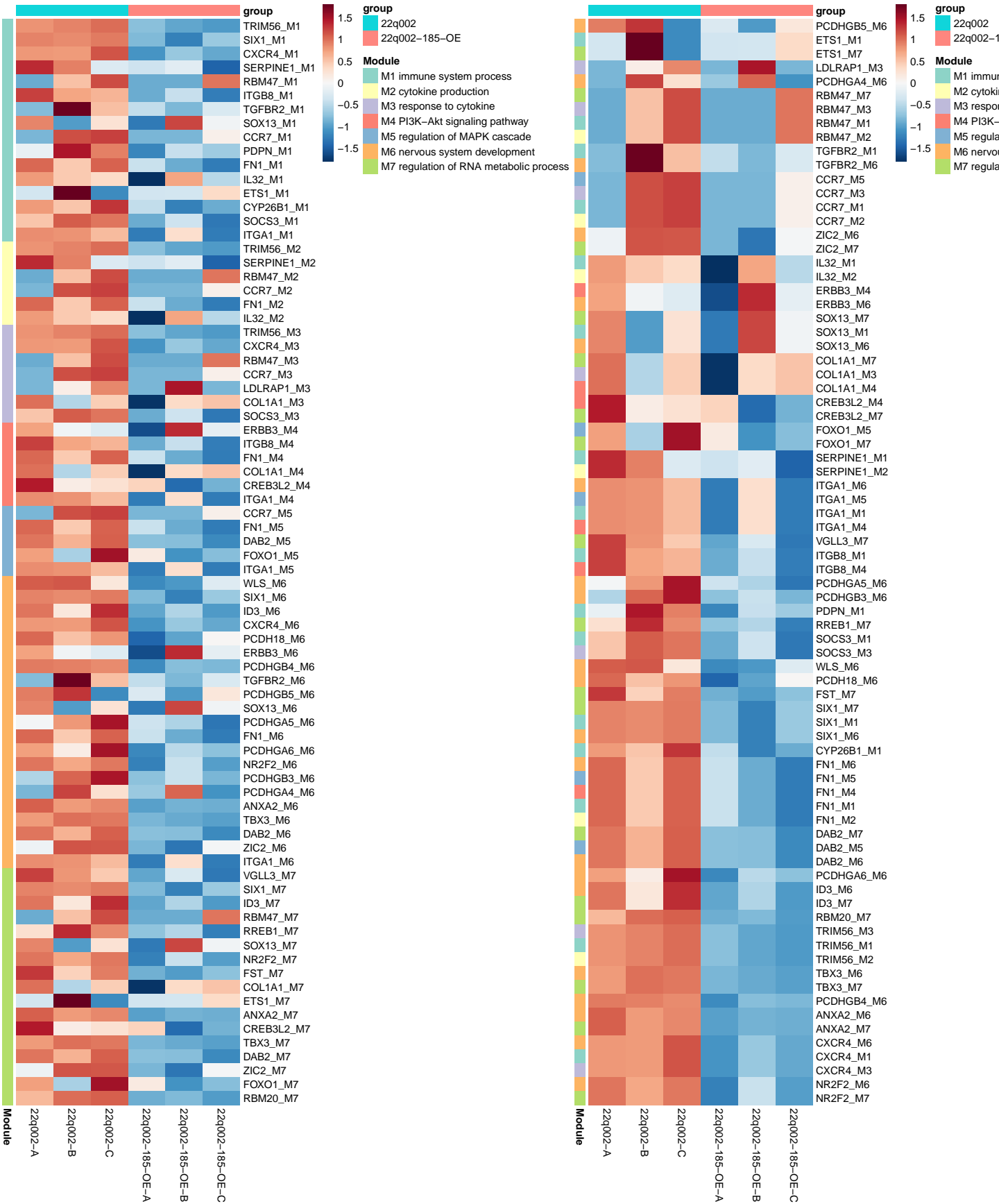
Sample 007



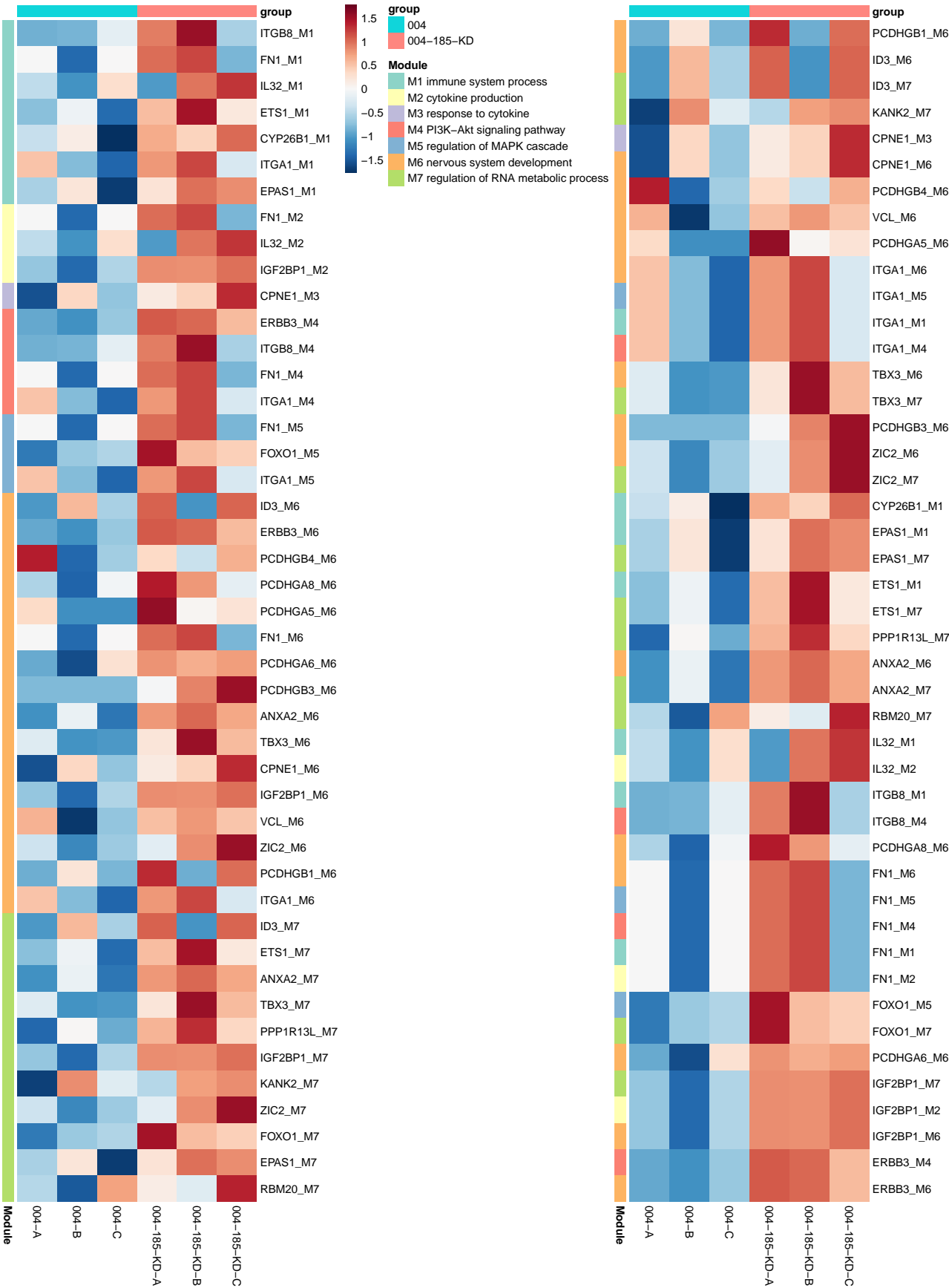
Sample 001



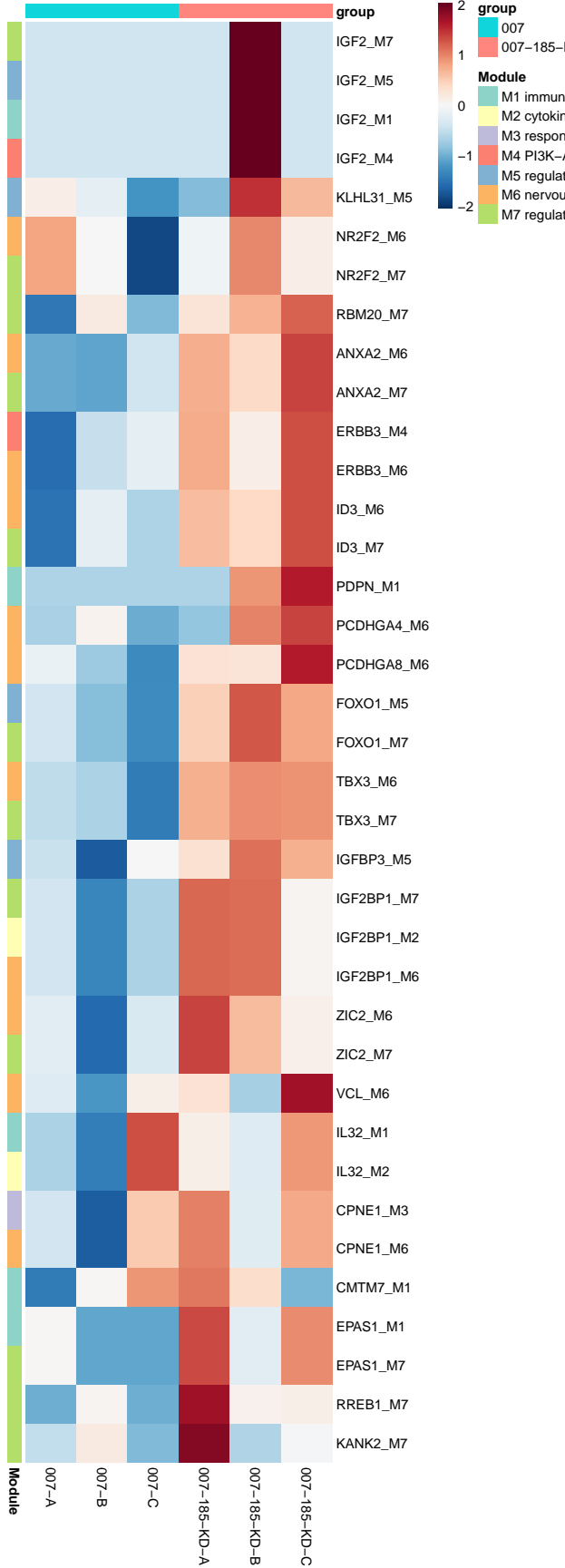
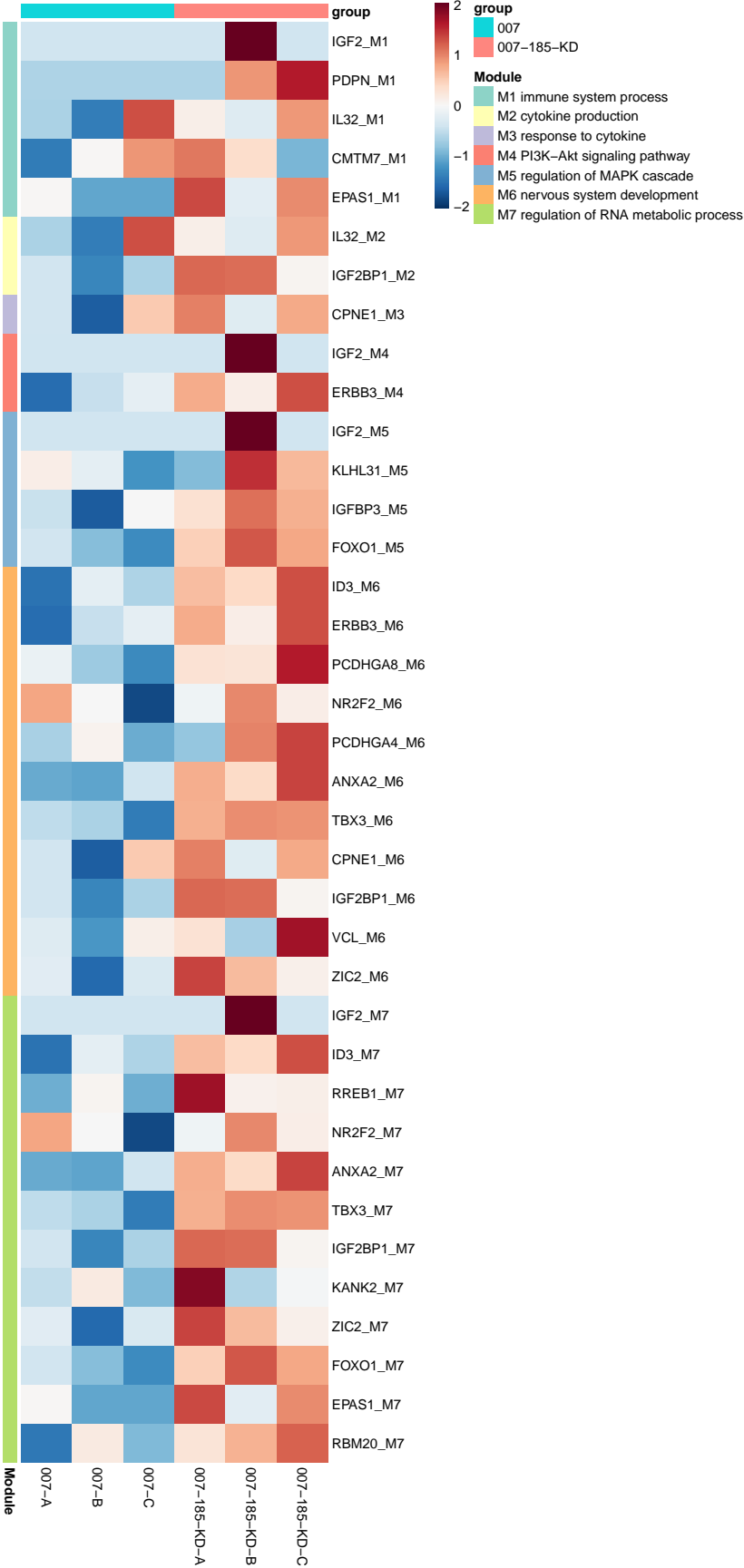
Sample 002



Sample 004



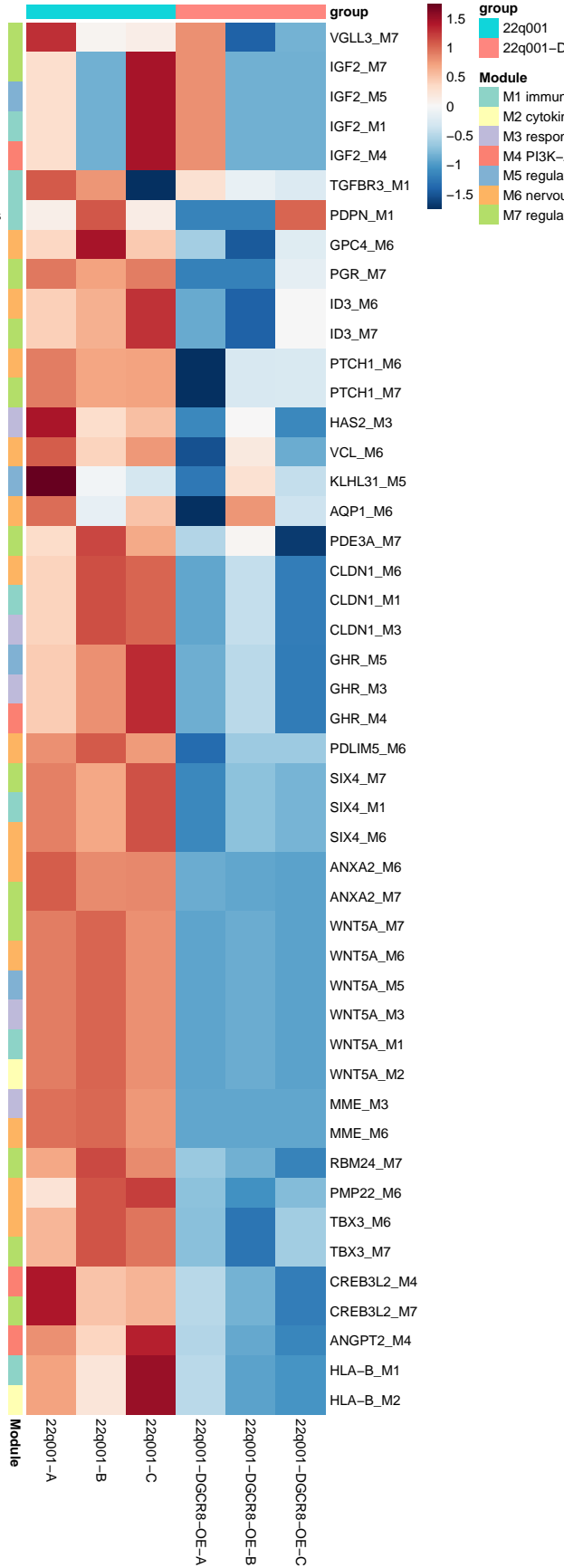
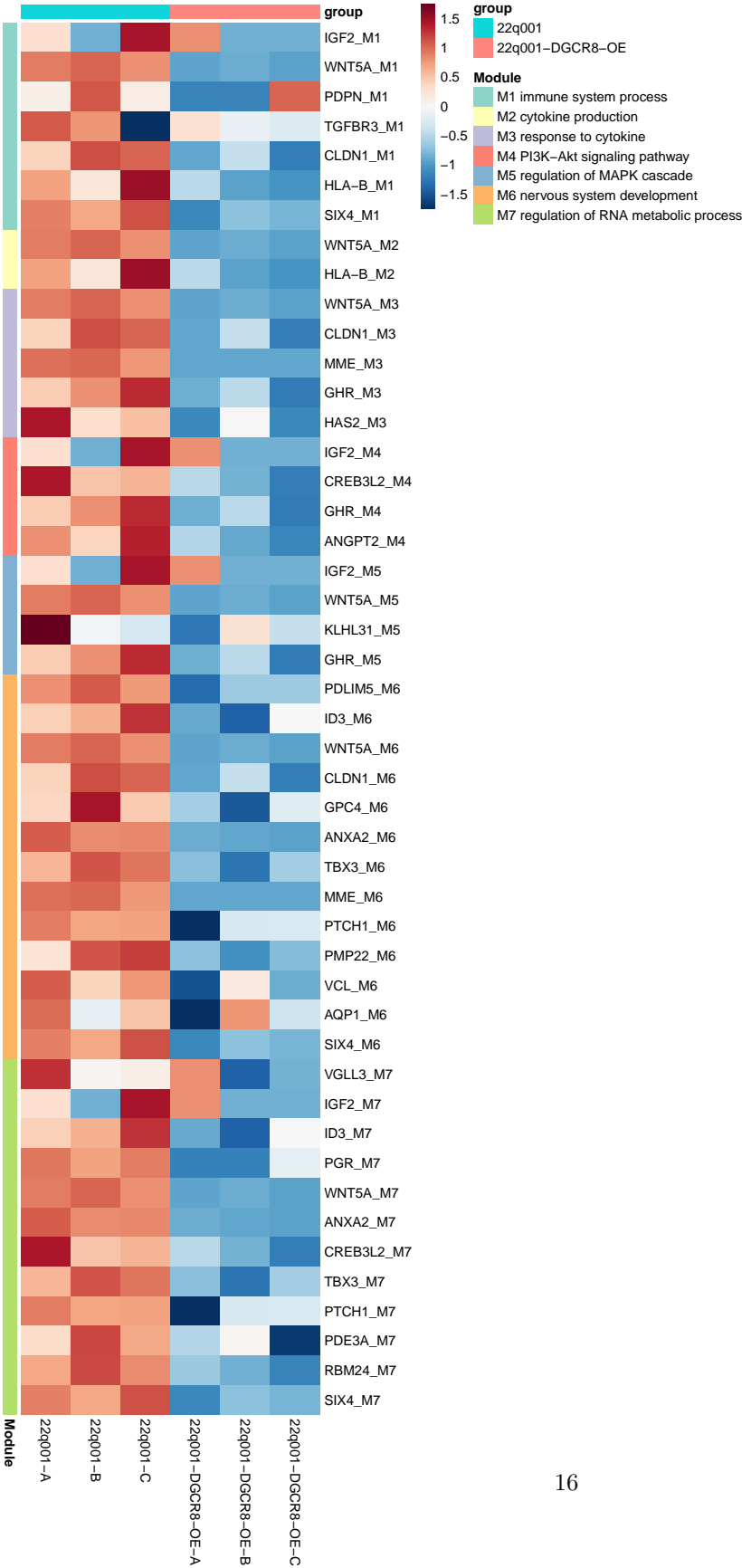
Sample 007



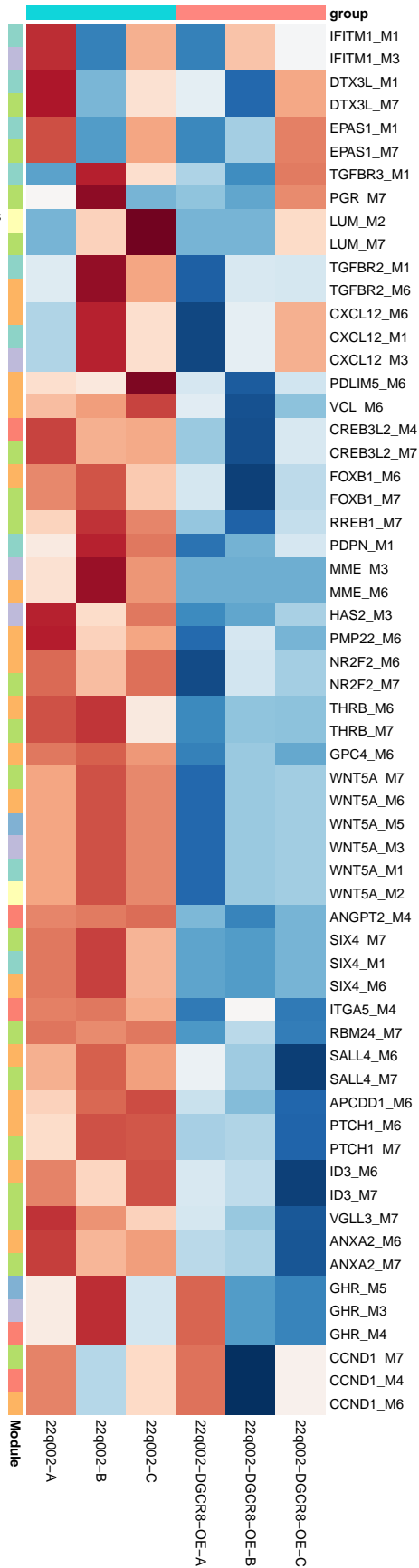
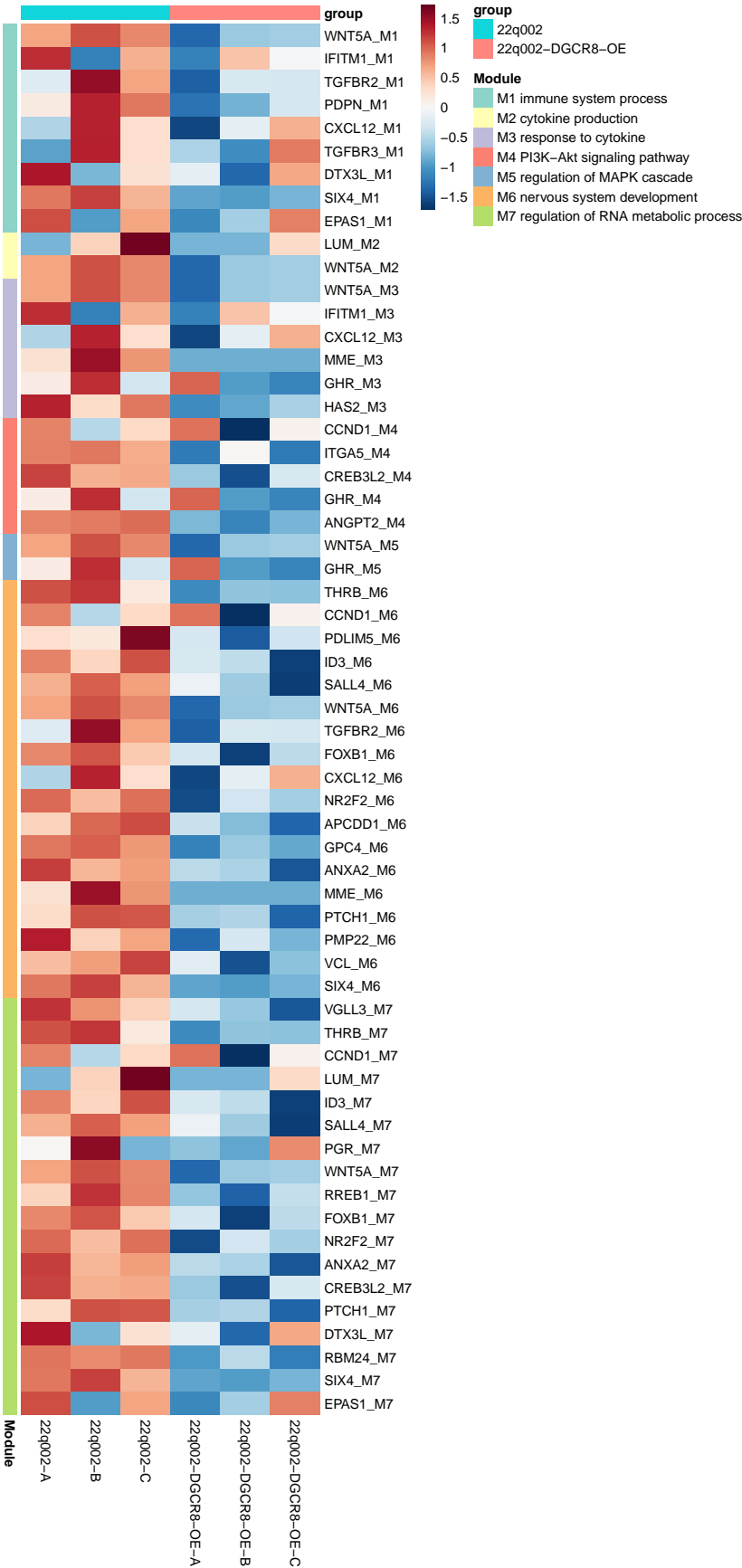
DGCR8

miRNA 128

Sample 001

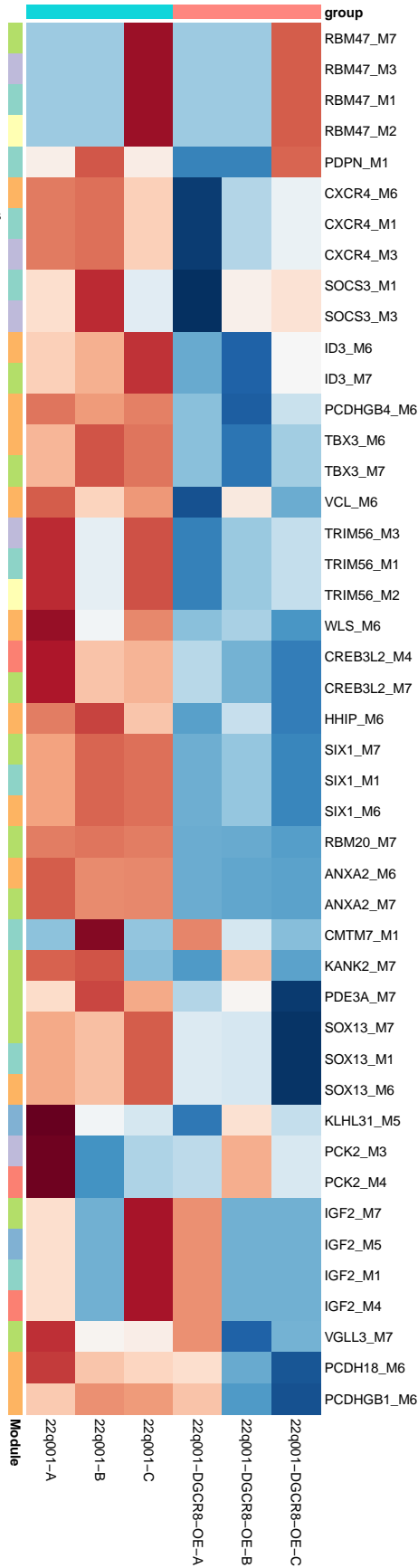
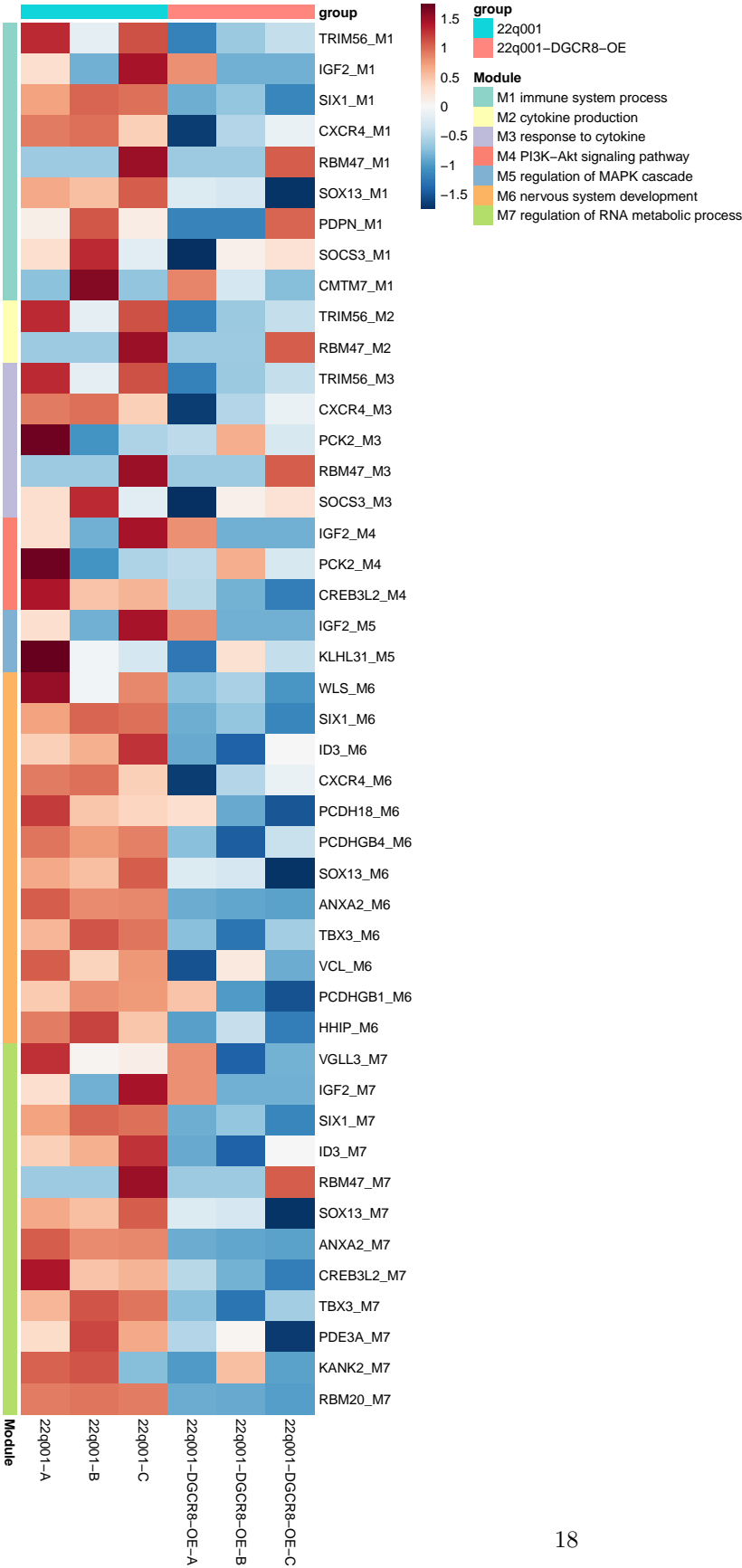


Sample 002

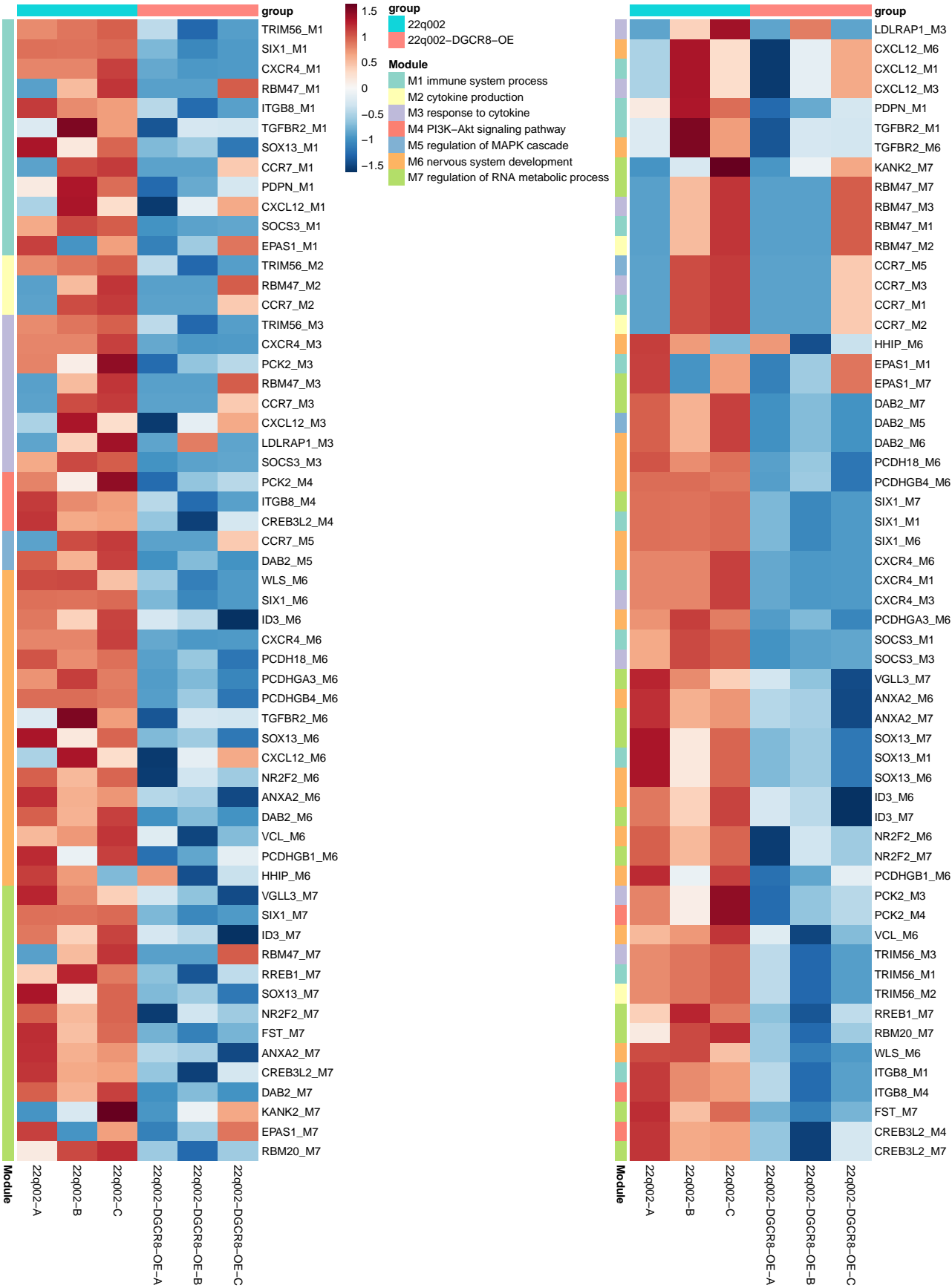


miRNA 185

Sample 001

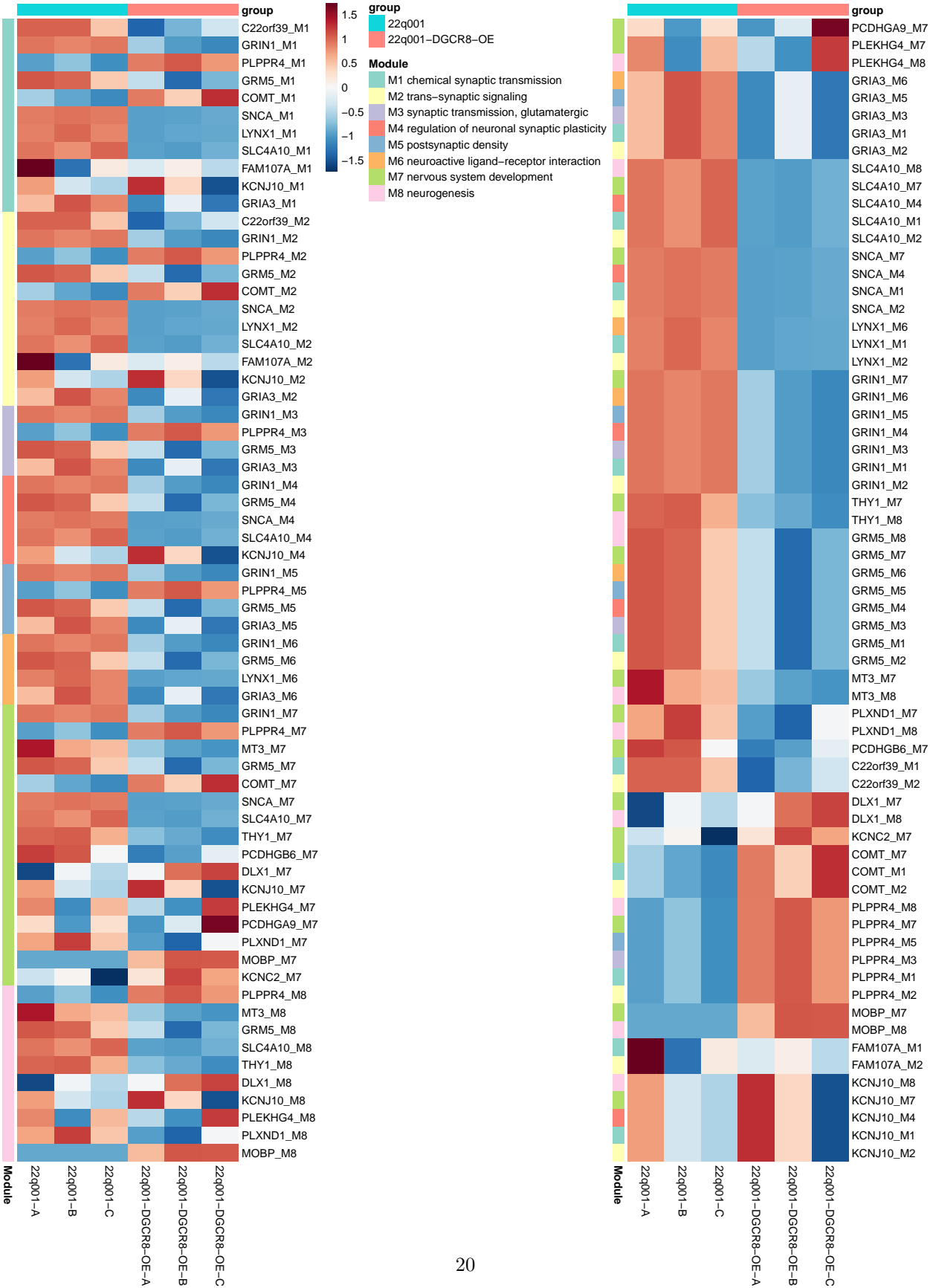


Sample 002

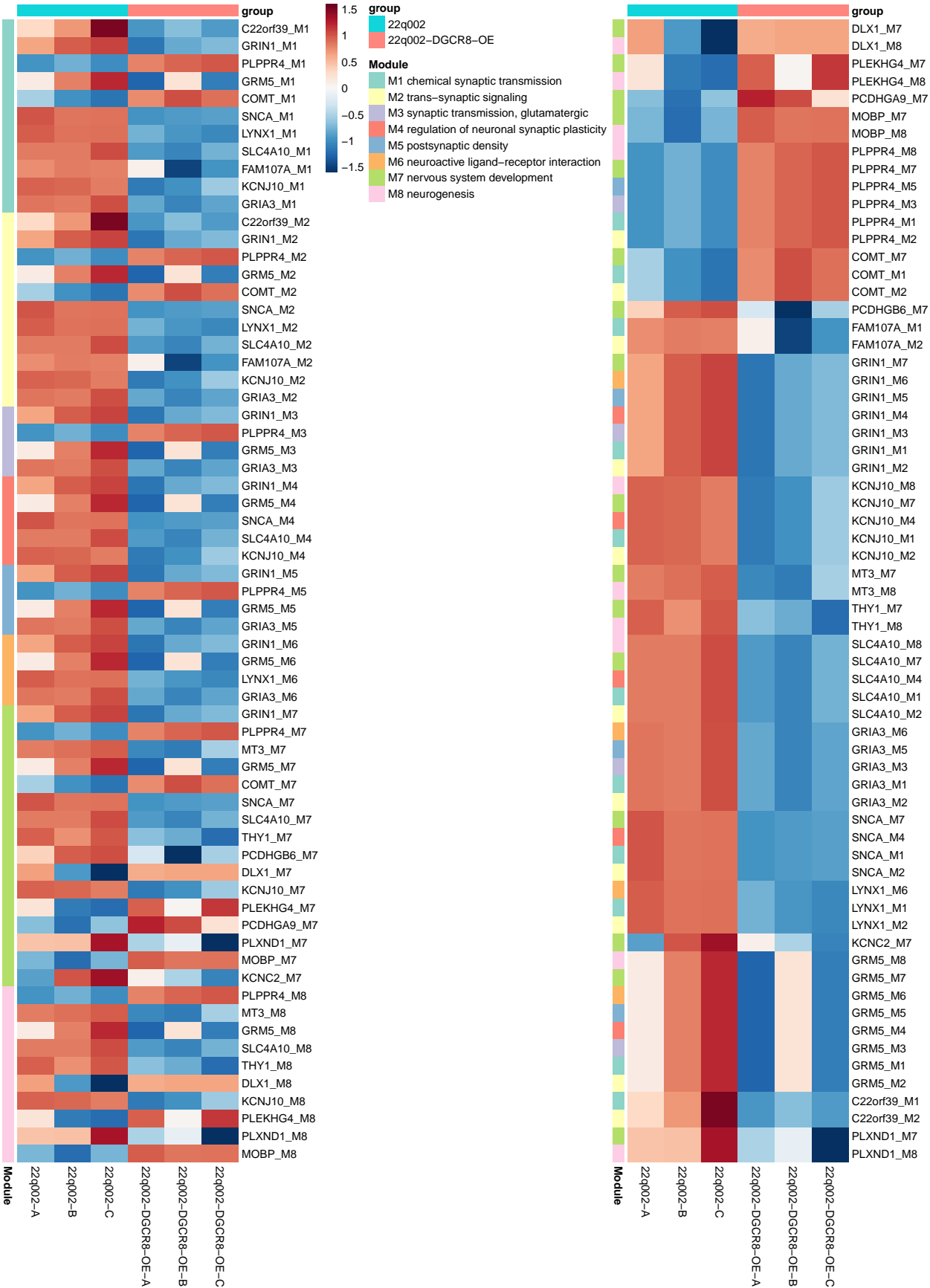


miRNA 214

Sample 001



Sample 002



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 data.table_1.17.4
## [17] org.Hs.eg.db_3.19.1 AnnotationDbi_1.66.0
## [19] clusterProfiler_4.12.6 ggfortify_0.4.17
## [21] EnhancedVolcano_1.22.0 ggrepel_0.9.6
## [23] apeglm_1.26.1 DESeq2_1.44.0
## [25] SummarizedExperiment_1.34.0 Biobase_2.64.0
## [27] MatrixGenerics_1.16.0 matrixStats_1.5.0
## [29] reshape2_1.4.4 Matrix_1.7-3
## [31] Signac_1.14.0 Seurat_5.3.0
## [33] SeuratObject_5.1.0 sp_2.2-0
## [35] RColorBrewer_1.1-3 pheatmap_1.0.12
## [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	