

Figruue for 2025-06-03

Ximing Ran

2025-06-03

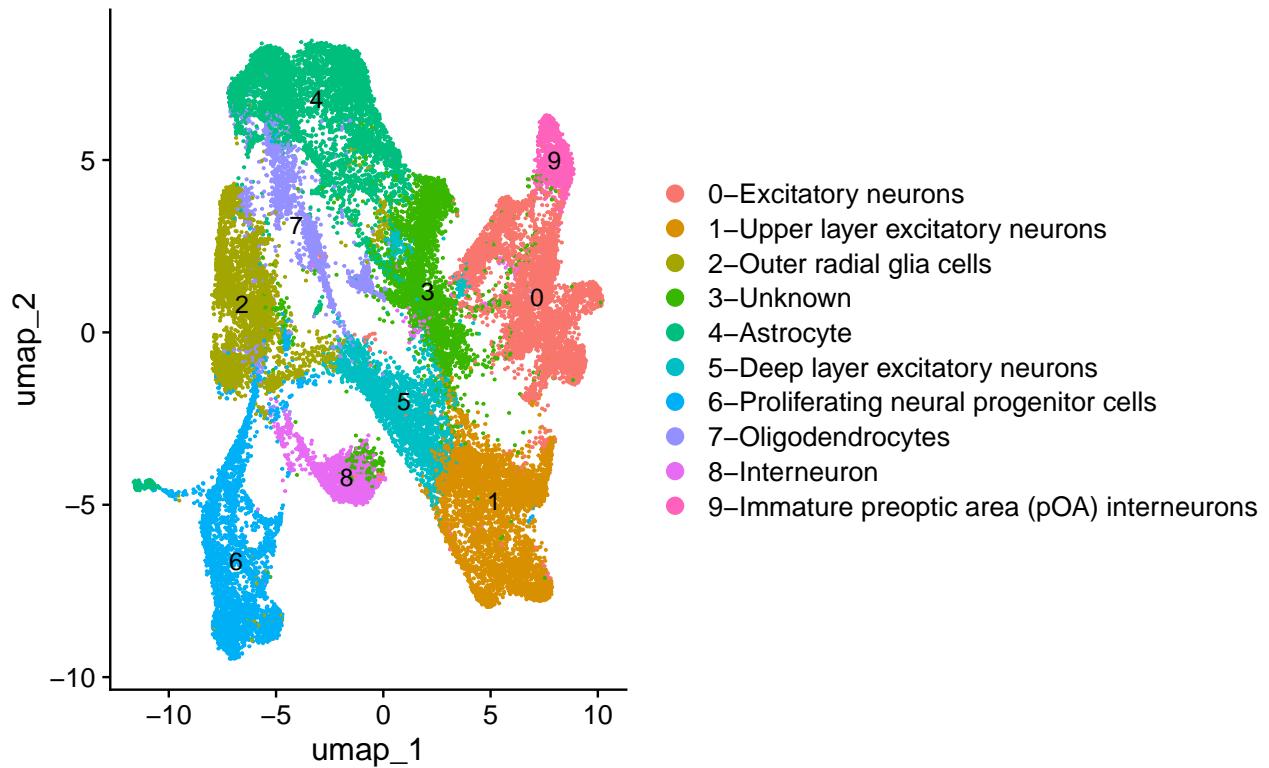
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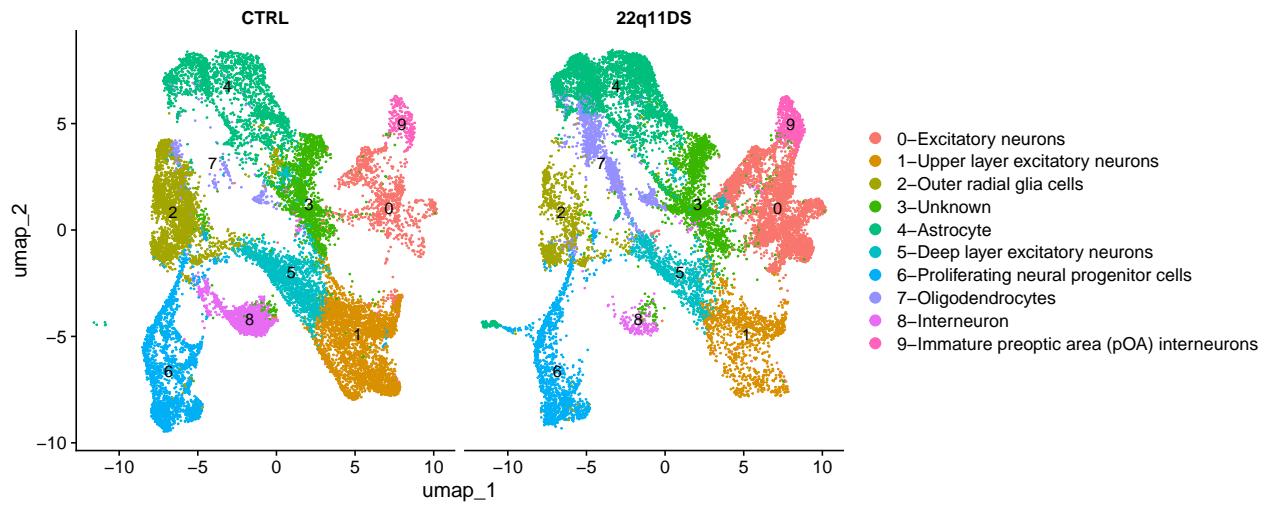
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1. Read the merged Data

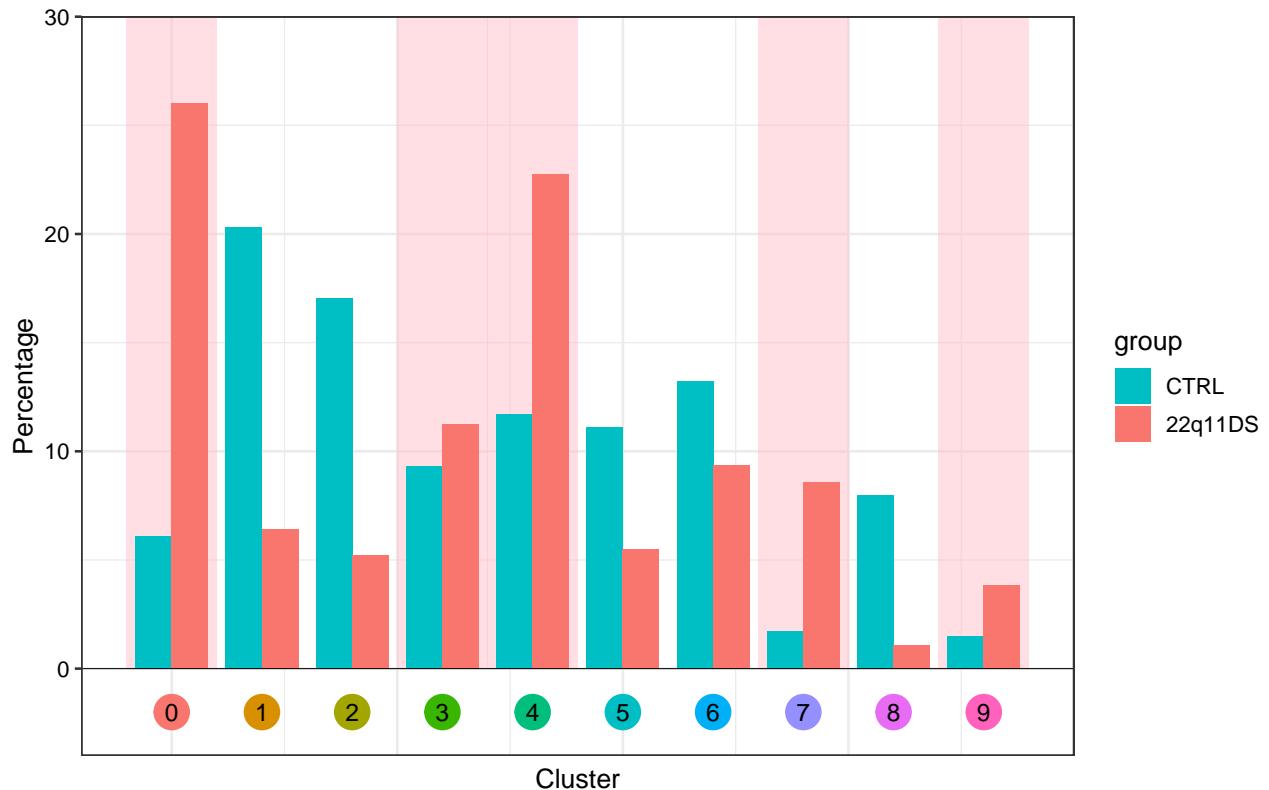
2. Plot the UMAP

```
##          0-Excitatory neurons      5608
##          1-Upper layer excitatory neurons    4626
##          2-Outer radial glia cells     3848
##          3-Unknown                  3576
##          4-Astrocyte                6009
##          5-Deep layer excitatory neurons   2880
##          6-Proliferating neural progenitor cells 3923
##          7-Oligodendrocytes            1802
##          8-Interneuron               1563
## 9-Immature preoptic area (pOA) interneurons  930
```





3. Plot the cell_type proportion



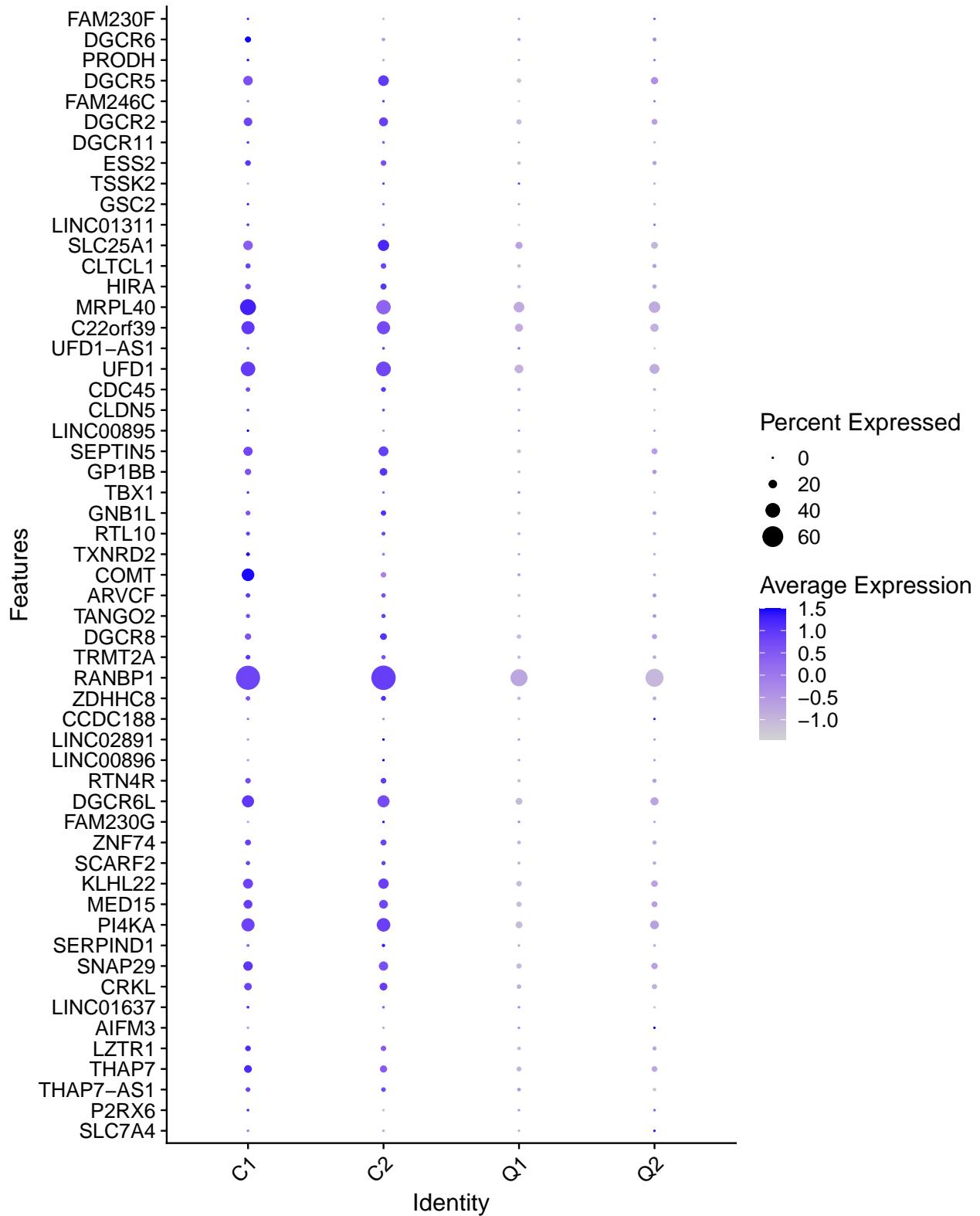
4. Plot the marker

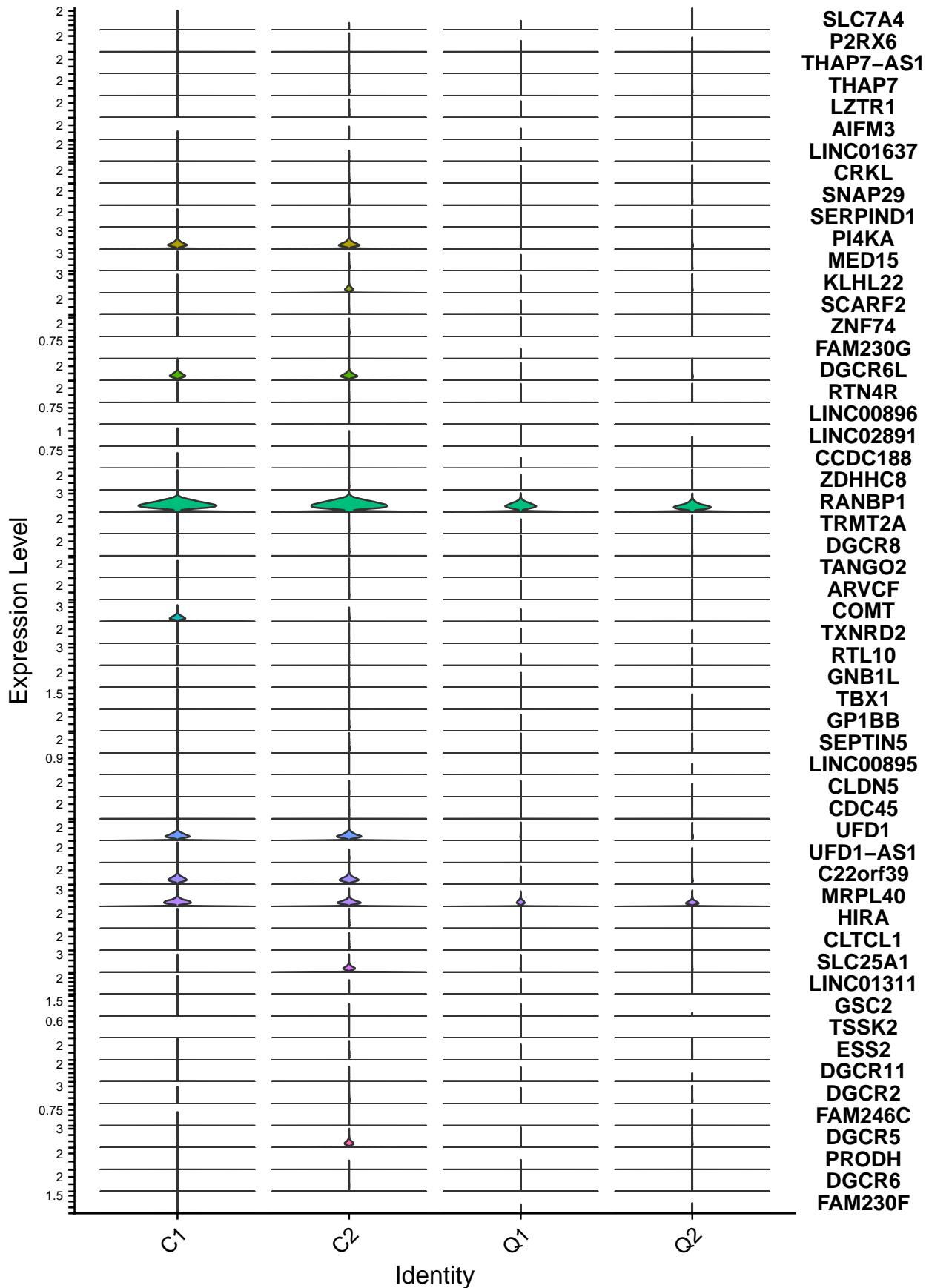
```
##          0-Excitatory neurons      1-Upper layer excitatory neurons
##                               5608                               4626
##          2-Outer radial glia cells      3-Unknown
##                               3848                               3576
##          4-Astrocyte      5-Deep layer excitatory neurons
```

##	6009	2880
## 6-Proliferating neural progenitor cells		7-Oligodendrocytes
##	3923	1802
##	8-Interneuron	9-Immature pOA interneurons
##	1563	930

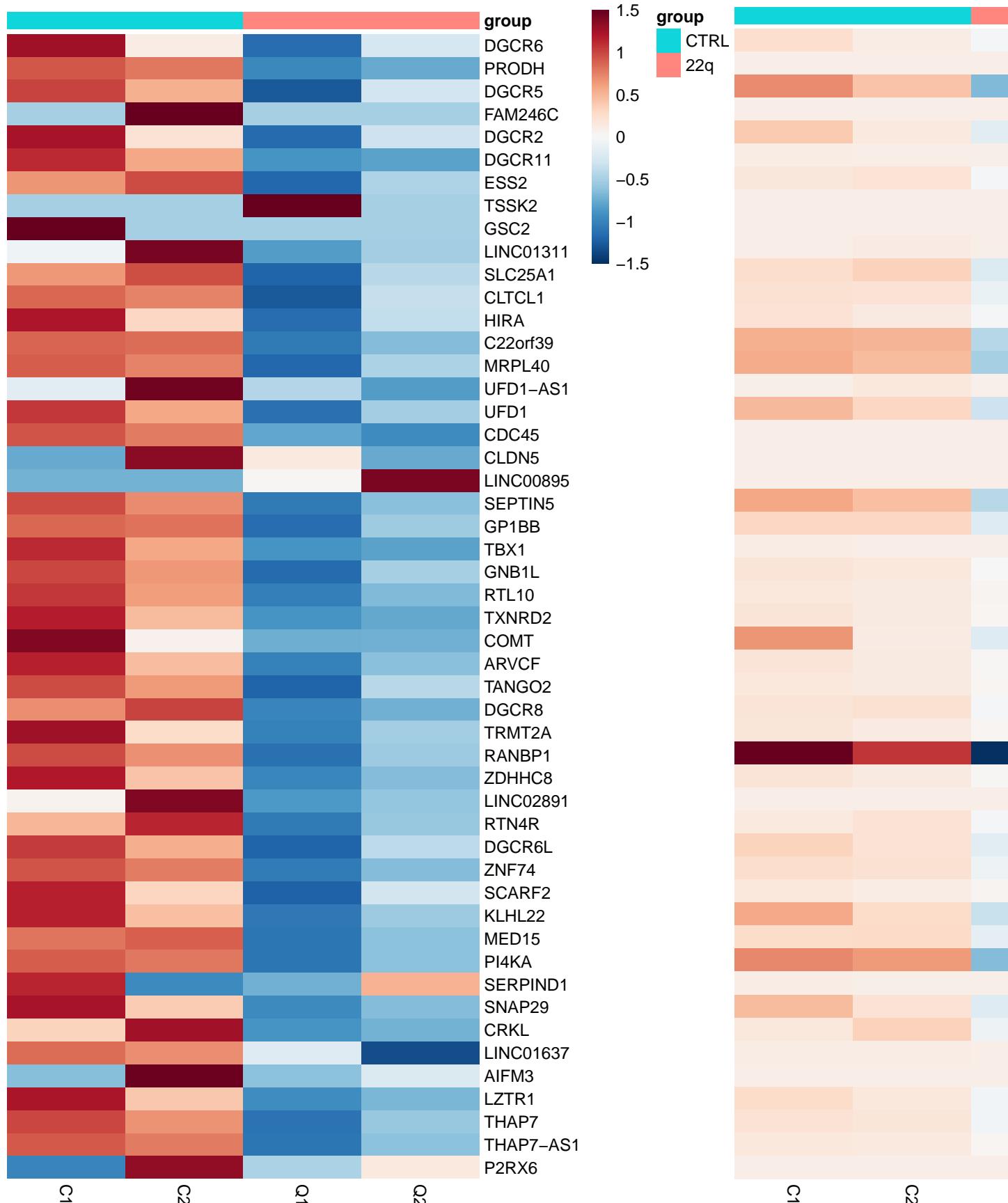
5. Plot for deleted region

```
## [1] "C1" "C2" "Q1" "Q2"
```

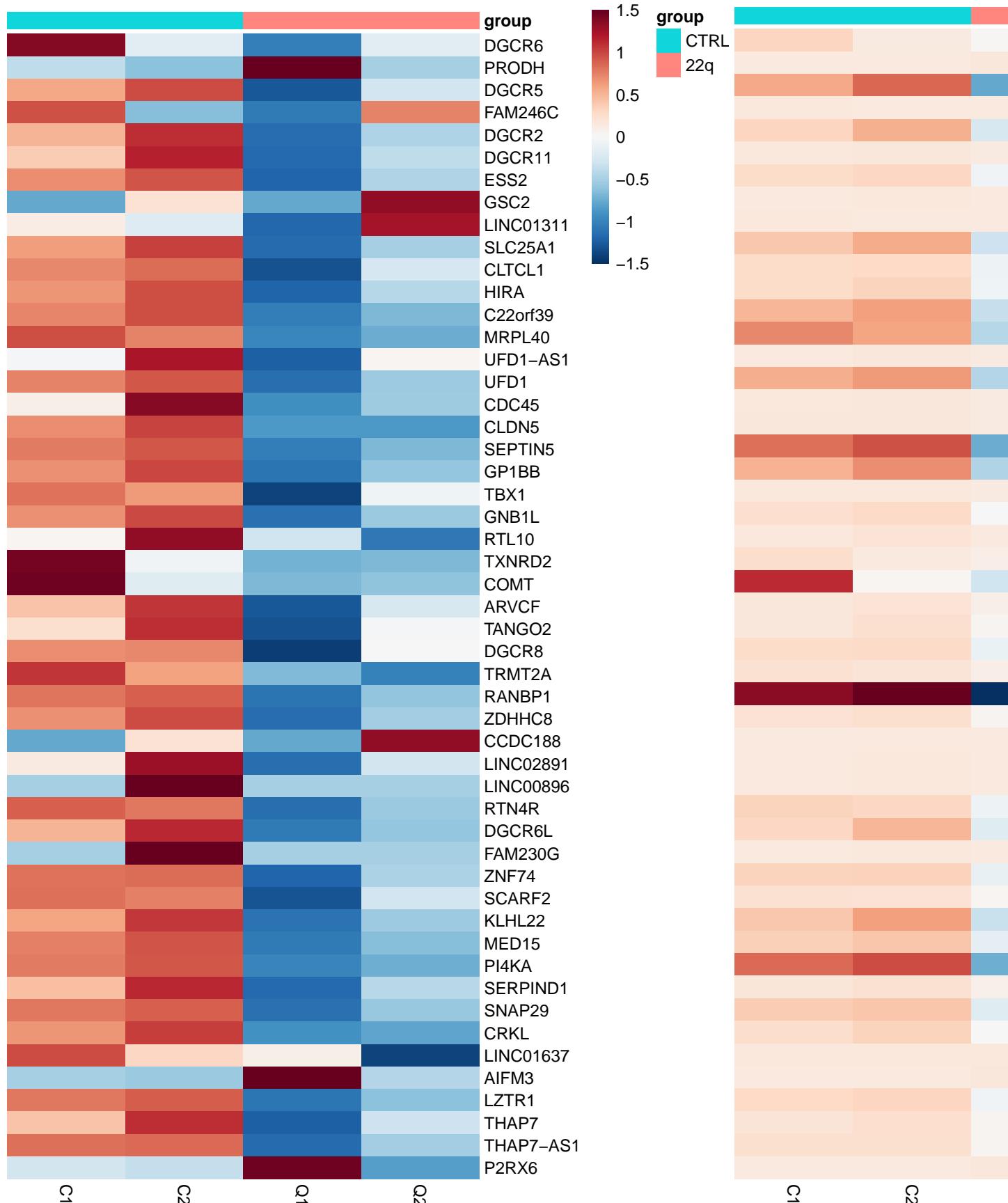




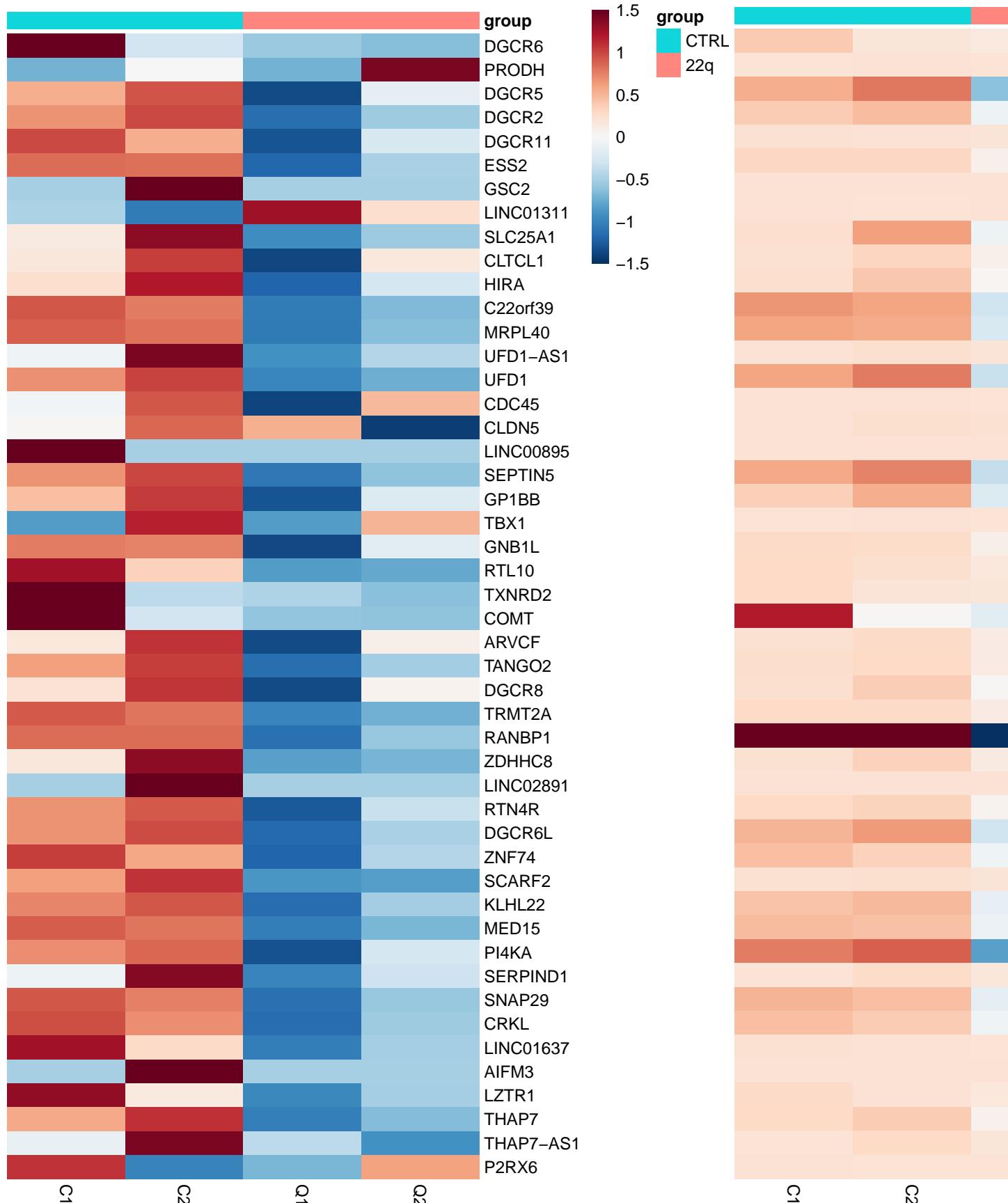
```
## [1] "Cluster 0"
```



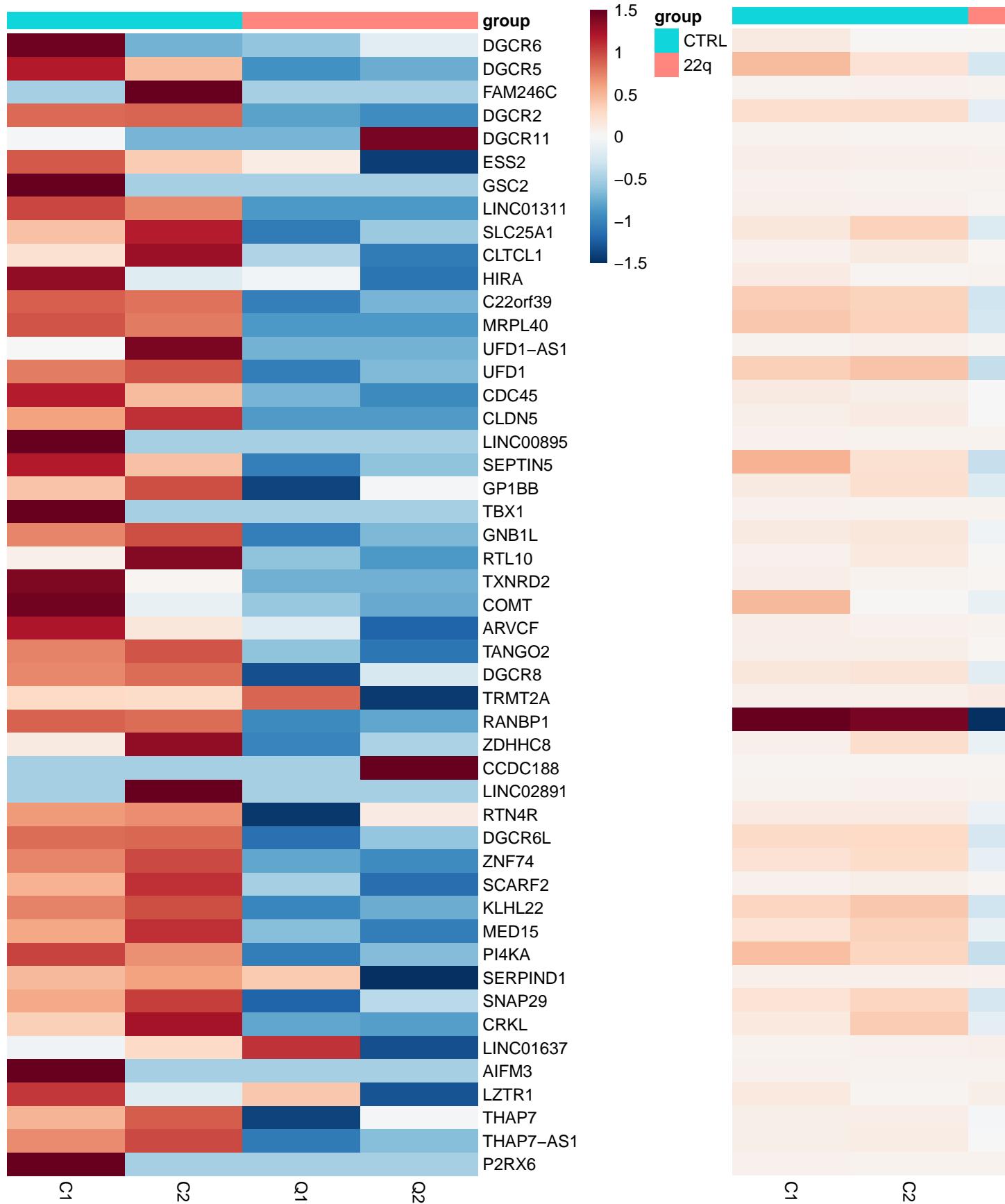
```
## [1] "Cluster 1"
```



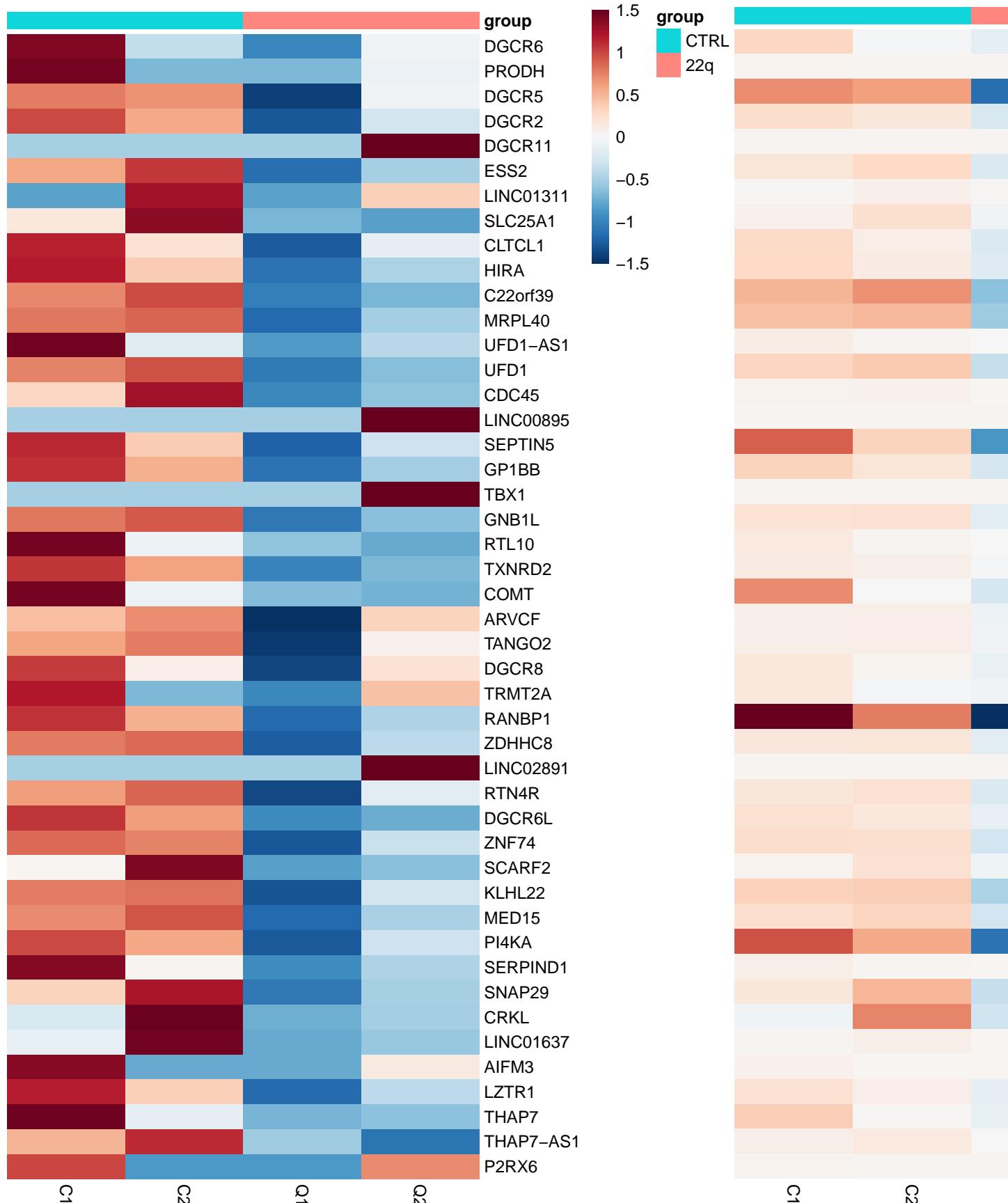
```
## [1] "Cluster 5"
```



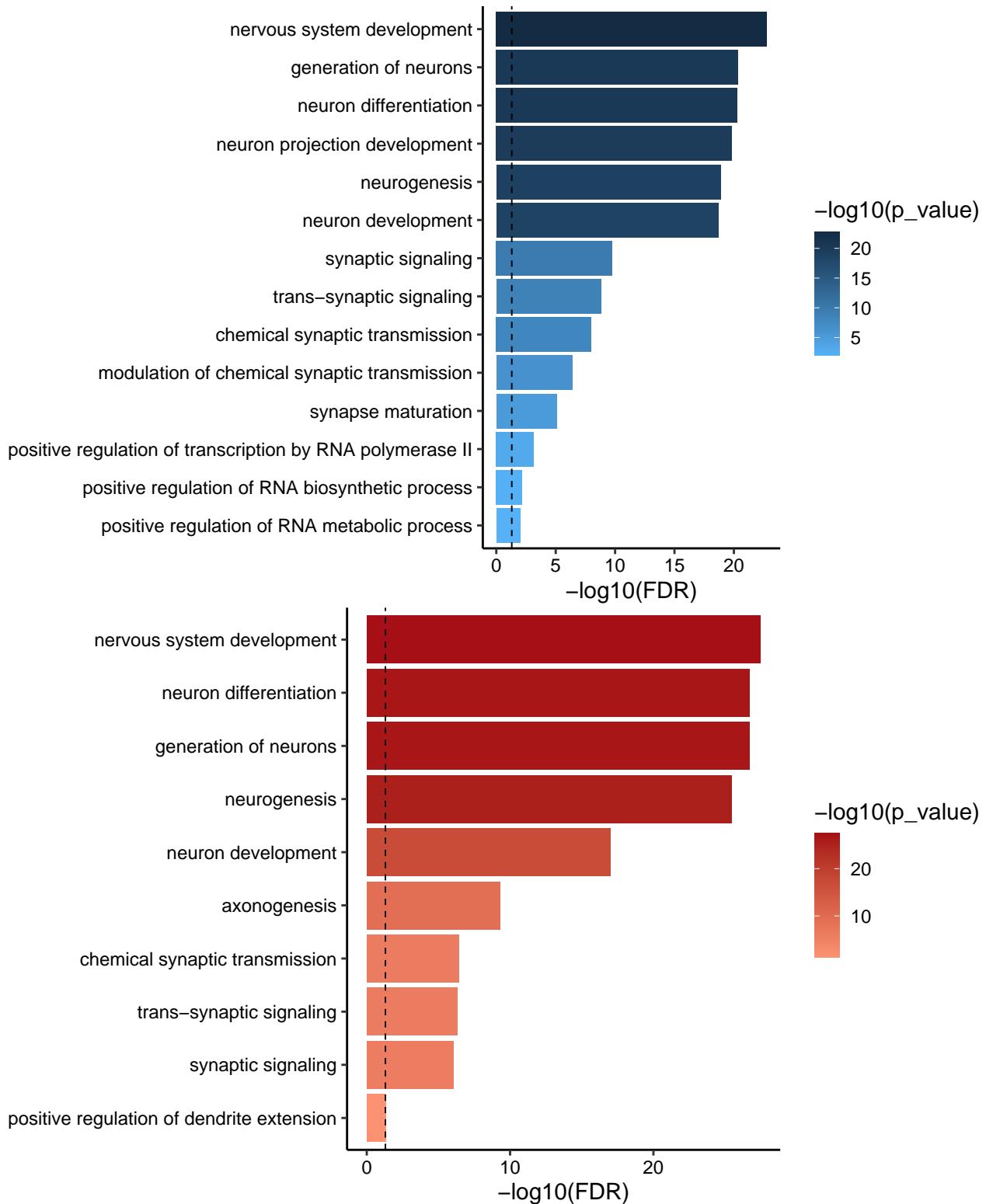
```
## [1] "Cluster 8"
```

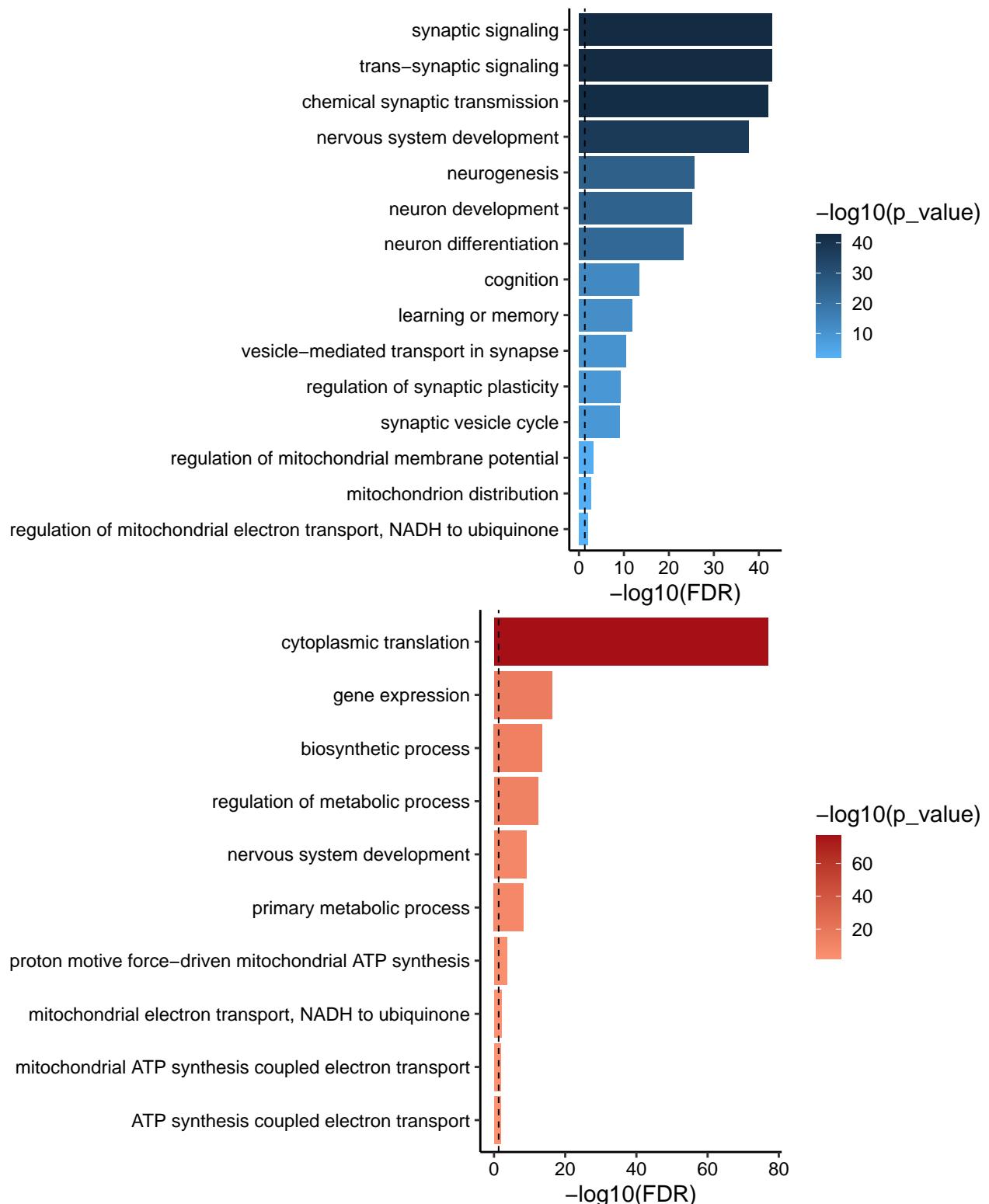


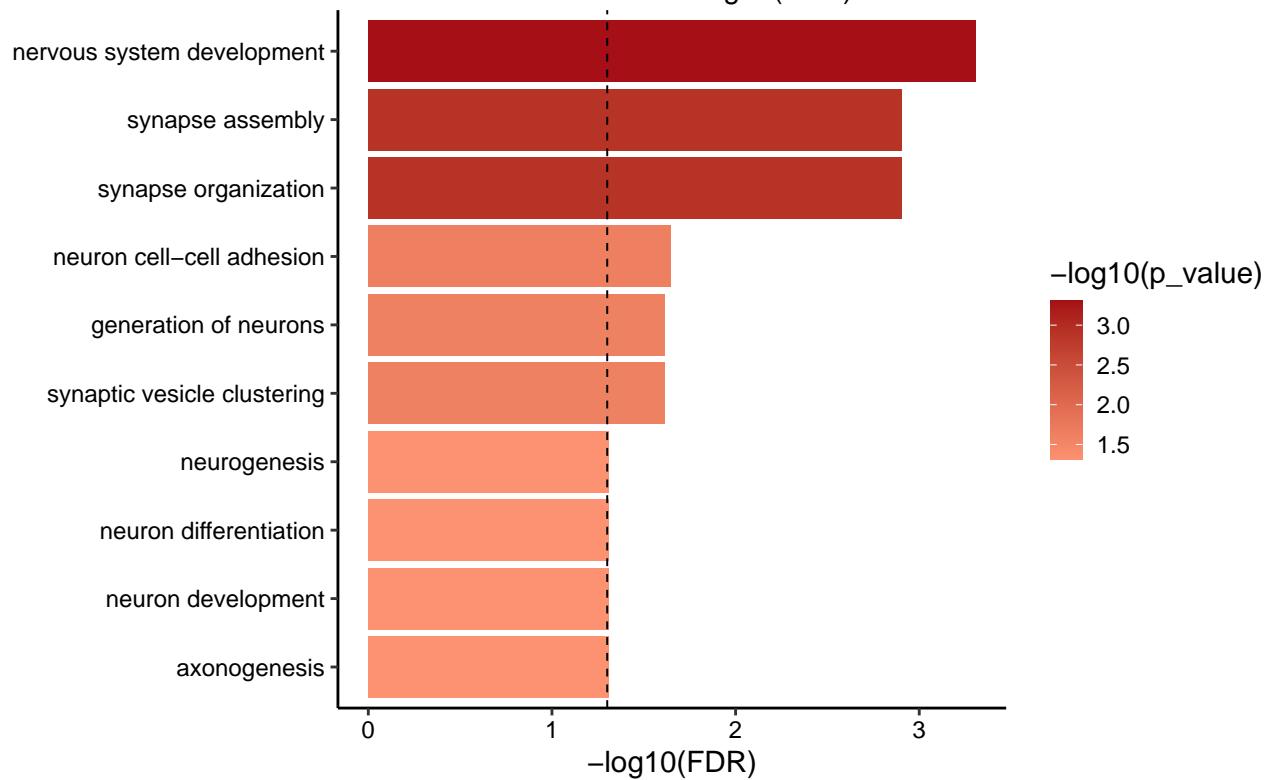
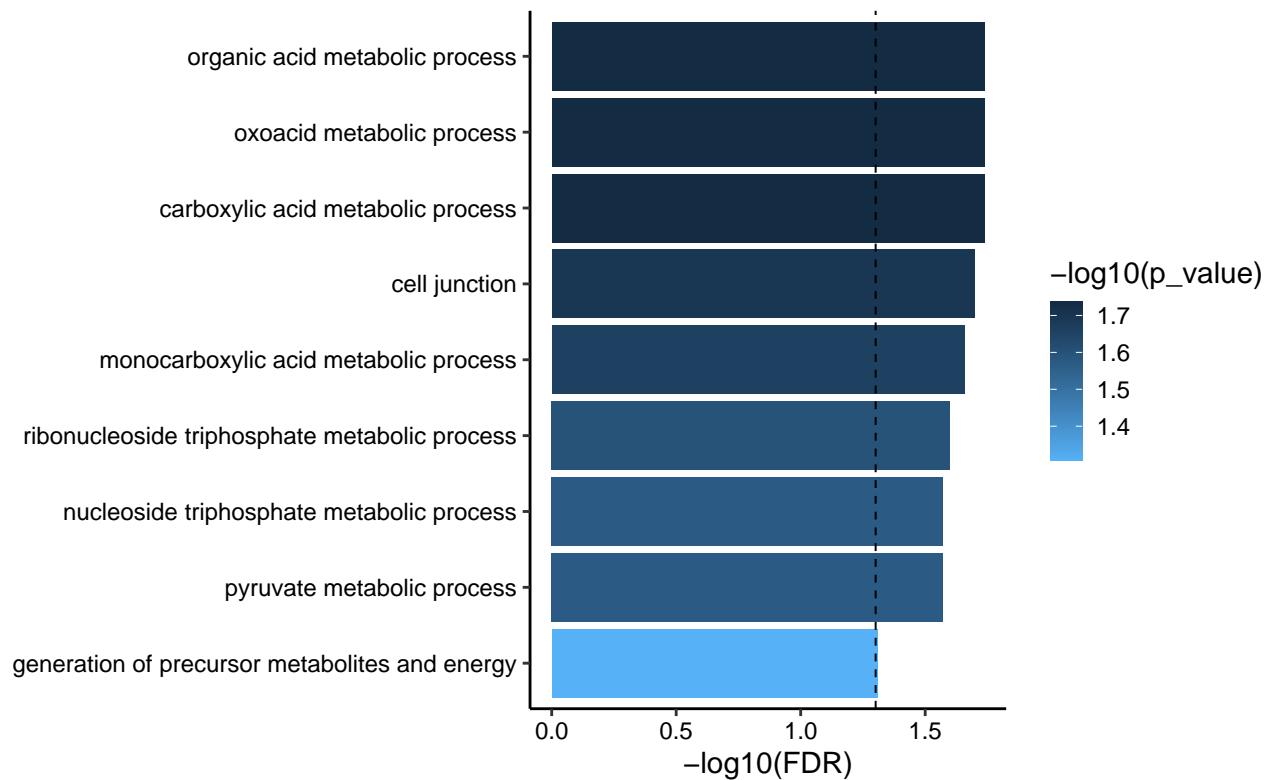
```
## [1] "Cluster 9"
```

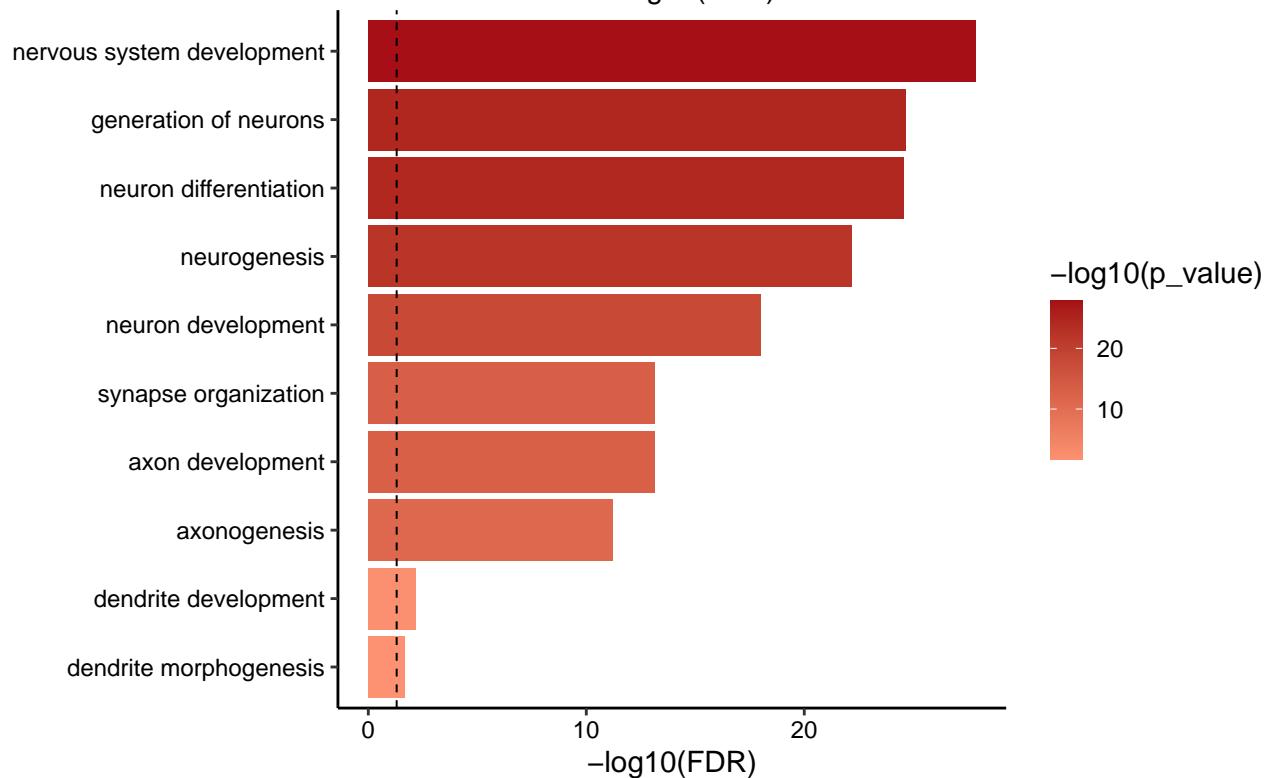
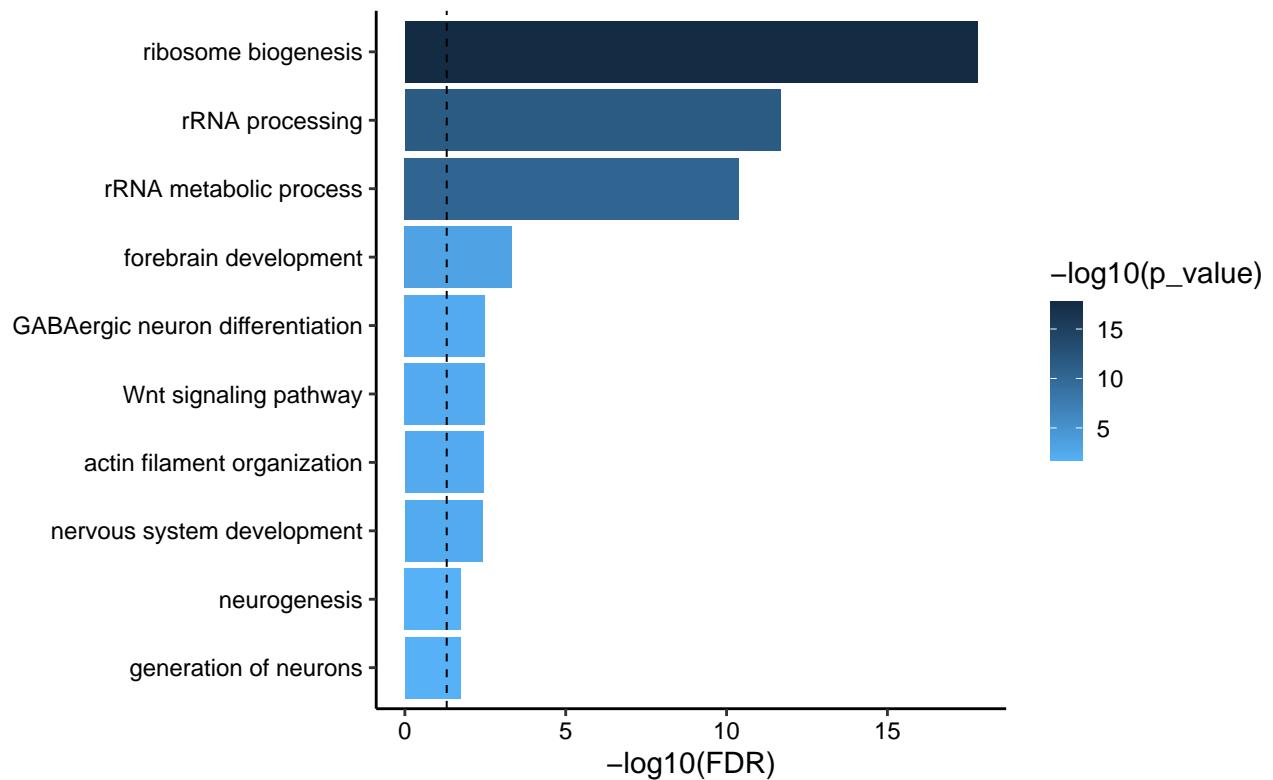


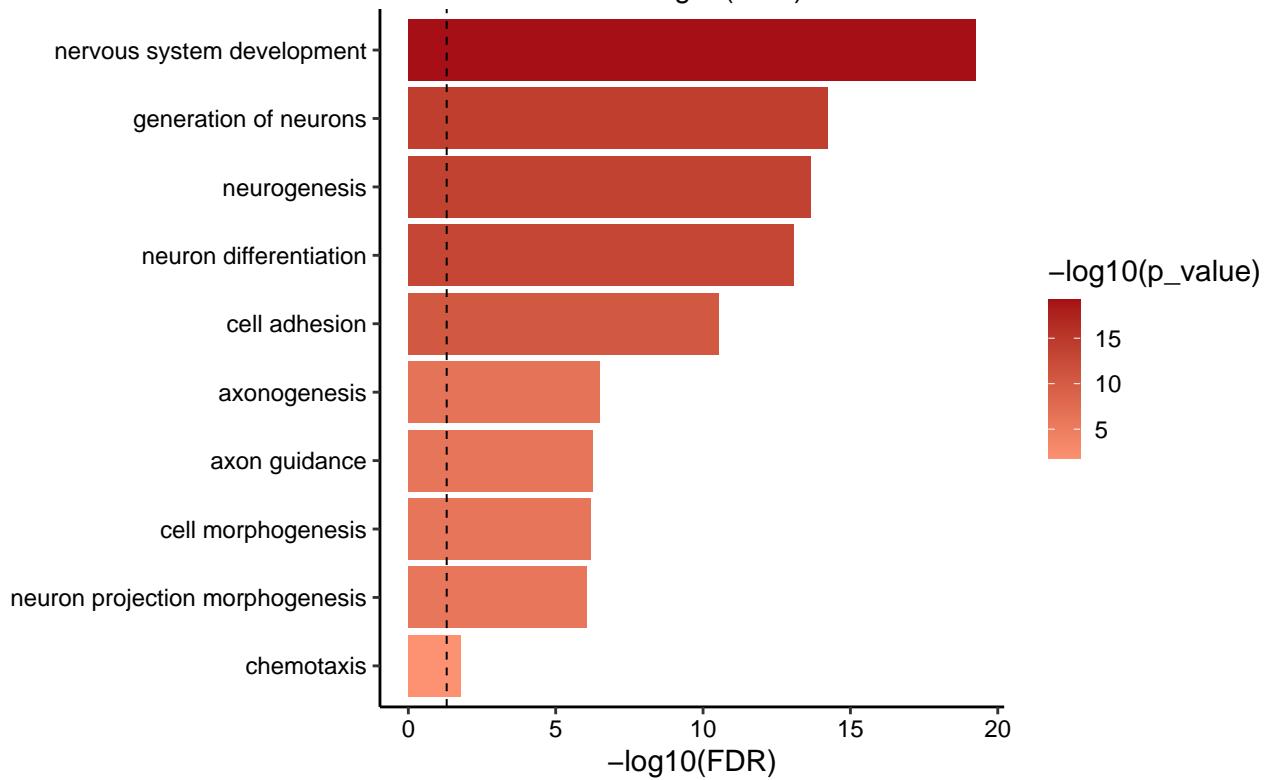
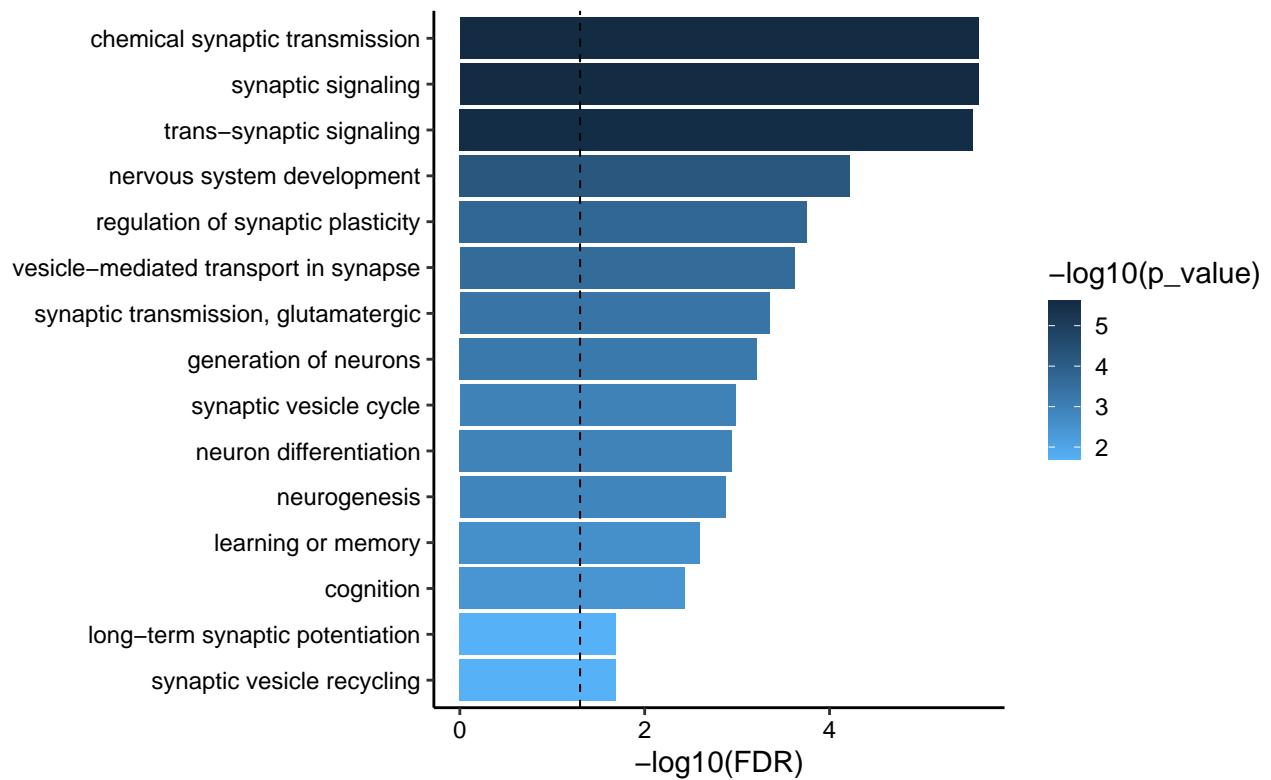
6. Pathway analysis











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] stats4      stats       graphics   grDevices  utils      datasets   methods
## [8] base
##
## other attached packages:
##  [1] Matrix_1.7-3           kableExtra_1.4.0
##  [3] extrafont_0.19          patchwork_1.3.0
##  [5] pheatmap_1.0.12          data.table_1.17.4
##  [7] harmony_1.2.3            Rcpp_1.0.14
##  [9] conflicted_1.2.0         openxlsx_4.2.8
## [11] Seurat_5.3.0             SeuratObject_5.1.0
## [13] sp_2.2-0                 AnnotationHub_3.12.0
## [15] BiocFileCache_2.12.0     dbplyr_2.5.0
## [17] simspec_0.0.0.9000       cowplot_1.1.3
## [19] EnsDb.Hsapiens.v86_2.99.0 ensemblldb_2.28.1
## [21] AnnotationFilter_1.28.0   GenomicFeatures_1.56.0
## [23] AnnotationDbi_1.66.0      Biobase_2.64.0
## [25] Signac_1.14.0             rtracklayer_1.64.0
## [27] GenomicRanges_1.56.2      GenomeInfoDb_1.40.1
## [29] IRanges_2.38.1            S4Vectors_0.42.1
## [31] BiocGenerics_0.50.0       knitr_1.50
## [33] lubridate_1.9.4          forcats_1.0.0
## [35] stringr_1.5.1             dplyr_1.1.4
## [37] purrrr_1.0.4              readr_2.1.5
## [39] tidyrr_1.3.1               tibble_3.2.1
## [41] ggplot2_3.5.2              tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
##  [1] RcppAnnoy_0.0.22        splines_4.4.0
##  [3] later_1.4.2              BiocIO_1.14.0
##  [5] bitops_1.0-9              filelock_1.0.3
##  [7] polyclip_1.10-7           XML_3.99-0.18
##  [9] fastDummies_1.7.5         lifecycle_1.0.4
## [11] rprojroot_2.0.4            globals_0.18.0
## [13] lattice_0.22-7             MASS_7.3-65
## [15] magrittr_2.0.3              plotly_4.10.4
## [17] rmarkdown_2.29              yaml_2.3.10
## [19] httpuv_1.6.16             sctransform_0.4.2
```

```

## [21] zip_2.3.2
## [23] spatstat.sparse_3.1-0
## [25] pbapply_1.7-2
## [27] RColorBrewer_1.1-3
## [29] zlibbioc_1.50.0
## [31] RCurl_1.98-1.17
## [33] GenomeInfoDbData_1.2.12
## [35] irlba_2.3.5.1
## [37] listenv_0.9.1
## [39] RSpectra_0.16-2
## [41] fitdistrplus_1.2-2
## [43] svglite_2.2.1
## [45] DelayedArray_0.30.1
## [47] xml2_1.3.8
## [49] UCSC.utils_1.0.0
## [51] spatstat.explore_3.4-3
## [53] GenomicAlignments_1.40.0
## [55] progressr_0.15.1
## [57] survival_3.8-3
## [59] tools_4.4.0
## [61] ica_1.0-3
## [63] Rttf2pt1_1.3.12
## [65] SparseArray_1.4.8
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## [69] withr_3.0.2
## [71] fastmap_1.2.0
## [73] timechange_0.3.0
## [75] mime_0.13
## [77] colorspace_2.1-1
## [79] tensor_1.5
## [81] dichromat_2.0-0.1
## [83] generics_0.1.4
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## [93] htmltools_0.5.8.1
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## [97] png_0.1-8
## [99] rstudioapi_0.17.1
## [101] reshape2_1.4.4
## [103] nlme_3.1-168
## [105] cachem_1.1.0
## [107] BiocVersion_3.19.1
## [109] parallel_4.4.0
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## [113] grid_4.4.0
## [115] RANN_2.6.2
## [117] xtable_1.8-4
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## [121] tinytex_0.57
## [123] compiler_4.4.0
## [125] rlang_1.1.6
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goftest_1.2-3
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RcppRoll_0.3.1
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jsonlite_2.0.0
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ragg_1.4.0
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BiocManager_1.30.25
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RSQLite_2.3.11
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scales_1.4.0
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cluster_2.1.8.1
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cli_3.6.5
Rsamtools_2.20.0
crayon_1.5.3
labeling_0.4.3

```

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## [131] deldir_2.0-4                       viridisLite_0.4.2
## [133] BiocParallel_1.38.0                 Biostrings_2.72.1
## [135] lazyeval_0.2.2                      spatstat.geom_3.4-1
## [137] RcppHNSW_0.6.0                      hms_1.1.3
## [139] bit64_4.6.0-1                      future_1.49.0
## [141] KEGGREST_1.44.1                     shiny_1.10.0
## [143] SummarizedExperiment_1.34.0          ROCR_1.0-11
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## [147] fastmatch_1.1-6                      bit_4.6.0
```