

# Differential Expression Analysis for bulk RNA-seq data

## 22q vs Control

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2025-05-15

## Contents

<b>1. Read the count data</b>	<b>2</b>
<b>2. Differential expression analysis</b>	<b>2</b>
<b>3. Visualization for results</b>	<b>3</b>
(1) Sample information . . . . .	3
(2) DEG visualization - Volcano plot and Heatmap . . . . .	5
(3) 22q gene visualization - Heatmap . . . . .	14
<b>4. GSVA analysis</b>	<b>16</b>
<b>5. Pathway Enrichment Analysis</b>	<b>17</b>
<b>Session information</b>	<b>25</b>

## 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. The final table will be stored in `results/02-DEG-Vehicle/synaptosomes_bulkRNA_counts.csv`.

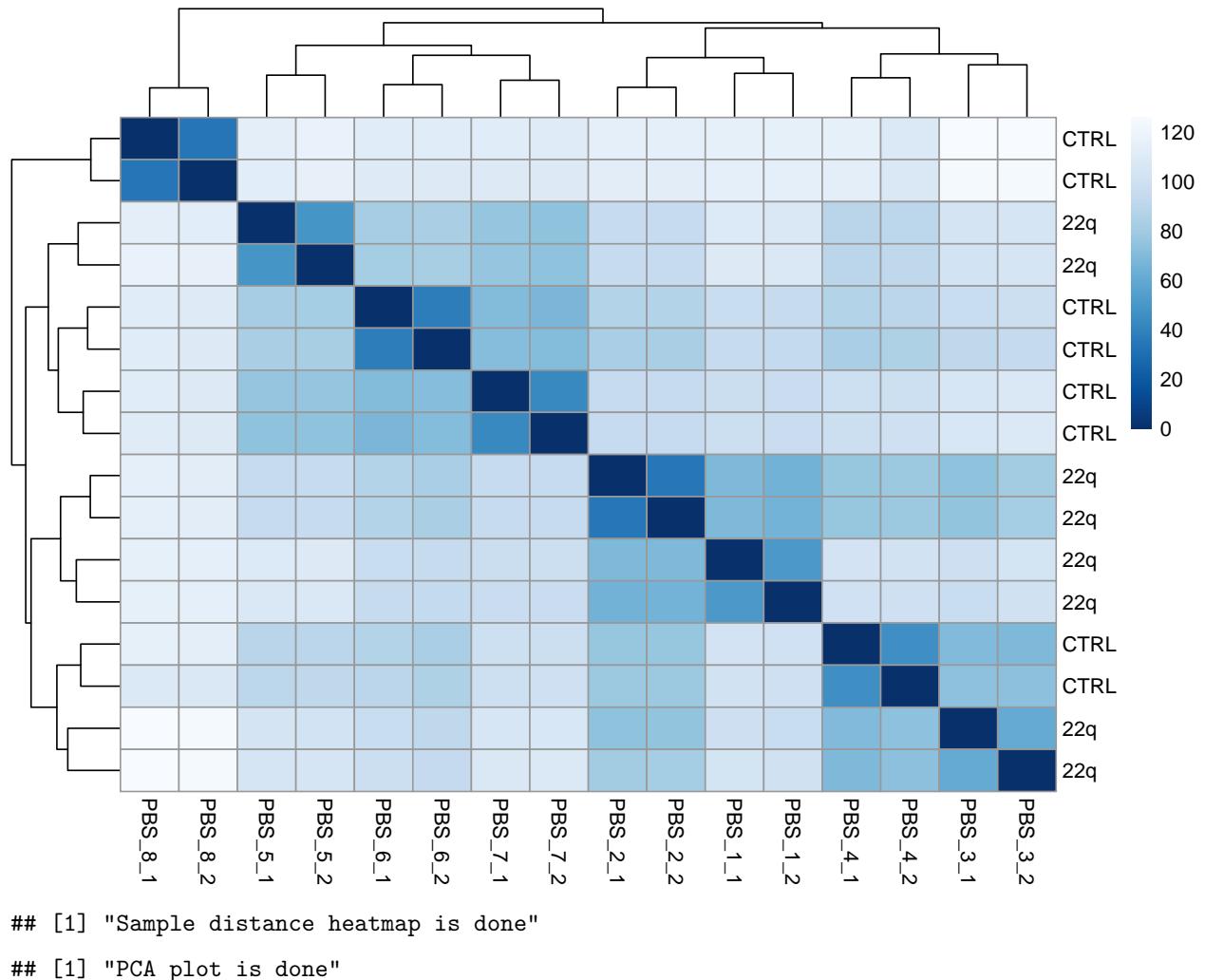
## 2. Differential expression analysis

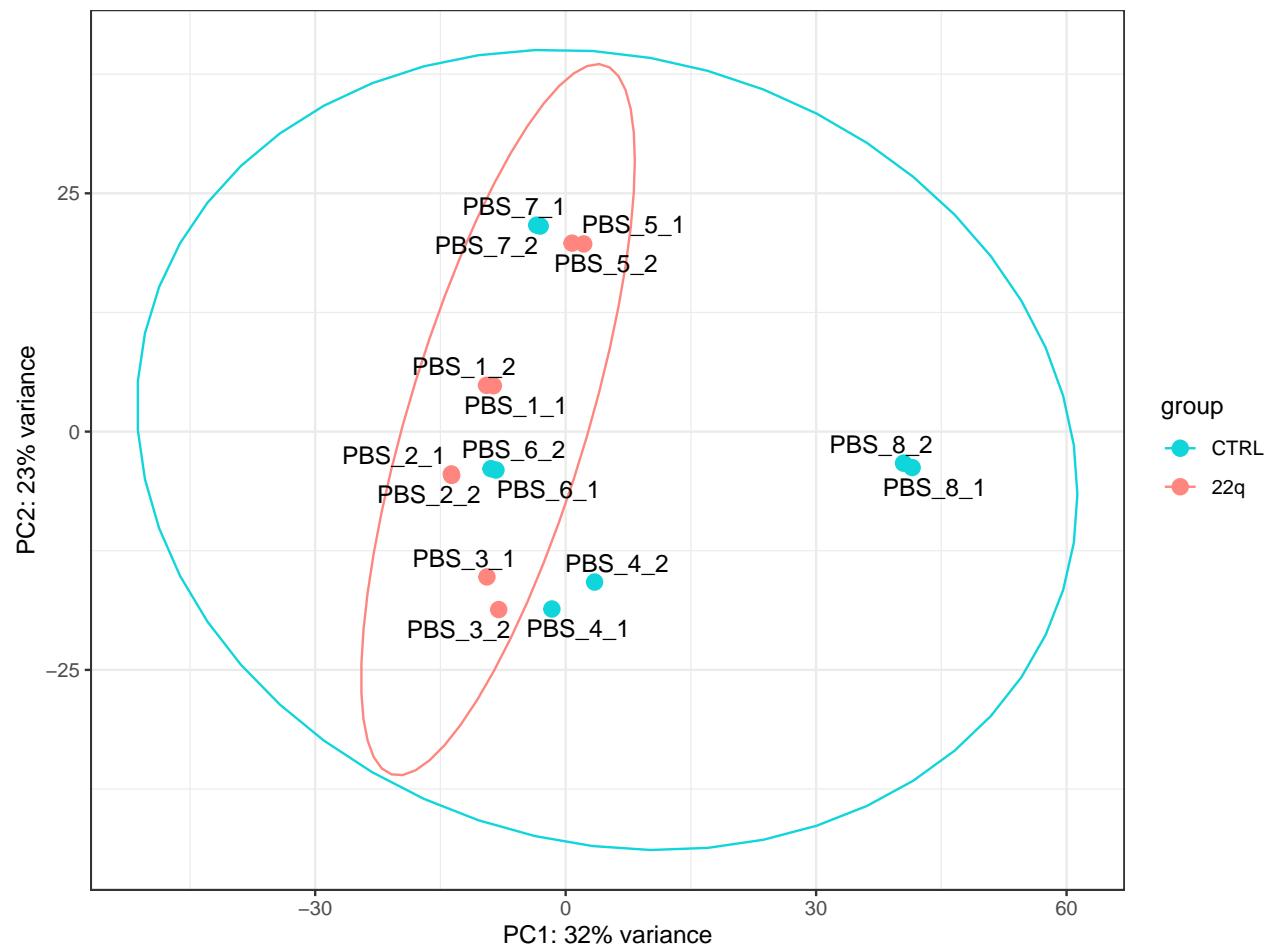
In this section, we will perform differential expression analysis using DESeq2. We will compare the 22q vs Control in the vehicle condition. The results will be stored in `results/02-DEG-Vehicle/DESeq2_results.csv`.

```
## [1] "DEG analysis is done"
```

### 3. Visualization for result

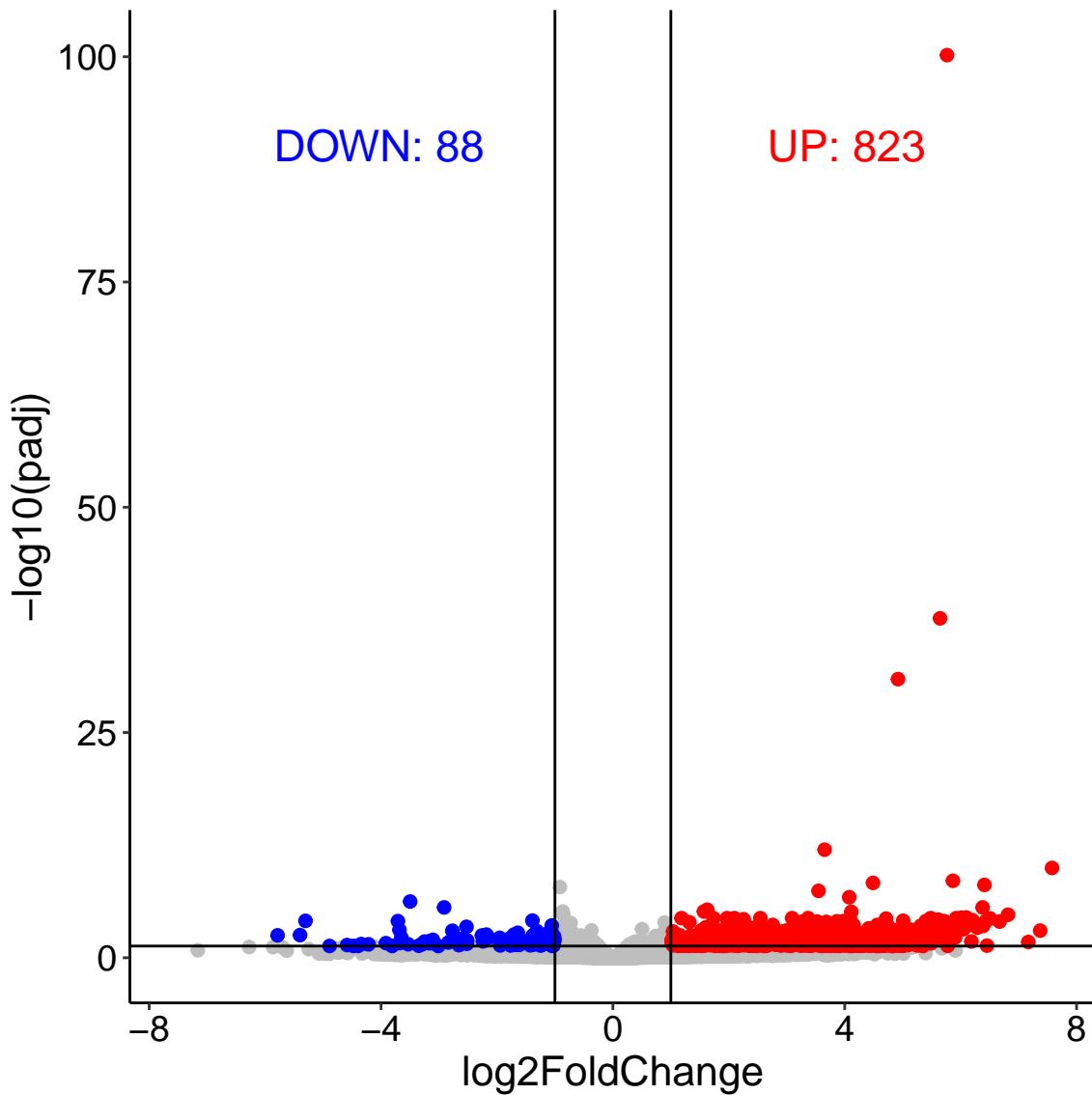
#### (1) Sample information



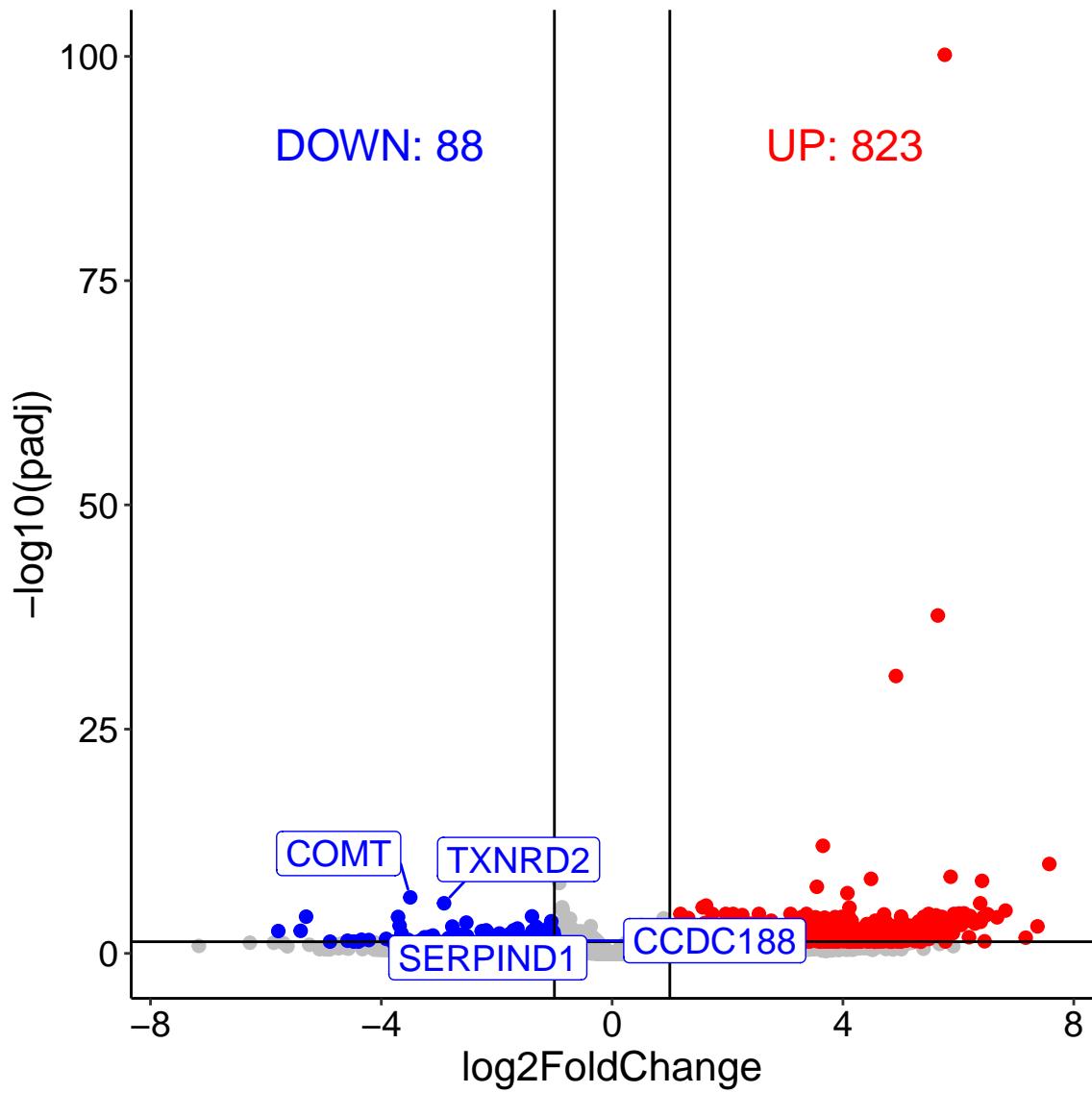


## (2) DEG visualization - Volcano plot and Heatmap

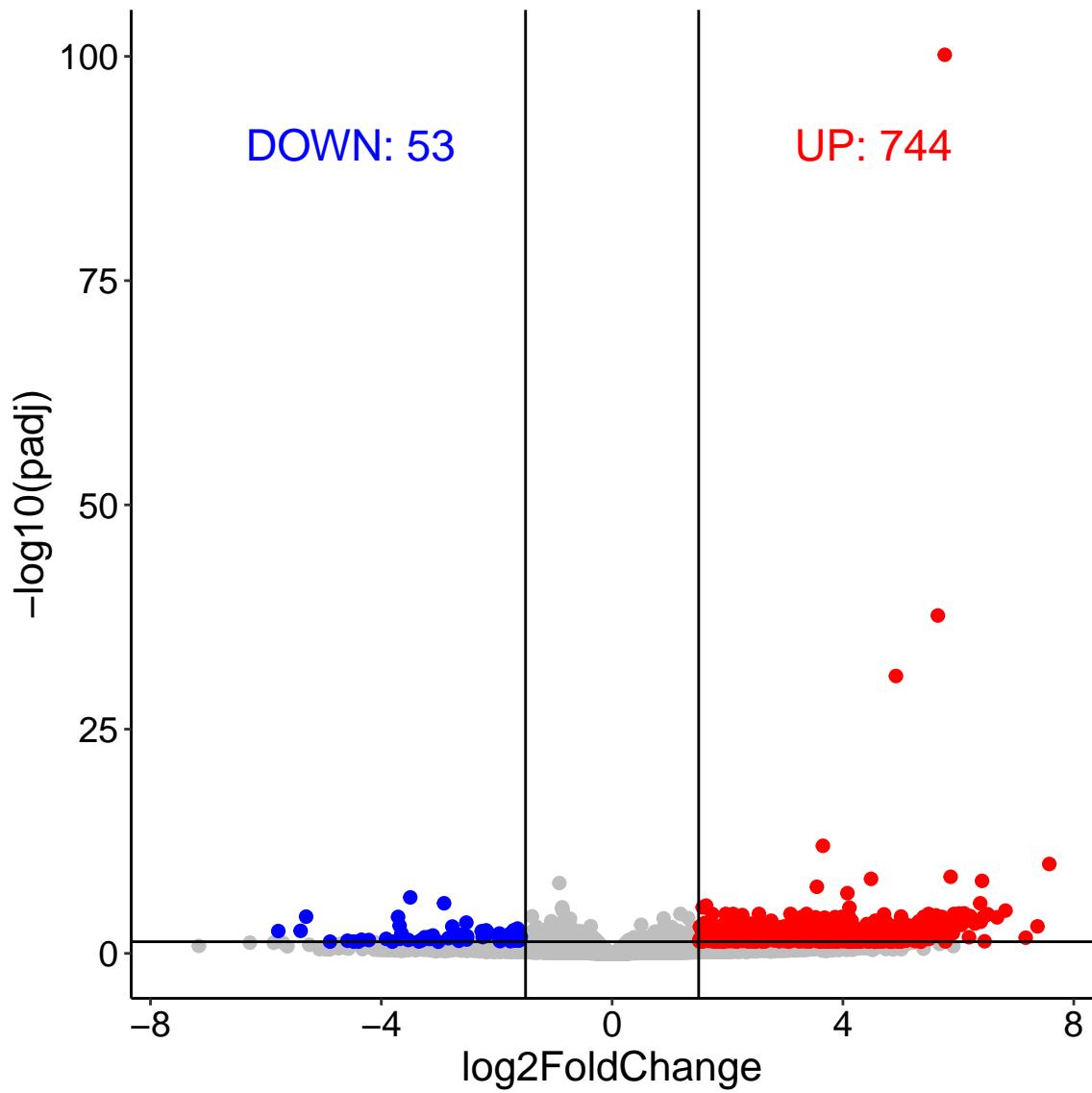
```
## [1] "Volcano plot for 02_volcano_plot_log2fc_1"
```



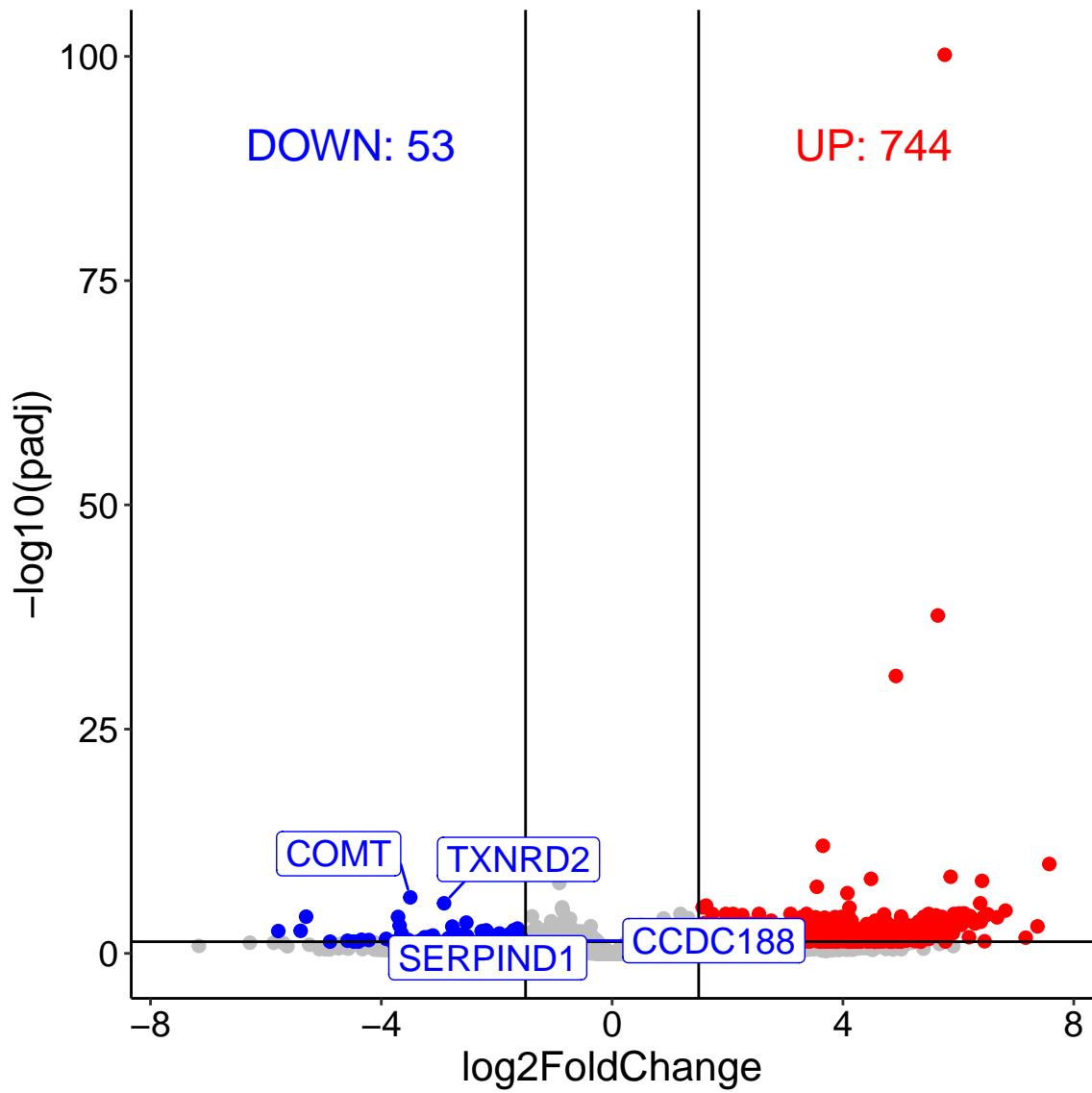
```
## [1] "Volcano plot for 02_volcano_plot_log2fc_1_with_22q_gene"
```



```
## [1] "Volcano plot for 03_volcano_plot_log2fc_1.5"
```



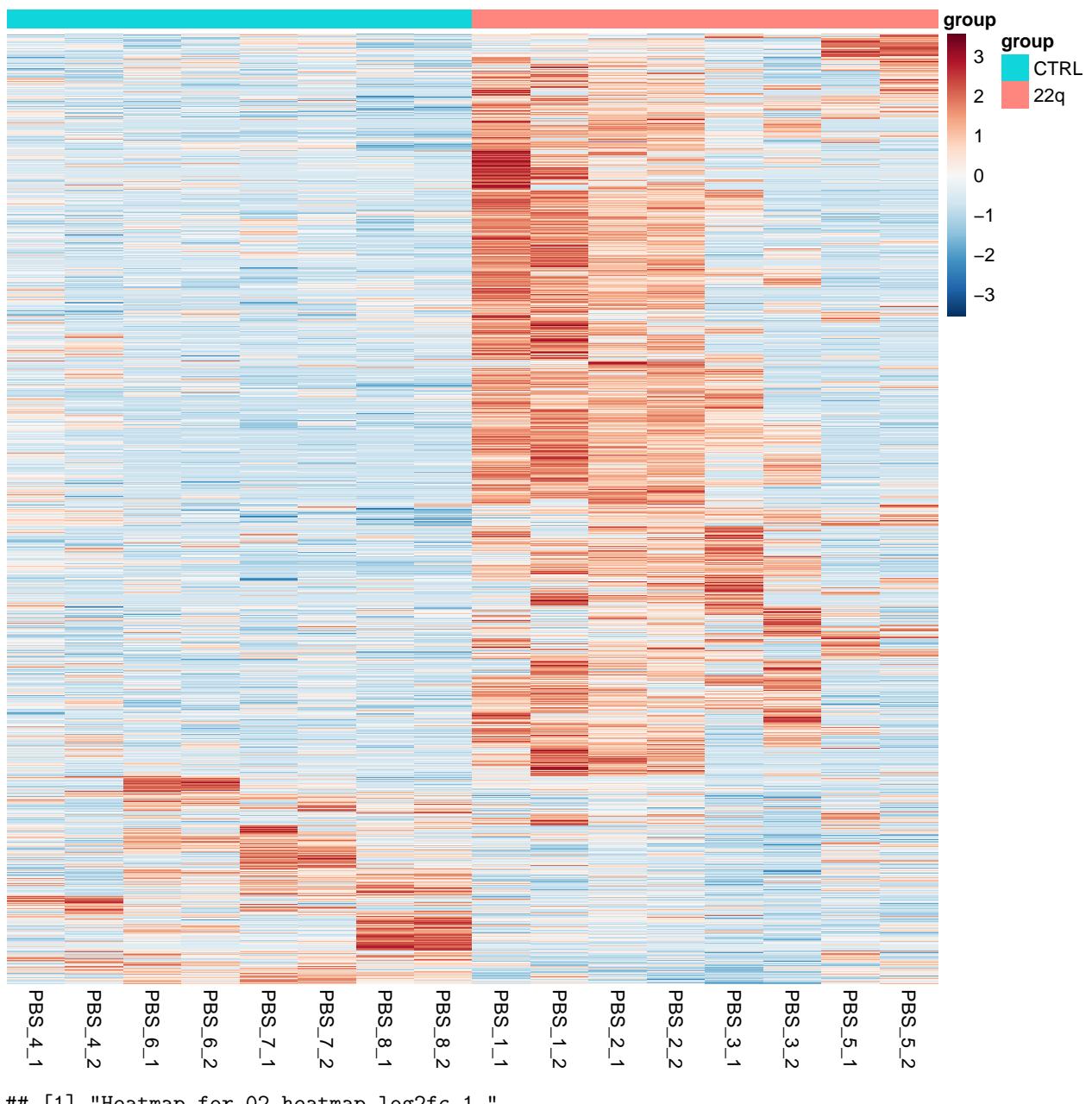
```
## [1] "Volcano plot for 03_volcano_plot_log2fc_1.5_with_22q_gene"
```



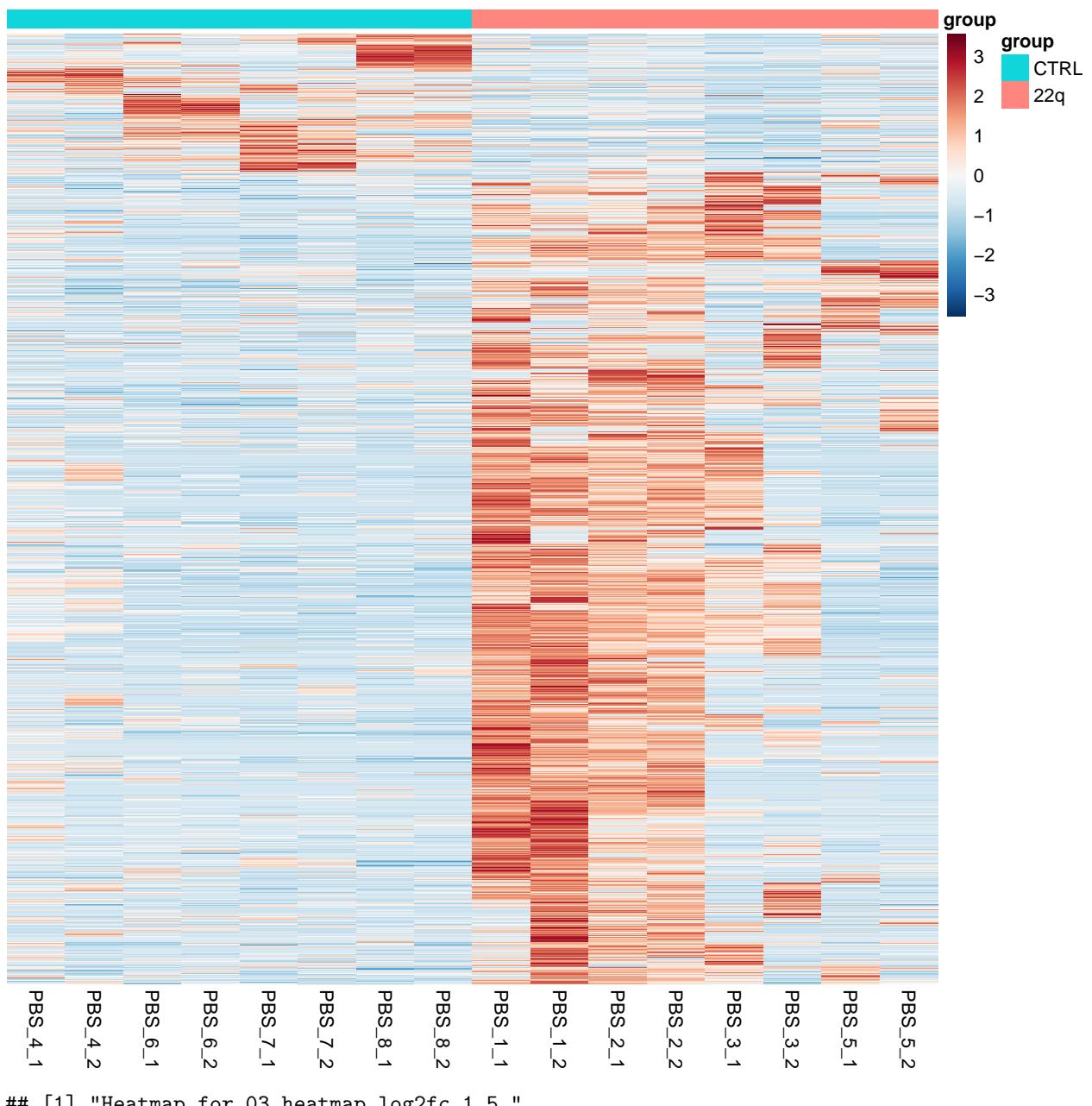
```
## [1] "Heatmap for 02_heatmap_log2fc_1 "
```

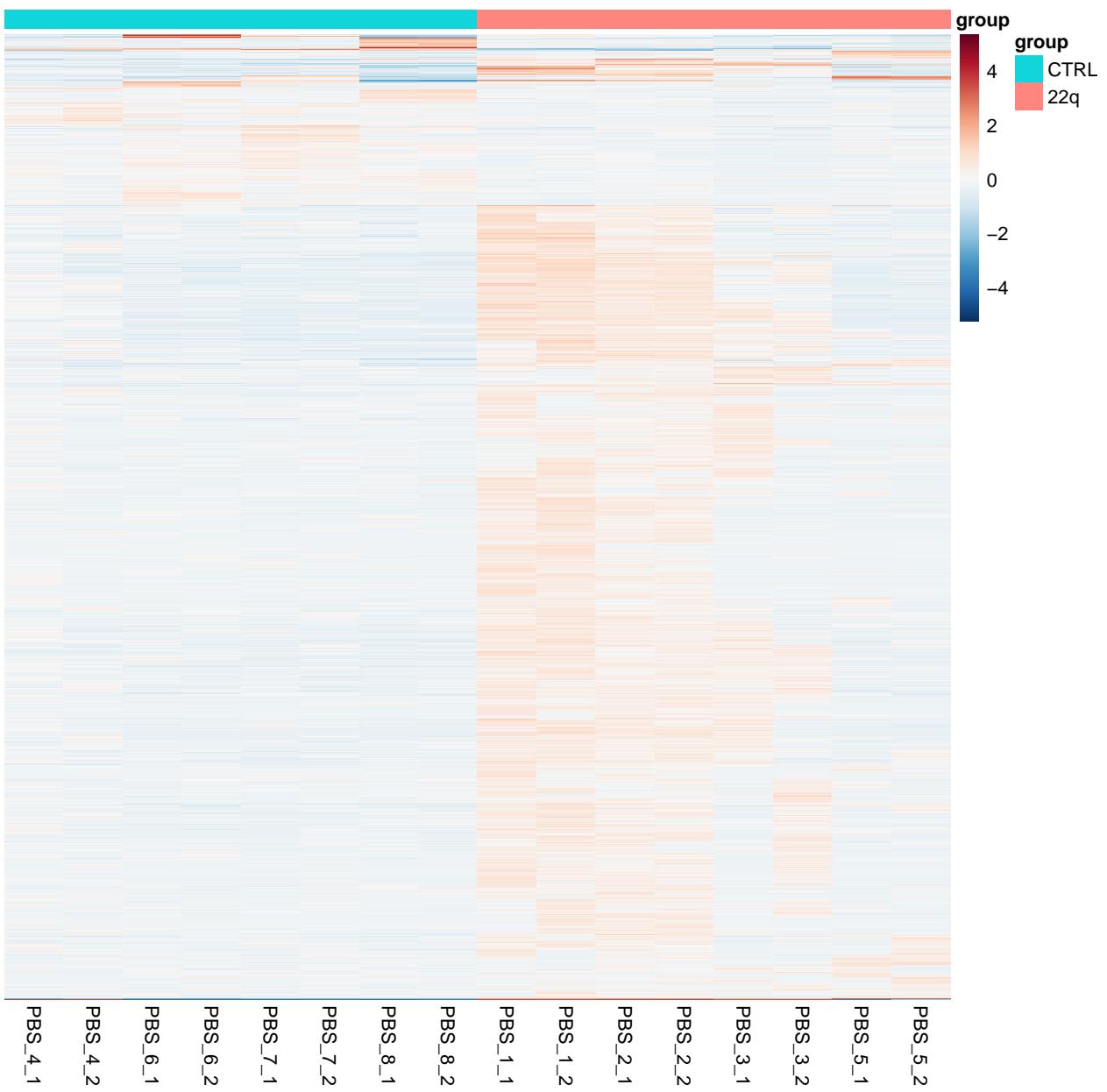


```
## [1] "Heatmap for 02_heatmap_log2fc_1_row "
```



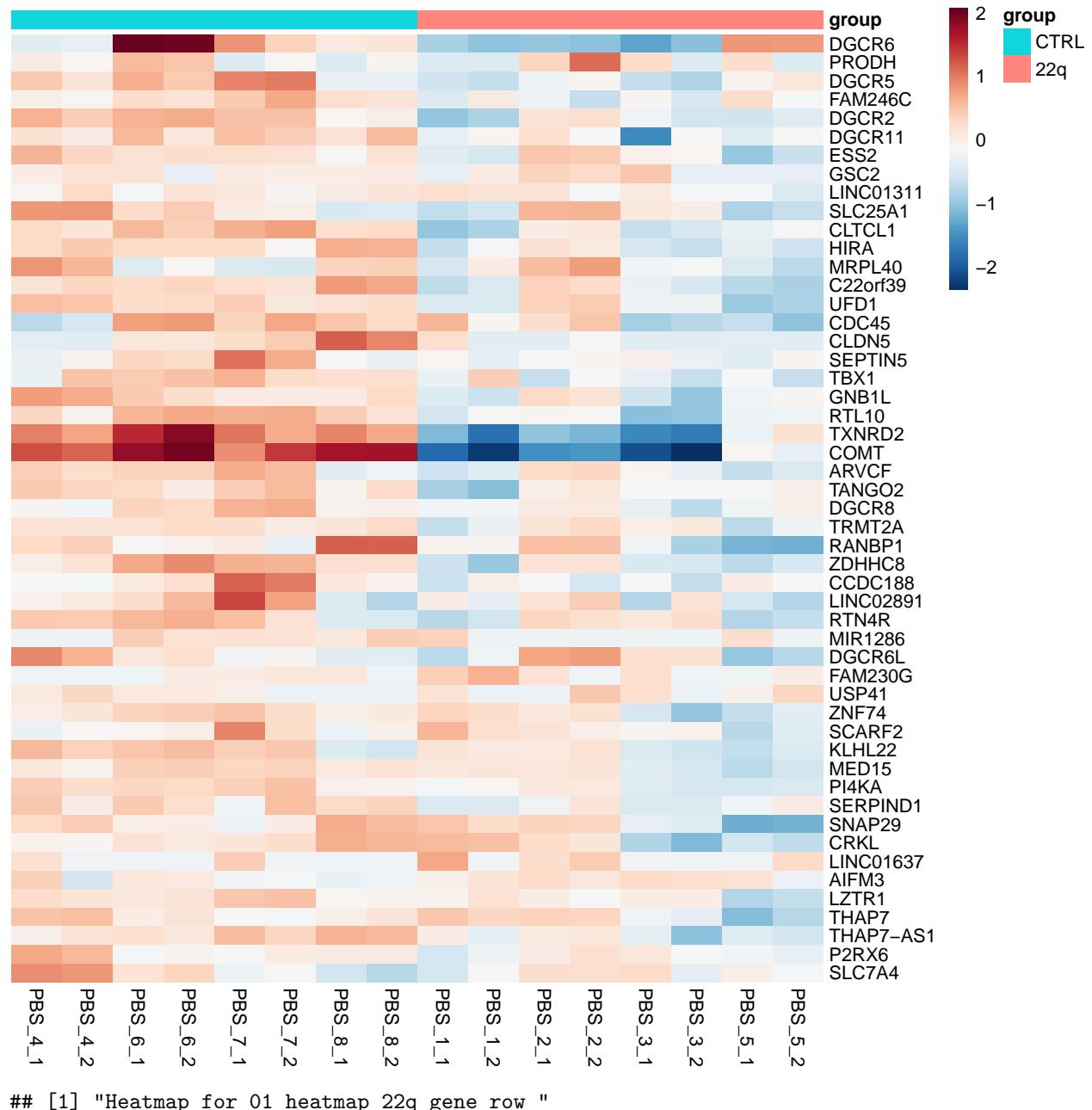




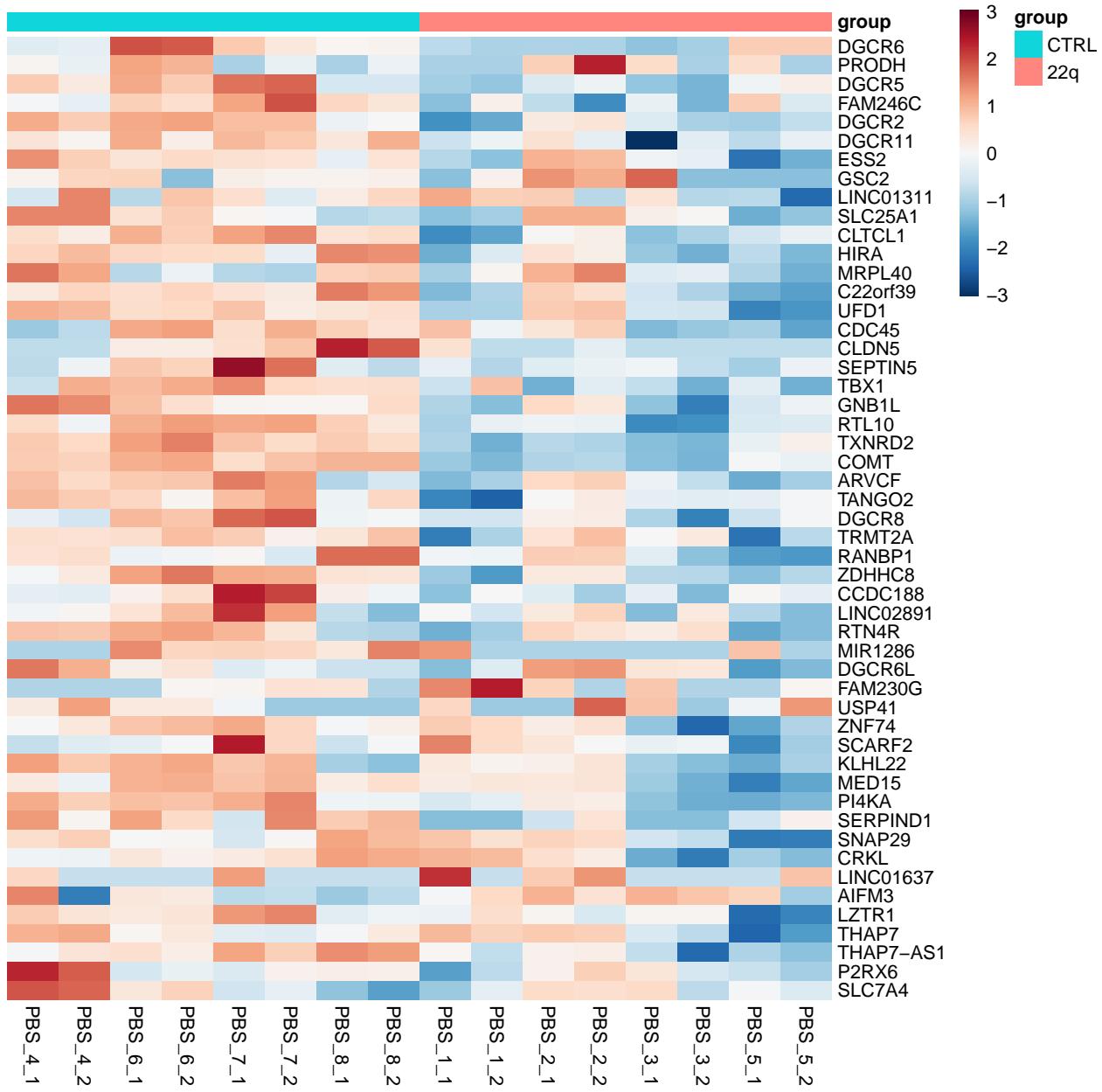


### (3) 22q gene visualization - Heatmap

```
## [1] "Heatmap for 01_heatmap_22q_gene "
```



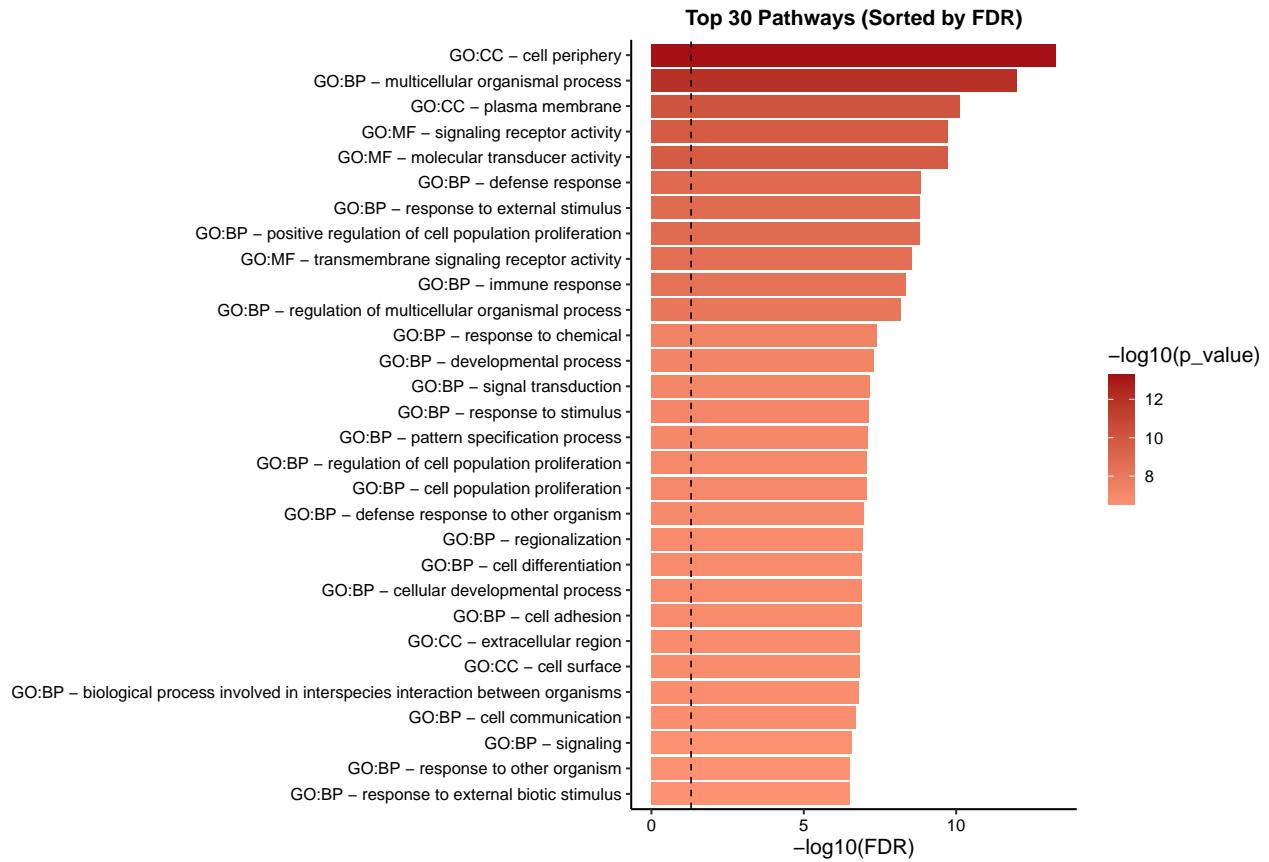
```
## [1] "Heatmap for 01_heatmap_22q_gene_row "
```



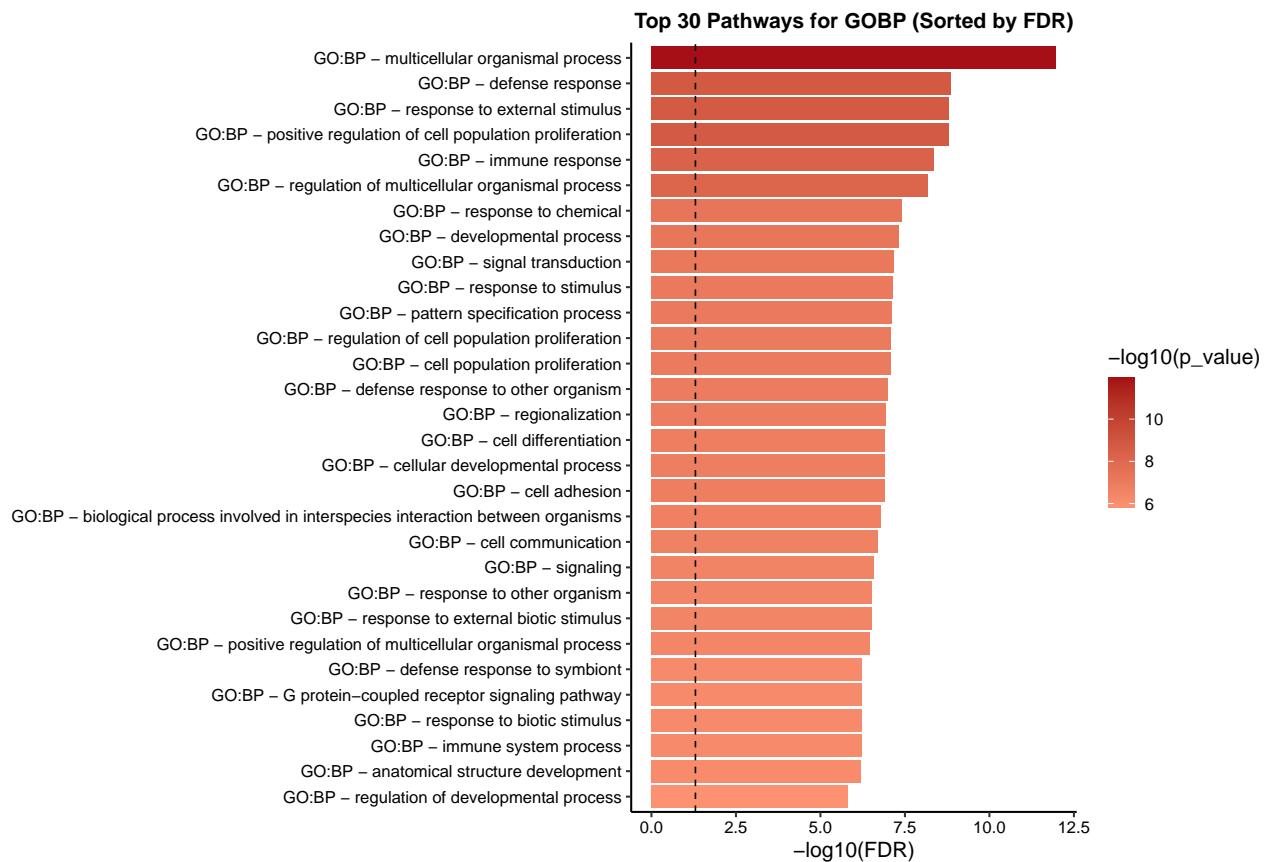
#### **4. GSVA analysis**

## 5. Pathway Enrichment Analysis

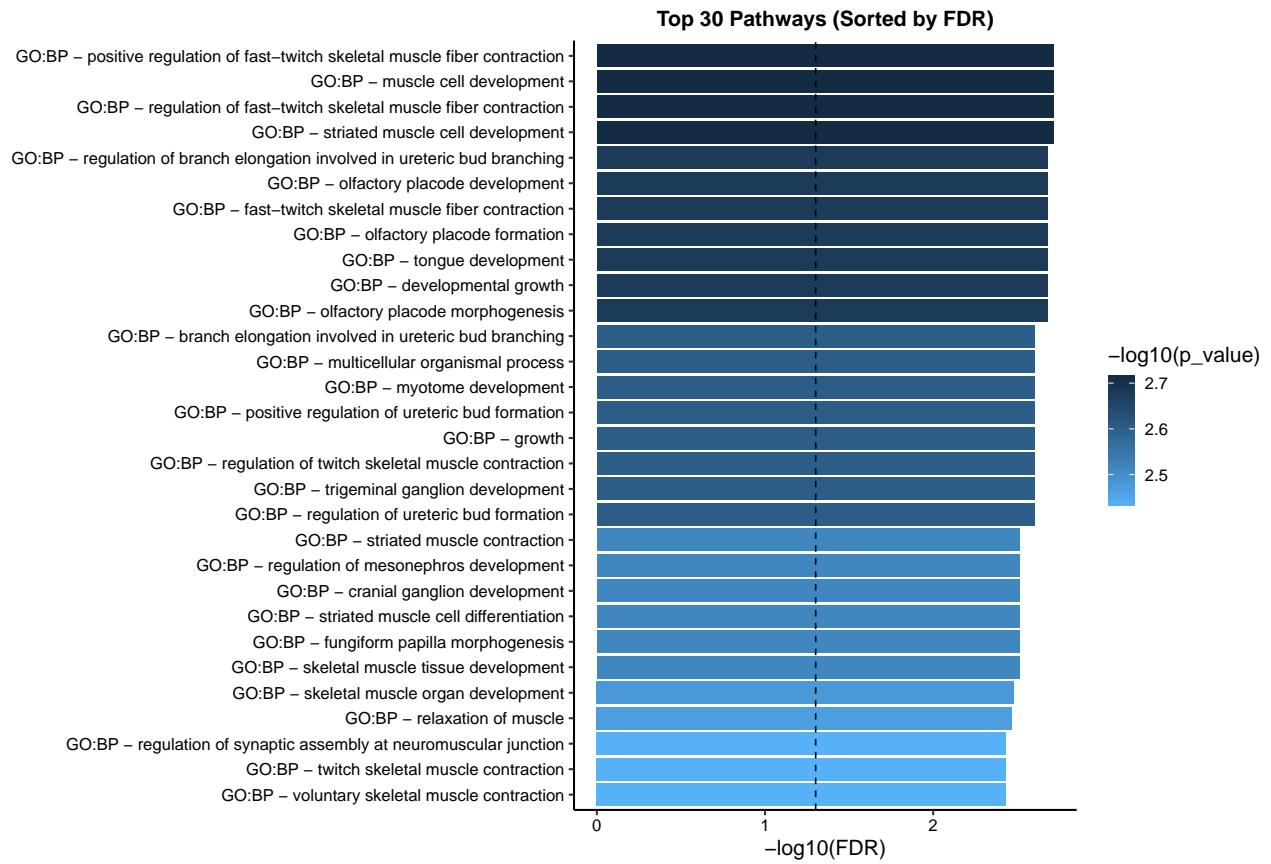
```
## [1] "Enrichment analysis for 01-DEG_1.0_up "
```



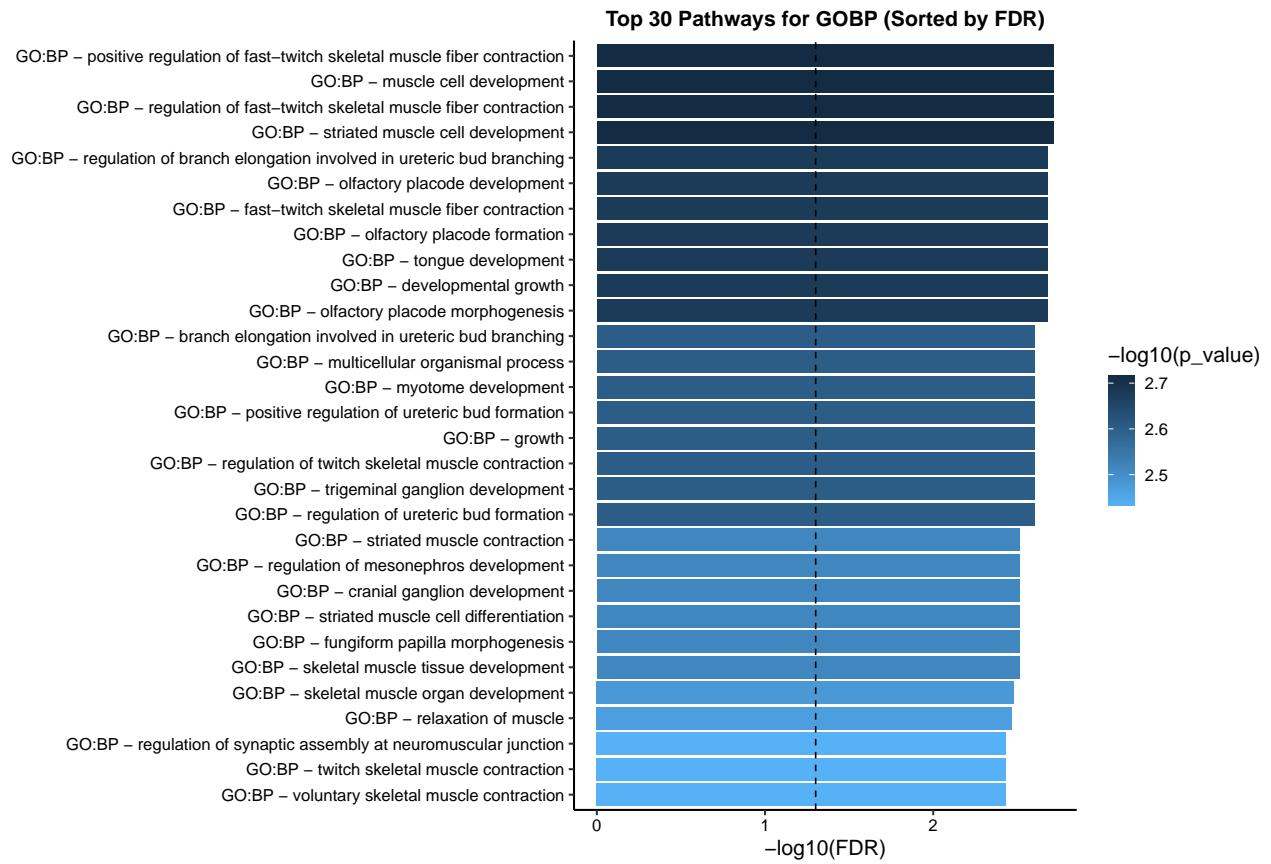
```
## [1] "Enrichment analysis for GOBP 01-DEG_1.0_up "
```



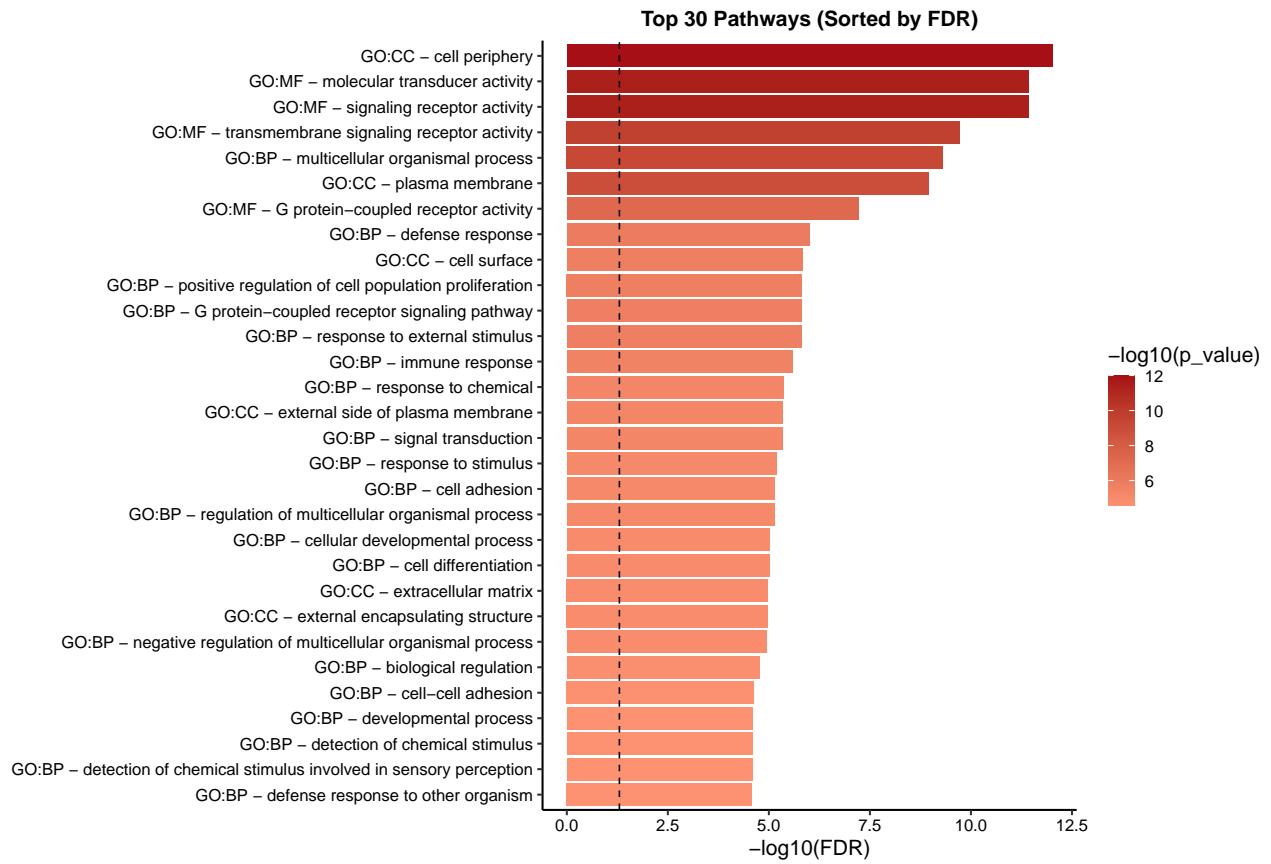
```
## [1] "Enrichment analysis for 01-DEG_1.0_down "
```



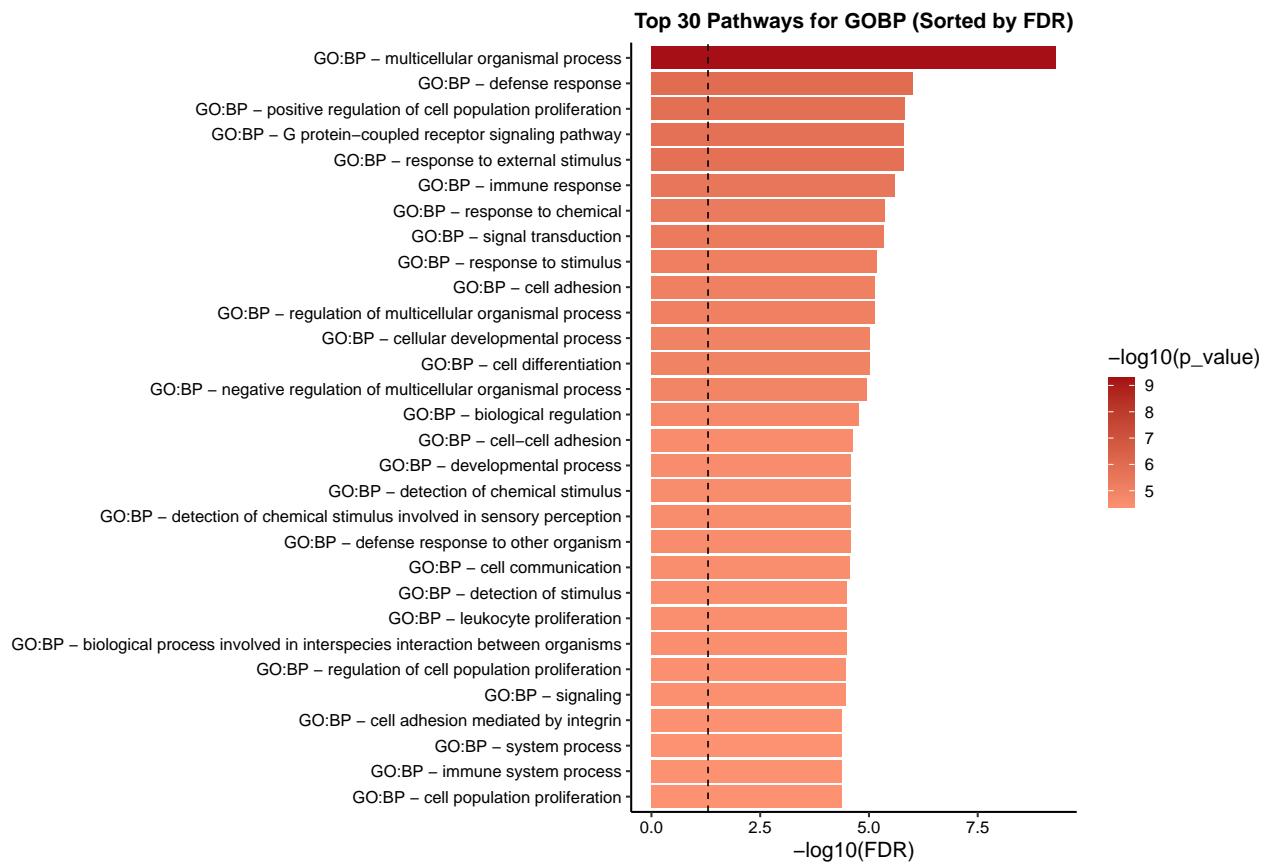
```
## [1] "Enrichment analysis for GOBP_01-DEG_1.0_down "
```



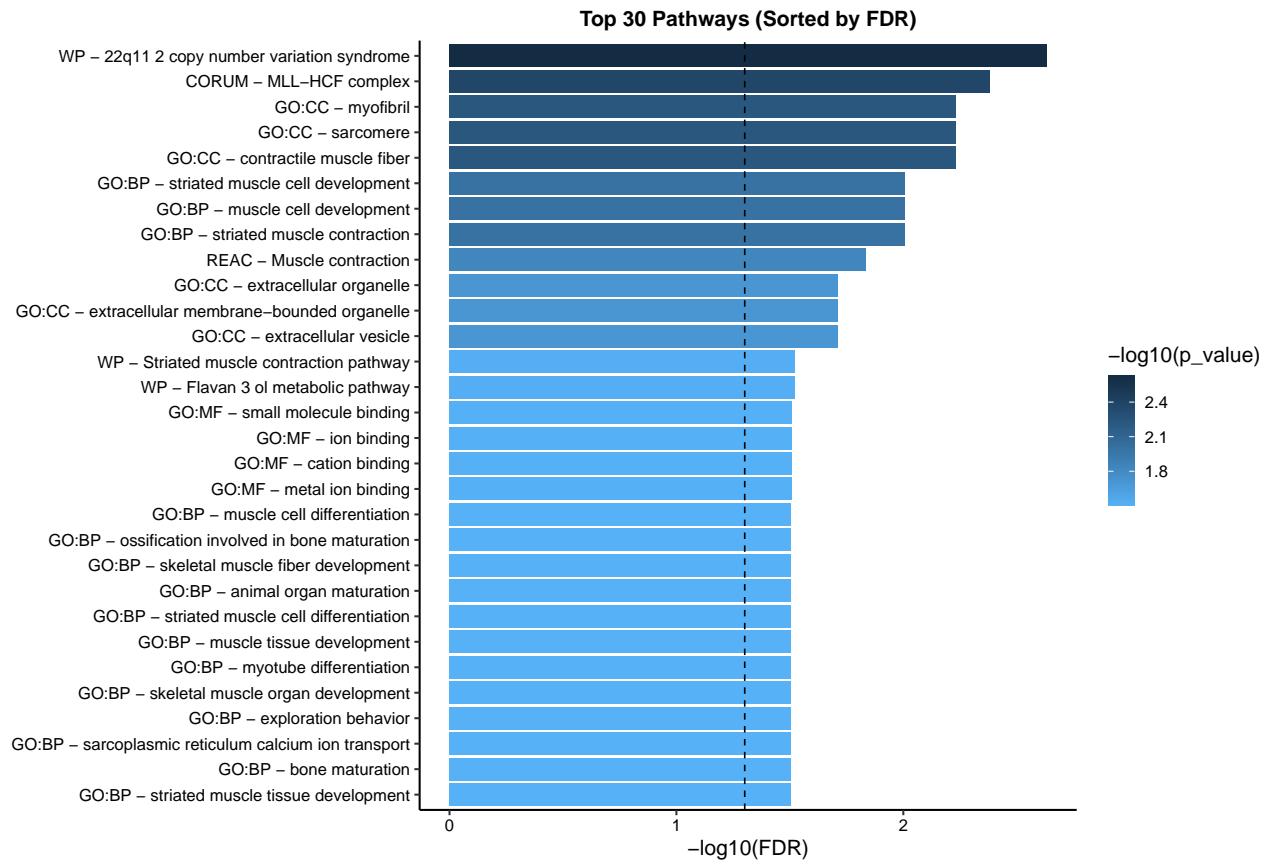
```
## [1] "Enrichment analysis for 02-DEG_1.5_up "
```



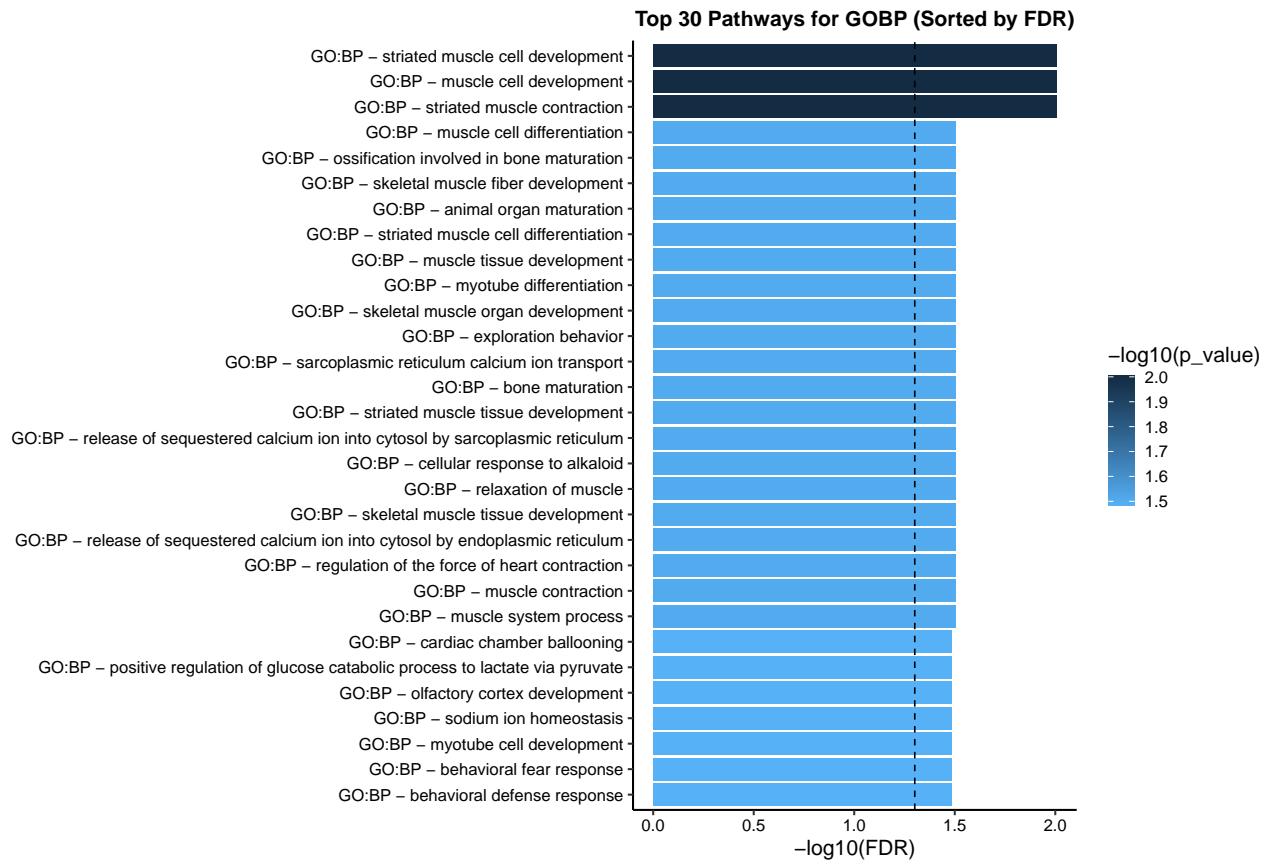
```
## [1] "Enrichment analysis for GOBP_02-DEG_1.5_up "
```



```
## [1] "Enrichment analysis for 02-DEG_1.5_down "
```



```
## [1] "Enrichment analysis for GOBP_02-DEG_1.5_down "
```



## 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] 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_1.17.2         org.Hs.eg.db_3.19.1
## [19] AnnotationDbi_1.66.0      clusterProfiler_4.12.6
## [21] ggrepify_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                purrrr_1.0.4
## [49] readr_2.1.5                tidyverse_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_3.3-3      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                 ggrepel_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_1.3.2
## [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_6.2.2
## [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_3.3-6
## [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_3.1-3     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          G0.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_3.4-2

```