Differential Expression Analysis for small RNA-seq data
Vehicle contition: 22q vs Control

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# Contents

1. Read the count data

In this section, we will read the clean count data from the synaptosomes_miRNARNA folder. The data is stored in the format of `.csv`. We will read the data and filter the columns based on the condition list. The final table will be stored in `results/02-DEM-Vehicle/DESeq2_results.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/01-DEM-Vehicle/DESeq2_results.csv`.
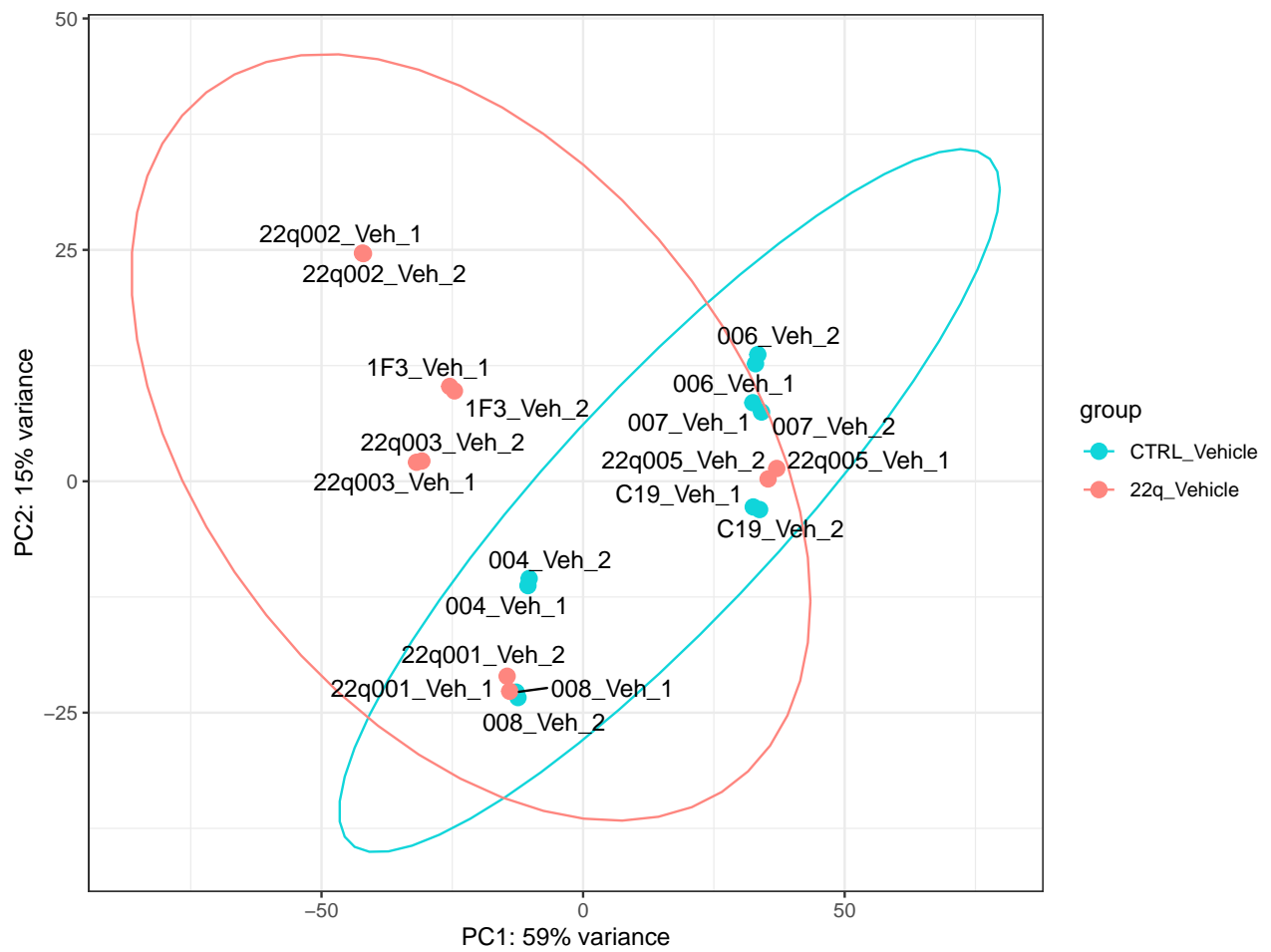
3. Visualization for reuslt

(1) Sample information
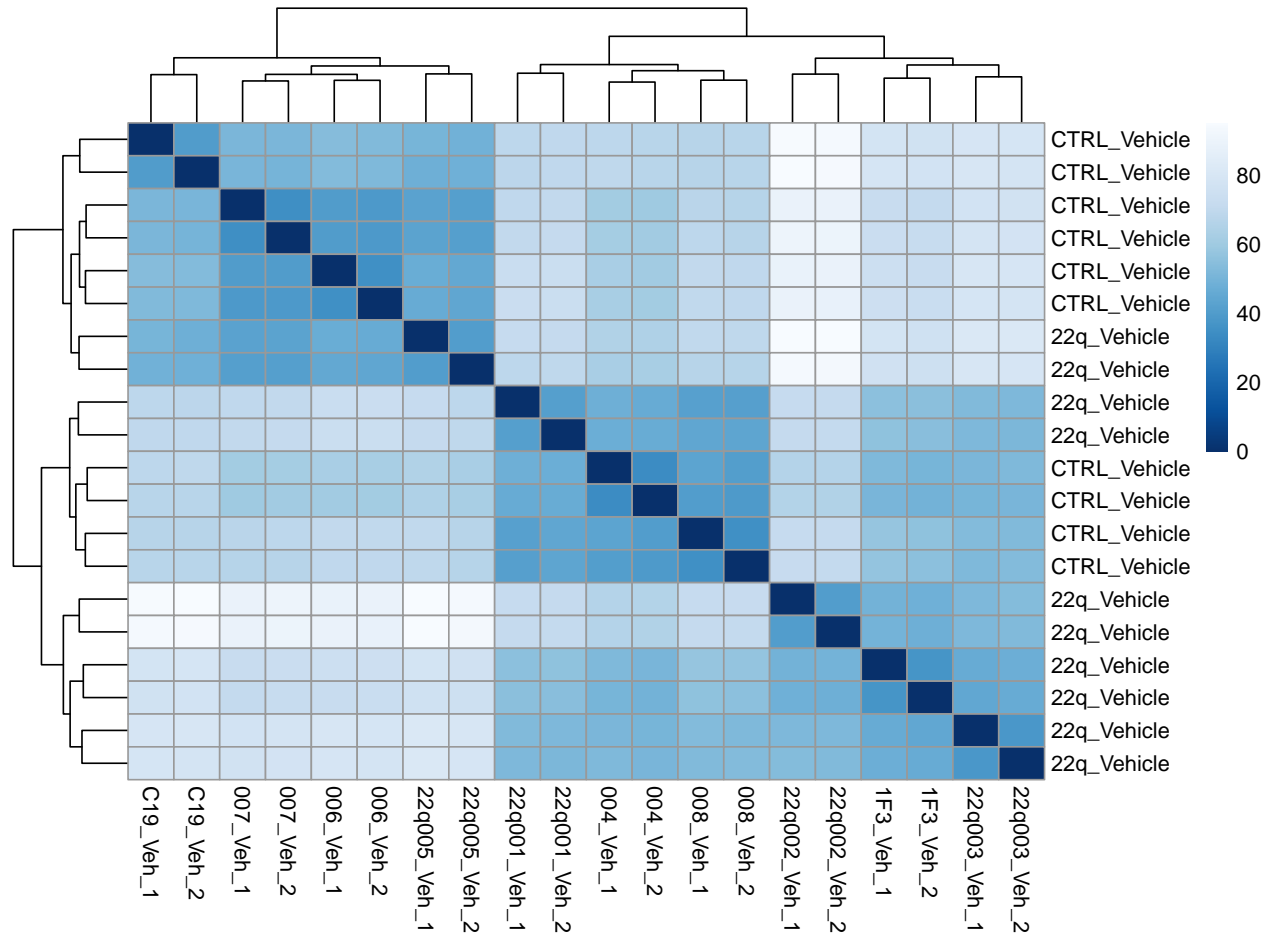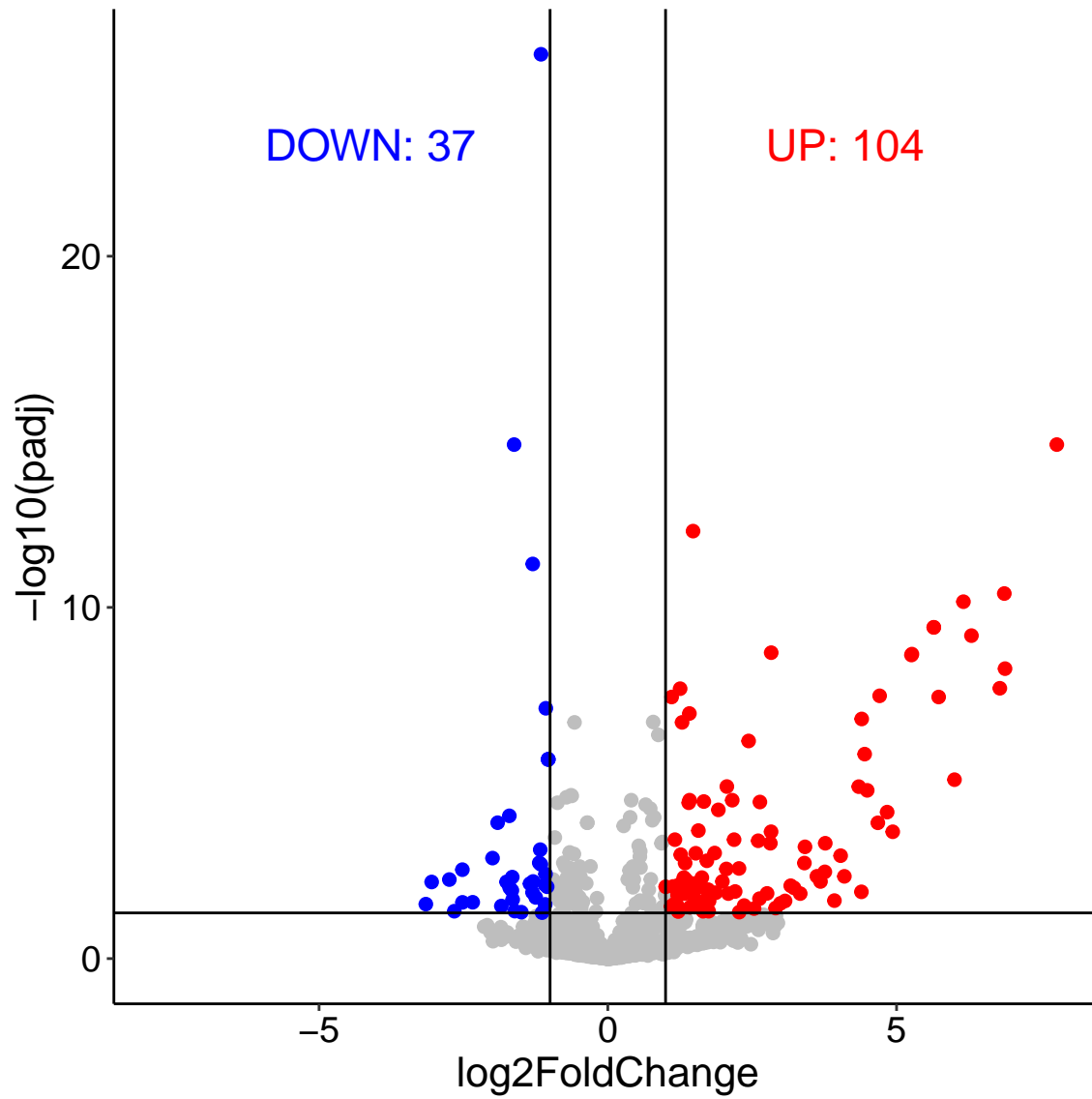


```
## [1] "Sample distance heatmap is done"
```

```
## [1] "PCA plot is done"
```

(2) DEM visualization - Volcano plot and Heatmap

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

`## [1] "Volcano plot for 02_volcano_plot_log2fc_1_with_label_miRNA"`
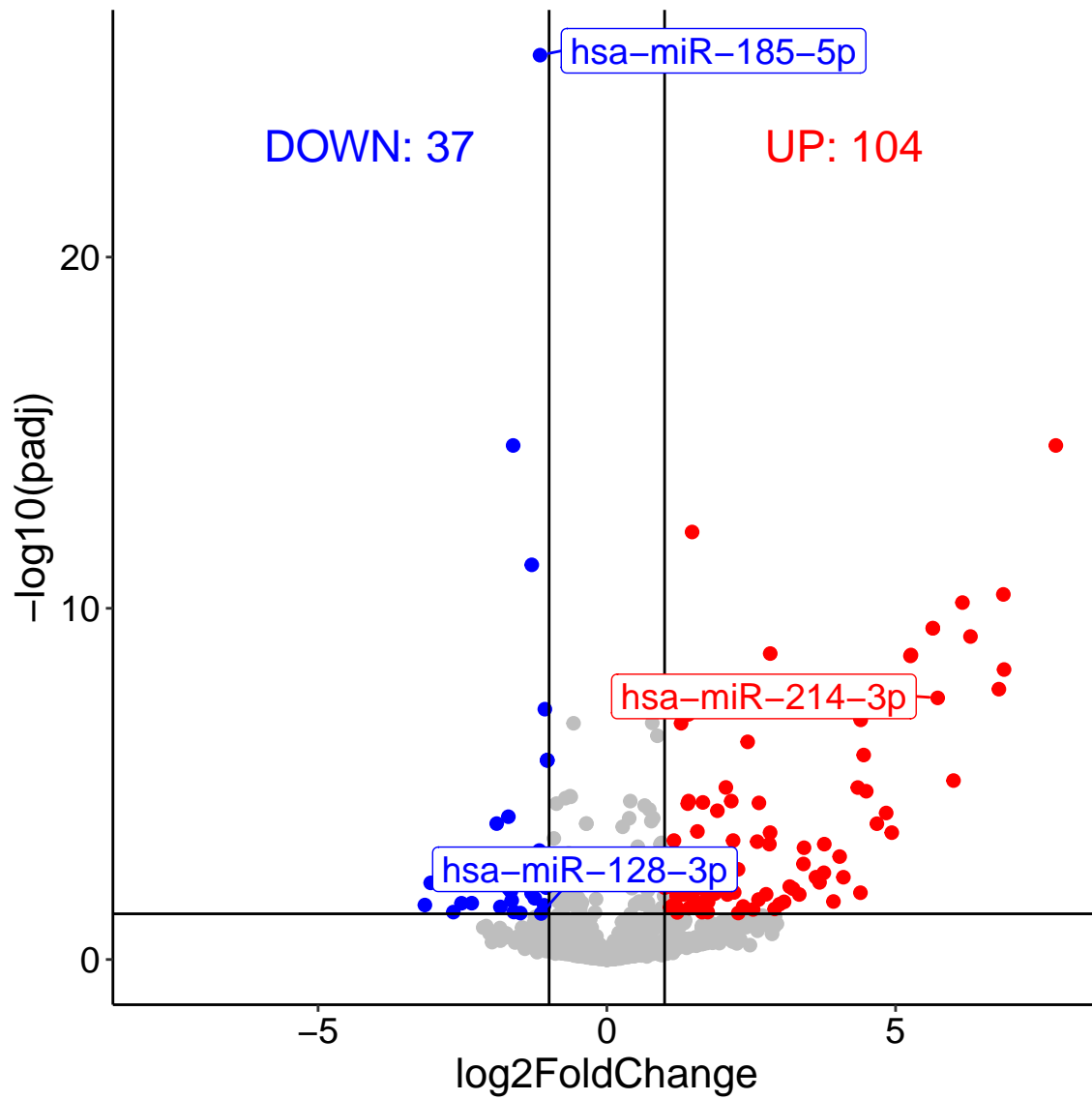
[1] "Volcano plot for 03_volcano_plot_log2fc_1.5"
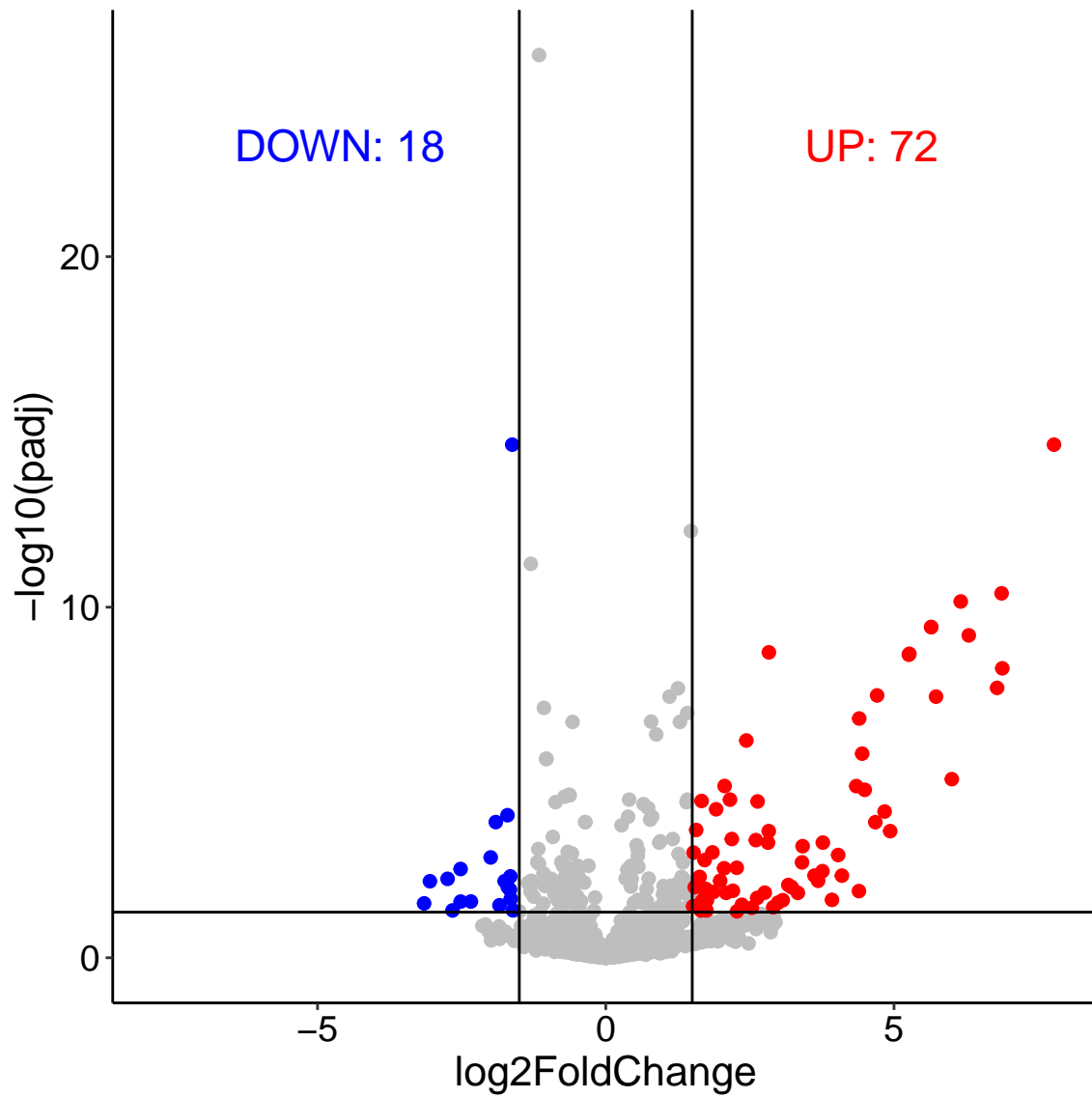
[1] "Volcano plot for 03_volcano_plot_log2fc_1.5_with_label_miRNA"
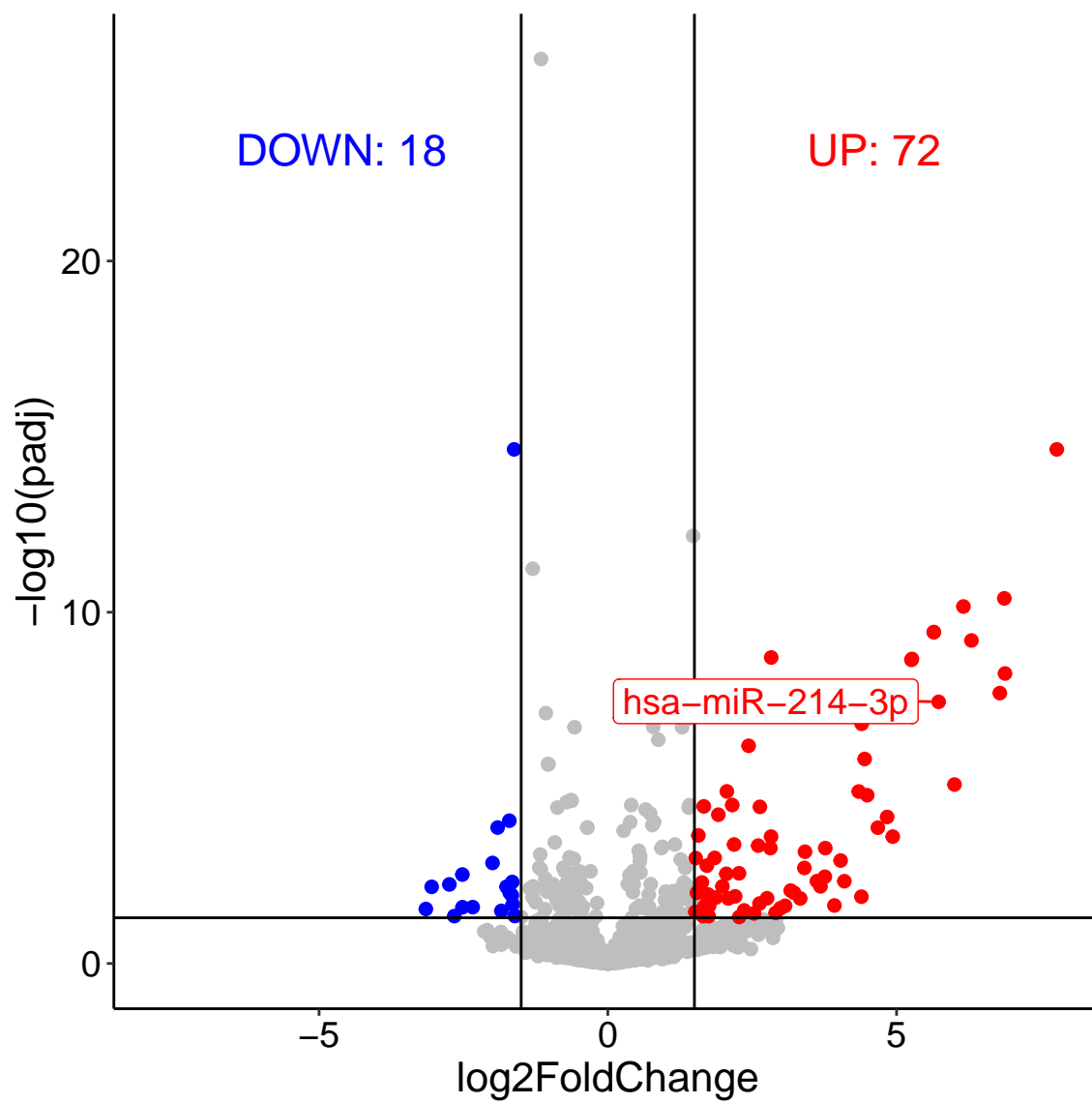
```
## [1] "Heatmap for 02_heatmap_log2fc_1 "
```
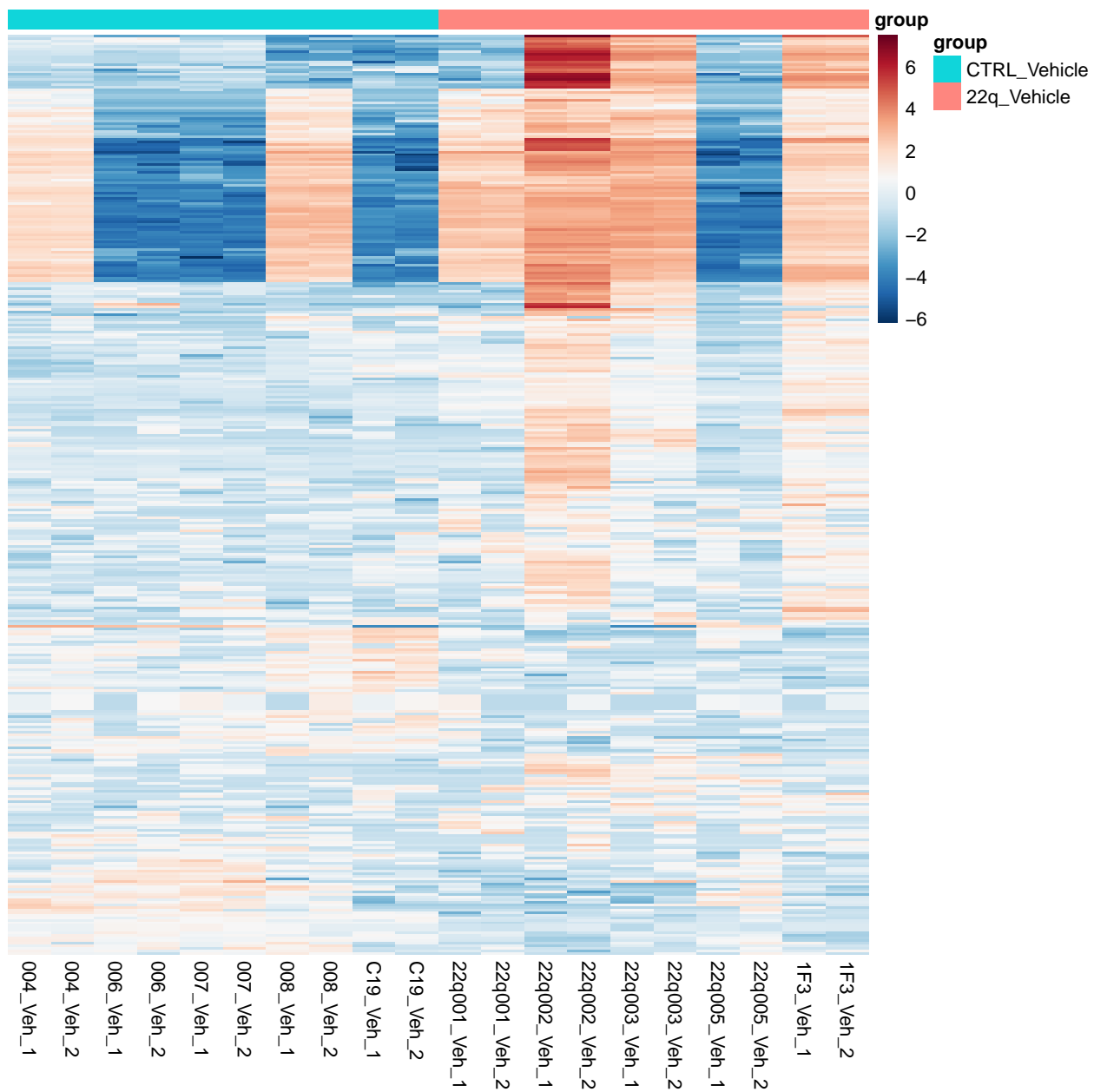
[1] "Heatmap for 02_heatmap_log2fc_1_row "
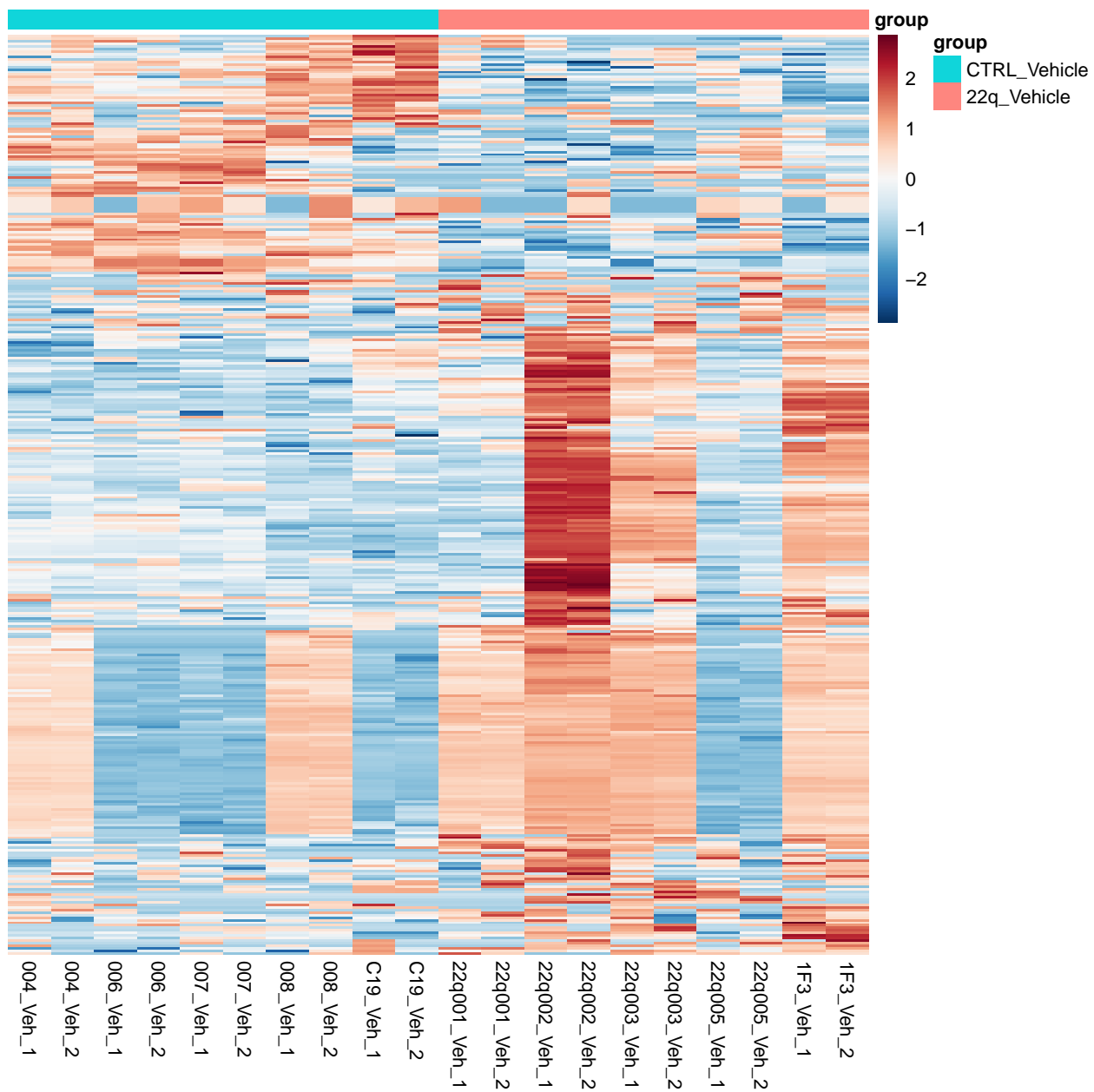
[1] "Heatmap for 02_heatmap_log2fc_1 "
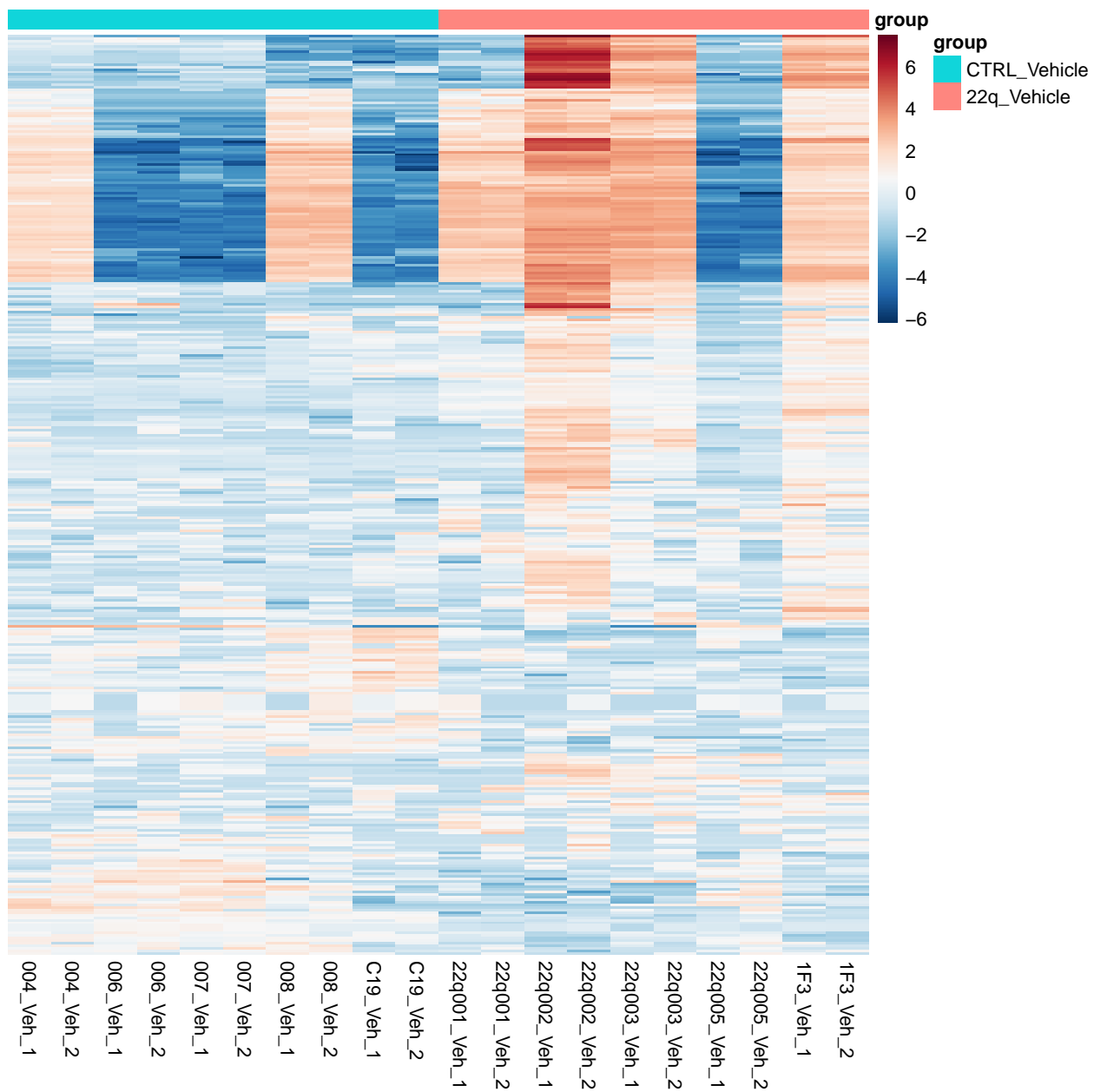
[1] "Heatmap for 03_heatmap_log2fc_1.5_row "
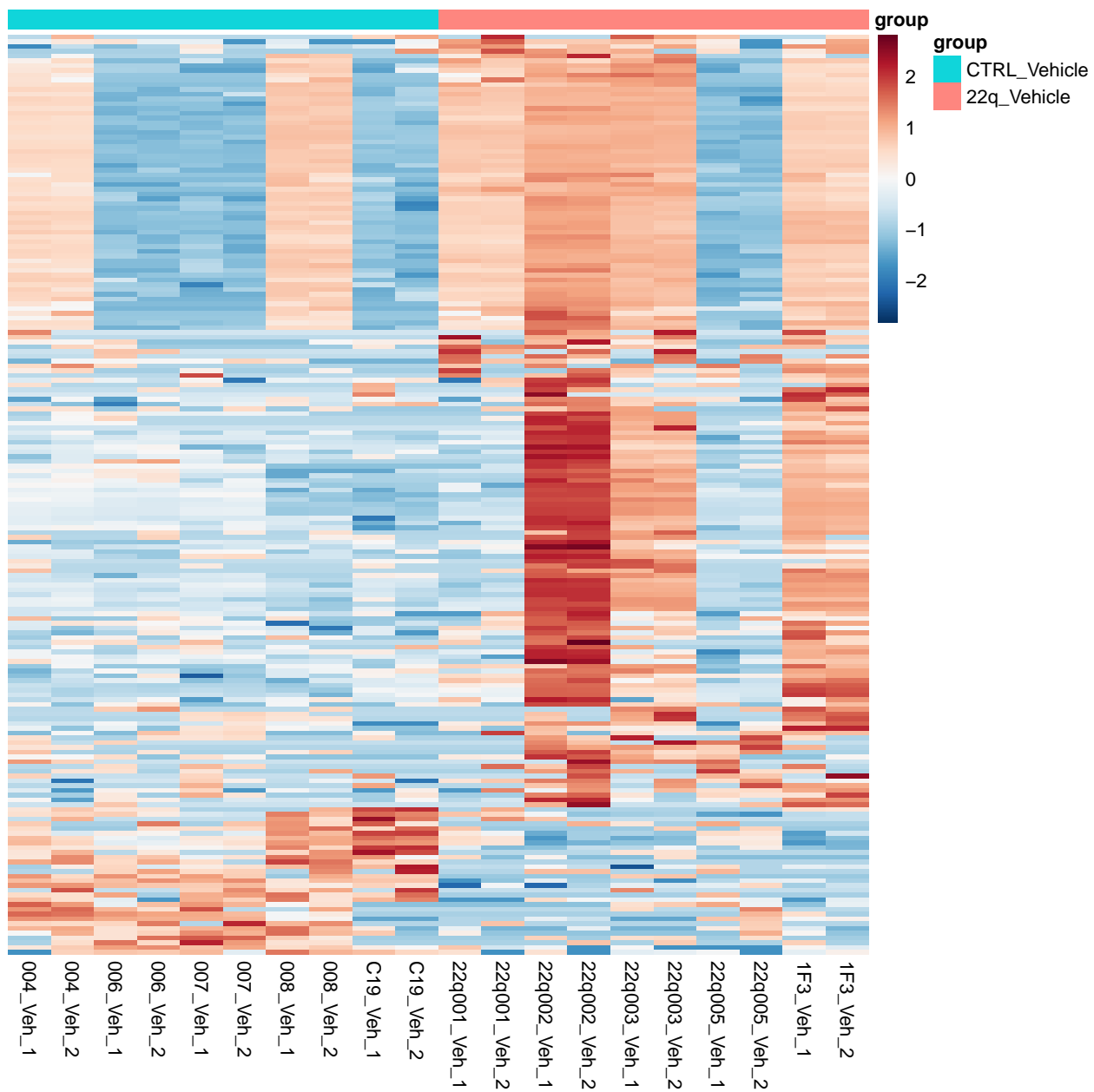
[1] "Heatmap for 03_heatmap_log2fc_1.5 "
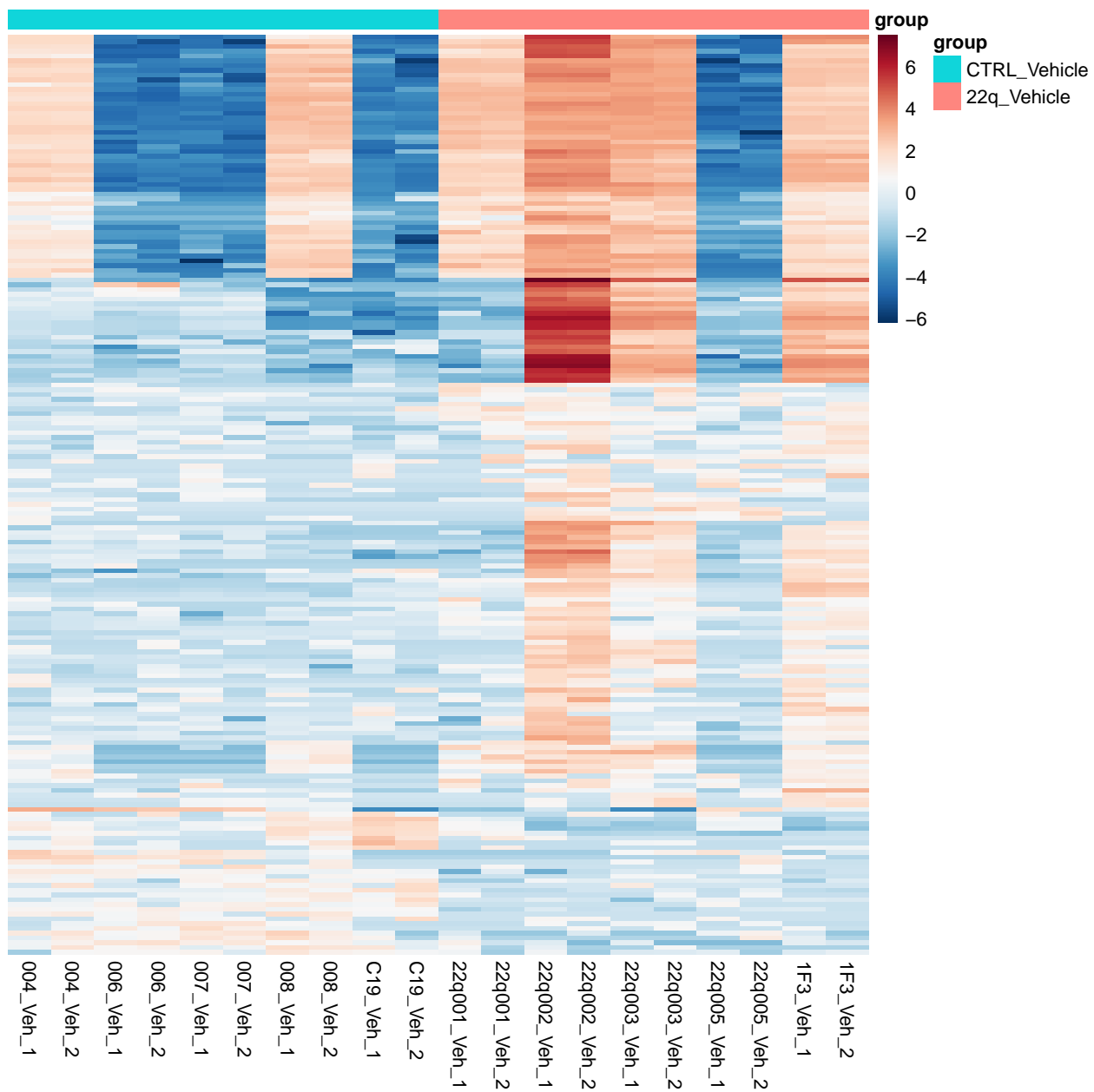
(3) 22q miRNA visualization - Heatmap

[1] "Heatmap for 01_heatmap_22q_gene "
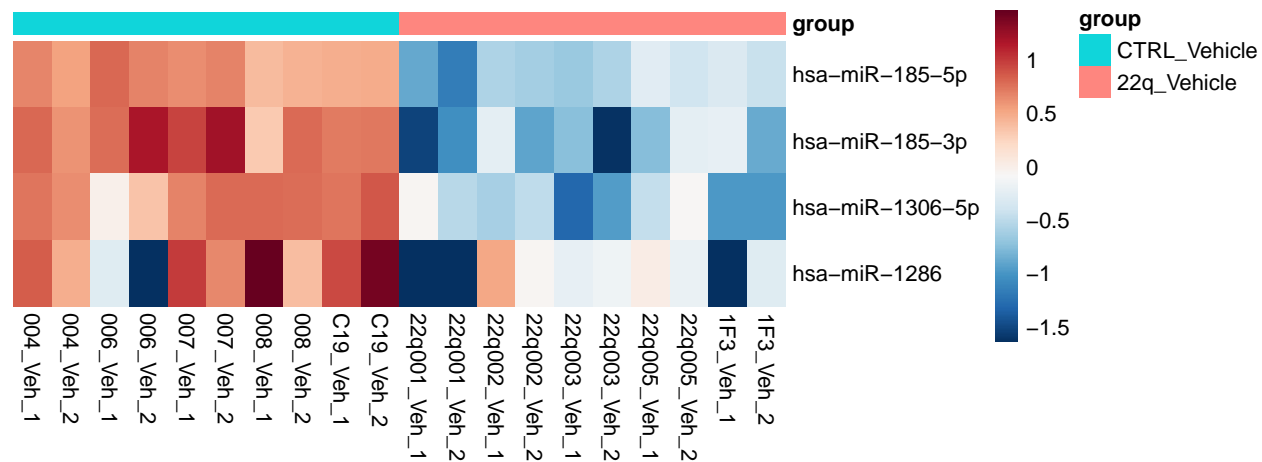
[1] "Heatmap for 01_heatmap_22q_gene_row "
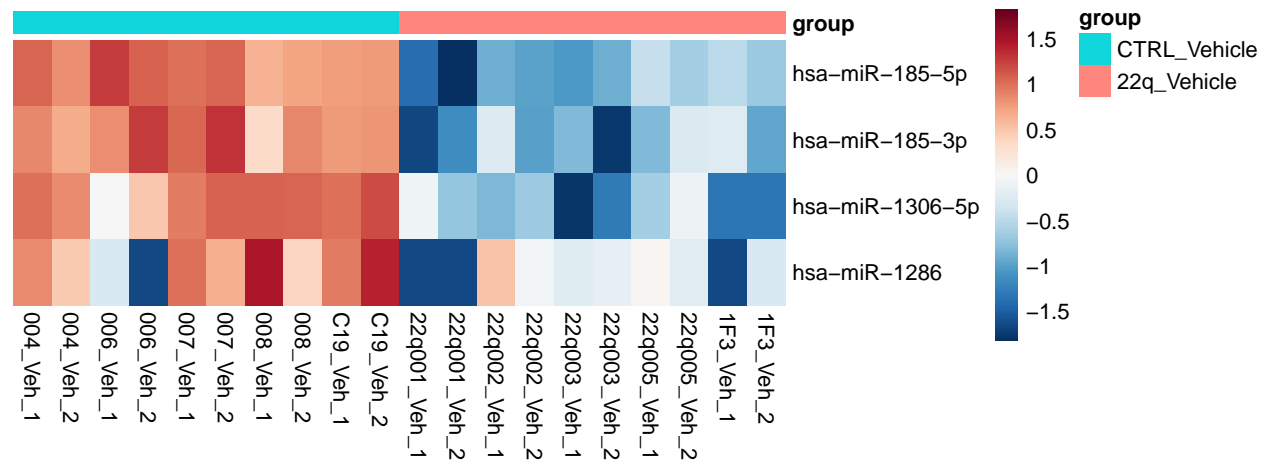
Session information

```
## 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_1.17.0        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_5.2.1
## [35] SeuratObject_5.0.2       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_3.5.1
## [53] 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] vctrs_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_1.6.15             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_1.3.3
##  [25] tidytree_0.4.6            zoo_1.8-13
##  [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_0.16.3            fitdistrplus_1.2-2
##  [37] rhdf5_2.48.0              rstudioapi_0.17.1
##  [39] UCSC.utils_1.0.0          miniUI_0.1.1.1
##  [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_1.6.5
## [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
```

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## [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] ggridges_0.5.6            progressr_0.15.1
## [139] ape_5.8-1                 jsonlite_2.0.0
## [141] RcppHNSW_0.6.0            bitops_1.0-9
## [143] bit64_4.6.0-1             Rtsne_0.17
## [145] yulab.utils_0.2.0         spatstat.utils_3.1-3
## [147] bdsmatrix_1.3-7           GOSemSim_2.30.2
## [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_0.56
## [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_1.34.0             rsvd_1.0.5
## [183] munsell_0.5.1             KernSmooth_2.23-26
## [185] htmlwidgets_1.6.4         fgsea_1.30.0
## [187] rlang_1.1.5               spatstat.sparse_3.1-0
## [189] spatstat.explore_3.4-2
```