

Upsetplot of DEG and DEM

Consider upregulated gene

Ximing Ran

2025-04-18

Contents

1. Read the DEG and DEM from the previous analysis	2
2. Predicted target miRNA of DEG	3
(a) Vene Plot	3
Plot for downregulated miRNA	3
Plot for upregulated miRNA	4
(b) Upset plot	5
Downregulated miRNA	5
Upregulated miRNA	6
Session information	7

1. Read the DEG and DEM from the previous analysis

```
## [1] "DEG label CTRL"
##
## down   up
##  177  214
## [1] "DEG label 22q"
##
## down   up
##    6    3
## [1] "DEM_Veh label"
##
## down   up
##   37  104
## [1] "DEM_TTX label"
##
## down   up
##   23   90
```

2. Predicted target miRNA of DEG

(a) Vene Plot

```
## [1] "DEM target CTRL up, DEG 214 , DEG target DEM 216 "
```

```
## [1] "DEM target CTRL down, DEG 173 , DEG target DEM 192 "
```

Plot for downregulated miRNA

```
## [1] "miRNA in overlap of all three"
```

```
## [1] "hsa-miR-128-3p" "hsa-miR-1286" "hsa-miR-1306-5p" "hsa-miR-139-5p"
```

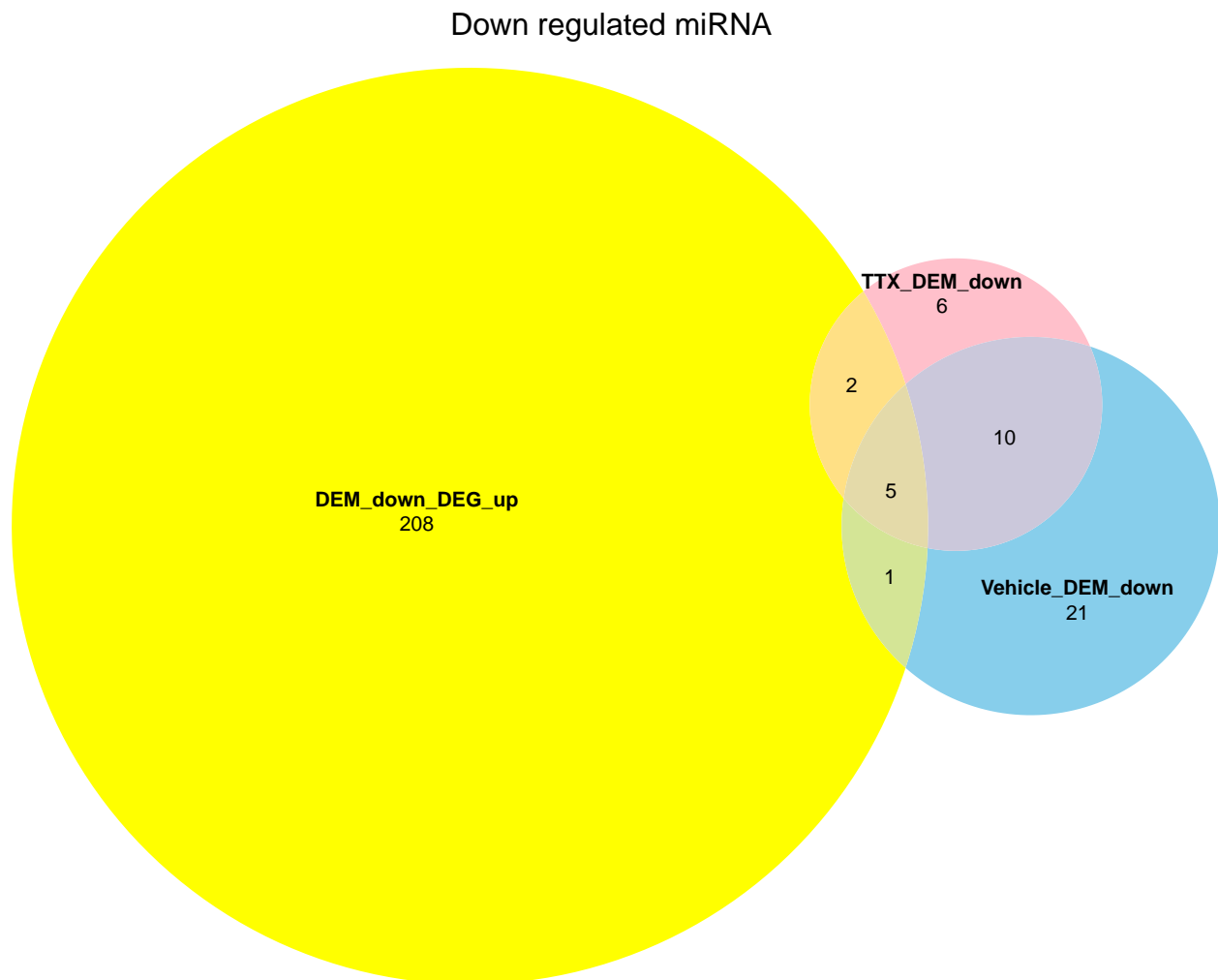
```
## [5] "hsa-miR-185-5p"
```

```
## pdf
```

```
## 2
```

```
## pdf
```

```
## 2
```



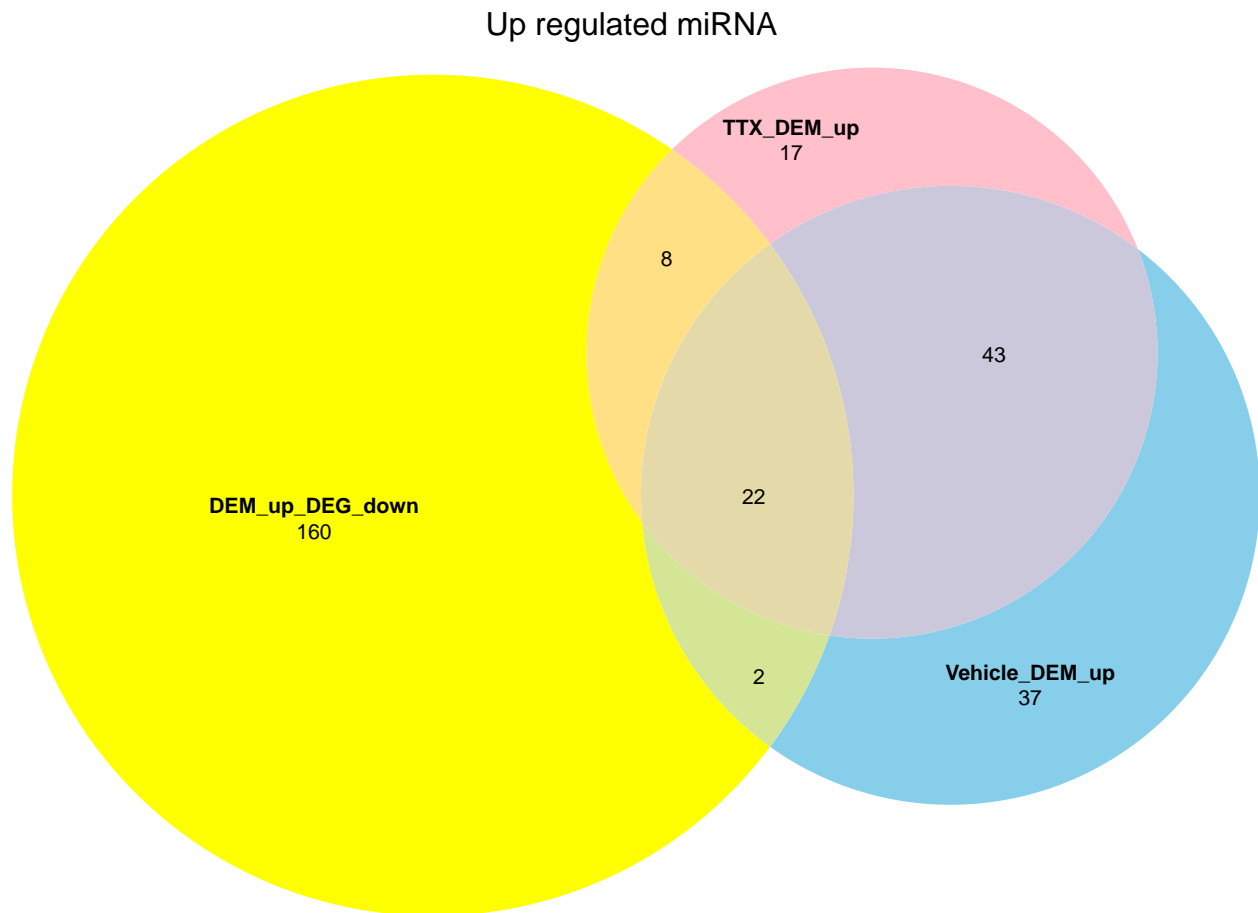
Plot for upregulated miRNA

```
## [1] "miRNA in overlap of all three"

## [1] "hsa-miR-1-3p"      "hsa-miR-106a-5p"  "hsa-miR-133a-3p"
## [4] "hsa-miR-133b"      "hsa-miR-143-3p"   "hsa-miR-145-5p"
## [7] "hsa-miR-148a-3p"   "hsa-miR-182-5p"   "hsa-miR-183-5p"
## [10] "hsa-miR-188-5p"    "hsa-miR-199a-3p"  "hsa-miR-199a-5p"
## [13] "hsa-miR-199b-3p"   "hsa-miR-199b-5p"  "hsa-miR-206"
## [16] "hsa-miR-20b-5p"    "hsa-miR-214-3p"   "hsa-miR-214-5p"
## [19] "hsa-miR-215-5p"    "hsa-miR-219a-2-3p" "hsa-miR-296-3p"
## [22] "hsa-miR-296-5p"

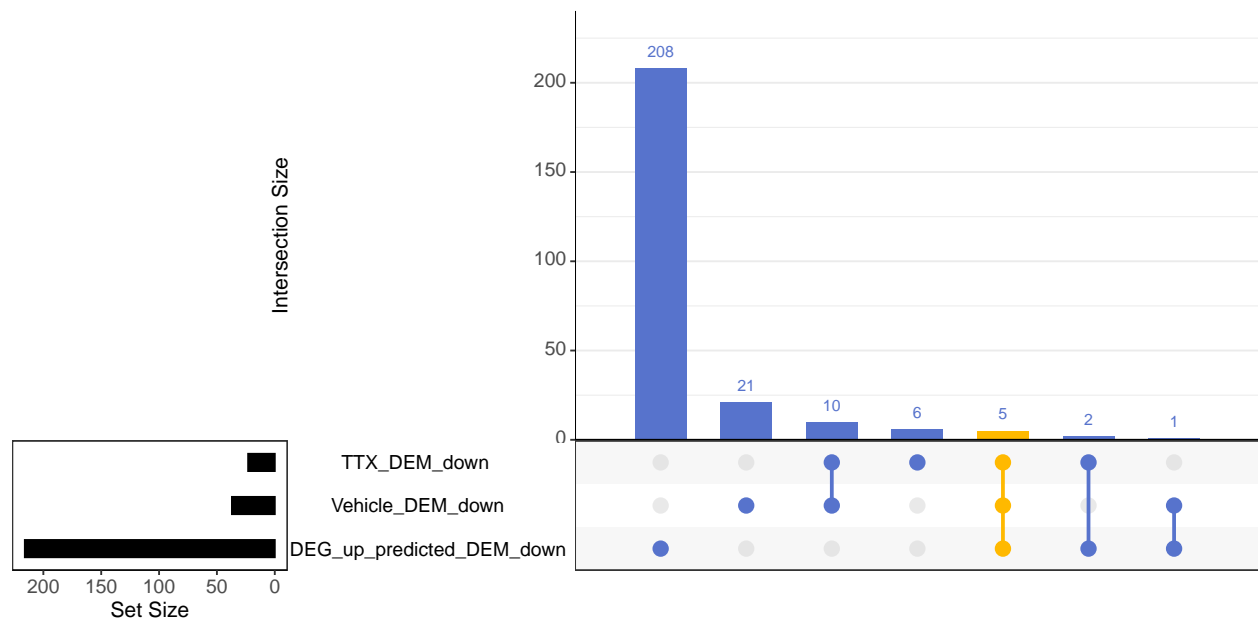
## pdf
## 2

## pdf
## 2
```



(b) Upset plot

Downregulated miRNA



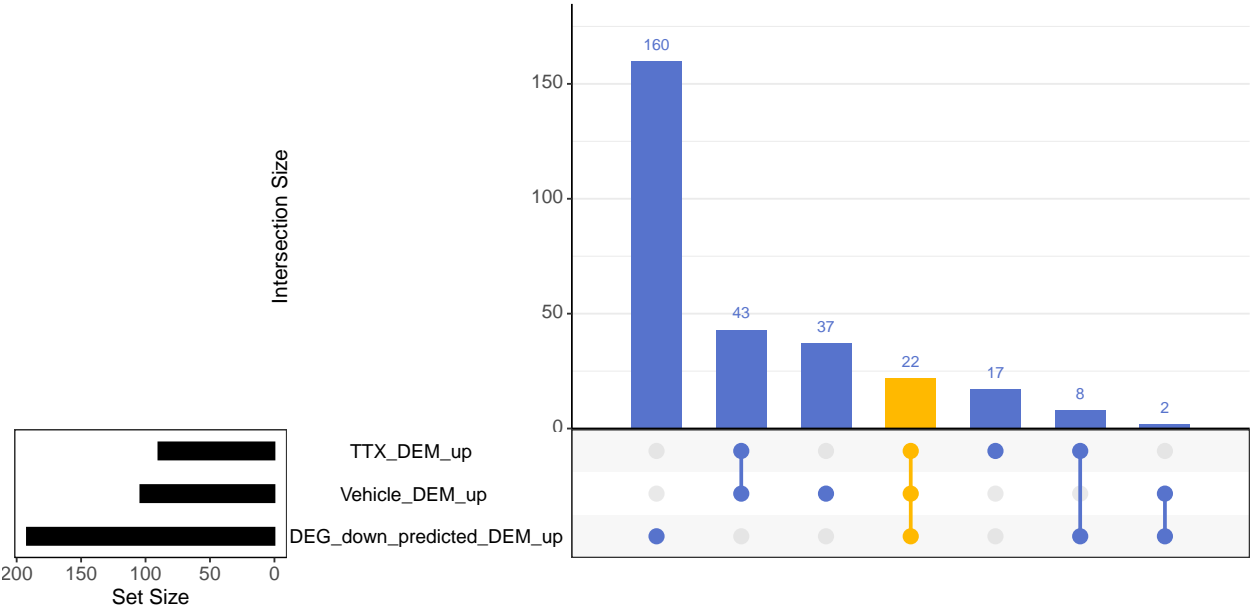
pdf

2

pdf

2

Upregulated miRNA



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] stats4      stats      graphics  grDevices  utils      datasets  methods
## [8] base
##
## other attached packages:
## [1] UpSetR_1.4.0      extrafont_0.19      eulerr_7.0.2
## [4] gprofiler2_0.2.3  rtracklayer_1.64.0  GenomicRanges_1.56.2
## [7] GenomeInfoDb_1.40.1 IRanges_2.38.1      S4Vectors_0.42.1
## [10] BiocGenerics_0.50.0 knitr_1.50          lubridate_1.9.4
## [13] forcats_1.0.0     stringr_1.5.1       dplyr_1.1.4
## [16] purrr_1.0.4       readr_2.1.5         tidyr_1.3.1
## [19] tibble_3.2.1      ggplot2_3.5.2       tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
## [1] tidyselect_1.2.1      viridisLite_0.4.2
## [3] farver_2.1.2          Biostings_2.72.1
## [5] bitops_1.0-9          fastmap_1.2.0
## [7] Rcurl_1.98-1.17       lazyeval_0.2.2
## [9] GenomicAlignments_1.40.0 XML_3.99-0.18
## [11] digest_0.6.37         timechange_0.3.0
## [13] lifecycle_1.0.4       polylabelr_0.3.0
## [15] magrittr_2.0.3        compiler_4.4.0
## [17] rlang_1.1.6           tools_4.4.0
## [19] yaml_2.3.10           data.table_1.17.0
## [21] labeling_0.4.3         S4Arrays_1.4.1
## [23] htmlwidgets_1.6.4     curl_6.2.2
## [25] here_1.0.1            DelayedArray_0.30.1
## [27] plyr_1.8.9            abind_1.4-8
## [29] BiocParallel_1.38.0   withr_3.0.2
## [31] polyclip_1.10-7       grid_4.4.0
## [33] colorspace_2.1-1      extrafontdb_1.0
## [35] scales_1.3.0          tinytex_0.57
## [37] SummarizedExperiment_1.34.0 cli_3.6.4
## [39] rmarkdown_2.29        crayon_1.5.3
## [41] generics_0.1.3        rstudioapi_0.17.1
## [43] httr_1.4.7            tzdb_0.5.0
## [45] rjson_0.2.23          zlibbioc_1.50.0
## [47] parallel_4.4.0        XVector_0.44.0
```

## [49] restfulr_0.0.15	matrixStats_1.5.0
## [51] vctrs_0.6.5	Matrix_1.7-3
## [53] jsonlite_2.0.0	hms_1.1.3
## [55] plotly_4.10.4	glue_1.8.0
## [57] codetools_0.2-20	stringi_1.8.7
## [59] gtable_0.3.6	BiocIO_1.14.0
## [61] UCSC.utils_1.0.0	munsell_0.5.1
## [63] pillar_1.10.2	htmltools_0.5.8.1
## [65] GenomeInfoDbData_1.2.12	R6_2.6.1
## [67] rprojroot_2.0.4	evaluate_1.0.3
## [69] Biobase_2.64.0	lattice_0.22-7
## [71] Rsamtools_2.20.0	Rcpp_1.0.14
## [73] gridExtra_2.3	SparseArray_1.4.8
## [75] Rttf2pt1_1.3.12	xfun_0.52
## [77] MatrixGenerics_1.16.0	pkgconfig_2.0.3