

# miRNA & mRNA regulation network

Vehicle contition: 22q vs Control

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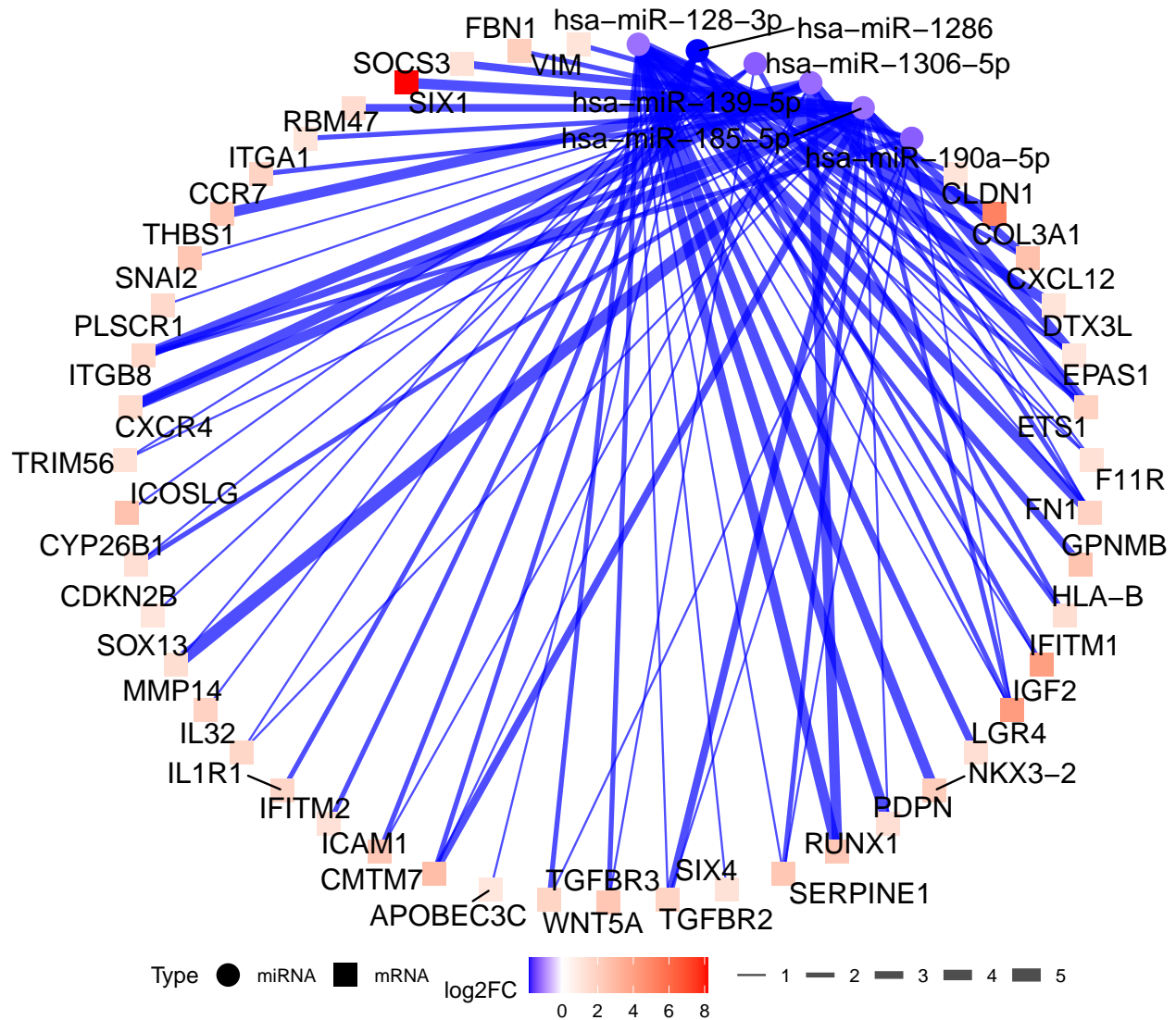
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## 1. Read the DEG and DEM from the previous analysis

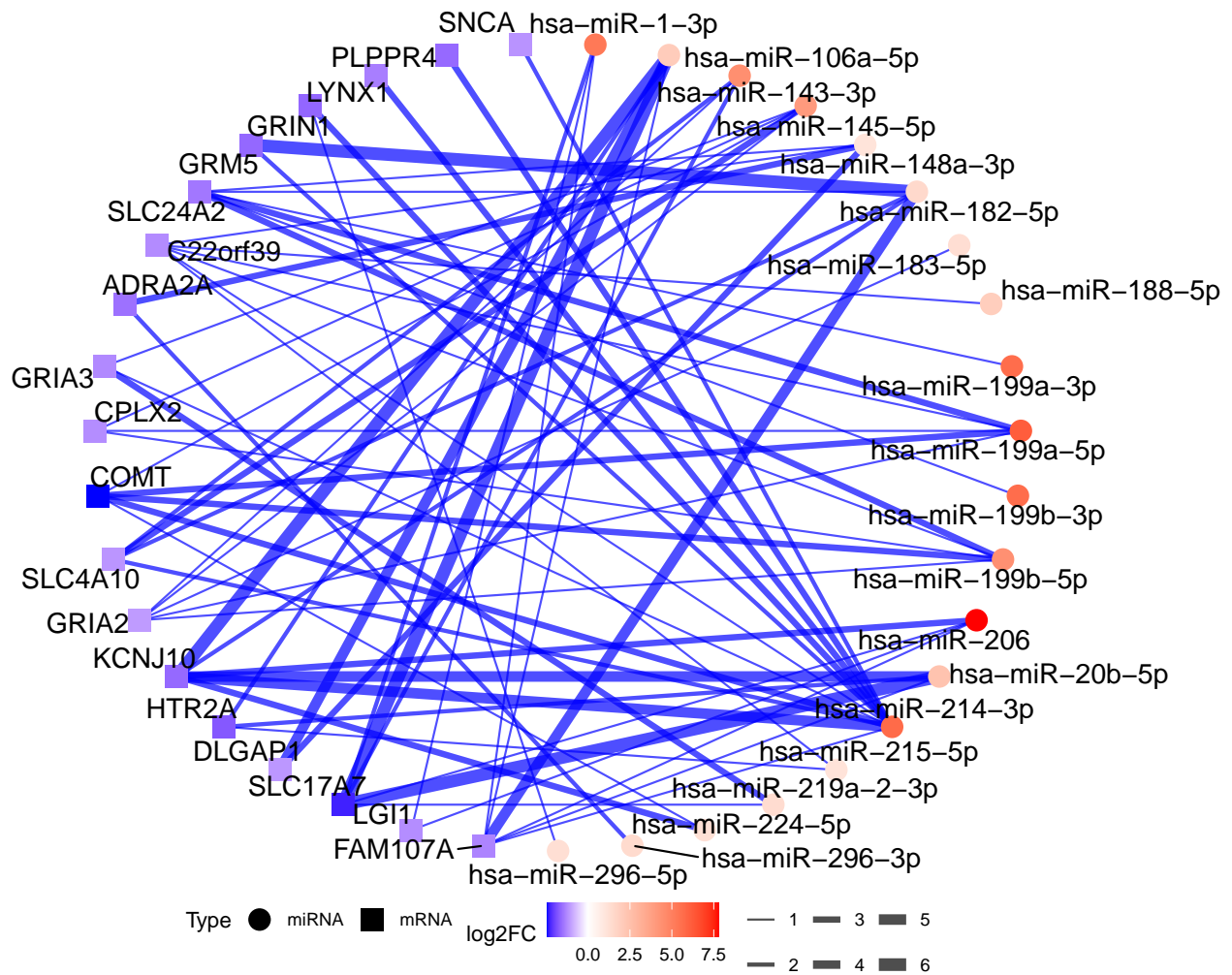
```
## [1] "DEG label"
##
## down   up
##  512  934
## [1] "DEM label"
##
## down   up
##   37  104
```

2. Load the ENCORI miRNA-target interaction data
3. Build newtork for miRNA and mRNA
4. Plot the network

## immune system process



# chemical synaptic transmission

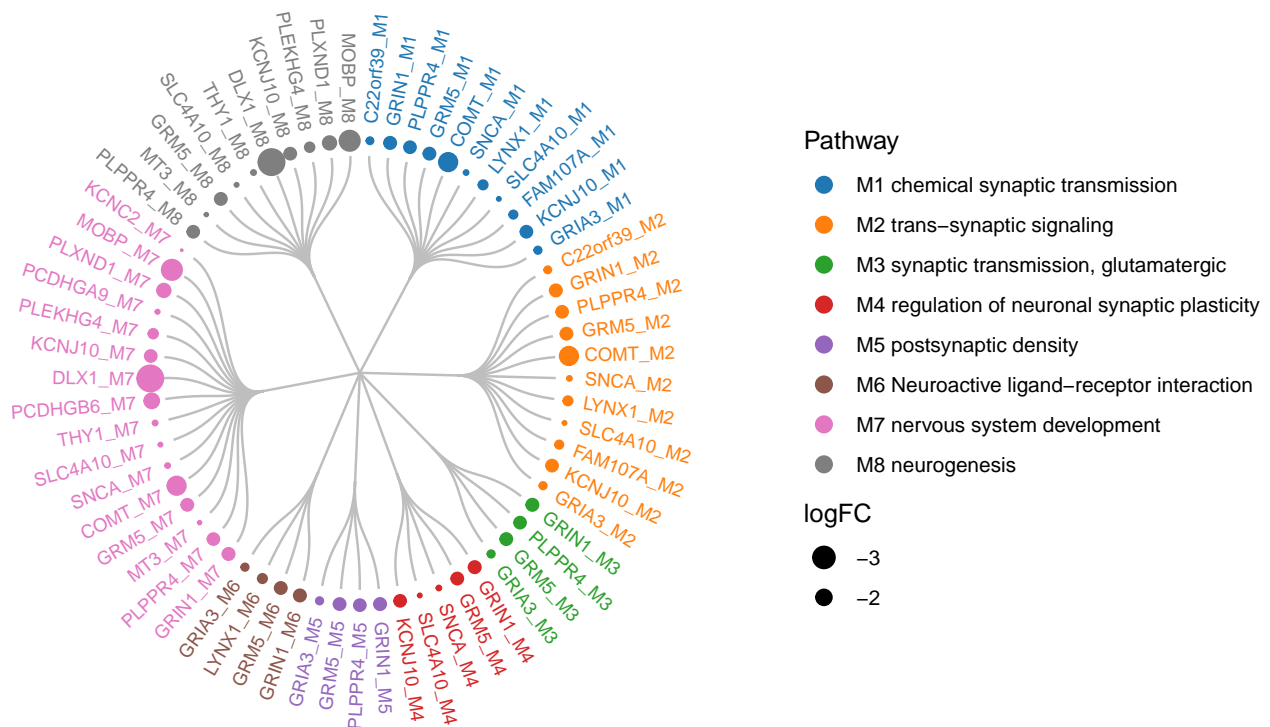


## 5. Plot the leaf network

### 5.1 Up-regulated miRNA and down-regulated gene

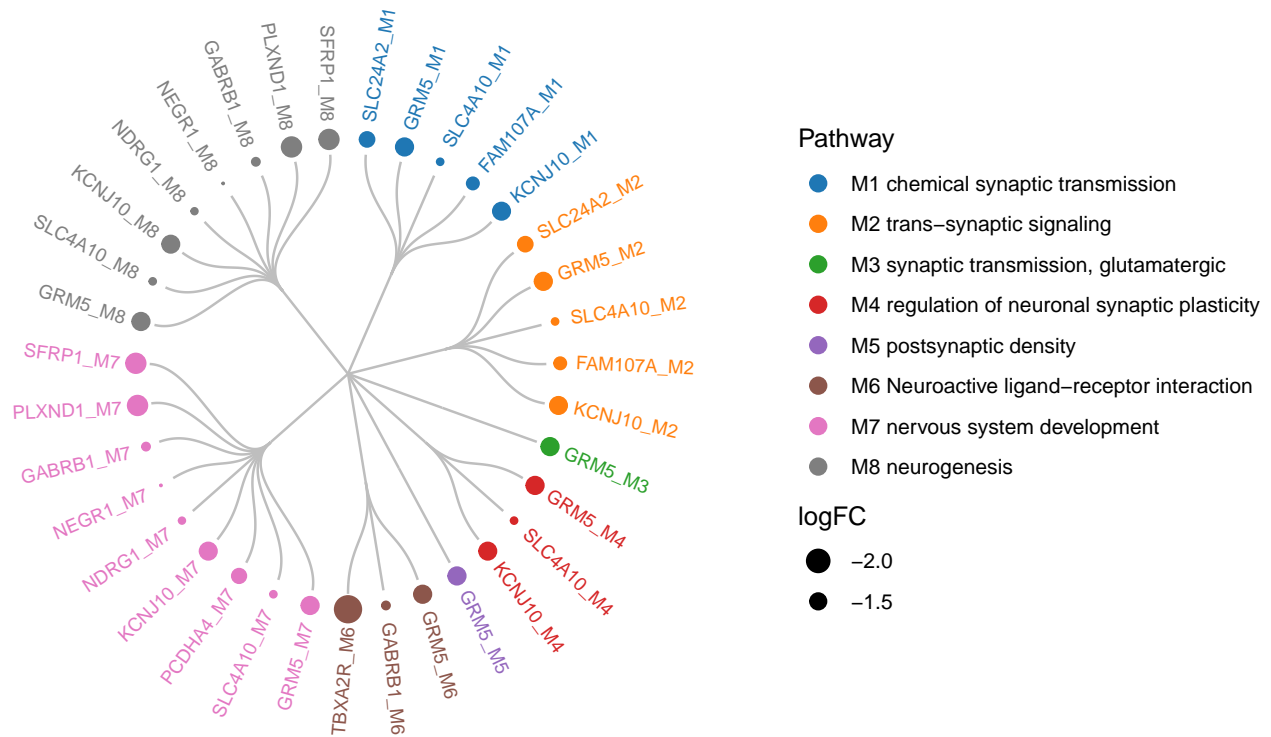
```
## [1] "hsa-mir-214-3p"
## [1] "chemical synaptic transmission"
## [1] "trans-synaptic signaling"
## [1] "synaptic transmission, glutamatergic"
## [1] "regulation of neuronal synaptic plasticity"
## [1] "postsynaptic density"
## [1] "Neuroactive ligand-receptor interaction"
## [1] "nervous system development"
## [1] "neurogenesis"
```

#### hsa-miR-214-3p



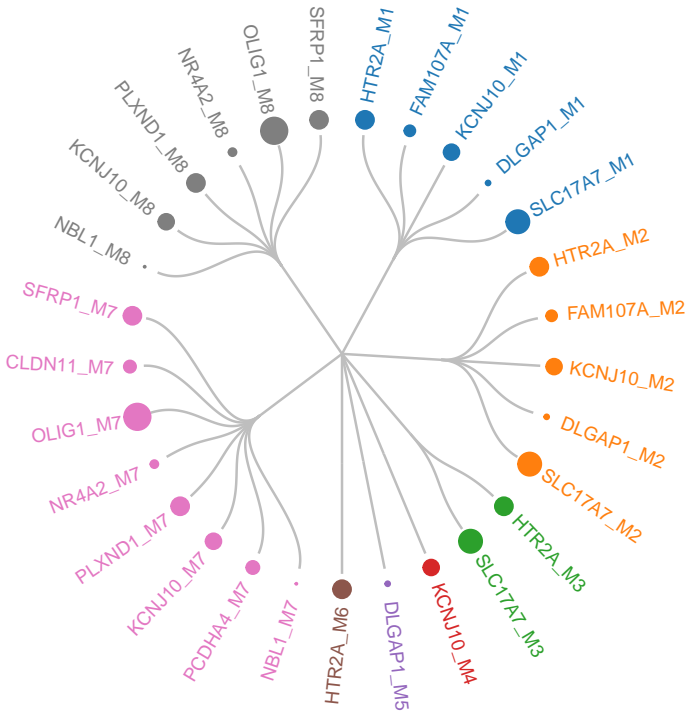
```
## [1] "hsa-mir-182-5p"
## [1] "chemical synaptic transmission"
## [1] "trans-synaptic signaling"
## [1] "synaptic transmission, glutamatergic"
## [1] "regulation of neuronal synaptic plasticity"
## [1] "postsynaptic density"
## [1] "Neuroactive ligand-receptor interaction"
## [1] "nervous system development"
## [1] "neurogenesis"
```

## hsa-miR-182-5p



```
## [1] "hsa-mir-106a-5p"
## [1] "chemical synaptic transmission"
## [1] "trans-synaptic signaling"
## [1] "synaptic transmission, glutamatergic"
## [1] "regulation of neuronal synaptic plasticity"
## [1] "postsynaptic density"
## [1] "Neuroactive ligand-receptor interaction"
## [1] "nervous system development"
## [1] "neurogenesis"
```

hsa-miR-106a-5p



Pathway

- M1 chemical synaptic transmission
- M2 trans-synaptic signaling
- M3 synaptic transmission, glutamatergic
- M4 regulation of neuronal synaptic plasticity
- M5 postsynaptic density
- M6 Neuroactive ligand-receptor interaction
- M7 nervous system development
- M8 neurogenesis

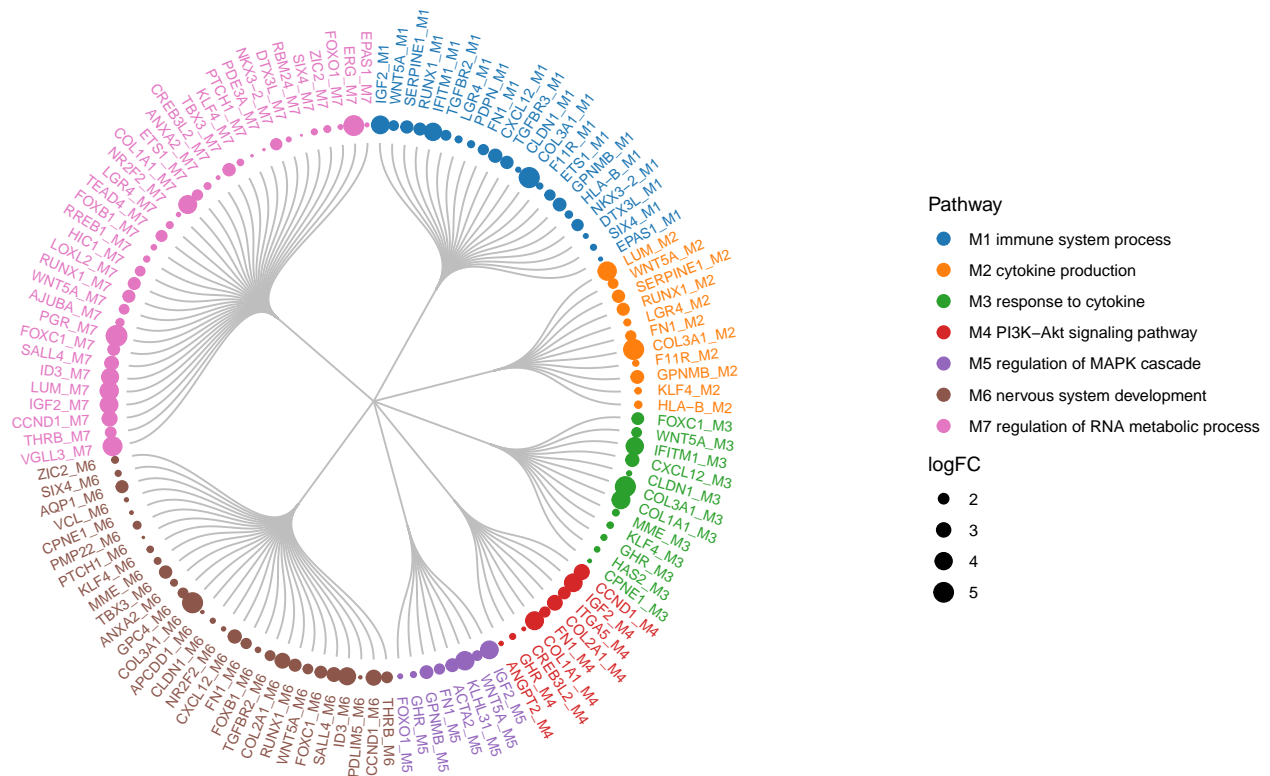
logFC

- 2.5
- 2.0
- 1.5

## 5.2 Down-regulated miRNA and up-regulated gene

```
## [1] "hsa-miR-128-3p"
## [1] "immune system process"
## [1] "cytokine production"
## [1] "response to cytokine"
## [1] "PI3K-Akt signaling pathway"
## [1] "regulation of MAPK cascade"
## [1] "nervous system development"
## [1] "regulation of RNA metabolic process"
```

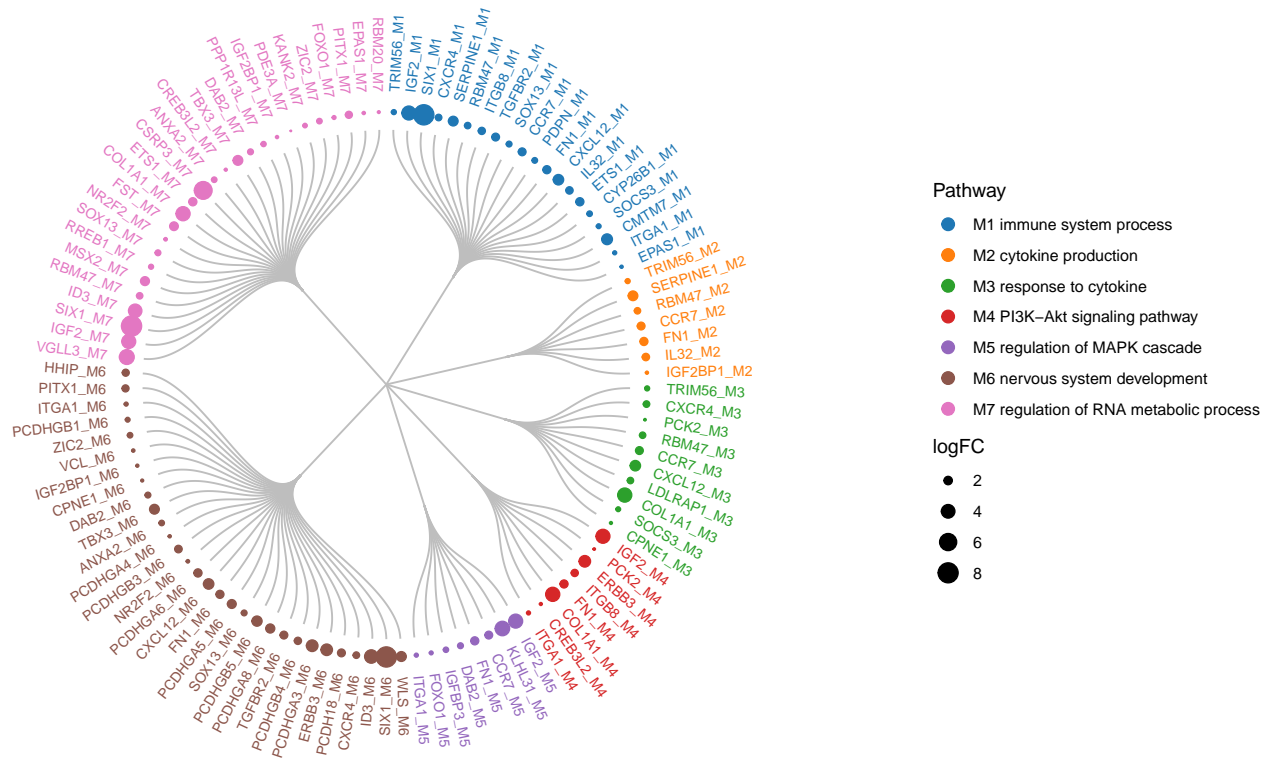
hsa-miR-128-3p



```
## [1] "hsa-miR-185-5p"
## [1] "immune system process"
## [1] "cytokine production"
## [1] "response to cytokine"
## [1] "PI3K-Akt signaling pathway"
## [1] "regulation of MAPK cascade"
## [1] "nervous system development"
## [1] "regulation of RNA metabolic process"
```



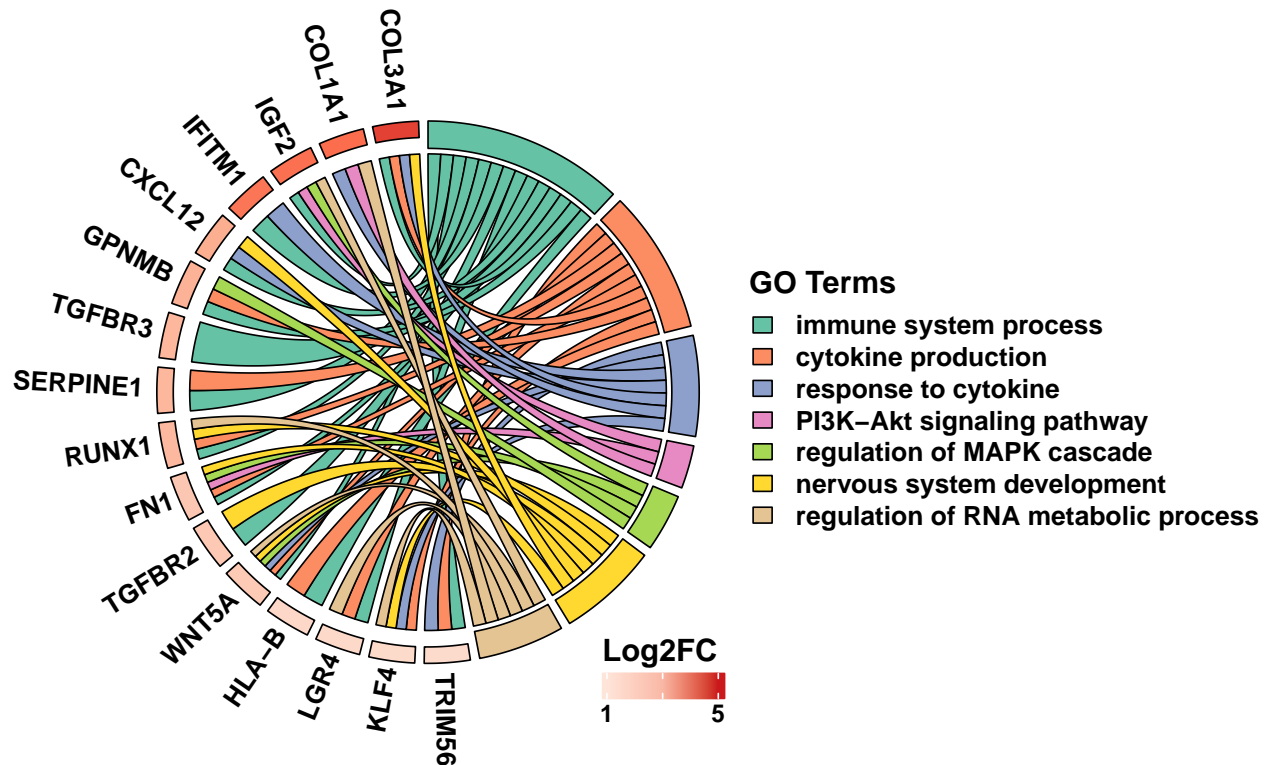
**hsa-miR-185-5p**



## 6. Plot the circos network

hsa-mir-128-3p

```
## [1] "hsa-mir-128-3p"
## [1] "TRIM56" "KLF4" "LGR4" "HLA-B" "WNT5A" "TGFB2"
## [7] "FN1" "RUNX1" "SERPINE1" "TGFB3" "GPNMB" "CXCL12"
## [13] "IFITM1" "IGF2" "COL1A1" "COL3A1"
## pdf
## 2
```



## hsa-mir-185-5p

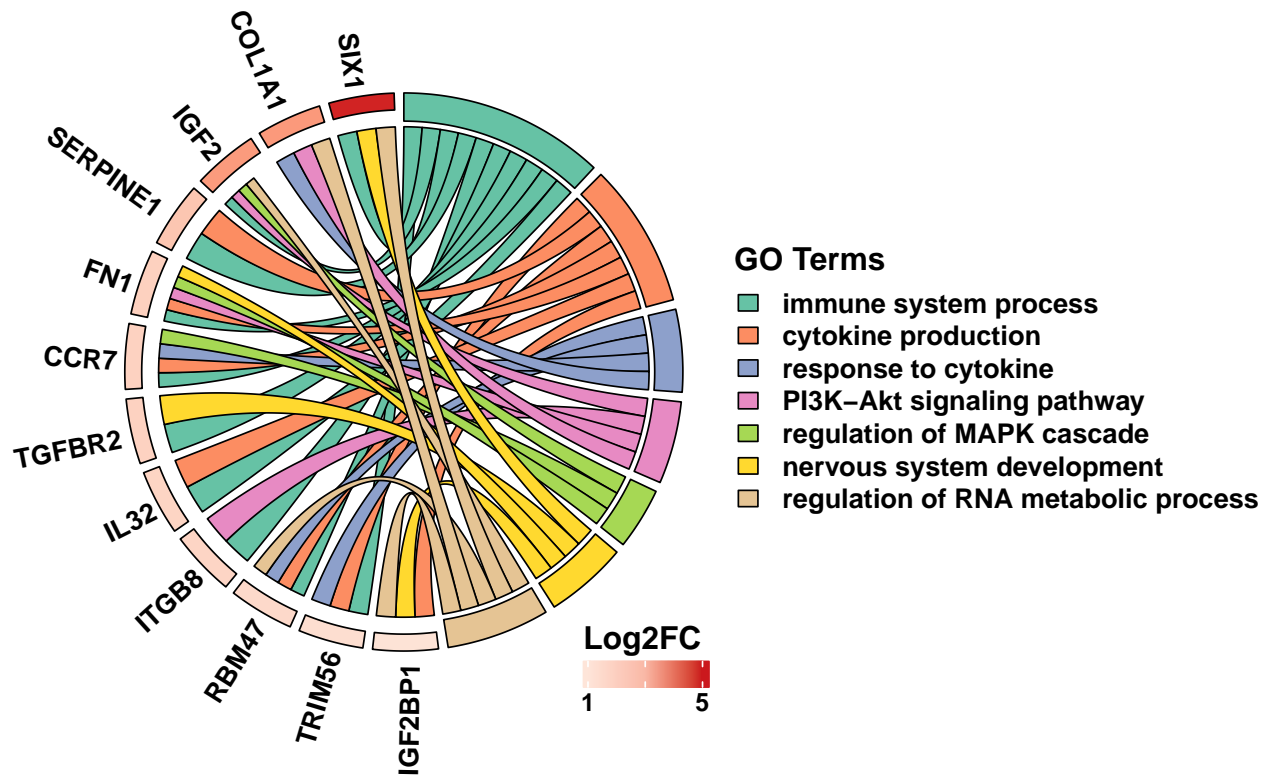
```
## [1] "hsa-mir-185-5p"
```

```
## [1] "IGF2BP1" "TRIM56" "RBM47" "ITGB8" "IL32" "TGFB2"
```

```
## [7] "CCR7" "FN1" "SERPINE1" "IGF2" "COL1A1" "SIX1"
```

```
## pdf
```

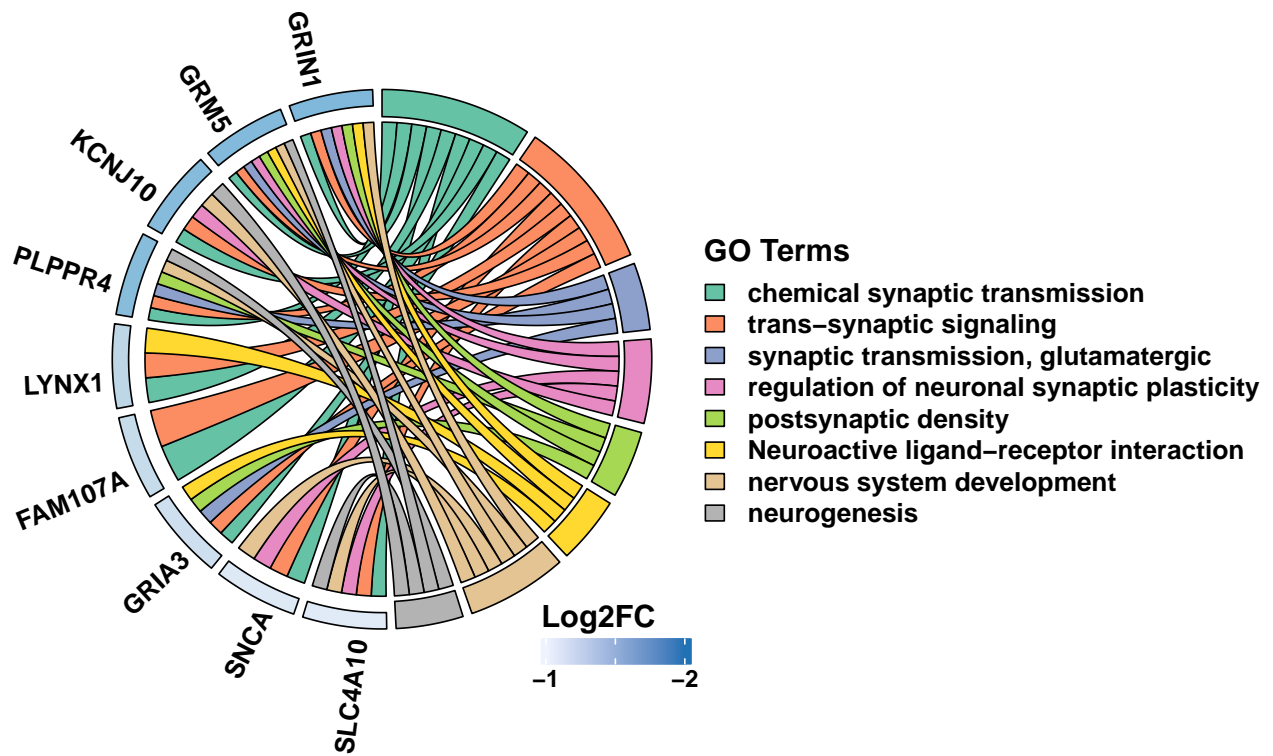
```
## 2
```



hsa-mir-214-3p

## pdf

## 2



## Session information

```
## R version 4.4.0 (2024-04-24)
## Platform: aarch64-apple-darwin20
## Running under: macOS Sonoma 14.3.1
##
## 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] grid      stats4    stats      graphics  grDevices  utils      datasets
## [8] methods   base
##
## other attached packages:
## [1] ComplexHeatmap_2.20.0 ggthemes_5.1.0      paletteer_1.6.0
## [4] scales_1.3.0          circlize_0.4.16     RColorBrewer_1.1-3
## [7] eulerr_7.0.2          extrafont_0.19      VennDiagram_1.7.3
## [10] futile.logger_1.4.3   gggraph_2.2.1       igraph_2.1.4
## [13] gprofiler2_0.2.3      data.table_1.16.4    pheatmap_1.0.12
## [16] reshape2_1.4.4        Matrix_1.7-2         ggsci_3.2.0
## [19] rtracklayer_1.64.0    GenomicRanges_1.56.2 GenomeInfoDb_1.40.1
## [22] IRanges_2.38.1        S4Vectors_0.42.1     BiocGenerics_0.50.0
## [25] knitr_1.49            lubridate_1.9.4      forcats_1.0.0
## [28] stringr_1.5.1         dplyr_1.1.4          purrr_1.0.4
## [31] readr_2.1.5           tidyr_1.3.1          tibble_3.2.1
## [34] ggplot2_3.5.1         tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
## [1] rstudioapi_0.17.1      jsonlite_1.9.0
## [3] shape_1.4.6.1          magrittr_2.0.3
## [5] farver_2.1.2           rmarkdown_2.29
## [7] GlobalOptions_0.1.2    BiocIO_1.14.0
## [9] zlibbioc_1.50.0        ragg_1.3.3
## [11] vctrs_0.6.5            memoise_2.0.1
## [13] Rsamtools_2.20.0       RCurl_1.98-1.16
## [15] tinytex_0.55           htmltools_0.5.8.1
## [17] S4Arrays_1.4.1         lambda.r_1.2.4
## [19] curl_6.2.1            SparseArray_1.4.8
## [21] htmlwidgets_1.6.4      plyr_1.8.9
## [23] futile.options_1.0.1    plotly_4.10.4
## [25] cachem_1.1.0           GenomicAlignments_1.40.0
## [27] iterators_1.0.14       lifecycle_1.0.4
## [29] pkgconfig_2.0.3        R6_2.6.1
## [31] fastmap_1.2.0          clue_0.3-66
## [33] GenomeInfoDbData_1.2.12 MatrixGenerics_1.16.0
## [35] digest_0.6.37          colorspace_2.1-1
## [37] rematch2_2.1.2         rprojroot_2.0.4
```

## [39] textshaping_1.0.0	labeling_0.4.3
## [41] timechange_0.3.0	httr_1.4.7
## [43] polyclip_1.10-7	abind_1.4-8
## [45] compiler_4.4.0	here_1.0.1
## [47] doParallel_1.0.17	withr_3.0.2
## [49] BiocParallel_1.38.0	viridis_0.6.5
## [51] ggforce_0.4.2	Rttf2pt1_1.3.12
## [53] MASS_7.3-64	DelayedArray_0.30.1
## [55] rjson_0.2.23	tools_4.4.0
## [57] extrafontdb_1.0	glue_1.8.0
## [59] restfulr_0.0.15	cluster_2.1.8
## [61] generics_0.1.3	gtable_0.3.6
## [63] tzdb_0.4.0	hms_1.1.3
## [65] tidygraph_1.3.1	XVector_0.44.0
## [67] foreach_1.5.2	ggrepel_0.9.6
## [69] pillar_1.10.1	tweenr_2.0.3
## [71] lattice_0.22-6	tidyselect_1.2.1
## [73] Biostrings_2.72.1	gridExtra_2.3
## [75] SummarizedExperiment_1.34.0	xfun_0.51
## [77] graphlayouts_1.2.2	Biobase_2.64.0
## [79] matrixStats_1.5.0	stringi_1.8.4
## [81] UCSC.utils_1.0.0	lazyeval_0.2.2
## [83] yaml_2.3.10	evaluate_1.0.3
## [85] codetools_0.2-20	cli_3.6.4
## [87] systemfonts_1.2.1	munsell_0.5.1
## [89] Rcpp_1.0.14	png_0.1-8
## [91] XML_3.99-0.18	parallel_4.4.0
## [93] bitops_1.0-9	viridisLite_0.4.2
## [95] crayon_1.5.3	GetoptLong_1.0.5
## [97] rlang_1.1.5	formatR_1.14