immgen data mir181

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Setup

path

```
setwd("D:/Krueger_Lab/Publications/miR181_paper/Supporting_scripts/immgen_data")
```

packages

```
library(reshape2)
library(ggplot2)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

data

```
immdat <- read.table("D:/Krueger_Lab/Publications/miR181_paper/Supporting_scripts/immgen_data/GSE144081_
                     header = T)
head(immdat[,1:5])
```

```
##         ID_REF        SPOT_ID         miRNA_pre_accession
## 1  miR-183-5p  mmu-miR-183-5p                    MI0000225
## 2  miR-877-5p  mmu-miR-877-5p                    MI0005553
## 3  miR-15b-5p  mmu-miR-15b-5p                    MI0000140
## 4    miR-9-3p    mmu-miR-9-3p MI0000157;MI0000720;MI0000721
## 5 miR-199a-5p mmu-miR-199a-5p           MI0000713;MI0000241
## 6  miR-369-5p  mmu-miR-369-5p                    MI0003535
##                                     miRNA_id              premiRNA
## 1                                 MIMAT0000212               mir-183
## 2                                 MIMAT0004861               mir-877
## 3                                 MIMAT0000124               mir-15b
## 4 MIMAT0000143;MIMAT0000143_1;MIMAT0000143_2 mir-9-2;mir-9-1;mir-9-3
## 5               MIMAT0000229;MIMAT0000229_1   mir-199a-2;mir-199a-1
## 6                                 MIMAT0003185               mir-369
```

mir181

```r
mirs <- c("miR-181a-5p", "miR-181b-5p")

mir181 <- immdat[immdat$ID_REF %in% mirs,]
```
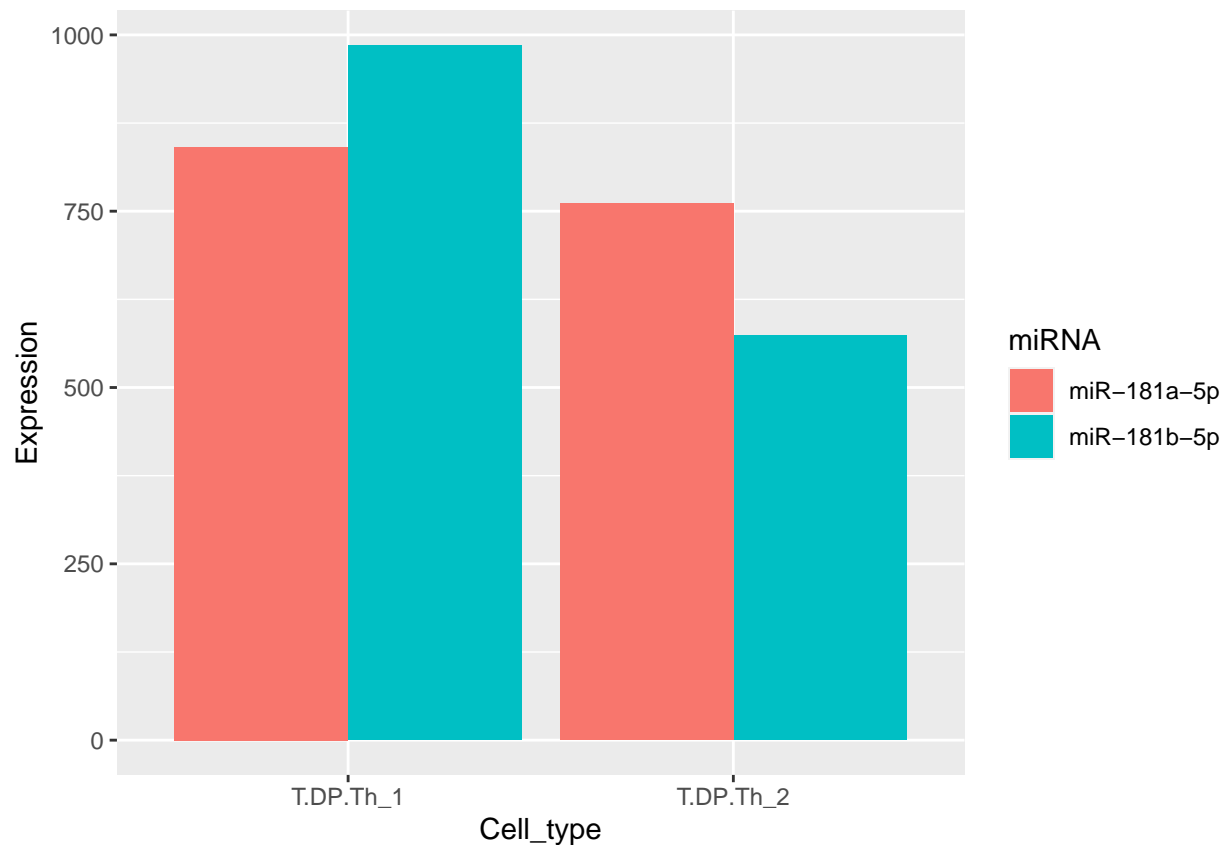
melt data

```r
mirmelt181 <- melt(mir181[,c(1, 9:149)])
```

```
## Using ID_REF as id variables
```

```r
colnames(mirmelt181) <- c("miRNA", "Cell_type", "Expression")
mirmelt181$Expression <- as.numeric(mirmelt181$Expression)
head(mirmelt181)
```

```
##          miRNA Cell_type Expression
## 1 miR-181b-5p    MF.PC_1   10.819646
## 2 miR-181a-5p    MF.PC_1    3.840292
## 3 miR-181b-5p    MF.PC_2    9.692904
## 4 miR-181a-5p    MF.PC_2   11.926901
## 5 miR-181b-5p    MF.PC_3    6.680114
## 6 miR-181a-5p    MF.PC_3    3.193117
```

plot

```r
cellselect <- c("T.DP.Th_1", "T.DP.Th_2")

mp181 <- ggplot(mirmelt181[mirmelt181$Cell_type %in% cellselect,], aes(y=Expression, x=Cell_type, fill=

mp181
```

all mirnas in DPs

data

```
dpset <- immdat[,c("ID_REF", "T.DP.Th_1", "T.DP.Th_2")]
head(dpset)
```

```
##         ID_REF    T.DP.Th_1    T.DP.Th_2
## 1  miR-183-5p    0.3613183    0.1079322
## 2  miR-877-5p    0.1658840    0.9912572
## 3  miR-15b-5p  326.2379386  420.9213534
## 4    miR-9-3p    0.1017251    0.1079322
## 5 miR-199a-5p    0.1055796    0.1086960
## 6  miR-369-5p    0.1017251    0.1079322
```

```
dpset$mean <- apply(dpset[,2:3], 1, mean)
dpset$stdiv <- apply(dpset[,2:3], 1, sd)

dpset <- dpset[order(dpset$mean, decreasing = T),]

dpmelt <- melt(dpset[1:10, 1:3])
```
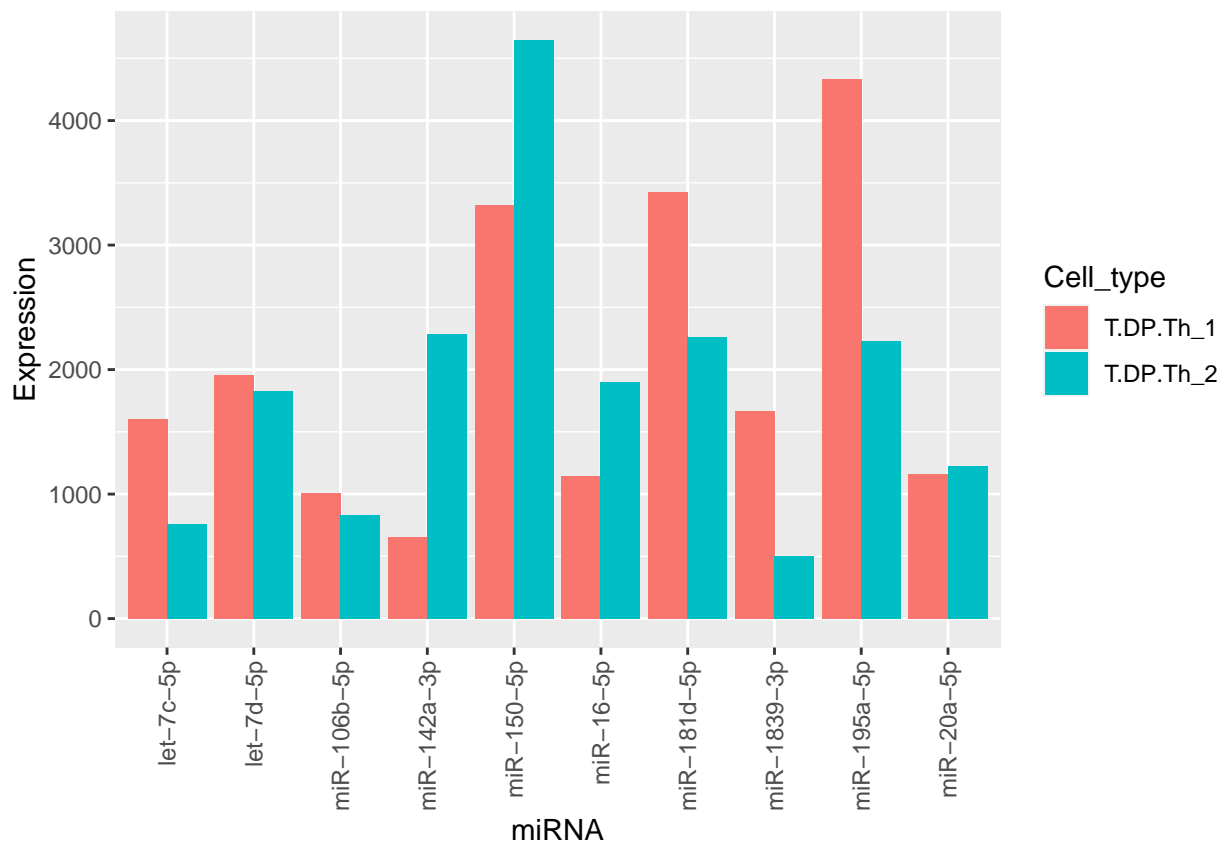
```
## Using ID_REF as id variables
```

```
colnames(dpmelt) <- c("miRNA", "Cell_type", "Expression")
head(dpmelt)
```

```
##        miRNA Cell_type Expression
## 1  miR-150-5p T.DP.Th_1  3325.0697
## 2 miR-195a-5p T.DP.Th_1  4330.8193
## 3 miR-181d-5p T.DP.Th_1  3428.5908
## 4   let-7d-5p T.DP.Th_1  1958.4029
## 5   miR-16-5p T.DP.Th_1  1146.9981
## 6 miR-142a-3p T.DP.Th_1   657.3647
```

plot

```
dpplot <- ggplot(dpmelt, aes(y=Expression, x=miRNA, fill=Cell_type)) +
  geom_bar(stat = "identity", position = "dodge") +
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust=1))
dpplot
```


export data

```
write.csv(dpset, "DPsets_immgen.csv")
```

session info

```
sessionInfo()
```

```
## R version 4.2.3 (2023-03-15 ucrt)
```

```
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 19044)
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=German_Germany.utf8  LC_CTYPE=German_Germany.utf8
## [3] LC_MONETARY=German_Germany.utf8 LC_NUMERIC=C
## [5] LC_TIME=German_Germany.utf8
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] dplyr_1.1.1   ggplot2_3.4.1  reshape2_1.4.4
##
## loaded via a namespace (and not attached):
##  [1] Rcpp_1.0.10      highr_0.10       compiler_4.2.3  pillar_1.9.0
##  [5] plyr_1.8.8       tools_4.2.3      digest_0.6.31   evaluate_0.20
##  [9] lifecycle_1.0.3 tibble_3.2.1     gtable_0.3.3    pkgconfig_2.0.3
## [13] rlang_1.1.0      cli_3.6.0        rstudioapi_0.14 yaml_2.3.7
## [17] xfun_0.37        fastmap_1.1.1    withr_2.5.0     stringr_1.5.0
## [21] knitr_1.42       generics_0.1.3   vctrs_0.6.1     grid_4.2.3
## [25] tidyselect_1.2.0 glue_1.6.2       R6_2.5.1        fansi_1.0.4
## [29] rmarkdown_2.21   farver_2.1.1     magrittr_2.0.3  scales_1.2.1
## [33] htmltools_0.5.4  colorspace_2.1-0 labeling_0.4.2  utf8_1.2.3
## [37] stringi_1.7.12   munsell_0.5.0
```