

Bound genes and gene regions of MREs

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1 Libraries and settings

```
# -----  
# libraries  
# -----  
library(tidyverse)  
library(GenomicRanges)  
library(colorspace)  
library(eulerr)  
library(gghalves)  
  
# -----  
# settings  
# -----  
out <- "/Users/melinaklostermann/Documents/projects/AgoCLIP_miR181/R_github/miR181_paper/Figure2/MRE_bo  
source("/Users/melinaklostermann/Documents/projects/R_general_functions/theme_paper.R")  
source("/Users/melinaklostermann/Documents/projects/AgoCLIP_miR181/mirko_files/mirECLIP/DifferentialBin  
  
# farben  
farbeneg <- "#B4B4B4"  
farbe1 <- "#0073C2FF" #WT farbe  
farbe2 <- "#EFC000FF"  
farbe3 <- "#CD534CFF" #miR181KO farbe  
farbe4 <- "#7AA6DCFF"  
farbe5 <- "#868686FF"  
farbe6 <- "#003C67FF"  
farbe7 <- "#8F7700FF"  
farbe8 <- "#3B3B3BFF"  
farbe9 <- "#A73030FF"
```

```

farbe10 <- "#4A6990FF"
farbe11 <- "#FF6F00FF"
farbe12 <- "#C71000FF"
farbe13 <- "#008EAOFF"
farbe14 <- "#8A4198FF"
farbe15 <- "#5A9599FF"
farbe16 <- "#FF6348FF"

```

2 What was done?

- the genotype and gene region of the mir 181 binding sites (union) are plotted (Figure2XX)

3 Files

```

# -----
# MREs
# -----

mir181_bs <- readRDS("/Users/melinaklostermann/Documents/projects/AgoCLIP_miR181/R_github/miR181_paper/1

```

4 Characterise MRE

4.1 mir181 bound genes - Figure 2A

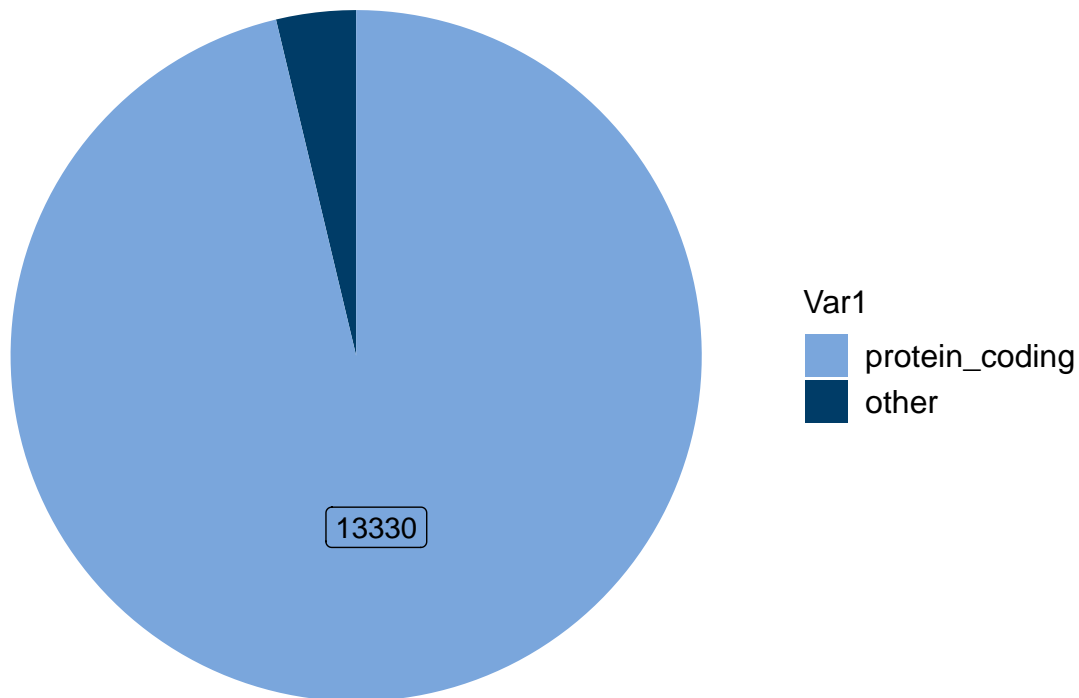
```

names(mir181_bs) <- 1:NROW(mir181_bs)
mir181_bs <- as.data.frame(mir181_bs)

gene_type_df <- mutate(mir181_bs, geneType = case_when(geneType != "protein_coding" ~ "other", T ~ "pro
gene_type_df <- table(gene_type_df$geneType) %>%
  as.data.frame(.)

p <- ggplot(gene_type_df, aes(y=Freq, x="", fill=Var1)) +
  geom_col()+
  coord_polar(theta="y") +
  # xlim(c(2, 4)) +
  geom_label(data = gene_type_df %>% subset(gene_type_df == "protein_coding"), aes(y=Freq, x="", fill=V
    position = position_stack(vjust = 0.5),
    show.legend = FALSE) +
  scale_fill_manual(values = c (farbe6, farbe4)) +
  theme_paper() +
  theme_nice_pie() +
  #theme(legend.position = "none") +
  guides(fill = guide_legend(reverse = TRUE)) +
  labs(y = NULL,
    x = NULL)
p

```



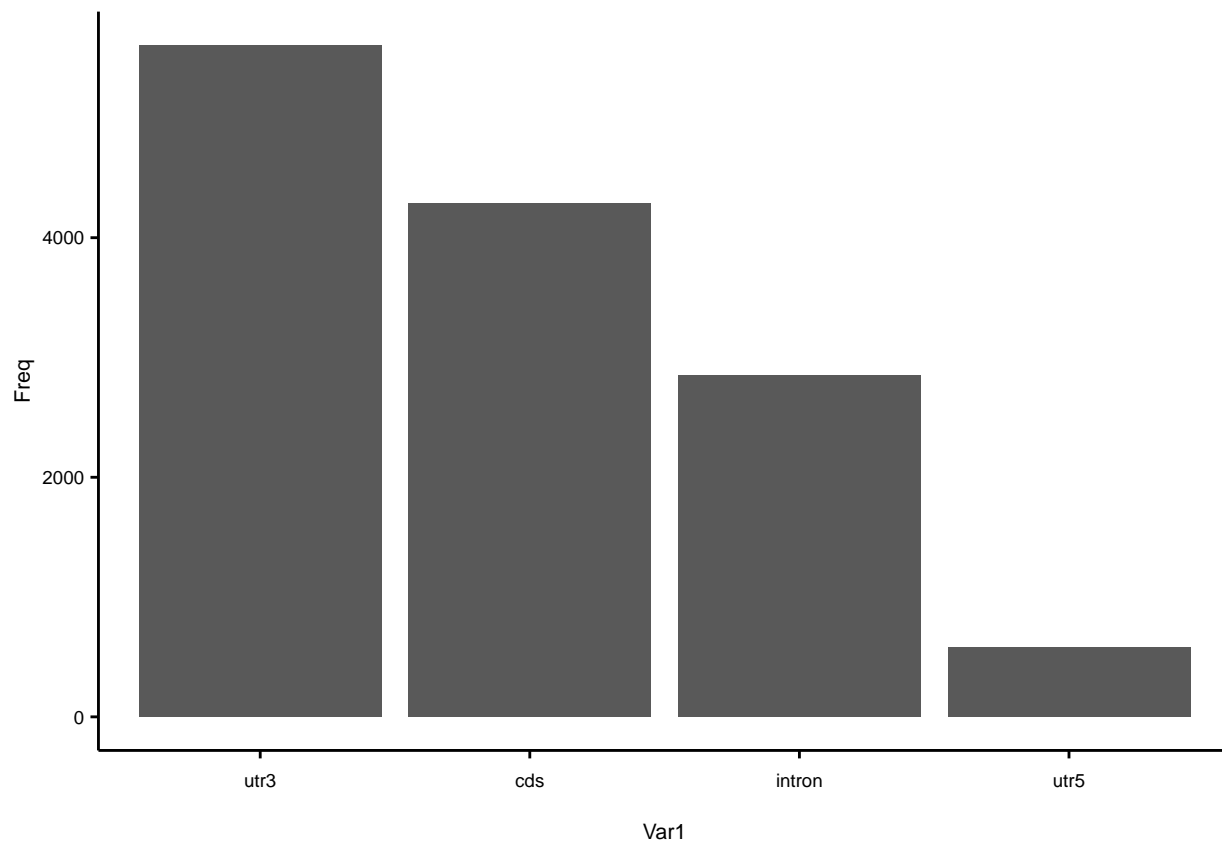
```
ggsave(p, filename = paste0(out, "Figure2A_bound_gene_types_miR181_BS", Sys.Date(), ".pdf"), width = un
```

4.2 mir181 bound regions - Figure 2B

```
gene_region_df <- table(mir181_bs$region) %>%
  as.data.frame(.) %>%
  arrange(desc(Freq))

gene_region_df$Var1 <- factor(gene_region_df$Var1, levels = gene_region_df$Var1)

p <- ggplot(gene_region_df %>% subset(Var1 != "outside"), aes(y=Freq, x=Var1)) +
  geom_col()+
  theme_paper()
p
```



```
ggsave(p, filename = paste0(out, "Figure2B_bound_gene_regions_miR181_BS", Sys.Date(), ".pdf"), width = 10, height = 10)
```

4.3 Relative maps of MRE position along gene - Figure 2 D

4.4 Seed distance to MRE - Figure 2 C

5 Session Info

```
sessionInfo()

## R version 4.2.2 (2022-10-31)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Big Sur ... 10.16
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.2/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.2/Resources/lib/libRlapack.dylib
##
## locale:
##  [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
##  [1] stats4      stats      graphics  grDevices  utils      datasets  methods
##  [8] base
##
## other attached packages:
##  [1] gghalves_0.1.4      eulerr_7.0.0        colorspace_2.1-0
```

```

## [4] GenomicRanges_1.50.2 GenomeInfoDb_1.34.7 IRanges_2.32.0
## [7] S4Vectors_0.36.1      BiocGenerics_0.44.0 forcats_0.5.2
## [10] stringr_1.5.0          dplyr_1.0.10        purrr_1.0.1
## [13] readr_2.1.3            tidyr_1.3.0          tibble_3.1.8
## [16] ggplot2_3.4.0          tidyverse_1.3.2      knitr_1.42
##
## loaded via a namespace (and not attached):
## [1] httr_1.4.4              jsonlite_1.8.4         carData_3.0-5
## [4] modelr_0.1.10           assertthat_0.2.1       highr_0.10
## [7] GenomeInfoDbData_1.2.9 googlesheets4_1.0.1    cellranger_1.1.0
## [10] yaml_2.3.7              pillar_1.8.1           backports_1.4.1
## [13] glue_1.6.2              digest_0.6.31          XVector_0.38.0
## [16] ggsignif_0.6.4          rvest_1.0.3            htmltools_0.5.4
## [19] pkgconfig_2.0.3         broom_1.0.3            haven_2.5.1
## [22] zlibbioc_1.44.0         scales_1.2.1           tzdb_0.3.0
## [25] timechange_0.2.0        googledrive_2.0.0      farver_2.1.1
## [28] generics_0.1.3          car_3.1-1              ellipsis_0.3.2
## [31] ggpubr_0.5.0            withr_2.5.0            cli_3.6.0
## [34] magrittr_2.0.3          crayon_1.5.2           readxl_1.4.1
## [37] evaluate_0.20           fs_1.6.0               fansi_1.0.4
## [40] rstatix_0.7.1           xml2_1.3.3             textshaping_0.3.6
## [43] tools_4.2.2             hms_1.1.2              gargle_1.2.1
## [46] lifecycle_1.0.3         munsell_0.5.0          reprex_2.0.2
## [49] compiler_4.2.2          systemfonts_1.0.4      rlang_1.0.6
## [52] grid_4.2.2              RCurl_1.98-1.9         rstudioapi_0.14
## [55] bitops_1.0-7            labeling_0.4.2          rmarkdown_2.20
## [58] gtable_0.3.1            abind_1.4-5            DBI_1.1.3
## [61] R6_2.5.1                lubridate_1.9.1        fastmap_1.1.0
## [64] utf8_1.2.2              ragg_1.2.5             stringi_1.7.12
## [67] Rcpp_1.0.10             vctrs_0.5.2            dbplyr_2.3.0
## [70] tidyselect_1.2.0        xfun_0.36

```