

Figure4_v2

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Setup

dir

```
setwd("D:/Krueger_Lab/Publications/miR181_paper/Figure4")
```

Packages

```
source("D:/Krueger_Lab/Publications/miR181_paper/Supporting_scripts/themes/theme_paper.R")
library(ggplot2)
library(rtracklayer)
```

```
## Loading required package: GenomicRanges
## Loading required package: stats4
## Loading required package: BiocGenerics
##
## Attaching package: 'BiocGenerics'
## The following objects are masked from 'package:stats':
## 
##     IQR, mad, sd, var, xtabs
## The following objects are masked from 'package:base':
## 
##     anyDuplicated, aperm, append, as.data.frame, basename, cbind,
##     colnames, dirname, do.call, duplicated, eval, evalq, Filter, Find,
##     get, grep, grepl, intersect, is.unsorted, lapply, Map, mapply,
##     match, mget, order, paste, pmax, pmax.int, pmin, pmin.int,
##     Position, rank, rbind, Reduce, rownames, sapply, setdiff, sort,
##     table, tapply, union, unique, unsplit, which.max, which.min
## Loading required package: S4Vectors
##
## Attaching package: 'S4Vectors'
## The following objects are masked from 'package:base':
## 
##     expand.grid, I, unname
## Loading required package: IRanges
##
## Attaching package: 'IRanges'
```

```

## The following object is masked from 'package:grDevices':
##
##      windows

## Loading required package: GenomeInfoDb
library(dplyr)

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:GenomicRanges':
##
##      intersect, setdiff, union

## The following object is masked from 'package:GenomeInfoDb':
##
##      intersect

## The following objects are masked from 'package:IRanges':
##
##      collapse, desc, intersect, setdiff, slice, union

## The following objects are masked from 'package:S4Vectors':
##
##      first, intersect, rename, setdiff, setequal, union

## The following objects are masked from 'package:BiocGenerics':
##
##      combine, intersect, setdiff, union

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

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

library(tibble)
library(Rtsne)
library(cliProfiler)
library(GenomicRanges)
library(cowplot)
library(eulerr)
library(readxl)

```

Data

```

#Ribo profiling
RNA <- read.csv("D:/Krueger_Lab/Publications/miR181_paper/Figure3/RNA_masterframe.csv")
RPF <- read.csv("D:/Krueger_Lab/Publications/miR181_paper/Figure3/RPF_masterframe.csv")

#load the gtf file to compare genes
gff23 <- import.gff3("D:/Krueger_Lab/Ribo_Profiling/run15112022M23/ref_genome/gencode.vM23.annotation.gff3")
gff23path <- file.path("D:/Krueger_Lab/Ribo_Profiling/run15112022M23/ref_genome", "gencode.vM23.annotation.gff3")

#targets
target <- readRDS("D:/Krueger_Lab/Publications/miR181_paper/Figure4/mir181_bs_with_seeds_transcripts.rds")

```

```

largetframe <- as.data.frame(larget)
table(largetframe$set)

##
##          ago_bs_mir181_chi    ago_bs_mir181_chi&mir181_enriched
##                      5725                                1061
##          mir181_enriched
##                      3458

largetframe <- largetframe[!(largetframe$set == "ago_bs_mir181_chi"),]

# modify dataset to only include working targetsets

#only use miR181_enriched und both
# largetframe <- largetframe[largetframe$set %in% c("mir181_enriched", "ago_bs_mir181_chi&mir181_enriched")]

#ms
MS <- as.data.frame(read_xlsx("D:/Krueger_Lab/Publications/miR181_paper/Figure3/MS_analysis.xlsx",
                               sheet = 2))
#adjust upper case lower case of gene names of MS data:
#function
capFirst <- function(s) {
  paste(toupper(substring(s, 1, 1)), substring(s, 2), sep = "")
}
MS$`Gene Symbol` <- tolower(MS$`Gene Symbol`)
MS$`Gene Symbol` <- capFirst(MS$`Gene Symbol`)
names(MS)[names(MS) == 'Gene Symbol'] <- 'gene_symbol'
names(MS)[names(MS) == 'P-value'] <- 'pvalue'
names(MS)[names(MS) == 'Log2(FC)'] <- 'log2FoldChange'

head(MS$gene_symbol)

## [1] "Ckb"      "Gnb4"     "Ccm2"     "Rnpep"    "Aldh1b1"   "Macf1"
#Translational efficiency
TE <- read.csv("D:/Krueger_Lab/Publications/miR181_paper_v07122022/Supporting scripts/deltaTE/TE_m23_genome.csv")

#MMsat4
repeat_masker <- readRDS("D:/Krueger_Lab/Publications/miR181_paper/Figure2/MMsat4/repeat_masker.rds")
MMSAT4 <- repeat_masker[repeat_masker$repName == "MMSAT4"]
MurSatRep1 <- repeat_masker[repeat_masker$repName == "MurSatRep1"]

```

colours

```

#colours
farbeneg <- "#b4b4b4"
farbe1 <- "#0073C2FF"
farbe2 <- "#EFC000FF"
farbe3 <- "#CD534CFF"
farbe4 <- "#7AA6DCFF"

```

```

farbe5 <- "#868686FF"
farbe6 <- "#003C67FF"
farbe7 <- "#8F7700FF"
farbe8 <- "#3B3B3BFF"
farbe9 <- "#A73030FF"
farbe10 <- "#4A6990FF"
farbe11 <- "#FF6FOOFF"
farbe12 <- "#C71000FF"
farbe13 <- "#008EA0FF"
farbe14 <- "#8A4198FF"
farbe15 <- "#5A9599FF"
farbe16 <- "#FF6348FF"

RNApcol <- "#b56504"
RNAncol <- "#027d73"
RPFpcol <- "#c4c404"
RPFncol <- "#8d0391"

```

axis limits

```

xlim <- 0.5
zoomfac <- 0.45

```

number of binding sites

```

bsnum <- as.data.frame(table(largetframe$geneName))
colnames(bsnum) <- c("gene_symbol", "BS_number")

```

wobble plot

ecdf

```

#RNA
RNA$wobble <- "Non-target"
RNA$wobble[RNA$gene_symbol %in% largetframe[is.na(largetframe$first_seed_200down.wobble) , "geneName"]] <- "Non-target"
RNA$wobble[RNA$gene_symbol %in% largetframe[largetframe$first_seed_200down.wobble == FALSE , "geneName"]] <- "Non-target"
RNA$wobble[RNA$gene_symbol %in% largetframe[largetframe$first_seed_200down.wobble == TRUE , "geneName"]] <- "Target"
RNA$wobble[RNA$gene_symbol %in% bsnum[bsnum$BS_number > 1 , "gene_symbol"]] <- "Multiple"

#RPF
RPF$wobble <- "Non-target"
RPF$wobble[RPF$gene_symbol %in% largetframe[is.na(largetframe$first_seed_200down.wobble) , "geneName"]] <- "Non-target"
RPF$wobble[RPF$gene_symbol %in% largetframe[largetframe$first_seed_200down.wobble == FALSE , "geneName"]] <- "Non-target"
RPF$wobble[RPF$gene_symbol %in% largetframe[largetframe$first_seed_200down.wobble == TRUE , "geneName"]] <- "Target"
RPF$wobble[RPF$gene_symbol %in% bsnum[bsnum$BS_number > 1 , "gene_symbol"]] <- "Multiple"

#MS
MS$wobble <- "Non-target"
MS$wobble[MS$gene_symbol %in% largetframe[is.na(largetframe$first_seed_200down.wobble) , "geneName"]] <- "Non-target"
MS$wobble[MS$gene_symbol %in% largetframe[largetframe$first_seed_200down.wobble == FALSE , "geneName"]] <- "Non-target"
MS$wobble[MS$gene_symbol %in% largetframe[largetframe$first_seed_200down.wobble == TRUE , "geneName"]] <- "Target"
MS$wobble[MS$gene_symbol %in% bsnum[bsnum$BS_number > 1 , "gene_symbol"]] <- "Multiple"

```

```

#TE
TE$wobble <- "Non-target"
TE$wobble[TE$gene_symbol %in% largetframe[is.na(largetframe$first_seed_200down.wobble) , "geneName"]] <-
TE$wobble[TE$gene_symbol %in% largetframe[largetframe$first_seed_200down.wobble == FALSE , "geneName"]] <-
TE$wobble[TE$gene_symbol %in% largetframe[largetframe$first_seed_200down.wobble == TRUE , "geneName"]] <-
TE$wobble[TE$gene_symbol %in% bsnum[bsnum$BS_number > 1 , "gene_symbol"]] <- "Multiple"

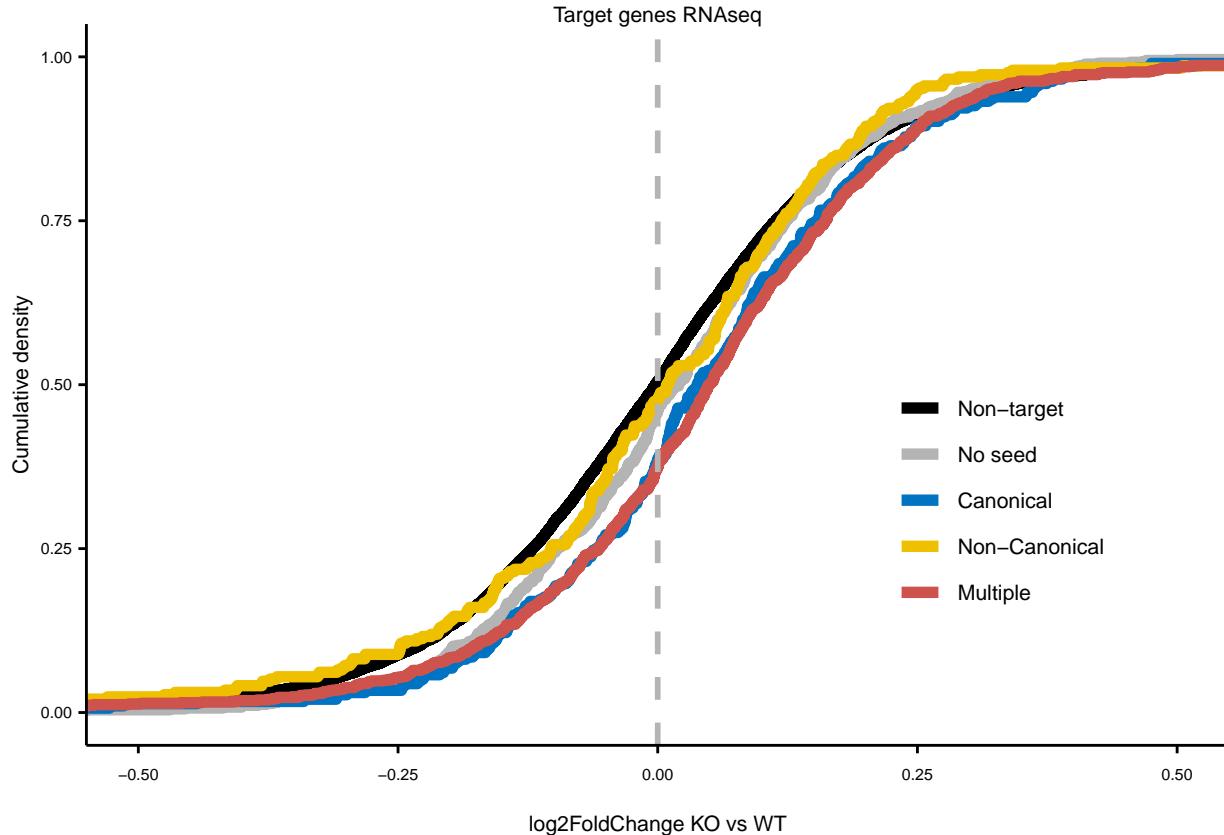
#ECDF

#RNA
wobbleecdfRNA <- ggplot(RNA, aes(as.numeric(log2FoldChange), colour=factor(wobble, levels = c("Non-target",
stat_ecdf(geom="step", linewidth=2) +
geom_vline(xintercept = 0, linewidth=1, linetype="dashed", colour=farbeneg) +
scale_colour_manual(values = c("black", farbeneg, farbe1, farbe2, farbe3)) +
coord_cartesian(xlim = c(-xlim, xlim)) +
theme_paper() +
scale_y_continuous("Cumulative density") + scale_x_continuous("log2FoldChange KO vs WT") +
ggtitle("Target genes RNAseq")

## Warning: The `size` argument of `element_line()` is deprecated as of ggplot2 3.4.0.
## i Please use the `linewidth` argument instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.

wobbleecdfRNA

```

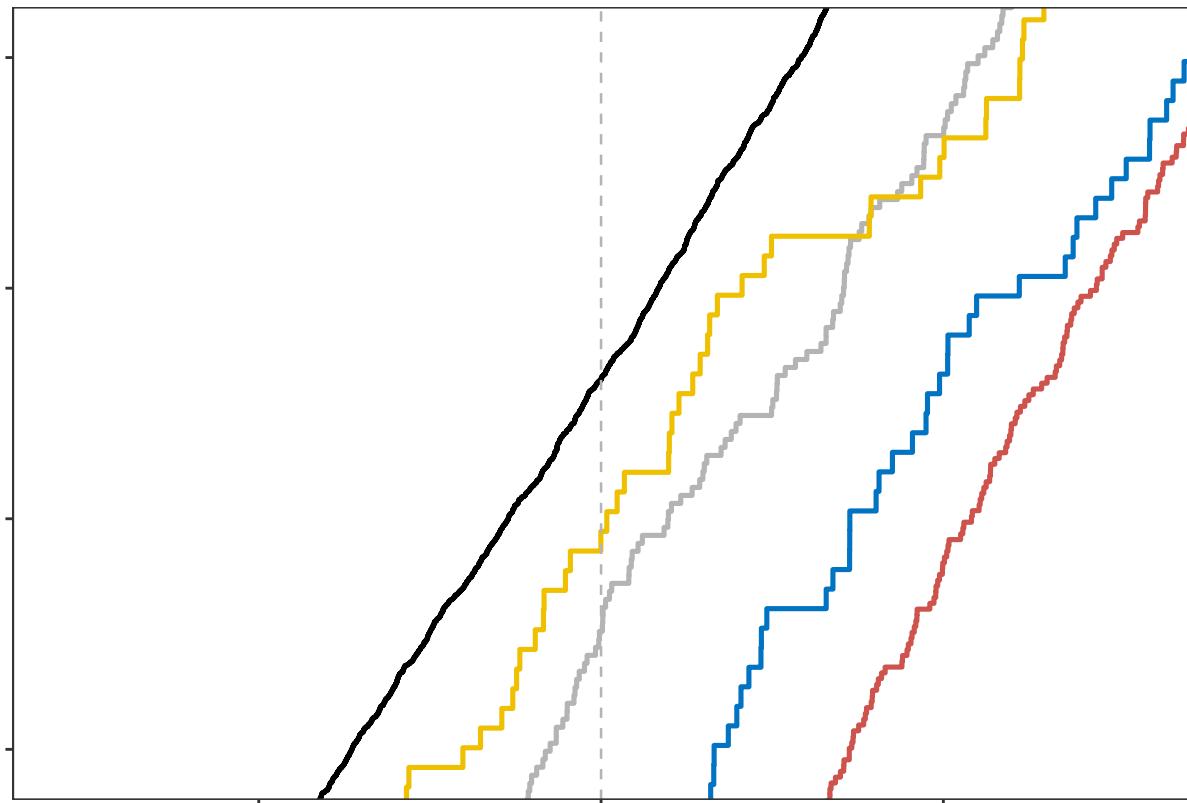


```

#zoom
wobbleecdfRNAZ <- ggplot(RNA, aes(as.numeric(log2FoldChange), colour=factor(wobble, levels = c("Non-target", "Target")))) +
  stat_ecdf(geom="step", linewidth=2*zoomfac) +
  geom_vline(xintercept = 0, linewidth=1*zoomfac, linetype="dashed", colour=farbeneg) +
  scale_colour_manual(values = c("black", farbeneg, farbe1, farbe2, farbe3)) +
  coord_cartesian(xlim = c(-(xlim/8), (xlim/8)), ylim = c(0.5-1/16, 0.5+1/16)) +
  theme_bw() +
  theme(legend.position = "none", axis.text = element_blank(), panel.grid = element_blank(),
        panel.background = element_rect(fill='transparent'), #transparent panel bg
        plot.background = element_rect(fill='transparent', color=NA)) +
  scale_y_continuous("") + scale_x_continuous("")

```

wobbleecdfRNAZ

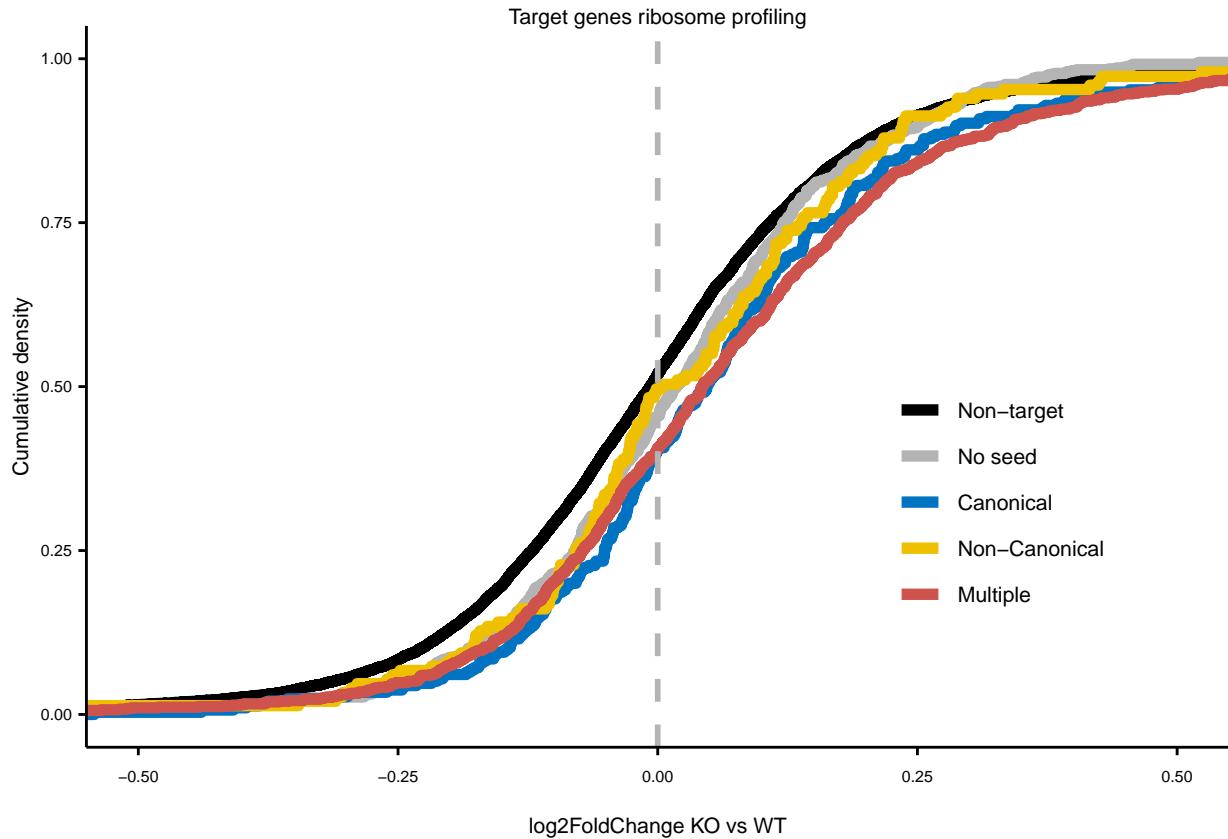


```

#RPF
wobbleecdfRPF <- ggplot(RPF, aes(as.numeric(log2FoldChange), colour=factor(wobble, levels = c("Non-target", "Target")))) +
  stat_ecdf(geom="step", linewidth=2) +
  geom_vline(xintercept = 0, linewidth=1, linetype="dashed", colour=farbeneg) +
  scale_colour_manual(values = c("black", farbeneg, farbe1, farbe2, farbe3)) +
  coord_cartesian(xlim = c(-xlim, xlim)) +
  theme_paper() +
  scale_y_continuous("Cumulative density") + scale_x_continuous("log2FoldChange K0 vs WT") +
  ggtitle("Target genes ribosome profiling")

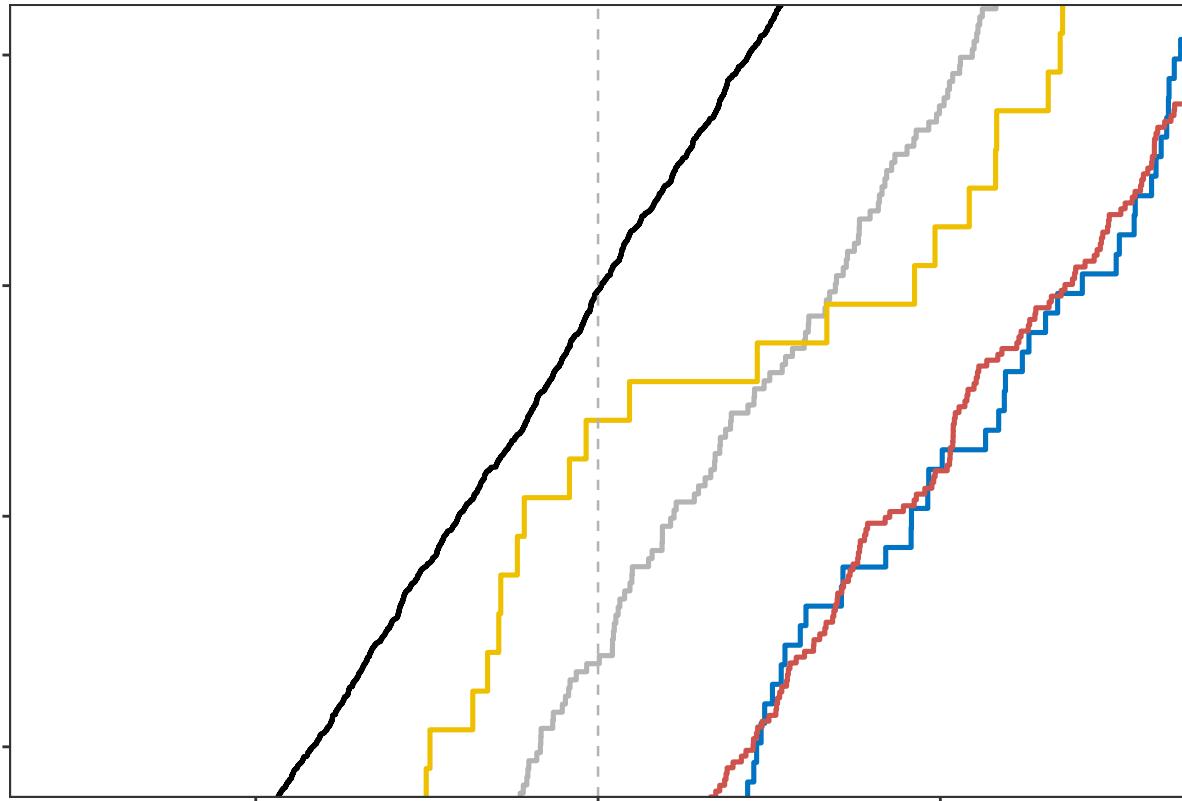
```

wobbleecdfRPF



```
#zoom
wobbleecdfRPFZ <- ggplot(RPF, aes(as.numeric(log2FoldChange), colour=factor(wobble, levels = c("Non-target", "No seed", "Canonical", "Non-Canonical", "Multiple")))) +
  stat_ecdf(geom="step", linewidth=2*zoomfac) +
  geom_vline(xintercept = 0, linewidth=1*zoomfac, linetype="dashed", colour=farbeneg) +
  scale_colour_manual(values = c("black", farbeneg, farbe1, farbe2, farbe3)) +
  coord_cartesian(xlim = c(-(xlim/8), (xlim/8)), ylim = c(0.5-1/16, 0.5+1/16)) +
  theme_bw() +
  theme(legend.position = "none", axis.text = element_blank(), panel.grid = element_blank(),
        panel.background = element_rect(fill='transparent'), #transparent panel bg
        plot.background = element_rect(fill='transparent', color=NA)) +
  scale_y_continuous("") + scale_x_continuous("")
```

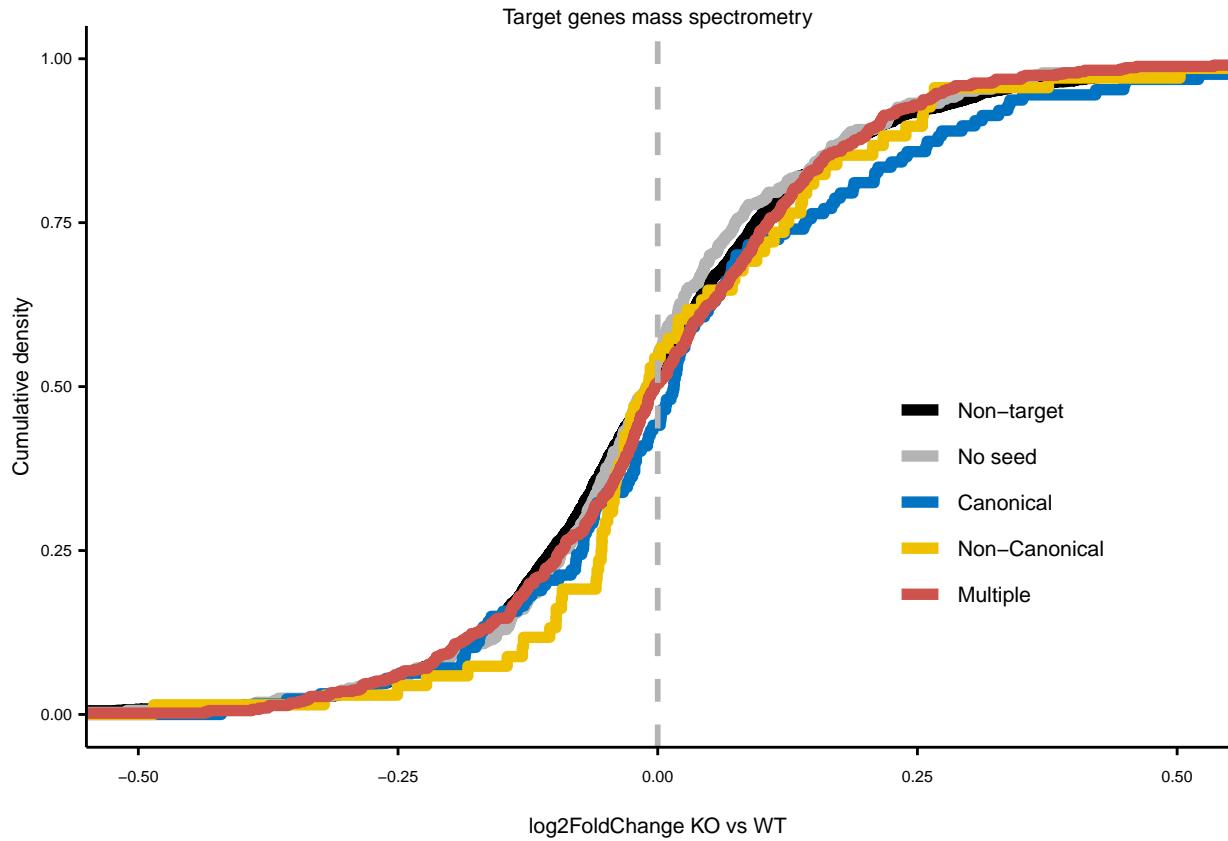
wobbleecdfRPFZ



```
#MS
```

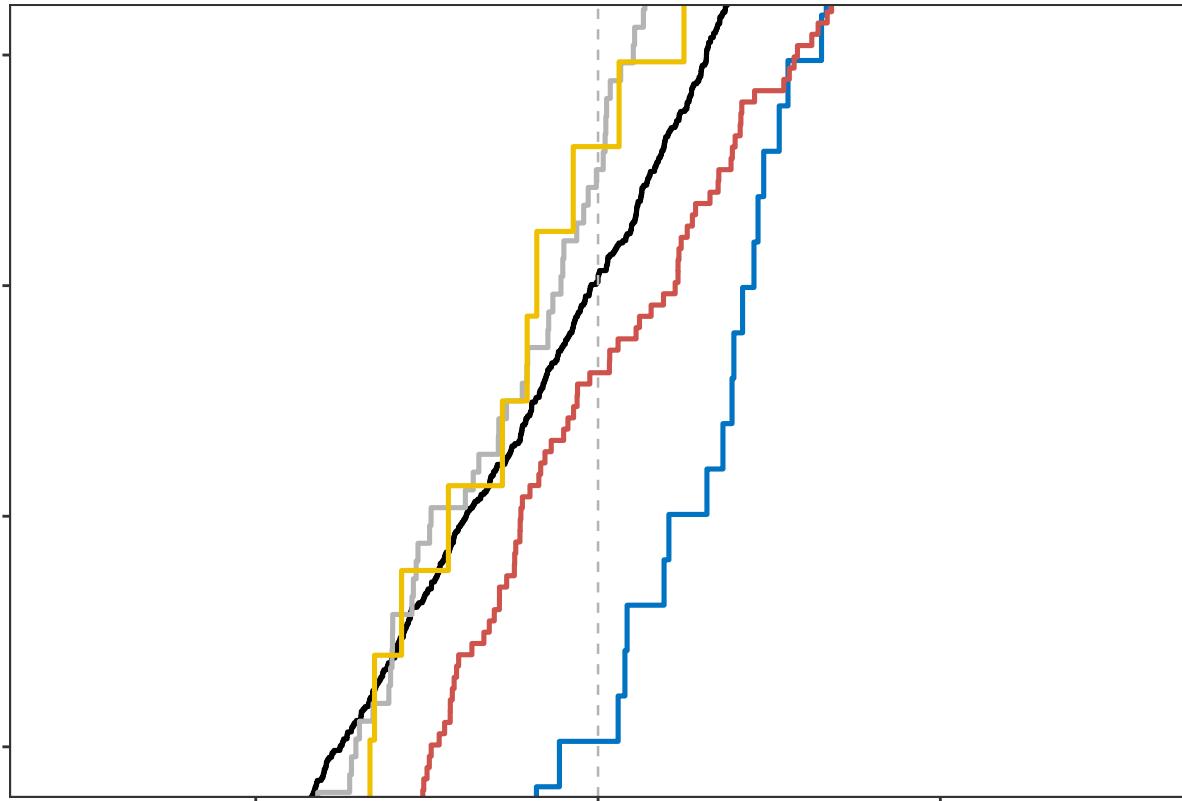
```
wobbleecdfMS <- ggplot(MS, aes(as.numeric(log2FoldChange), colour=factor(wobble, levels = c("Non-target", "farbeneg", "farbe1", "farbe2", "farbe3")))) +  
  stat_ecdf(geom="step", linewidth=2) +  
  geom_vline(xintercept = 0, linewidth=1, linetype="dashed", colour=farbeneg) +  
  scale_colour_manual(values = c("black", farbeneg, farbe1, farbe2, farbe3)) +  
  coord_cartesian(xlim = c(-xlim, xlim)) +  
  theme_paper() +  
  scale_y_continuous("Cumulative density") + scale_x_continuous("log2FoldChange K0 vs WT") +  
  ggtitle("Target genes mass spectrometry")
```

```
wobbleecdfMS
```



```
#zoom
wobbleecdfMSZ <- ggplot(MS, aes(as.numeric(log2FoldChange), colour=factor(wobble, levels = c("Non-target", "No seed", "Canonical", "Non-Canonical", "Multiple")))) +
  stat_ecdf(geom="step", linewidth=2*zoomfac) +
  geom_vline(xintercept = 0, linewidth=1*zoomfac, linetype="dashed", colour=farbeneg) +
  scale_colour_manual(values = c("black", farbeneg, farbe1, farbe2, farbe3)) +
  coord_cartesian(xlim = c(-(xlim/8), (xlim/8)), ylim = c(0.5-1/16, 0.5+1/16)) +
  theme_bw() +
  theme(legend.position = "none", axis.text = element_blank(), panel.grid = element_blank(),
        panel.background = element_rect(fill='transparent'), #transparent panel bg
        plot.background = element_rect(fill='transparent', color=NA)) +
  scale_y_continuous("") + scale_x_continuous("")
```

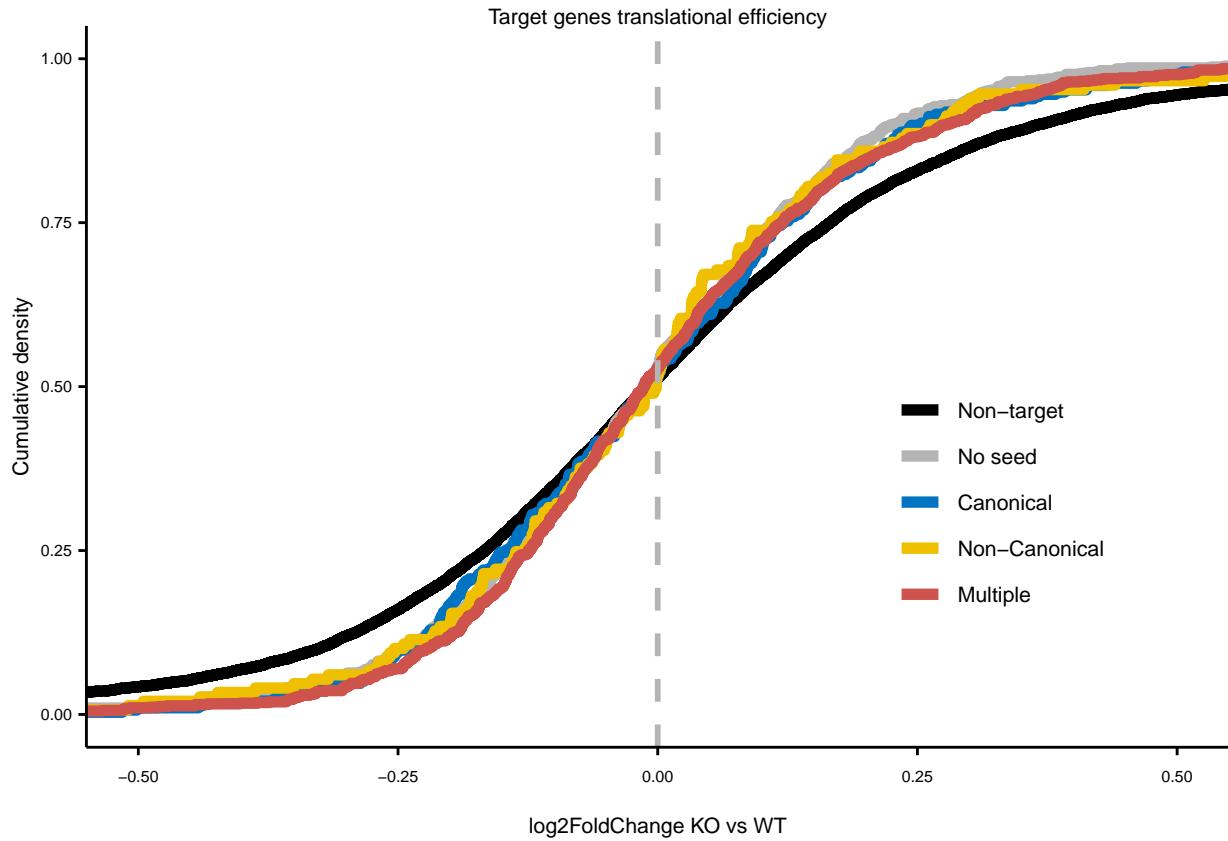
wobbleecdfMSZ



#TE

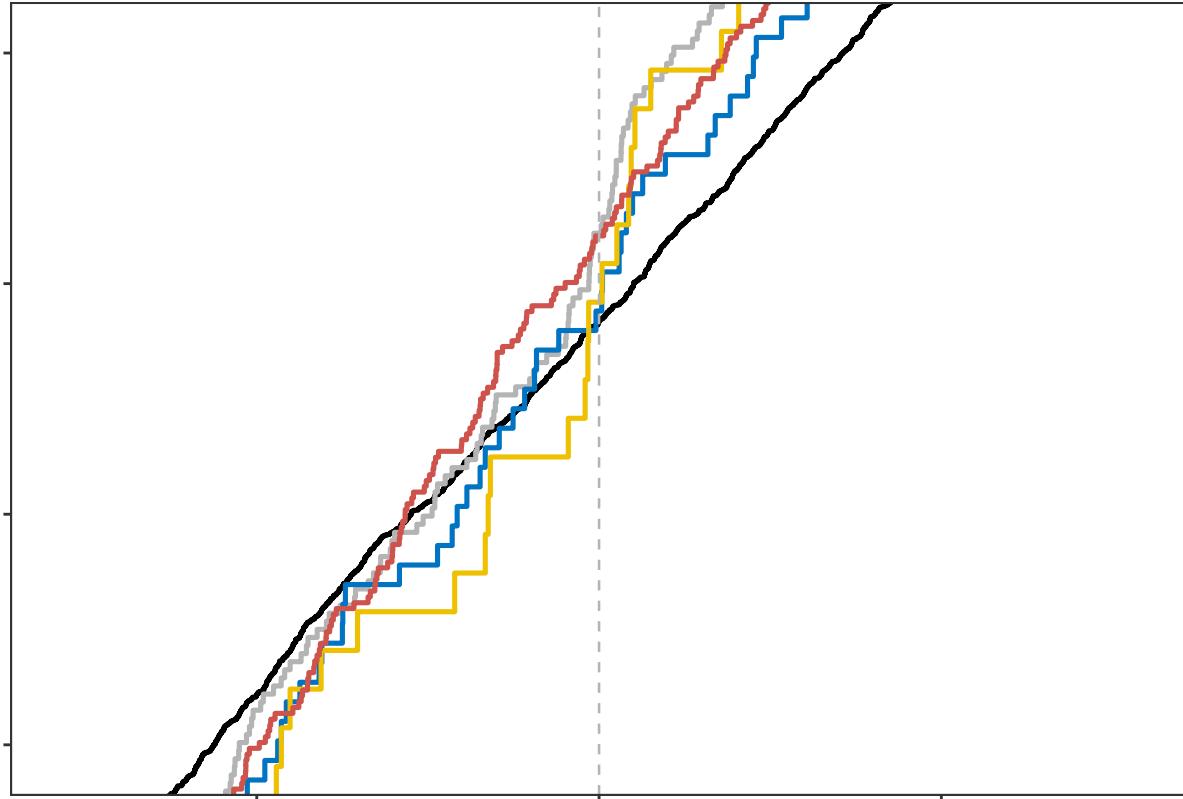
```
wobbleecdfTE <- ggplot(TE, aes(as.numeric(log2FoldChange), colour=factor(wobble, levels = c("Non-target", "Target", "Regulated", "Unregulated")))) +
  stat_ecdf(geom="step", linewidth=2) +
  geom_vline(xintercept = 0, linewidth=1, linetype="dashed", colour=farbeneg) +
  scale_colour_manual(values = c("black", farbeneg, farbe1, farbe2, farbe3)) +
  coord_cartesian(xlim = c(-10, 10)) +
  theme_paper() +
  scale_y_continuous("Cumulative density") +
  scale_x_continuous("log2FoldChange K0 vs WT") +
  ggtitle("Target genes translational efficiency")
```

wobbleecdfTE



```
#zoom
wobbleecdfTEZ <- ggplot(TE, aes(as.numeric(log2FoldChange), colour=factor(wobble, levels = c("Non-target", "No seed", "Canonical", "Non-Canonical", "Multiple")))) +
  stat_ecdf(geom="step", linewidth=2*zoomfac) +
  geom_vline(xintercept = 0, linewidth=1*zoomfac, linetype="dashed", colour=farbeneg) +
  scale_colour_manual(values = c("black", farbeneg, farbe1, farbe2, farbe3)) +
  coord_cartesian(xlim = c(-(xlim/8), (xlim/8)), ylim = c(0.5-1/16, 0.5+1/16)) +
  theme_bw() +
  theme(legend.position = "none", axis.text = element_blank(), panel.grid = element_blank(),
        panel.background = element_rect(fill='transparent'), #transparent panel bg
        plot.background = element_rect(fill='transparent', color=NA)) +
  scale_y_continuous("") + scale_x_continuous("")
```

wobbleecdfTEZ



```

#export RNA
pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/wobbleECDF_RNA.pdf", width=2, height = 2)
wobbleecdfRNA
dev.off()

## pdf
## 2
pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/wobbleECDF_RNA_zoom.pdf", width=2*zoomfac, height
wobbleecdfRNAZ
dev.off()

## pdf
## 2
#export RPF
pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/wobbleECDF_RPF.pdf", width=2, height = 2)
wobbleecdfRPF
dev.off()

## pdf
## 2
pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/wobbleECDF_RPF_zoom.pdf", width=2*zoomfac, height
wobbleecdfRPFZ
dev.off()

## pdf
## 2

```

```

#export MS
pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/wobbleECDF_MS.pdf", width=2, height = 2)
wobbleecdfMS
dev.off()

## pdf
## 2

pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/wobbleECDF_MS_zoom.pdf", width=2*zoomfac, height =
wobbleecdfMSZ
dev.off()

## pdf
## 2

#export TE
pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/wobbleECDF_TE.pdf", width=2, height = 2)
wobbleecdfTE
dev.off()

## pdf
## 2

pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/wobbleECDF_TE_zoom.pdf", width=2*zoomfac, height =
wobbleecdfTEZ
dev.off()

## pdf
## 2

table(RPF$wobble)

##
##      Canonical      Multiple      No seed Non-Canonical      Non-target
##            295           990          713            149          9222

```

by type of MRE (wobble and non wobble combined)

```

#RNA
RNA$MREtype <- "Non-target"
RNA$MREtype [RNA$gene_symbol %in% targetframe[is.na(targetframe$first_seed_200down.type), "geneName"]] <-
RNA$MREtype [RNA$gene_symbol %in% targetframe[targetframe$first_seed_200down.type == "seed_6mer", "geneName"]]
RNA$MREtype [RNA$gene_symbol %in% targetframe[targetframe$first_seed_200down.type == "seed_7mer_a1", "geneName"]]
RNA$MREtype [RNA$gene_symbol %in% targetframe[targetframe$first_seed_200down.type == "seed_7mer_m8", "geneName"]]
RNA$MREtype [RNA$gene_symbol %in% targetframe[targetframe$first_seed_200down.type == "seed_8mer", "geneName"]]
RNA$MREtype [RNA$gene_symbol %in% targetframe[targetframe$first_seed_200down.type == "seed_alt_38", "geneName"]]
RNA$MREtype [RNA$gene_symbol %in% bsnum[bsnum$BS_number > 1, "gene_symbol"]] <- "Multiple"

#RPF
RPF$MREtype <- "Non-target"
RPF$MREtype [RPF$gene_symbol %in% targetframe[is.na(targetframe$first_seed_200down.type), "geneName"]] <-
RPF$MREtype [RPF$gene_symbol %in% targetframe[targetframe$first_seed_200down.type == "seed_6mer", "geneName"]]
RPF$MREtype [RPF$gene_symbol %in% targetframe[targetframe$first_seed_200down.type == "seed_7mer_a1", "geneName"]]
RPF$MREtype [RPF$gene_symbol %in% targetframe[targetframe$first_seed_200down.type == "seed_7mer_m8", "geneName"]]
RPF$MREtype [RPF$gene_symbol %in% targetframe[targetframe$first_seed_200down.type == "seed_8mer", "geneName"]]
RPF$MREtype [RPF$gene_symbol %in% targetframe[targetframe$first_seed_200down.type == "seed_alt_38", "geneName"]]

```

```

RPF$MREtype[RPF$gene_symbol %in% bsnum[bsnum$BS_number > 1, "gene_symbol"]] <- "Multiple"

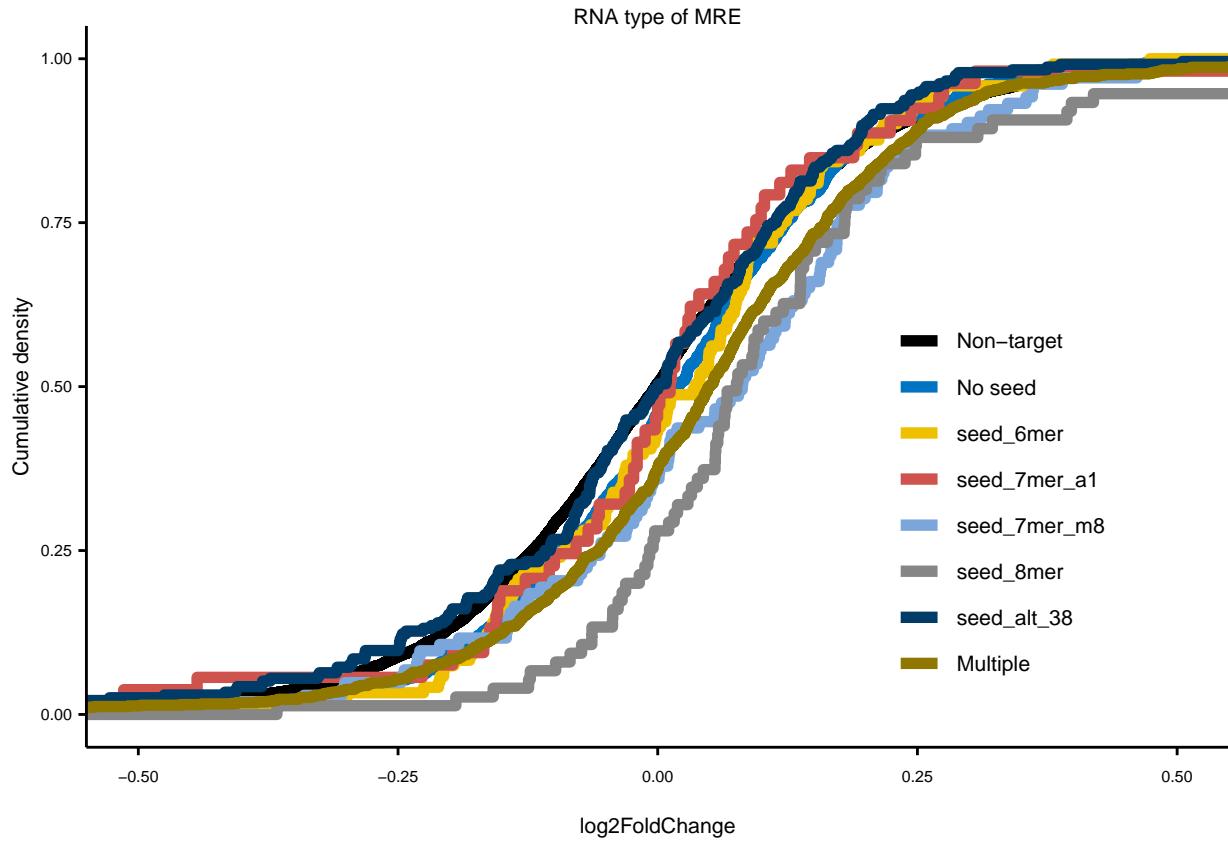
#MS
MS$MREtype <- "Non-target"
MS$MREtype [MS$gene_symbol %in% largetframe[is.na(largetframe$first_seed_200down.type), "geneName"]]] <- "Non-target"
MS$MREtype [MS$gene_symbol %in% largetframe[largetframe$first_seed_200down.type == "seed_6mer", "geneName"]]
MS$MREtype [MS$gene_symbol %in% largetframe[largetframe$first_seed_200down.type == "seed_7mer_a1", "geneName"]]
MS$MREtype [MS$gene_symbol %in% largetframe[largetframe$first_seed_200down.type == "seed_7mer_m8", "geneName"]]
MS$MREtype [MS$gene_symbol %in% largetframe[largetframe$first_seed_200down.type == "seed_8mer", "geneName"]]
MS$MREtype [MS$gene_symbol %in% largetframe[largetframe$first_seed_200down.type == "seed_alt_38", "geneName"]]
MS$MREtype [MS$gene_symbol %in% bsnum[bsnum$BS_number > 1, "gene_symbol"]]] <- "Multiple"

#TE
TE$MREtype <- "Non-target"
TE$MREtype [TE$gene_symbol %in% largetframe[is.na(largetframe$first_seed_200down.type), "geneName"]]] <- "Non-target"
TE$MREtype [TE$gene_symbol %in% largetframe[largetframe$first_seed_200down.type == "seed_6mer", "geneName"]]
TE$MREtype [TE$gene_symbol %in% largetframe[largetframe$first_seed_200down.type == "seed_7mer_a1", "geneName"]]
TE$MREtype [TE$gene_symbol %in% largetframe[largetframe$first_seed_200down.type == "seed_7mer_m8", "geneName"]]
TE$MREtype [TE$gene_symbol %in% largetframe[largetframe$first_seed_200down.type == "seed_8mer", "geneName"]]
TE$MREtype [TE$gene_symbol %in% largetframe[largetframe$first_seed_200down.type == "seed_alt_38", "geneName"]]
TE$MREtype [TE$gene_symbol %in% bsnum[bsnum$BS_number > 1, "gene_symbol"]]] <- "Multiple"

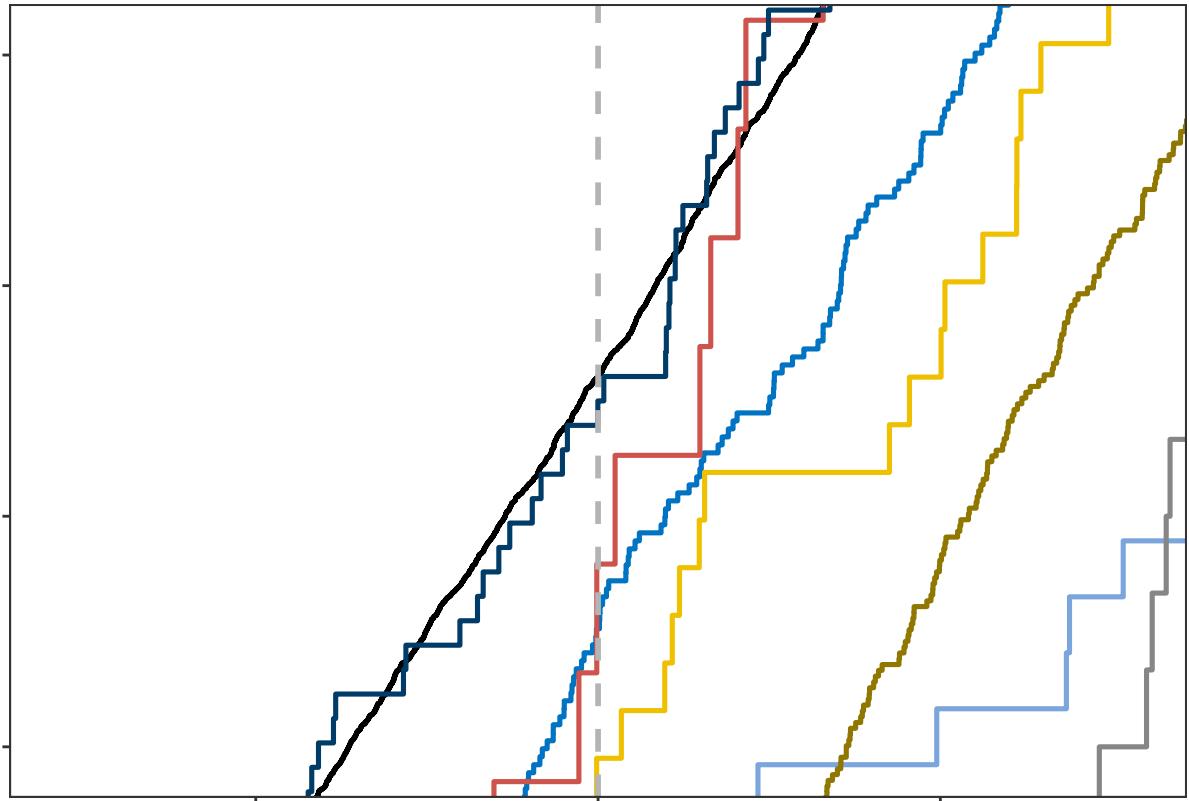
# ecdf plots
#RNA
typeECDFRNA <- ggplot(RNA, aes(as.numeric(log2FoldChange),
                                colour=factor(MREtype, levels = c("Non-target", "No seed", "seed_6mer", "seed_7mer", "seed_8mer", "seed_7mer_a1", "seed_7mer_m8", "seed_alt_38"))),
                                stat_ecdf(geom="step", linewidth=2) +
                                scale_colour_manual(values = c("black", farbe1, farbe2, farbe3, farbe4, farbe5, farbe6, farbe7)) +
                                coord_cartesian(xlim = c(-xlim, xlim)) +
                                theme_paper() +
                                scale_y_continuous("Cumulative density") + scale_x_continuous("log2FoldChange") +
                                ggtitle("RNA type of MRE"))

typeECDFRNA

```



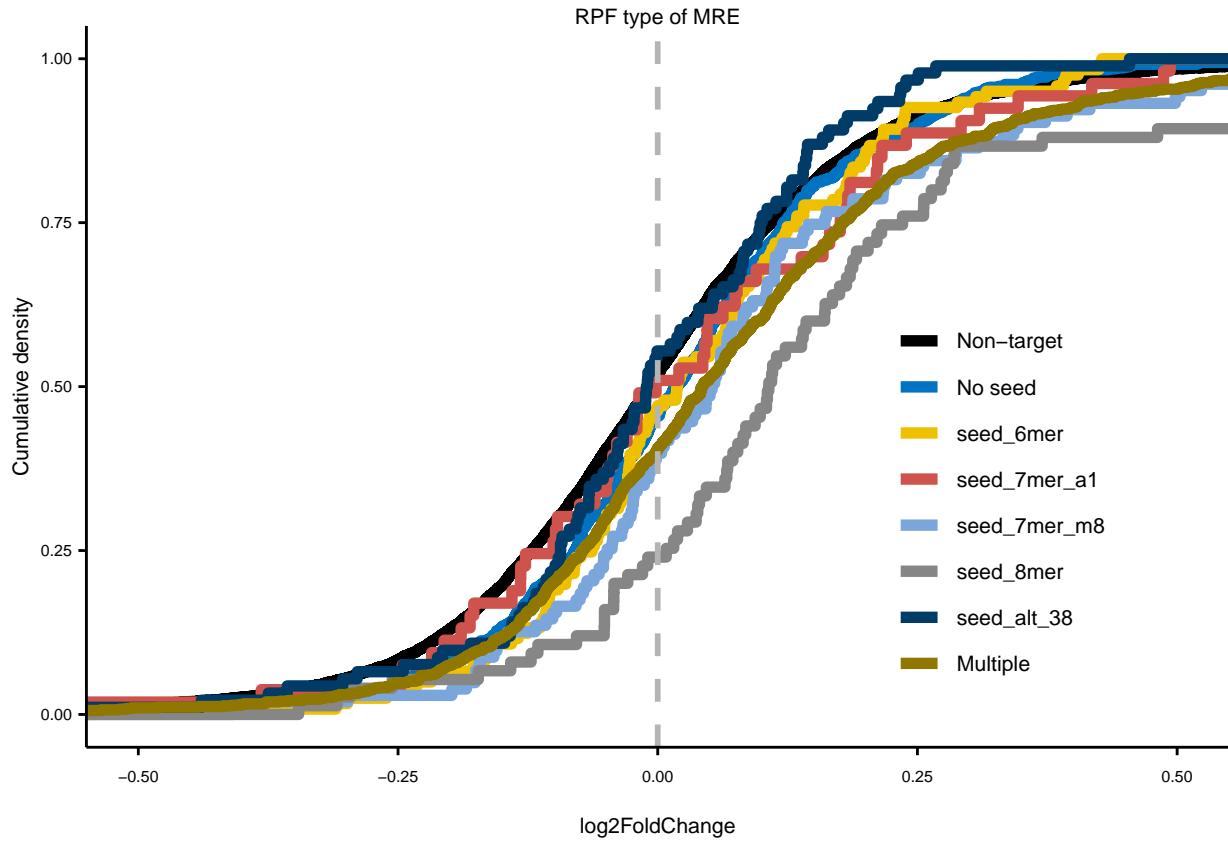
```
# zoom
typeECDFRNAZ <- ggplot(RNA, aes(as.numeric(log2FoldChange),
                                colour=factor(MREtype, levels = c("Non-target", "No seed", "seed_6mer", "seed_7mer_a1", "seed_7mer_m8", "seed_8mer", "seed_alt_38", "Multiple")),
                                stat_ecdf(geom="step", linewidth=2*zoomfac) +
                                geom_vline(xintercept = 0, linewidth=1, linetype="dashed", colour=farbeneg) +
                                scale_colour_manual(values = c("black", farbe1, farbe2, farbe3, farbe4, farbe5, farbe6, farbe7)) +
                                coord_cartesian(xlim = c(-xlim/8), (xlim/8)), ylim = c(0.5-1/16, 0.5+1/16)) +
                                theme_bw() +
                                theme(legend.position = "none", axis.text = element_blank(), panel.grid = element_blank(),
                                      panel.background = element_rect(fill='transparent'), #transparent panel bg
                                      plot.background = element_rect(fill='transparent', color=NA)) +
                                scale_y_continuous("") + scale_x_continuous(""))
typeECDFRNAZ
```



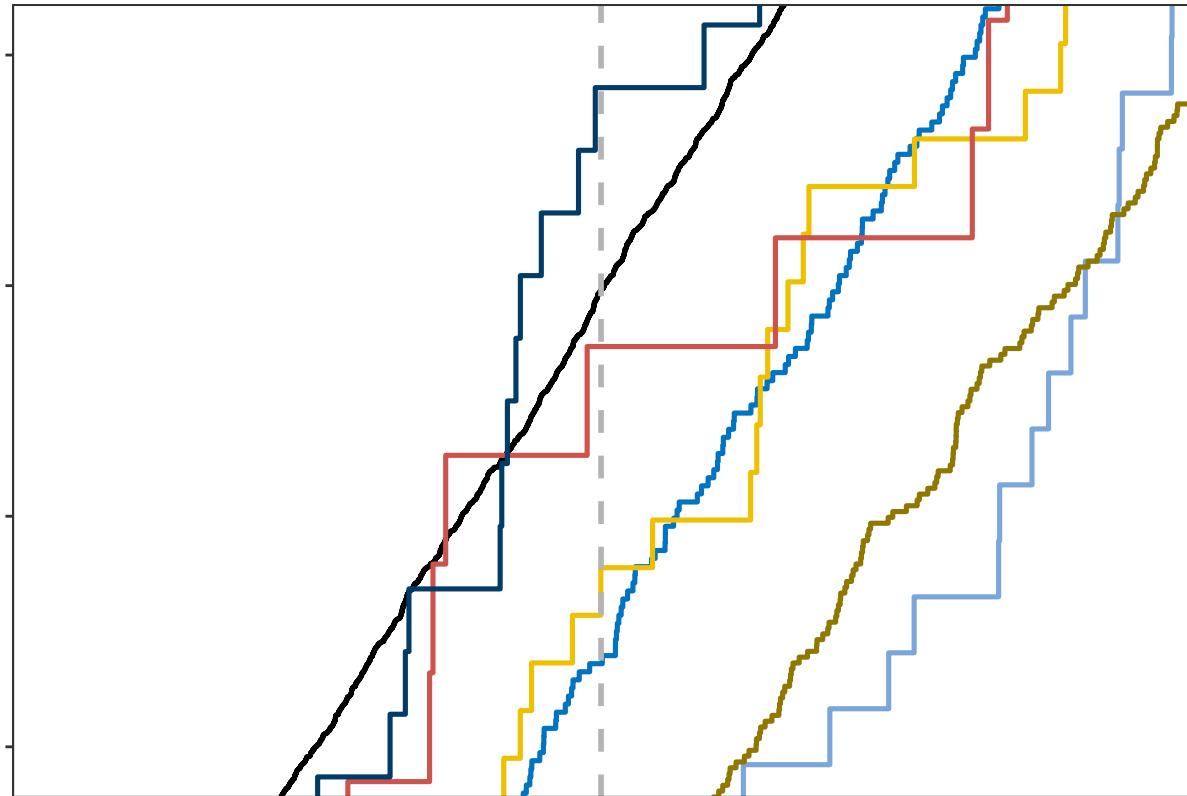
#RPF

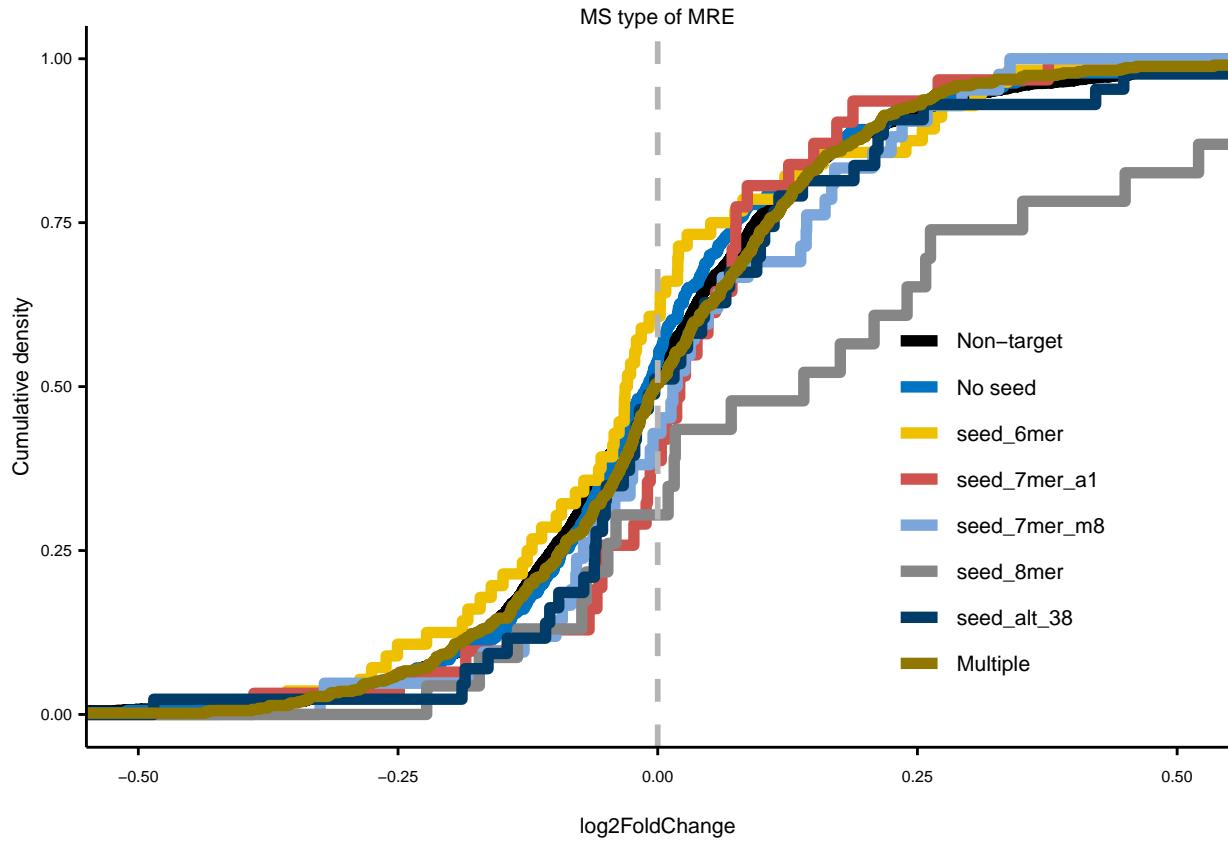
```
typeECDFRPF <- ggplot(RPF, aes(as.numeric(log2FoldChange),
                                colour=factor(MREtype, levels = c("Non-target", "No seed", "seed_6mer", "seed_8mer", "seed_10mer", "seed_12mer", "seed_14mer")),
                                stat_ecdf(geom="step", linewidth=2) +
                                geom_vline(xintercept = 0, linewidth=1, linetype="dashed", colour=farbeneg) +
                                scale_colour_manual(values = c("black", farbe1, farbe2, farbe3, farbe4, farbe5, farbe6, farbe7)) +
                                coord_cartesian(xlim = c(-xlim, xlim)) +
                                theme_paper() +
                                scale_y_continuous("Cumulative density") + scale_x_continuous("log2FoldChange") +
                                ggtitle("RPF type of MRE"))

typeECDFRPF
```

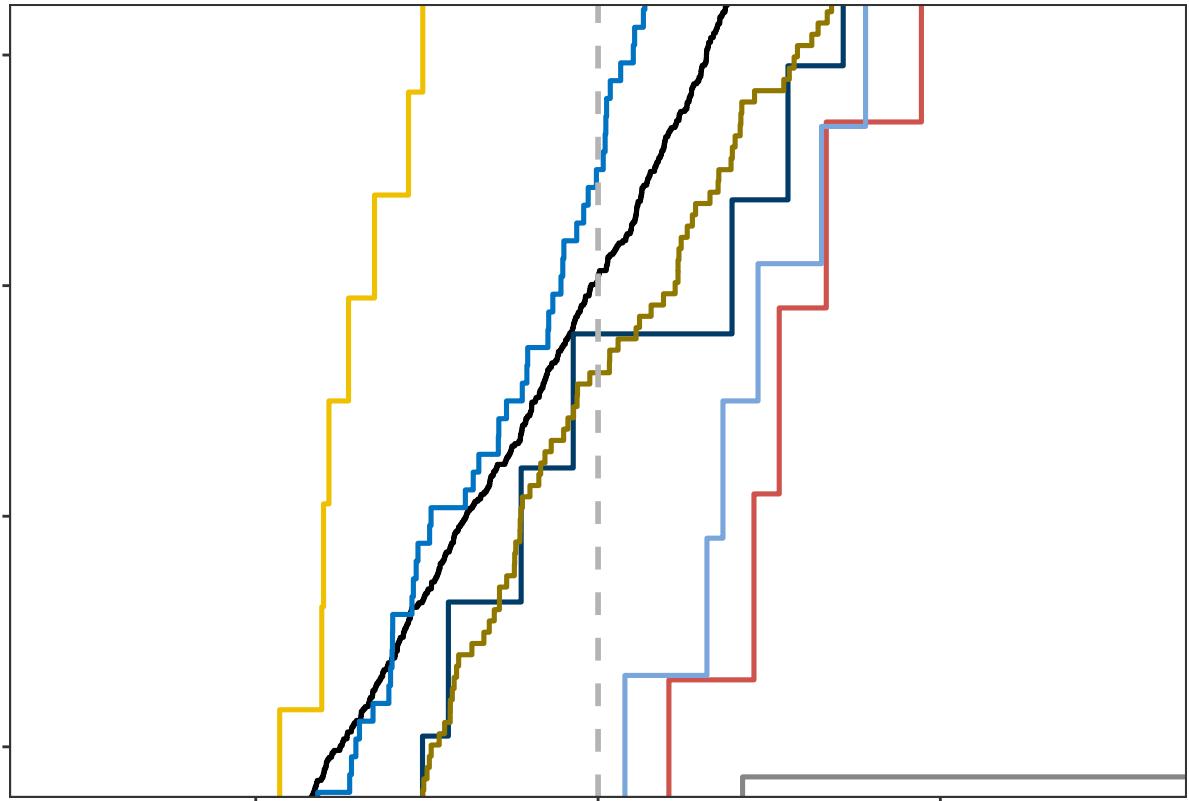


```
# zoom
typeECDFRPFZ <- ggplot(RPF, aes(as.numeric(log2FoldChange),
                                colour=factor(MREtype, levels = c("Non-target", "No seed", "seed_6mer", "seed_7mer_a1", "seed_7mer_m8", "seed_8mer", "seed_alt_38", "Multiple")),
                                stat_ecdf(geom="step", linewidth=2*zoomfac) +
                                geom_vline(xintercept = 0, linewidth=1, linetype="dashed", colour=farbeneg) +
                                scale_colour_manual(values = c("black", farbe1, farbe2, farbe3, farbe4, farbe5, farbe6, farbe7)) +
                                coord_cartesian(xlim = c(-xlim/8), (xlim/8)), ylim = c(0.5-1/16, 0.5+1/16)) +
                                theme_bw() +
                                theme(legend.position = "none", axis.text = element_blank(), panel.grid = element_blank(),
                                      panel.background = element_rect(fill='transparent'), #transparent panel bg
                                      plot.background = element_rect(fill='transparent', color=NA)) +
                                scale_y_continuous("") + scale_x_continuous(""))
typeECDFRPFZ
```



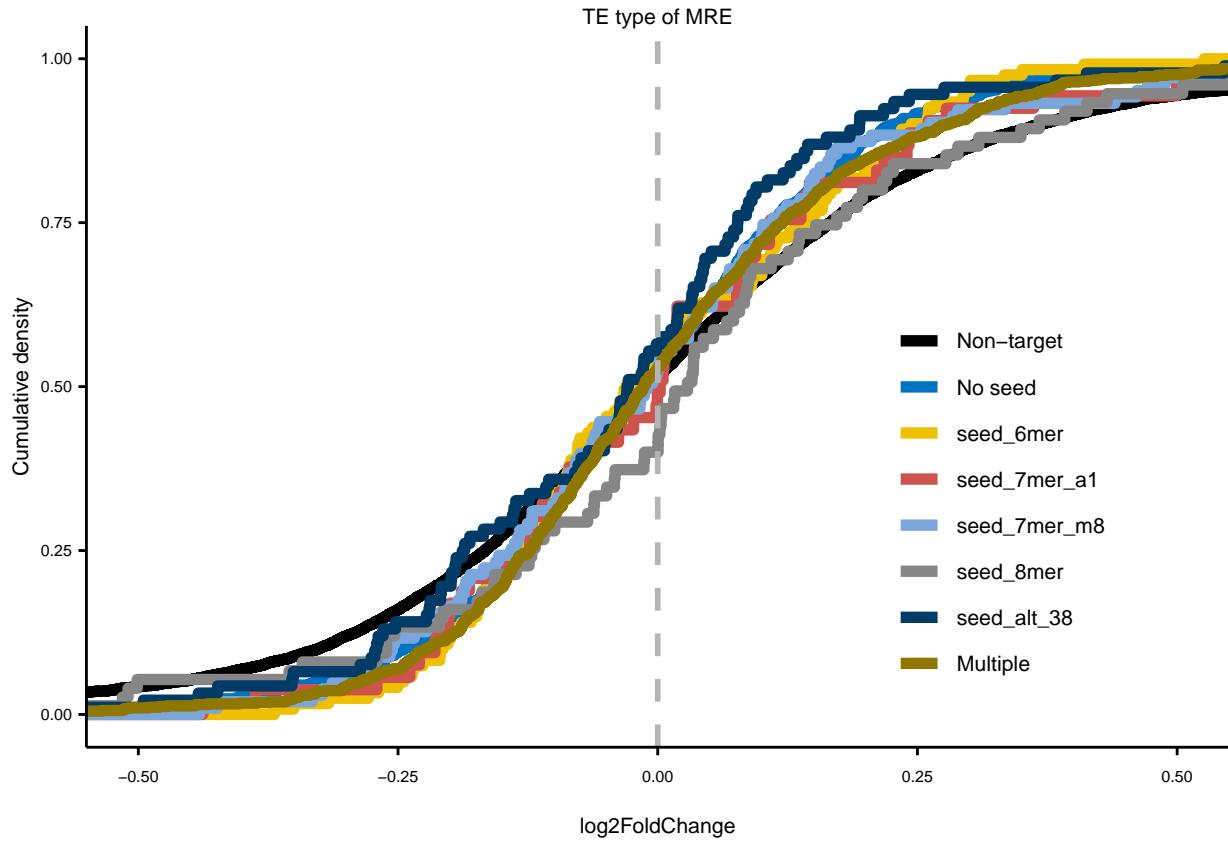


```
# zoom
typeECDFMSZ <- ggplot(MS, aes(as.numeric(log2FoldChange),
                           colour=factor(MREtype, levels = c("Non-target", "No seed", "seed_6mer", "seed_7mer_a1", "seed_7mer_m8", "seed_8mer", "seed_alt_38", "Multiple")),
                           stat_ecdf(geom="step", linewidth=2*zoomfac) +
                           geom_vline(xintercept = 0, linewidth=1, linetype="dashed", colour=farbeneg) +
                           scale_colour_manual(values = c("black", farbe1, farbe2, farbe3, farbe4, farbe5, farbe6, farbe7)) +
                           coord_cartesian(xlim = c(-xlim/8), (xlim/8)), ylim = c(0.5-1/16, 0.5+1/16)) +
                           theme_bw() +
                           theme(legend.position = "none", axis.text = element_blank(), panel.grid = element_blank(),
                           panel.background = element_rect(fill='transparent'), #transparent panel bg
                           plot.background = element_rect(fill='transparent', color=NA)) +
                           scale_y_continuous("") + scale_x_continuous(""))
typeECDFMSZ
```

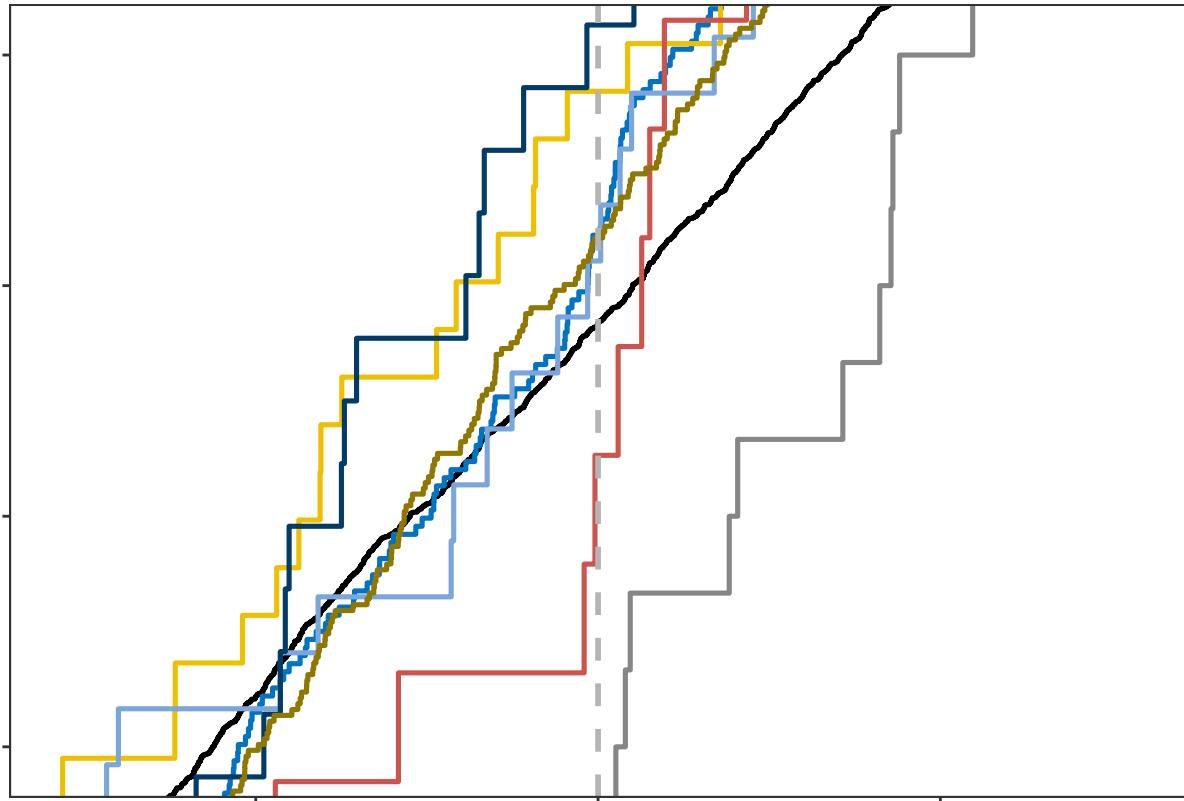


```
#TE
typeECDFTE <- ggplot(TE, aes(as.numeric(log2FoldChange),
                           colour=factor(MREtype, levels = c("Non-target", "No seed", "seed_6mer", "seed_7mer", "seed_8mer", "seed_9mer", "seed_10mer")),
                           stat_ecdf(geom="step", linewidth=2) +
                           geom_vline(xintercept = 0, linewidth=1, linetype="dashed", colour=farbeneg) +
                           scale_colour_manual(values = c("black", farbe1, farbe2, farbe3, farbe4, farbe5, farbe6, farbe7)) +
                           coord_cartesian(xlim = c(-xlim, xlim)) +
                           theme_paper() +
                           scale_y_continuous("Cumulative density") + scale_x_continuous("log2FoldChange") +
                           ggtitle("TE type of MRE"))

typeECDFTE
```



```
# zoom
typeECDFTEZ <- ggplot(TE, aes(as.numeric(log2FoldChange),
                           colour=factor(MREtype, levels = c("Non-target", "No seed", "seed_6mer", "seed_7mer_a1", "seed_7mer_m8", "seed_8mer", "seed_alt_38", "Multiple")),
                           stat_ecdf(geom="step", linewidth=2*zoomfac) +
                           geom_vline(xintercept = 0, linewidth=1, linetype="dashed", colour=farbeneg) +
                           scale_colour_manual(values = c("black", farbe1, farbe2, farbe3, farbe4, farbe5, farbe6, farbe7)) +
                           coord_cartesian(xlim = c(-xlim/8, (xlim/8)), ylim = c(0.5-1/16, 0.5+1/16)) +
                           theme_bw() +
                           theme(legend.position = "none", axis.text = element_blank(), panel.grid = element_blank(),
                                 panel.background = element_rect(fill='transparent'), #transparent panel bg
                                 plot.background = element_rect(fill='transparent', color=NA)) +
                           scale_y_continuous("") + scale_x_continuous(""))
typeECDFTEZ
```



```

#export RNA
pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/typeECDF_RNA.pdf", width=2, height = 2)
typeECDFRNA
dev.off()

## pdf
## 2
pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/typeECDF_RNA_zoom.pdf", width=2*zoomfac, height =
typeECDFRNAZ
dev.off()

## pdf
## 2
#export RPF
pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/typeECDF_RPF.pdf", width=2, height = 2)
typeECDFRPF
dev.off()

## pdf
## 2
pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/typeECDF_RPF_zoom.pdf", width=2*zoomfac, height =
typeECDFRPFZ
dev.off()

## pdf
## 2

```

```

#export MS
pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/typeECDF_MS.pdf", width=2, height = 2)
typeECDFMS
dev.off()

## pdf
## 2
pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/typeECDF_MS_zoom.pdf", width=2*zoomfac, height = 2)
typeECDFMSZ
dev.off()

## pdf
## 2
#export TE
pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/typeECDF_TE.pdf", width=2, height = 2)
typeECDFTE
dev.off()

## pdf
## 2
pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/typeECDF_TE_zoom.pdf", width=2*zoomfac, height = 2)
typeECDFTEZ
dev.off()

## pdf
## 2
table(RPF$MREtype)

##
##      Multiple      No seed   Non-target   seed_6mer   seed_7mer_a1   seed_7mer_m8
##      990          713       9222        121           53            103
##      seed_8mer   seed_alt_38
##      75           92

```

mmsat4

```

mmsat4frame <- as.data.frame(subsetByOverlaps(gff23, MMSAT4))

#RNA
RNA$tvsmmssat4 <- "Non-target"
RNA$tvsmmssat4[RNA$gene_symbol %in% mmsat4frame$gene_name] <- "MMsat4"
RNA$tvsmmssat4[RNA$gene_symbol %in% targetframe$geneName] <- "miR-181 target"
RNA$tvsmmssat4[RNA$gene_symbol %in% targetframe$geneName & RNA$gene_symbol %in% mmsat4frame$gene_name] <-
table(RNA$tvsmmssat4)

##
##      both miR-181 target      MMsat4      Non-target
##      81       2079        163        10978

#RPF
RPF$tvsmmssat4 <- "Non-target"
RPF$tvsmmssat4[RPF$gene_symbol %in% mmsat4frame$gene_name] <- "MMsat4"
RPF$tvsmmssat4[RPF$gene_symbol %in% targetframe$geneName] <- "miR-181 target"

```

```

RPF$tvsmmsat4[RPF$gene_symbol %in% targetframe$geneName & RPF$gene_symbol %in% mmsat4frame$gene_name] <-  

table(RPF$tvsmmsat4)

##  

##          both miR-181 target      MMsat4     Non-target  

##          79           2068       152        9070

#MS  

MS$tvsmmsat4 <- "Non-target"  

MS$tvsmmsat4[MS$gene_symbol %in% mmsat4frame$gene_name] <- "MMsat4"  

MS$tvsmmsat4[MS$gene_symbol %in% targetframe$geneName] <- "miR-181 target"  

MS$tvsmmsat4[MS$gene_symbol %in% targetframe$geneName & MS$gene_symbol %in% mmsat4frame$gene_name] <- "Targeted"  

table(MS$tvsmmsat4)

##  

##          both miR-181 target      Non-target  

##          1           1029       2499

#TE  

TE$tvsmmsat4 <- "Non-target"  

TE$tvsmmsat4[TE$gene_symbol %in% mmsat4frame$gene_name] <- "MMsat4"  

TE$tvsmmsat4[TE$gene_symbol %in% targetframe$geneName] <- "miR-181 target"  

TE$tvsmmsat4[TE$gene_symbol %in% targetframe$geneName & TE$gene_symbol %in% mmsat4frame$gene_name] <- "Targeted"  

table(TE$tvsmmsat4)

##  

##          both miR-181 target      MMsat4     Non-target  

##          79           2068       152        9070

#RNA  

to1ECDFRNA <- ggplot(RNA, aes(as.numeric(log2FoldChange), colour=factor(tvsmmsat4, levels = c("Non-target", "Targeted")))) +  

stat_ecdf(geom="step", linewidth=2*zoomfac) +  

geom_vline(xintercept = 0, linewidth=1*zoomfac, linetype="dashed", colour=farbeneg) +  

scale_colour_manual(values = c("black", farbe1, farbe3, RPFncol)) +  

coord_cartesian(xlim = c(-xlim, xlim)) +  

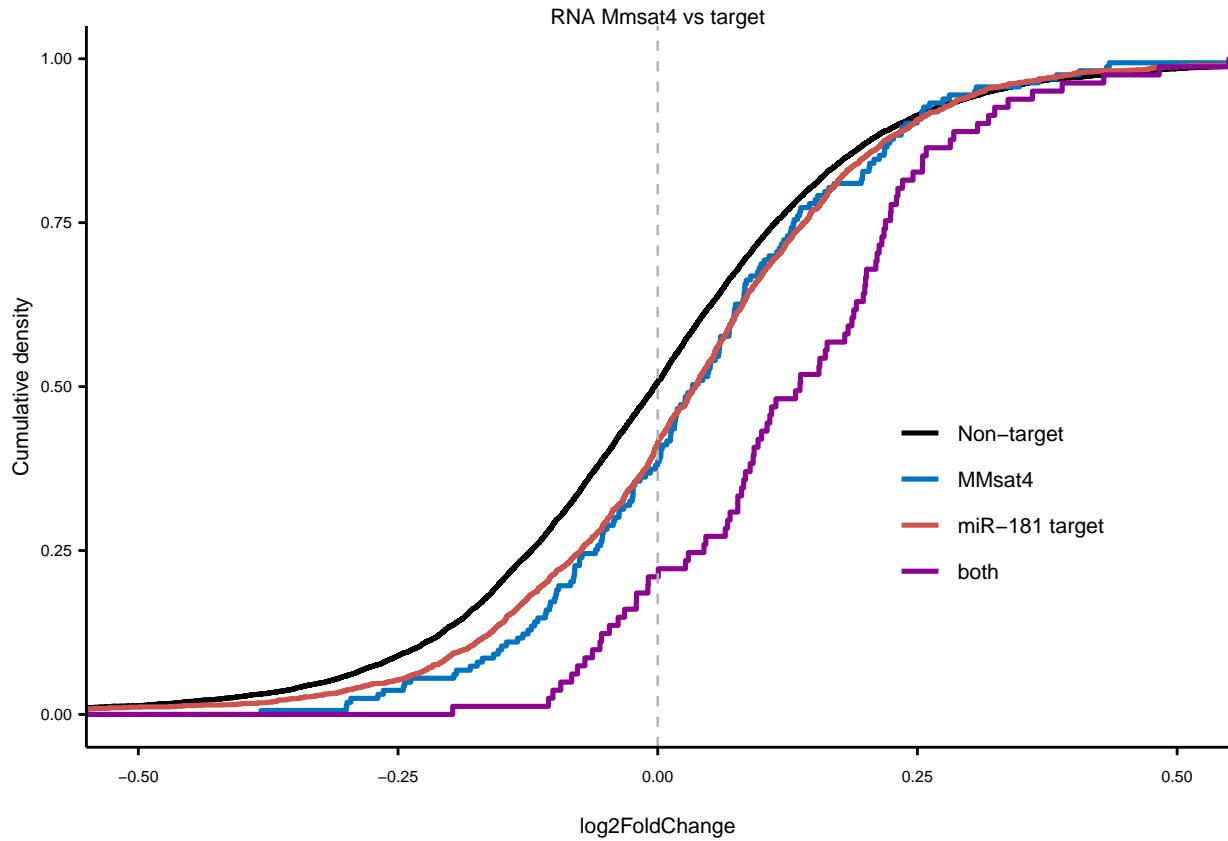
theme_paper() +  

scale_y_continuous("Cumulative density") + scale_x_continuous("log2FoldChange") +  

ggtitle("RNA Mmsat4 vs target")

to1ECDFRNA

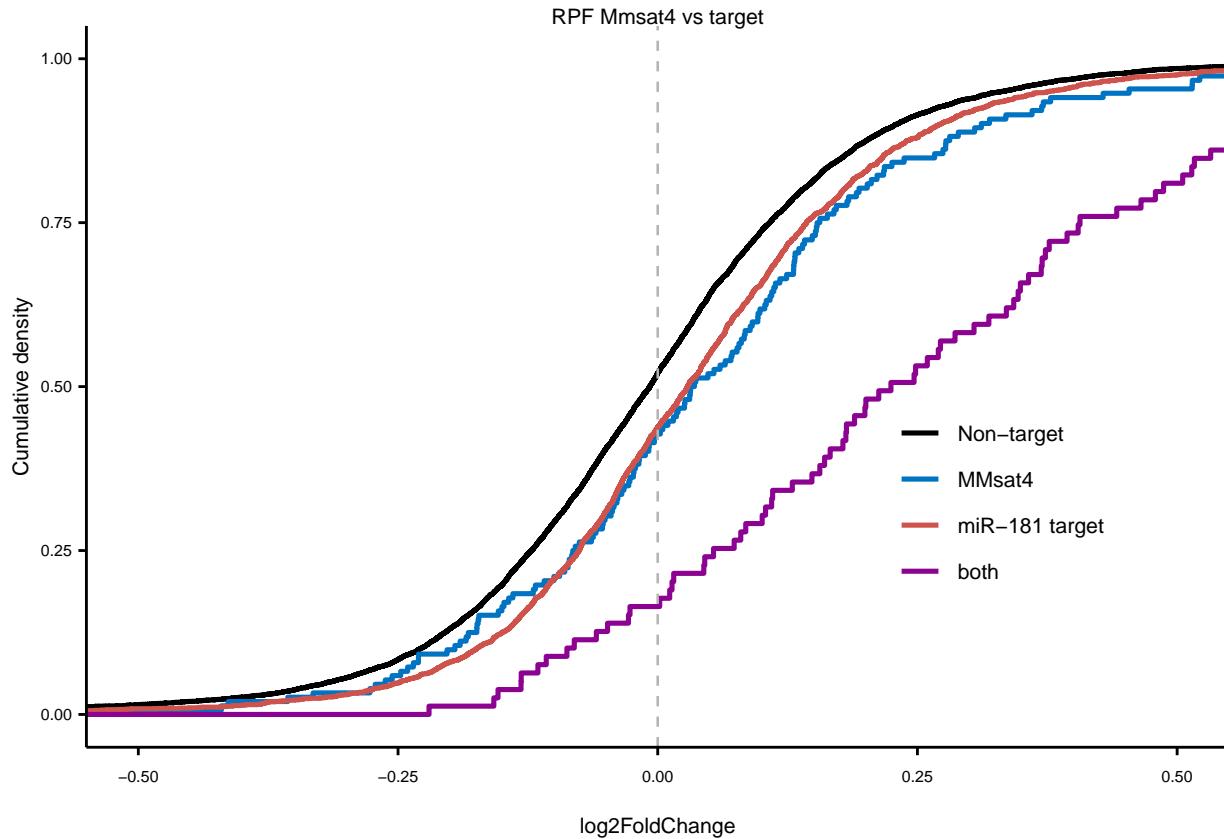
```



#RPF

```
to1ECDFRPF <- ggplot(RPF, aes(as.numeric(log2FoldChange), colour=factor(tvsmmsat4, levels = c("Non-target", "MMsat4", "miR-181 target", "both")))) +  
  stat_ecdf(geom="step", linewidth=2*zoomfac) +  
  geom_vline(xintercept = 0, linewidth=1*zoomfac, linetype="dashed", colour=farbeneg) +  
  scale_colour_manual(values = c("black", farbe1, farbe3, RPFncol)) +  
  coord_cartesian(xlim = c(-xlim, xlim)) +  
  theme_paper() +  
  scale_y_continuous("Cumulative density") + scale_x_continuous("log2FoldChange") +  
  ggtitle("RPF Mmsat4 vs target")
```

to1ECDFRPF



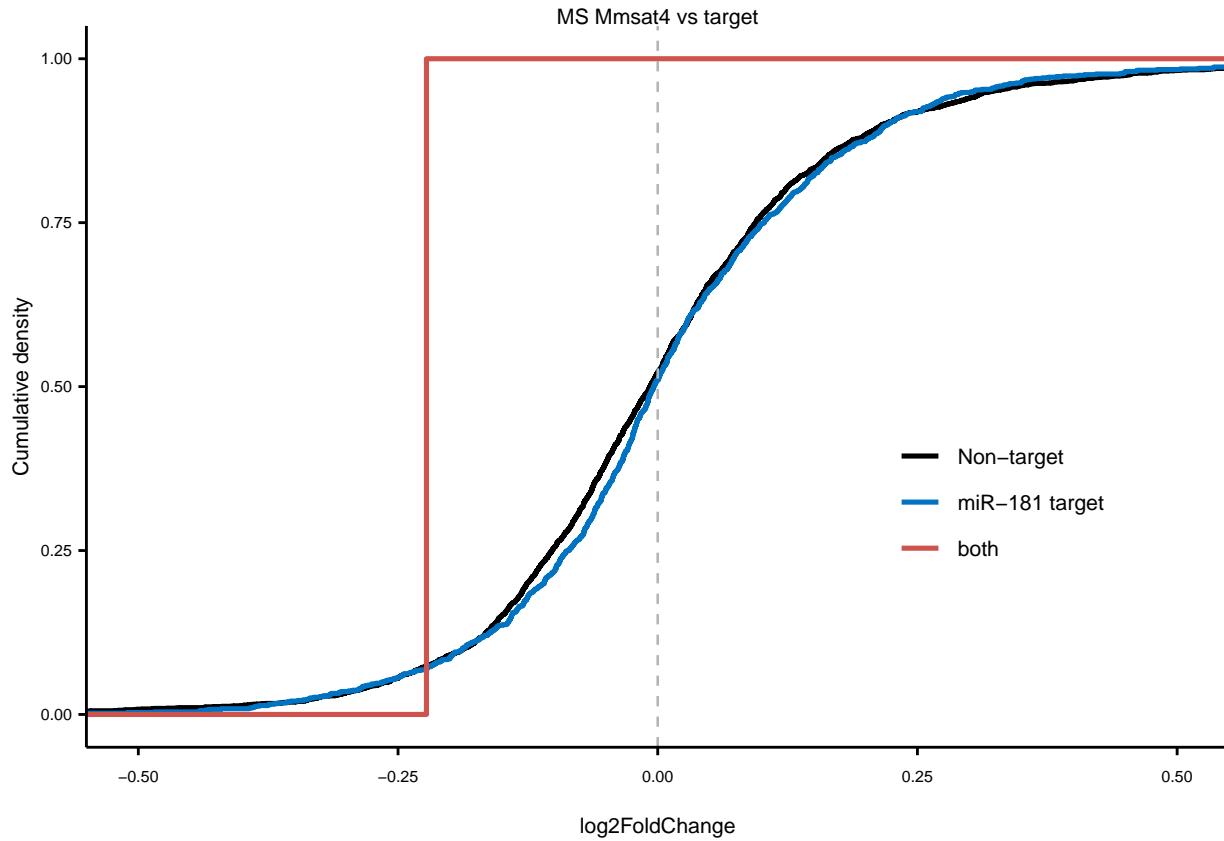
#MS

```

to1ECDFMS <- ggplot(MS, aes(as.numeric(log2FoldChange), colour=factor(tvsmmsat4, levels = c("Non-target",
  stat_ecdf(geom="step", linewidth=2*zoomfac) +
  geom_vline(xintercept = 0, linewidth=1*zoomfac, linetype="dashed", colour=farbeneg) +
  scale_colour_manual(values = c("black", farbe1, farbe3, RPFncol)) +
  coord_cartesian(xlim = c(-xlim, xlim)) +
  theme_paper() +
  scale_y_continuous("Cumulative density") + scale_x_continuous("log2FoldChange") +
  ggtitle("MS Mmsat4 vs target"))

to1ECDFMS

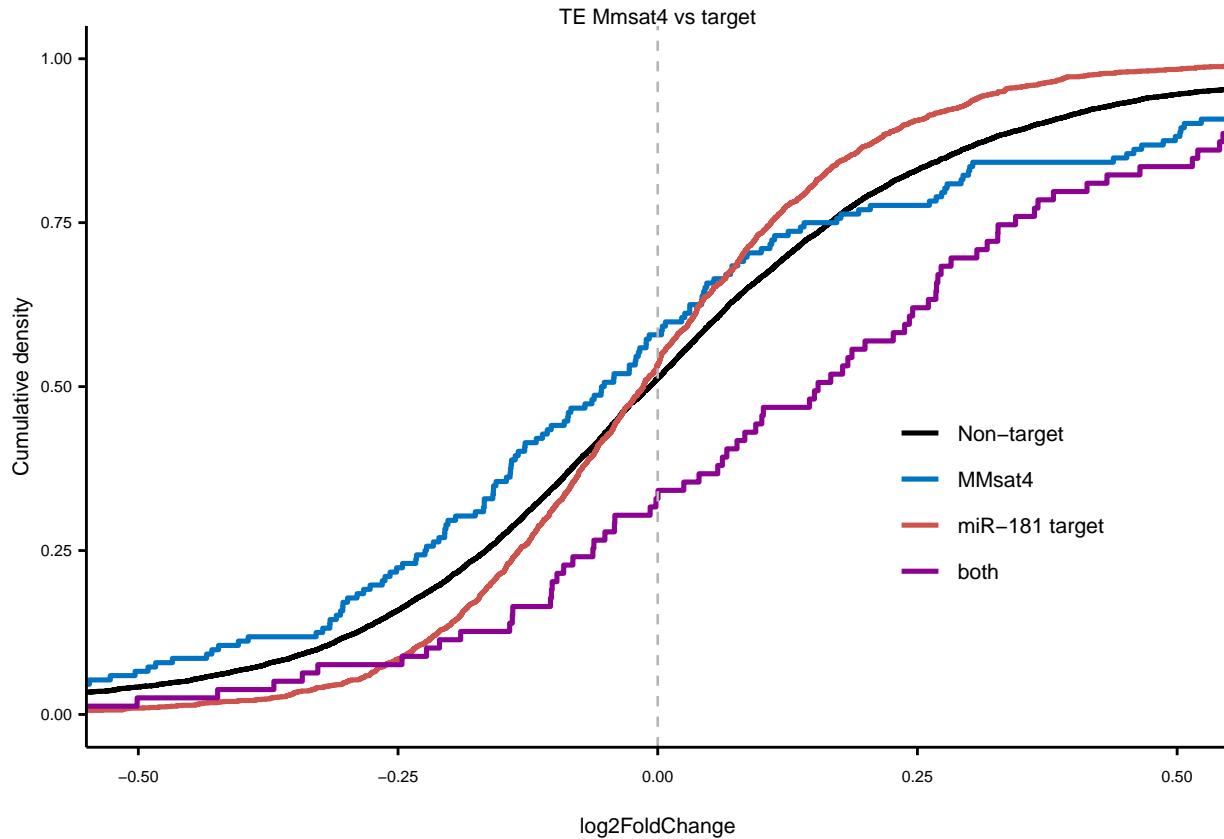
```



```
#TE
```

```
to1ECDFTE <- ggplot(TE, aes(as.numeric(log2FoldChange), colour=factor(tvsmmsat4, levels = c("Non-target", "miR-181 target", "both")))) +  
  stat_ecdf(geom="step", linewidth=2*zoomfac) +  
  geom_vline(xintercept = 0, linewidth=1*zoomfac, linetype="dashed", colour=farbeneg) +  
  scale_colour_manual(values = c("black", farbe1, farbe3, RPFncol)) +  
  coord_cartesian(xlim = c(-xlim, xlim)) +  
  theme_paper() +  
  scale_y_continuous("Cumulative density") + scale_x_continuous("log2FoldChange") +  
  ggtitle("TE Mmsat4 vs target")
```

```
to1ECDFTE
```



```

#export RNA
pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/MMSAT4ECDF_RNA.pdf", width=2, height = 2)
toECDFRNA
dev.off()

## pdf
## 2

#export RPF
pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/MMSAT4ECDF_RPF.pdf", width=2, height = 2)
toECDFRPF
dev.off()

## pdf
## 2

#export MS
pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/MMSAT4ECDF_MS.pdf", width=2, height = 2)
toECDFMS
dev.off()

## pdf
## 2

#export TE
pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/MMSAT4ECDF_TE.pdf", width=2, height = 2)
toECDFTE
dev.off()

```

```

## pdf
## 2





```

MurSatRep1

```

MurSatRep1frame <- as.data.frame(subsetByOverlaps(gff23, MurSatRep1))

#RNA
RNA$tvsMurSatRep1 <- "Non-target"
RNA$tvsMurSatRep1[RNA$gene_symbol %in% MurSatRep1frame$gene_name] <- "MurSatRep1"
RNA$tvsMurSatRep1[RNA$gene_symbol %in% largetframe$geneName] <- "miR-181 target"
RNA$tvsMurSatRep1[RNA$gene_symbol %in% largetframe$geneName & RNA$gene_symbol %in% MurSatRep1frame$gene_


#RPF



```

RPF$tvsMurSatRep1 <- "Non-target"
RPF$tvsMurSatRep1[RPF$gene_symbol %in% MurSatRep1frame$gene_name] <- "MurSatRep1"
RPF$tvsMurSatRep1[RPF$gene_symbol %in% largetframe$geneName] <- "miR-181 target"
RPF$tvsMurSatRep1[RPF$gene_symbol %in% largetframe$geneName & RPF$gene_symbol %in% MurSatRep1frame$gene_

#MS


```

MS$tvsMurSatRep1 <- "Non-target"
MS$tvsMurSatRep1[MS$gene_symbol %in% MurSatRep1frame$gene_name] <- "MurSatRep1"
MS$tvsMurSatRep1[MS$gene_symbol %in% largetframe$geneName] <- "miR-181 target"
MS$tvsMurSatRep1[MS$gene_symbol %in% largetframe$geneName & MS$gene_symbol %in% MurSatRep1frame$gene_


#TE



```

TE$tvsMurSatRep1 <- "Non-target"
TE$tvsMurSatRep1[TE$gene_symbol %in% MurSatRep1frame$gene_name] <- "MurSatRep1"
TE$tvsMurSatRep1[TE$gene_symbol %in% largetframe$geneName] <- "miR-181 target"
TE$tvsMurSatRep1[TE$gene_symbol %in% largetframe$geneName & TE$gene_symbol %in% MurSatRep1frame$gene_


```

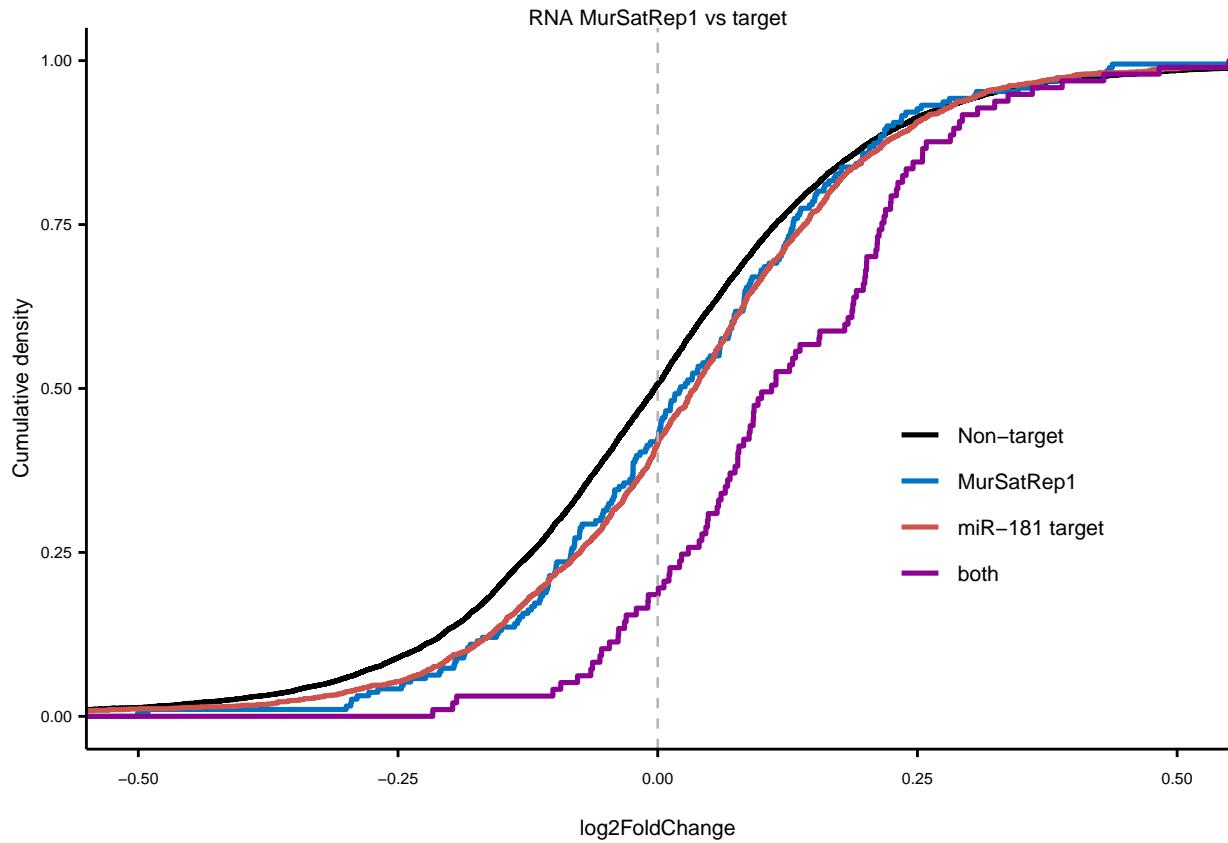

```


```


```

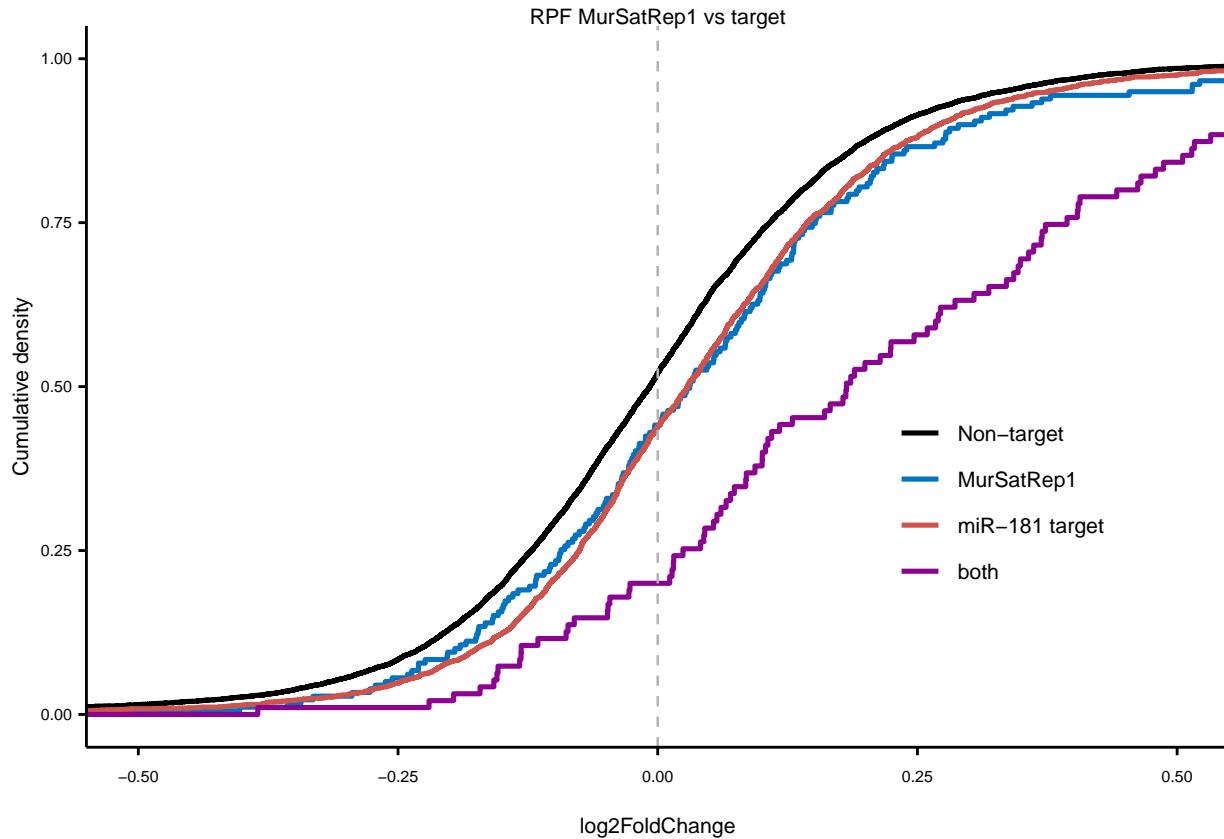
```
#RNA
murECDFRNA <- ggplot(RNA, aes(as.numeric(log2FoldChange), colour=factor(tvsMurSatRep1, levels = c("Non-
stat_ecdf(geom="step", linewidth=2*zoomfac) +
geom_vline(xintercept = 0, linewidth=1*zoomfac, linetype="dashed", colour=farbeneg) +
scale_colour_manual(values = c("black", farbe1, farbe3, RPFncol)) +
coord_cartesian(xlim = c(-xlim, xlim)) +
theme_paper() +
scale_y_continuous("Cumulative density") + scale_x_continuous("log2FoldChange") +
ggtitle("RNA MurSatRep1 vs target")
```

murECDFRNA



```
#RPF
murECDFRPF <- ggplot(RPF, aes(as.numeric(log2FoldChange), colour=factor(tvsMurSatRep1, levels = c("Non-
stat_ecdf(geom="step", linewidth=2*zoomfac) +
geom_vline(xintercept = 0, linewidth=1*zoomfac, linetype="dashed", colour=farbeneg) +
scale_colour_manual(values = c("black", farbe1, farbe3, RPFncol)) +
coord_cartesian(xlim = c(-xlim, xlim)) +
theme_paper() +
scale_y_continuous("Cumulative density") + scale_x_continuous("log2FoldChange") +
ggtitle("RPF MurSatRep1 vs target")
```

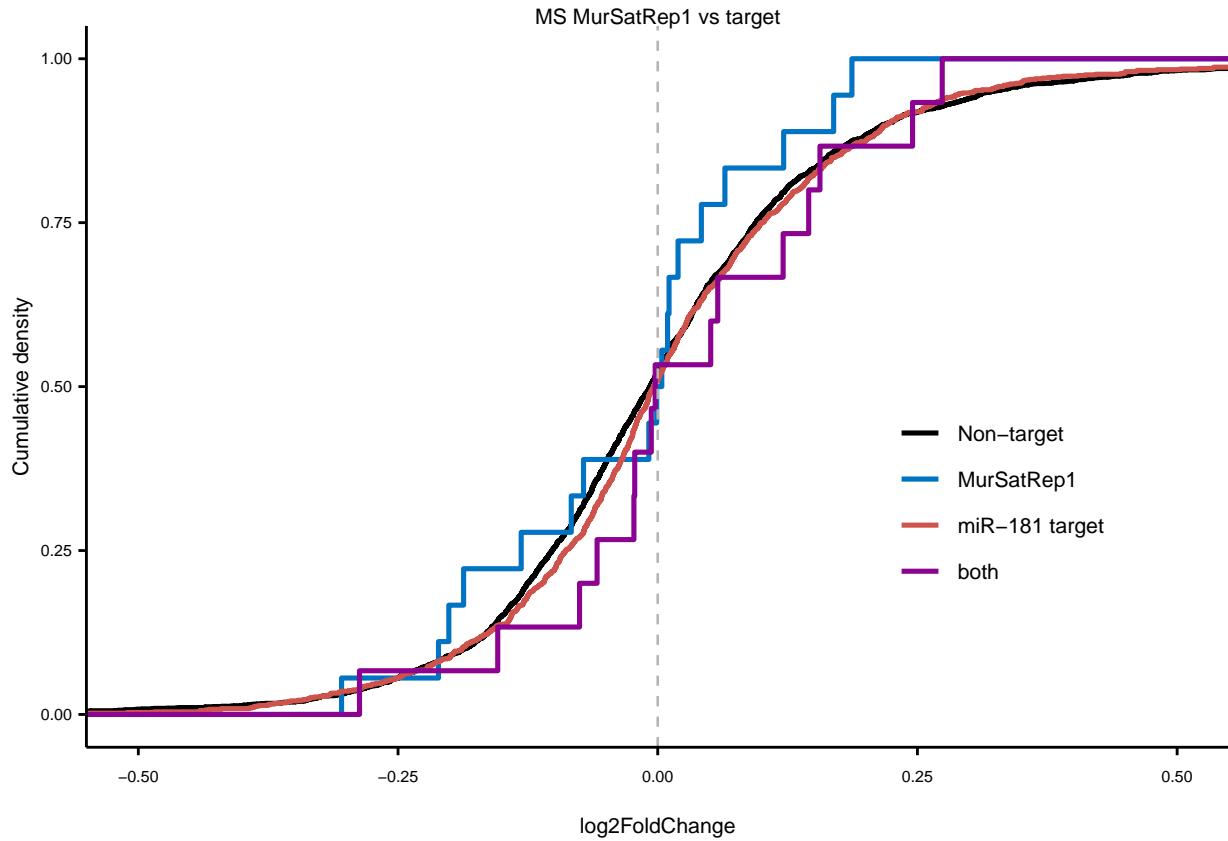
murECDFRPF



```
#MS
```

```
murECDFMS <- ggplot(MS, aes(as.numeric(log2FoldChange), colour=factor(tvsMurSatRep1, levels = c("Non-target", "MurSatRep1", "miR-181 target", "both")))) +  
  stat_ecdf(geom="step", linewidth=2*zoomfac) +  
  geom_vline(xintercept = 0, linewidth=1*zoomfac, linetype="dashed", colour=farbeneg) +  
  scale_colour_manual(values = c("black", farbe1, farbe3, RPFncol)) +  
  coord_cartesian(xlim = c(-xlim, xlim)) +  
  theme_paper() +  
  scale_y_continuous("Cumulative density") + scale_x_continuous("log2FoldChange") +  
  ggtitle("MS MurSatRep1 vs target")
```

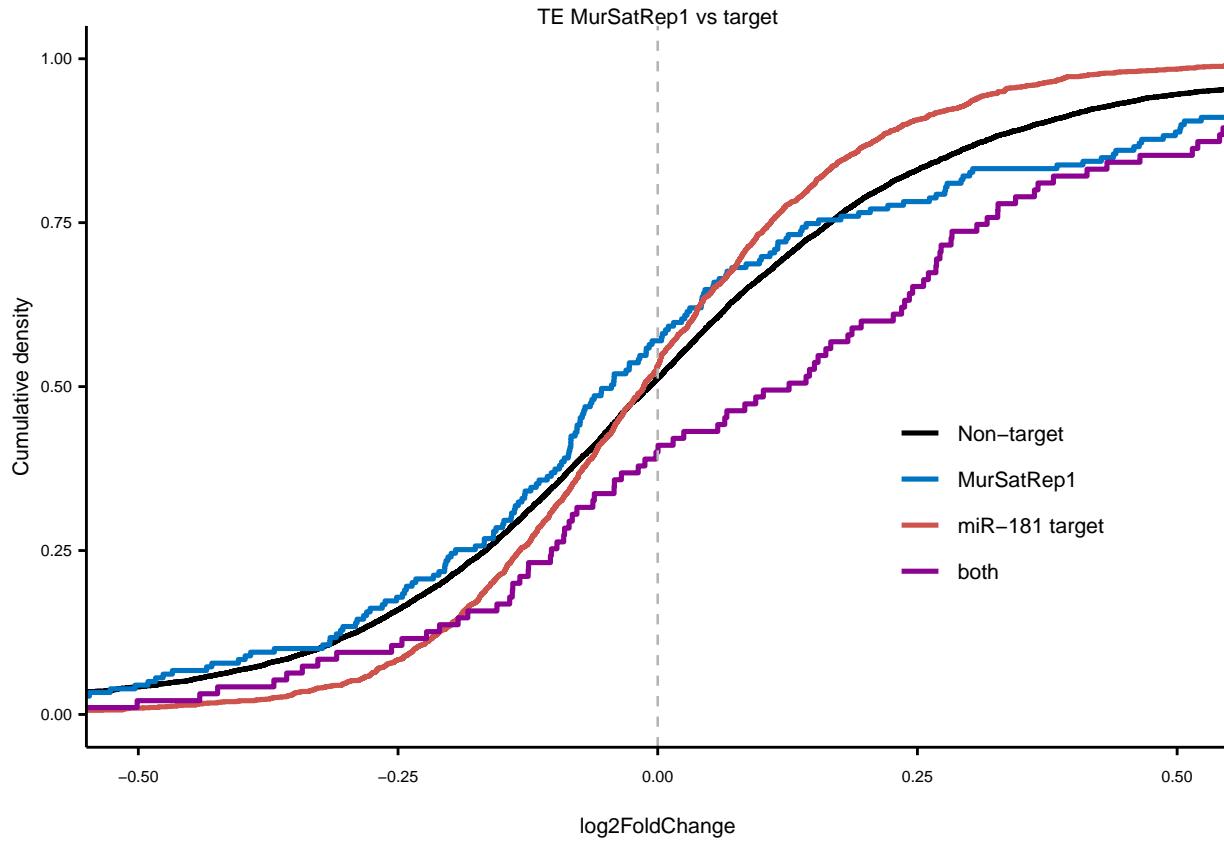
```
murECDFMS
```



```
#TE
```

```
murECDFTE <- ggplot(TE, aes(as.numeric(log2FoldChange), colour=factor(tvsMurSatRep1, levels = c("Non-target", "MurSatRep1", "miR-181 target", "both")))) +  
  stat_ecdf(geom="step", linewidth=2*zoomfac) +  
  geom_vline(xintercept = 0, linewidth=1*zoomfac, linetype="dashed", colour=farbeneg) +  
  scale_colour_manual(values = c("black", farbe1, farbe3, RPFncol)) +  
  coord_cartesian(xlim = c(-xlim, xlim)) +  
  theme_paper() +  
  scale_y_continuous("Cumulative density") + scale_x_continuous("log2FoldChange") +  
  ggtitle("TE MurSatRep1 vs target")
```

```
murECDFTE
```



```

#export RNA
pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/mursatrep1ECDF_RNA.pdf", width=2, height = 2)
murECDFRNA
dev.off()

## pdf
## 2

#export RPF
pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/mursatrep1ECDF_RPF.pdf", width=2, height = 2)
murECDFRPF
dev.off()

## pdf
## 2

#export MS
pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/mursatrep1ECDF_MS.pdf", width=2, height = 2)
murECDFMS
dev.off()

## pdf
## 2

#export TE
pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/mursatrep1ECDF_TE.pdf", width=2, height = 2)
murECDFTE
dev.off()

```

```

## pdf
## 2





```

metagene plot

```

MMSAT4$id <- "MMSat4"
MurSatRep1$id <- "MurSatRep1"

metaob <- c(MMSAT4, MurSatRep1)

metael <- metaGeneProfile(object = metaob, annotation = gff23path, group = "id")
metasat4 <- metaGeneProfile(object = MMSAT4, annotation = gff23path)
metamur <- metaGeneProfile(object = MurSatRep1, annotation = gff23path)

metasat4

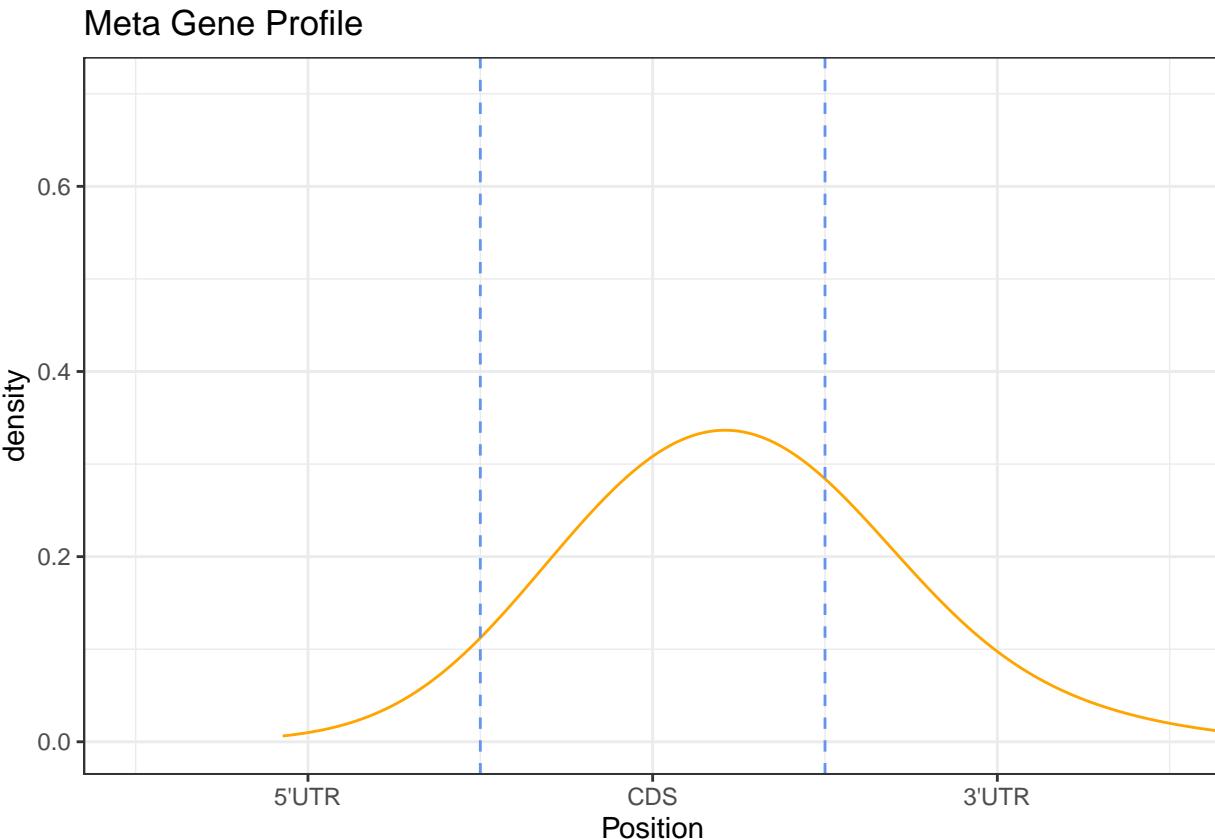
## $Peaks
## GRanges object with 1693 ranges and 17 metadata columns:
##           seqnames      ranges strand |   swScore  milliDiv
##           <Rle>      <IRanges> <Rle> | <integer> <numeric>
## [1]     chr1    49003992-49004114 - |    272    295
## [2]     chr1    49004329-49004605 - |    402    284
## [3]     chr1    82366411-82366554 - |    395    248
## [4]     chr1    86014673-86014899 - |    382    314
## [5]     chr1    117749987-117750291 - |    312    304
## ...
## [1689] chr4_KZ289068_fix    531409-532565 + |   1261    87
## [1690] chr7_JH792828_fix  149909-150032 + |   282    294
## [1691] chr7_JH792828_fix  150332-150465 + |   262    358
## [1692] chr7_JH792828_fix  150584-150721 + |   228    306
## [1693] chrY_JH792832_fix  349767-349817 + |   230    180
##   milliDel milliIns genoLeft repName repClass repFamily
##   <numeric> <numeric> <integer> <character> <character> <character>
## [1]      57       8 -146467857  MMSAT4 Satellite  Satellite
## [2]      32      27 -146467366  MMSAT4 Satellite  Satellite
## [3]      42      21 -113105417  MMSAT4 Satellite  Satellite
## [4]       0       0 -109457072  MMSAT4 Satellite  Satellite
## [5]      30      27 -77721680  MMSAT4 Satellite  Satellite
## ...
## [1689]      0       0      -7  MMSAT4 Satellite  Satellite
## [1690]      40      40 -323706  MMSAT4 Satellite  Satellite
## [1691]      0       0 -323273  MMSAT4 Satellite  Satellite
## [1692]      22      29 -323017  MMSAT4 Satellite  Satellite
## [1693]      0      20 -194372  MMSAT4 Satellite  Satellite
##   repStart repEnd repLeft      id center location
##   <integer> <integer> <integer> <character> <integer> <character>
## [1]      -5     163      35 MMsat4  49004054      NO
## [2]     -13     278       1 MMsat4  49004467      NO
## [3]      0     168      22 MMsat4  82366483      NO

```

```

##      [4]      0     227      1    MMsat4  86014787      NO
##      [5]      0     305      1    MMsat4 117750139      NO
##      ...
## [1689]      1    1157      0    MMsat4  531987      NO
## [1690]     31     154     -14   MMsat4 149971      NO
## [1691]     31     164     -4    MMsat4 150399      NO
## [1692]     31     167     -1    MMsat4 150653      NO
## [1693]    115     164     -4    MMsat4 349793      NO
##           Gene_ID Transcript_ID  Position
##           <character> <character> <numeric>
##      [1]      Nan      <NA>      5
##      [2]      Nan      <NA>      5
##      [3]      Nan      <NA>      5
##      [4]      Nan      <NA>      5
##      [5]      Nan      <NA>      5
##      ...
## [1689]     Nan      <NA>      5
## [1690]     Nan      <NA>      5
## [1691]     Nan      <NA>      5
## [1692]     Nan      <NA>      5
## [1693]     Nan      <NA>      5
##
## -----
## seqinfo: 239 sequences (1 circular) from mm10 genome
##
## $Plot

```



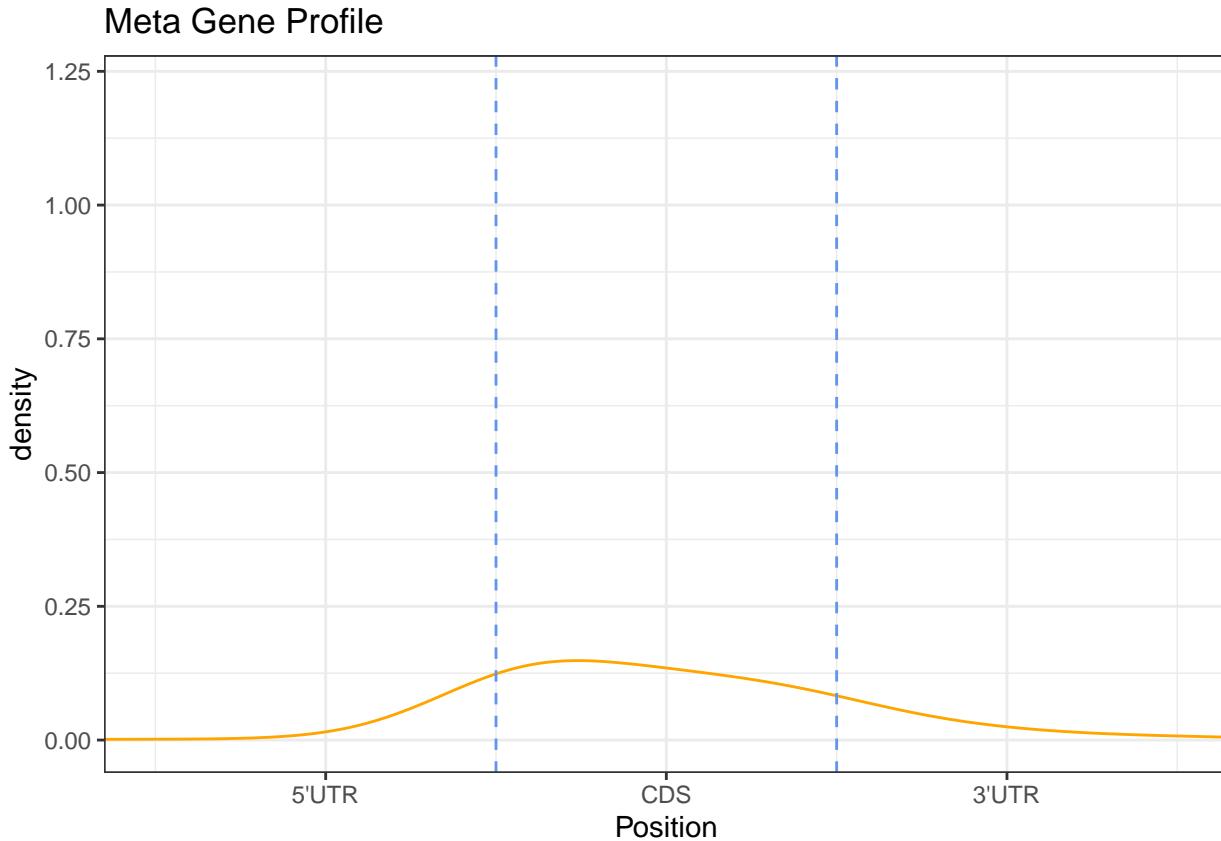
```
metamur
```

```
## $Peaks
## GRanges object with 2701 ranges and 17 metadata columns:
##          seqnames      ranges strand |  swScore  milliDiv
##             <Rle>      <IRanges> <Rle> | <integer> <numeric>
## [1]       chr1 3950995-3951044   - |    249     220
## [2]       chr1 7035216-7035274   - |    270     107
## [3]       chr1 11458214-11458331  - |    564     188
## [4]       chr1 49004231-49004449  - |    255     303
## [5]       chr1 49004708-49004792  - |    281     286
## ...
## ...       ...   ...   ... | ...
## [2697] chrY_JH584301_random 71770-71865  + |    247     302
## [2698] chr3_KZ289066_fix   325612-325675 + |    385     172
## [2699] chr4_KZ289068_fix   110486-110611 + |    259     344
## [2700] chr16_KB469741_fix  436227-436289 + |    236     254
## [2701] chrY_JH792832_fix   347783-347884 + |    295     290
##      milliDel milliIns genoLeft repName repClass repFamily
##      <numeric> <numeric> <integer> <character> <character> <character>
## [1]       0       0 -191520927 MurSatRep1 Unknown  Unknown
## [2]      85      51 -188436697 MurSatRep1 Unknown  Unknown
## [3]      68       8 -184013640 MurSatRep1 Unknown  Unknown
## [4]      91      50 -146467522 MurSatRep1 Unknown  Unknown
## [5]      12      12 -146467179 MurSatRep1 Unknown  Unknown
## ...
## ...       ...   ...   ... | ...
## [2697]     10      0 -188010 MurSatRep1 Unknown  Unknown
## [2698]     0       0 -13559 MurSatRep1 Unknown  Unknown
## [2699]     8       8 -421961 MurSatRep1 Unknown  Unknown
## [2700]     45      0 -69587 MurSatRep1 Unknown  Unknown
## [2701]     10      20 -196305 MurSatRep1 Unknown  Unknown
##      repStart repEnd repLeft id center location
##      <integer> <integer> <integer> <character> <integer> <character>
## [1]     -1395    742    693 MurSatRep1 3951020 NO
## [2]     -1845    292    232 MurSatRep1 7035246 NO
## [3]     -1868    269    145 MurSatRep1 11458273 NO
## [4]      0      2137   1910 MurSatRep1 49004341 NO
## [5]     -1409    728    644 MurSatRep1 49004750 NO
## ...
## ...       ...   ...   ... | ...
## [2697]     627    723   -1414 MurSatRep1 71818 NO
## [2698]     220    283   -1854 MurSatRep1 325644 NO
## [2699]     620    745   -1392 MurSatRep1 110549 NO
## [2700]     201    266   -1871 MurSatRep1 436259 NO
## [2701]     627    727   -1410 MurSatRep1 347834 NO
##      Gene_ID Transcript_ID Position
##      <character> <character> <numeric>
## [1]     Nan      <NA>      5
## [2]     Nan      <NA>      5
## [3]     Nan      <NA>      5
## [4]     Nan      <NA>      5
## [5]     Nan      <NA>      5
## ...
## ...       ...   ...   ...
## [2697]     Nan      <NA>      5
## [2698]     Nan      <NA>      5
## [2699]     Nan      <NA>      5
```

```

## [2700]      Nan      <NA>      5
## [2701]      Nan      <NA>      5
##
## -----
## seqinfo: 239 sequences (1 circular) from mm10 genome
##
## $Plot

```



```

metael

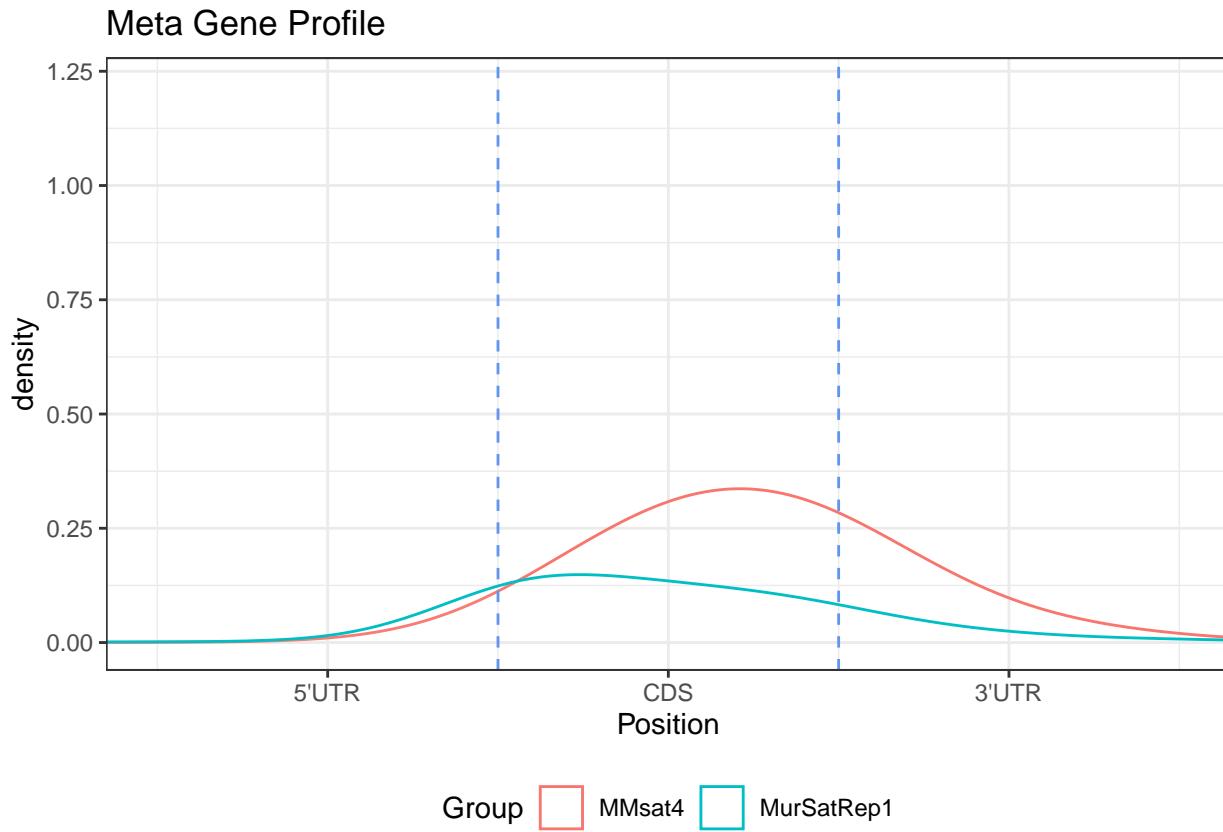
## $Peaks
## GRanges object with 4394 ranges and 17 metadata columns:
##           seqnames      ranges strand |  swScore  milliDiv
##           <Rle>      <IRanges> <Rle> | <integer> <numeric>
## [1]     chr1    49003992-49004114   - |    272    295
## [2]     chr1    49004329-49004605   - |    402    284
## [3]     chr1    82366411-82366554   - |    395    248
## [4]     chr1    86014673-86014899   - |    382    314
## [5]     chr1  117749987-117750291   - |    312    304
## ...
## [4390] chrY_JH584301_random  71770-71865   + |    247    302
## [4391] chr3_KZ289066_fix   325612-325675   + |    385    172
## [4392] chr4_KZ289068_fix   110486-110611   + |    259    344
## [4393] chr16_KB469741_fix  436227-436289   + |    236    254
## [4394] chrY_JH792832_fix  347783-347884   + |    295    290
##     milliDel milliIns  genoLeft   repName   repClass  repFamily
##     <numeric> <numeric> <integer> <character> <character> <character>
## [1]      57        8   -146467857    MMSAT4   Satellite  Satellite

```

```

##      [2]      32      27 -146467366      MMSAT4 Satellite Satellite
##      [3]      42      21 -113105417      MMSAT4 Satellite Satellite
##      [4]      0       0 -109457072      MMSAT4 Satellite Satellite
##      [5]      30      27 -77721680      MMSAT4 Satellite Satellite
##      ...
##      ...      ...      ...      ...      ...      ...
## [4390]     10      0   -188010 MurSatRep1 Unknown Unknown
## [4391]     0       0   -13559 MurSatRep1 Unknown Unknown
## [4392]     8       8  -421961 MurSatRep1 Unknown Unknown
## [4393]    45      0   -69587 MurSatRep1 Unknown Unknown
## [4394]    10     20  -196305 MurSatRep1 Unknown Unknown
##      repStart repEnd repLeft      id center location
##      <integer> <integer> <integer> <character> <integer> <character>
##      [1]     -5     163      35 MMsat4 49004054 NO
##      [2]    -13     278      1 MMsat4 49004467 NO
##      [3]      0     168      22 MMsat4 82366483 NO
##      [4]      0     227      1 MMsat4 86014787 NO
##      [5]      0     305      1 MMsat4 117750139 NO
##      ...
##      ...      ...      ...      ...      ...
## [4390]    627     723   -1414 MurSatRep1 71818 NO
## [4391]    220     283   -1854 MurSatRep1 325644 NO
## [4392]    620     745   -1392 MurSatRep1 110549 NO
## [4393]    201     266   -1871 MurSatRep1 436259 NO
## [4394]    627     727   -1410 MurSatRep1 347834 NO
##      Gene_ID Transcript_ID Position
##      <character> <character> <numeric>
##      [1]     Nan      <NA>      5
##      [2]     Nan      <NA>      5
##      [3]     Nan      <NA>      5
##      [4]     Nan      <NA>      5
##      [5]     Nan      <NA>      5
##      ...
##      ...      ...      ...
## [4390]     Nan      <NA>      5
## [4391]     Nan      <NA>      5
## [4392]     Nan      <NA>      5
## [4393]     Nan      <NA>      5
## [4394]     Nan      <NA>      5
##
## -----
## seqinfo: 239 sequences (1 circular) from mm10 genome
##
## $Plot

```



```
pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/metagene_profile_both.pdf", width=2, height = 2)
metael
```

```
## $Peaks
## GRanges object with 4394 ranges and 17 metadata columns:
##           seqnames      ranges strand |   swScore   milliDiv
##           <Rle>      <IRanges> <Rle> |   <integer> <numeric>
## [1]     chr1    49003992-49004114   - |     272    295
## [2]     chr1    49004329-49004605   - |     402    284
## [3]     chr1    82366411-82366554   - |     395    248
## [4]     chr1    86014673-86014899   - |     382    314
## [5]     chr1  117749987-117750291   - |     312    304
## ...
## ...
## [4390] chrY_JH584301_random    71770-71865   + |     247    302
## [4391] chr3_KZ289066_fix     325612-325675   + |     385    172
## [4392] chr4_KZ289068_fix     110486-110611   + |     259    344
## [4393] chr16_KB469741_fix    436227-436289   + |     236    254
## [4394] chrY_JH792832_fix     347783-347884   + |     295    290
##   milliDel milliIns genoLeft repName repClass repFamily
##   <numeric> <numeric> <integer> <character> <character> <character>
## [1]      57       8 -146467857   MMSAT4 Satellite  Satellite
## [2]      32      27 -146467366   MMSAT4 Satellite  Satellite
## [3]      42      21 -113105417   MMSAT4 Satellite  Satellite
## [4]       0       0 -109457072   MMSAT4 Satellite  Satellite
## [5]      30      27 -77721680   MMSAT4 Satellite  Satellite
## ...
## ...
## [4390]     10       0 -188010 MurSatRep1 Unknown   Unknown
```

```

## [4391]      0      0   -13559 MurSatRep1    Unknown Unknown
## [4392]      8      8   -421961 MurSatRep1    Unknown Unknown
## [4393]     45      0   -69587 MurSatRep1    Unknown Unknown
## [4394]     10     20  -196305 MurSatRep1    Unknown Unknown
##           repStart   repEnd   repLeft      id   center location
## <integer> <integer> <integer> <character> <integer> <character>
## [1]       -5     163      35 MMsat4 49004054      NO
## [2]      -13     278      1 MMsat4 49004467      NO
## [3]       0     168      22 MMsat4 82366483      NO
## [4]       0     227      1 MMsat4 86014787      NO
## [5]       0     305      1 MMsat4 117750139     NO
## ...
## [4390]     ...     ...     ...     ...     ...
## [4391]     220     283   -1854 MurSatRep1 71818      NO
## [4392]     620     745   -1392 MurSatRep1 325644      NO
## [4393]     201     266   -1871 MurSatRep1 436259      NO
## [4394]     627     727   -1410 MurSatRep1 347834      NO
##           Gene_ID Transcript_ID Position
## <character> <character> <numeric>
## [1]      Nan      <NA>      5
## [2]      Nan      <NA>      5
## [3]      Nan      <NA>      5
## [4]      Nan      <NA>      5
## [5]      Nan      <NA>      5
## ...
## [4390]     ...     ...
## [4391]     Nan      <NA>      5
## [4392]     Nan      <NA>      5
## [4393]     Nan      <NA>      5
## [4394]     Nan      <NA>      5
##
## -----
## seqinfo: 239 sequences (1 circular) from mm10 genome
##
## $Plot
dev.off()

## pdf
## 2

```

venn diagram

```

vset <- list(mmsat4frame[!duplicated(mmsat4frame$gene_name), "gene_name"], MurSatRep1frame[!duplicated(MurSatRep1frame$gene_name)], MurSatRep1frame[!duplicated(MurSatRep1frame$gene_name)])
names(vset) <- c("MMSAT4", "MurSatRep1")

vplot <- plot(euler(vset, shape = "ellipse"), quantities = TRUE, main="Genes by contained motifs" , fill=TRUE)

pdf("D:/Krueger_Lab/Publications/miR181_paper/Figure4/Venn_motif.pdf", width=2, height = 2)
vplot
dev.off()

## pdf
## 2

```

Sequence overlap mmsat4 mursatrep1

Just check to make sure these are not the same

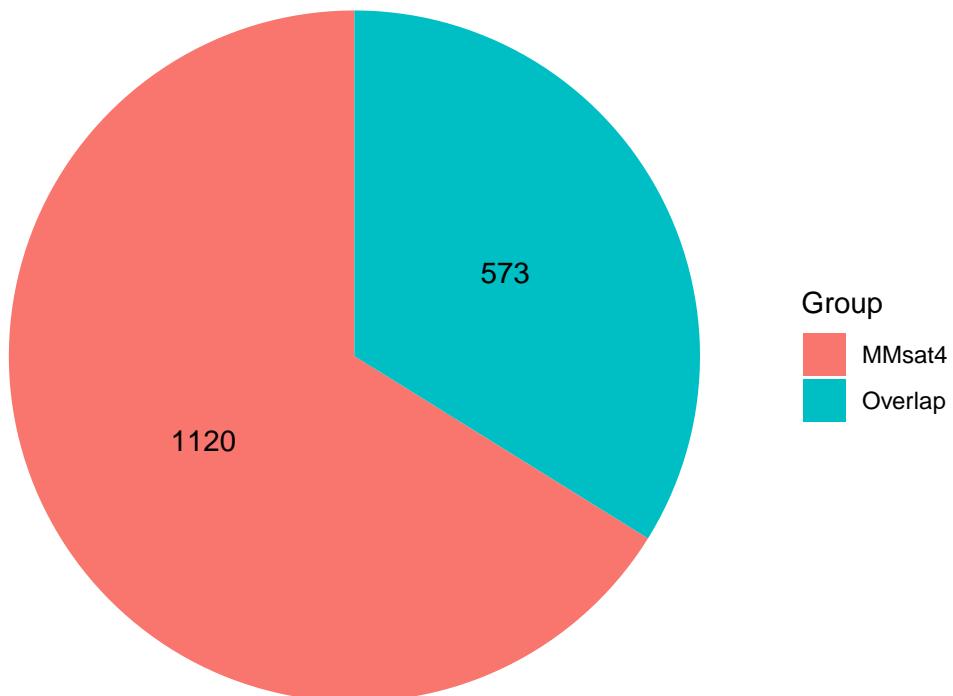
```
olmmsat4 <- subsetByOverlaps(MMSAT4, MurSatRep1)
olmursatrep1 <- subsetByOverlaps(MurSatRep1, MMSAT4)

#make pie charts
pimmsat <- data.frame(c("MMSat4", "Overlap"),
                        c(length(MMSAT4)-length(olmmsat4), length(olmmsat4)))
colnames(pimmsat) <- c("Group", "Count")

pimursatrep1 <- data.frame(c("MurSatRep1", "Overlap"),
                            c(length(MurSatRep1)-length(olmursatrep1), length(olmursatrep1)))
colnames(pimursatrep1) <- c("Group", "Count")

pimmsatP <- ggplot(pimmsat, aes(x="", y=Count, fill=Group)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar("y", start = 0) +
  theme_void() +
  geom_text(aes(label = Count),
            position = position_stack(vjust = 0.5))

pimmsatP
```

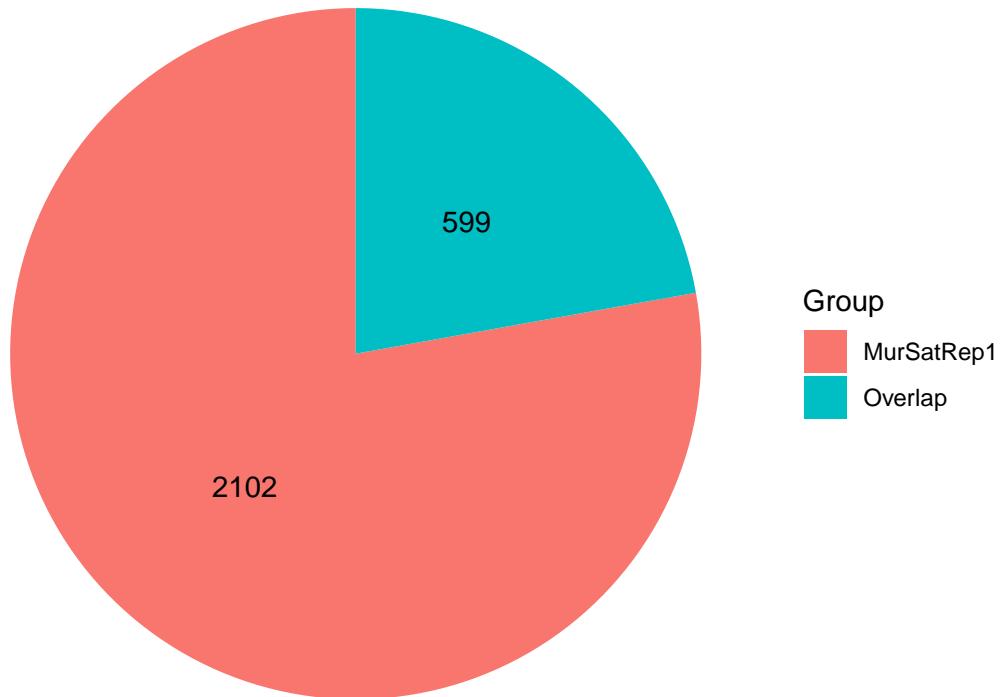


```

pimursatrep1P <- ggplot(pimursatrep1, aes(x="", y=Count, fill=Group)) +
  geom_bar(stat = "identity", width = 1) +
  coord_polar("y", start = 0) +
  theme_void() +
  geom_text(aes(label = Count),
            position = position_stack(vjust = 0.5))

pimursatrep1P

```



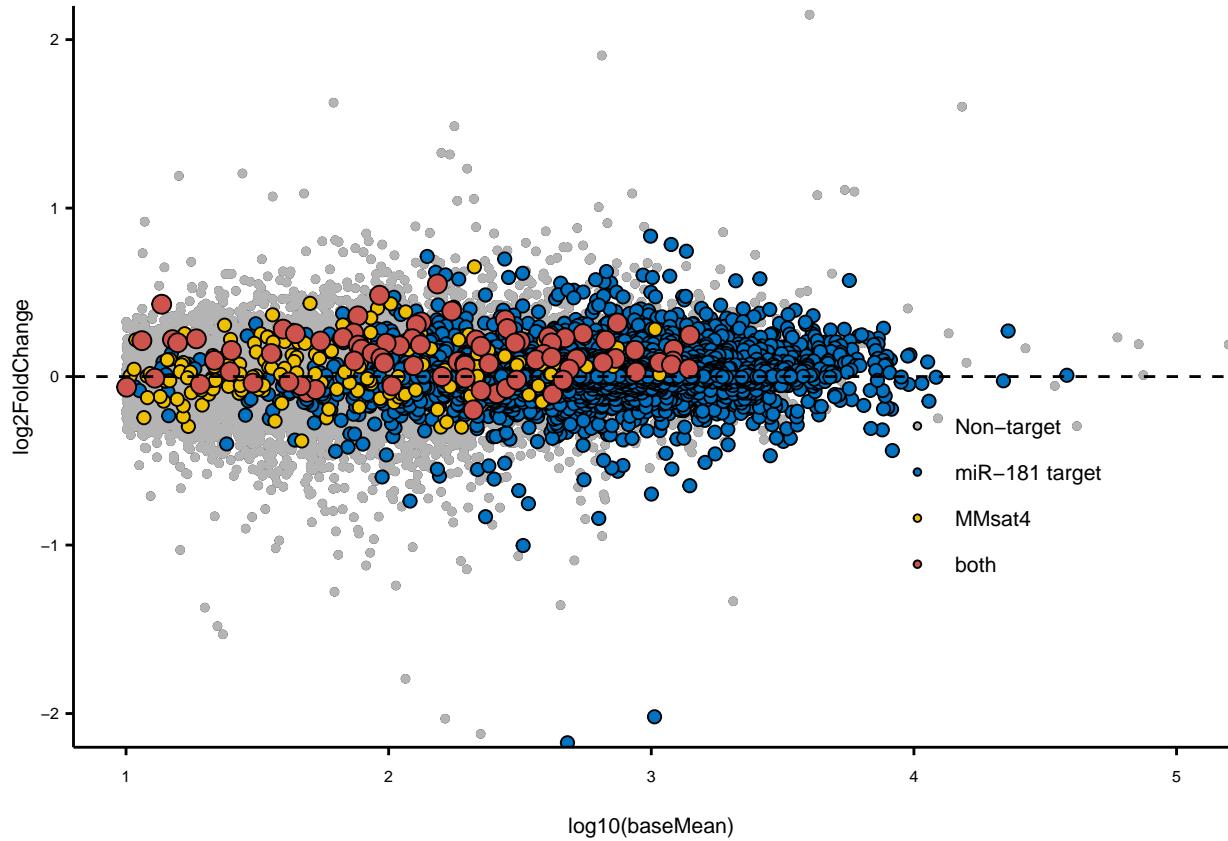
MAplots of targets with satellites

```

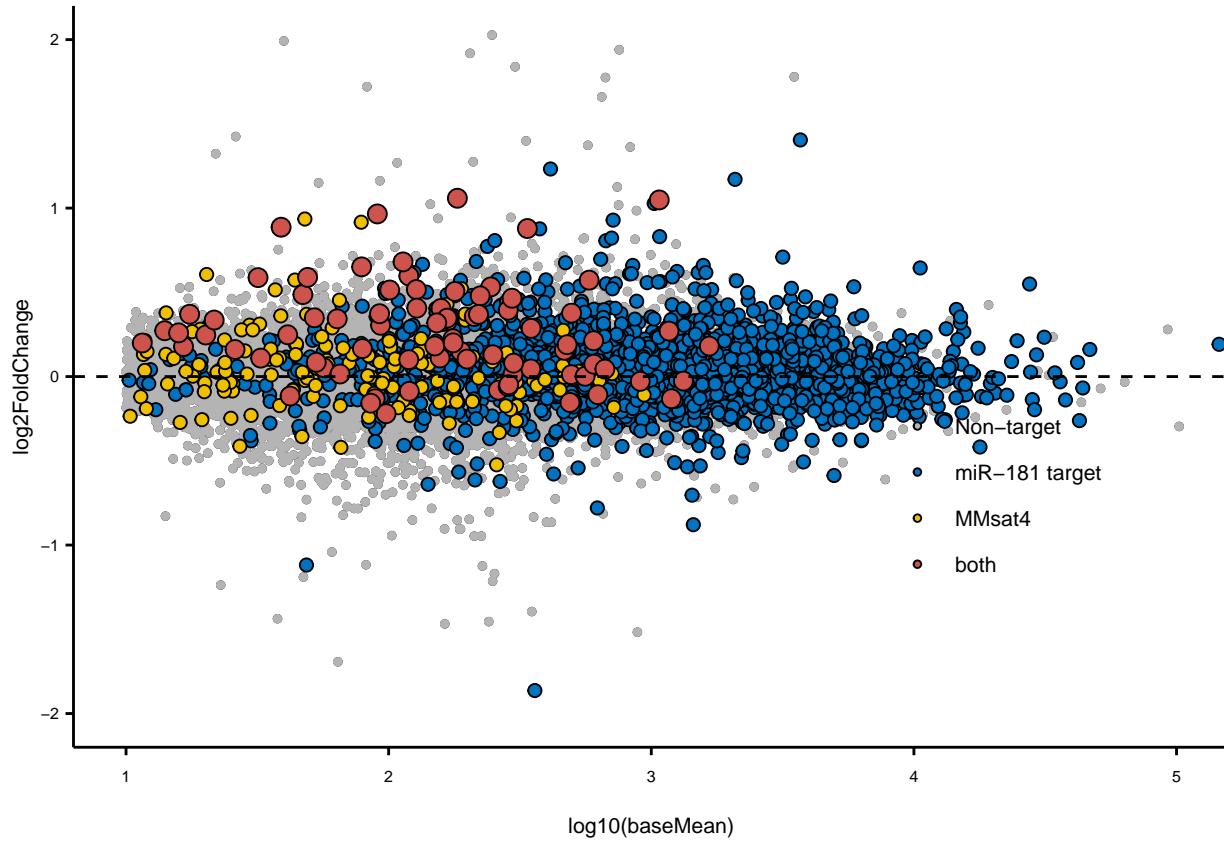
#mmsat4 RNA
MAmmsat4RNA <- ggplot(RNA, aes(x=log10(baseMean), y=log2FoldChange, fill=factor(tvsmmsat4, levels = c("Non-target", "miR-181 target", "MMsat4", "both")))) +
  geom_point(shape=21, size=1) +
  scale_fill_manual(values = c(farbeneg, farbe1, farbe2, farbe3)) +
  geom_point(data = RNA[RNA$tvsmmsat4=="Non-target",], aes(x=log10(baseMean), y=log2FoldChange), shape=21, color="black") +
  geom_point(data = RNA[RNA$tvsmmsat4=="miR-181 target",], aes(x=log10(baseMean), y=log2FoldChange), shape=21, color="red") +
  geom_point(data = RNA[RNA$tvsmmsat4=="MMsat4",], aes(x=log10(baseMean), y=log2FoldChange), shape=21, color="blue") +
  geom_point(data = RNA[RNA$tvsmmsat4=="both",], aes(x=log10(baseMean), y=log2FoldChange), shape=21, color="green") +
  geom_hline(yintercept = 0, linetype="dashed", colour="black")+
  theme_paper() +
  coord_cartesian(ylim = c(-2,2), xlim = c(1,5))

MAmmsat4RNA

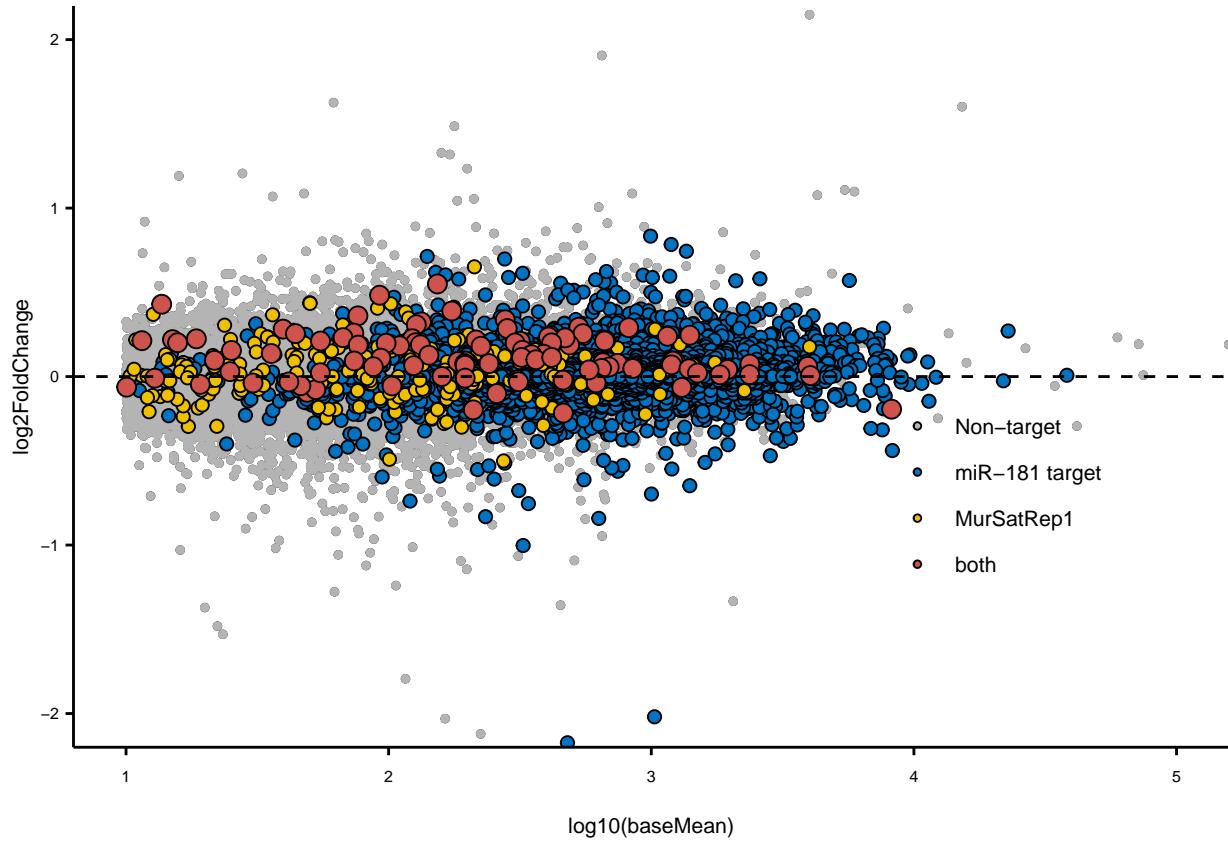
```



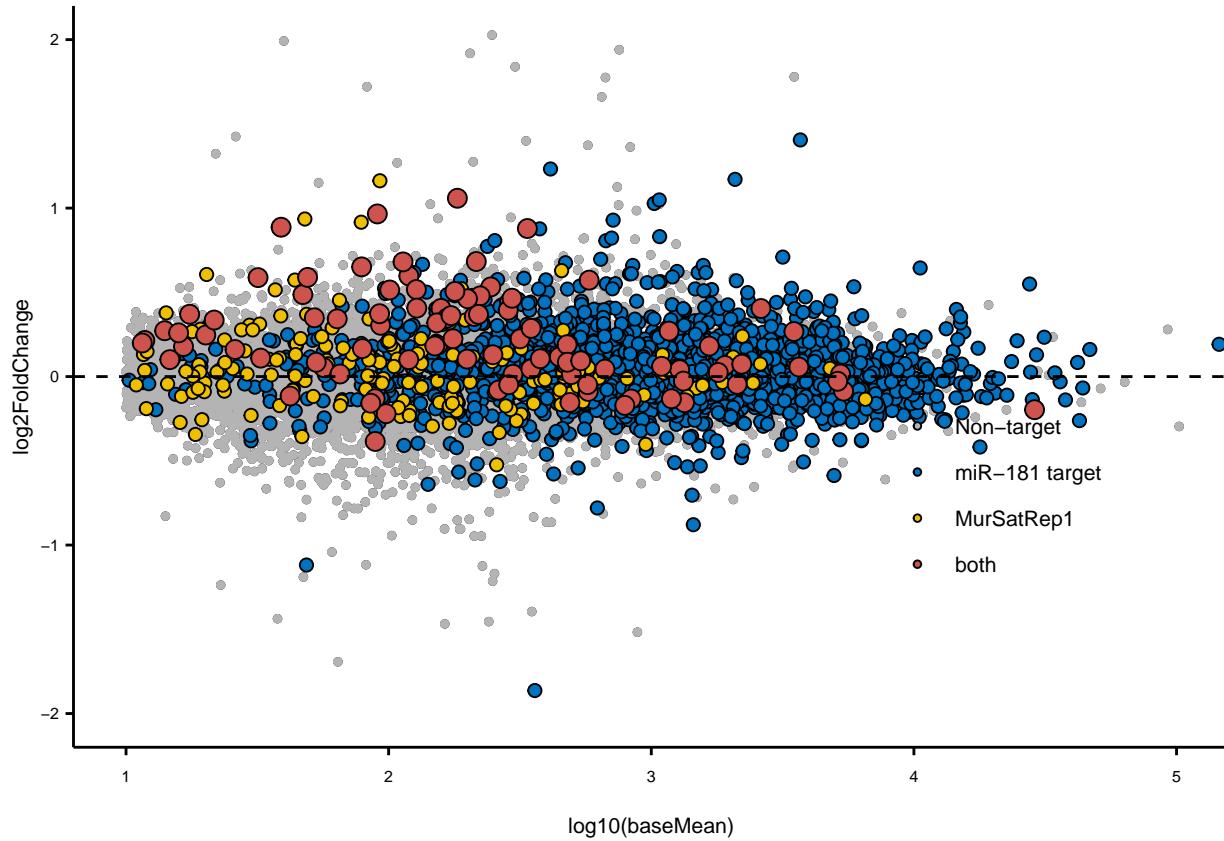
```
##mmsat4 RPF
MAmmsat4RPF <- ggplot(RPF, aes(x=log10(baseMean), y=log2FoldChange, fill=factor(tvsmmsat4, levels = c("Non-target", "miR-181 target", "MMsat4", "both")))) +
  geom_point(shape=21, size=1) +
  scale_fill_manual(values = c(farbeneg, farbe1, farbe2, farbe3)) +
  geom_point(data = RPF[RPF$tvsmmsat4=="Non-target",], aes(x=log10(baseMean), y=log2FoldChange), shape=21, colour="black") +
  geom_point(data = RPF[RPF$tvsmmsat4=="miR-181 target",], aes(x=log10(baseMean), y=log2FoldChange), shape=21, colour="blue") +
  geom_point(data = RPF[RPF$tvsmmsat4=="MMsat4"], aes(x=log10(baseMean), y=log2FoldChange), shape=21, colour="yellow") +
  geom_point(data = RPF[RPF$tvsmmsat4=="both"], aes(x=log10(baseMean), y=log2FoldChange), shape=21, colour="red") +
  geom_hline(yintercept = 0, linetype="dashed", colour="black") +
  theme_paper() +
  coord_cartesian(ylim = c(-2,2), xlim = c(1,5))
MAmmsat4RPF
```



```
#Mursatrep1 RNA
MAmursatrep1RNA <- ggplot(RNA, aes(x=log10(baseMean), y=log2FoldChange, fill=factor(tvsMurSatRep1, levels=c("Non-target", "miR-181 target", "MMSat4", "both")))) +
  geom_point(shape=21, size=1) +
  scale_fill_manual(values = c(farbeneg, farbe1, farbe2, farbe3)) +
  geom_point(data = RNA[RNA$tvsmurSatRep1=="Non-target",], aes(x=log10(baseMean), y=log2FoldChange), shape=21) +
  geom_point(data = RNA[RNA$tvsmurSatRep1=="miR-181 target",], aes(x=log10(baseMean), y=log2FoldChange), shape=21) +
  geom_point(data = RNA[RNA$tvsmurSatRep1=="MMSatRep1",], aes(x=log10(baseMean), y=log2FoldChange), shape=21) +
  geom_point(data = RNA[RNA$tvsmurSatRep1=="both",], aes(x=log10(baseMean), y=log2FoldChange), shape=21) +
  geom_hline(yintercept = 0, linetype="dashed", colour="black") +
  theme_paper() +
  coord_cartesian(ylim = c(-2,2), xlim = c(1,5))
MAmursatrep1RNA
```



```
#Mursatrep1 RPF
MAmursatrep1RPF <- ggplot(RPF, aes(x=log10(baseMean), y=log2FoldChange, fill=factor(tvsMurSatRep1, levels=c("Non-target", "miR-181 target", "MurSatRep1", "both")))) +
  geom_point(shape=21, size=1) +
  scale_fill_manual(values = c(farbeneg, farbe1, farbe2, farbe3)) +
  geom_point(data = RPF[RPF$tvsmurSatRep1=="Non-target",], aes(x=log10(baseMean), y=log2FoldChange), shape=21) +
  geom_point(data = RPF[RPF$tvsmurSatRep1=="miR-181 target",], aes(x=log10(baseMean), y=log2FoldChange), shape=21) +
  geom_point(data = RPF[RPF$tvsmurSatRep1=="MurSatRep1",], aes(x=log10(baseMean), y=log2FoldChange), shape=21) +
  geom_point(data = RPF[RPF$tvsmurSatRep1=="both",], aes(x=log10(baseMean), y=log2FoldChange), shape=21) +
  geom_hline(yintercept = 0, linetype="dashed", colour="black") +
  theme_paper() +
  coord_cartesian(ylim = c(-2,2), xlim = c(1,5))
MAmursatrep1RPF
```



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 19045)
##
## 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] stats4      stats       graphics    grDevices   utils       datasets   methods
## [8] base
##
## other attached packages:
## [1] readxl_1.4.2        eulerr_7.0.0          cowplot_1.1.1
## [4] cliProfiler_1.4.0    Rtsne_0.16            tibble_3.2.1
## [7] dplyr_1.1.2         rtracklayer_1.58.0   GenomicRanges_1.50.2
## [10] GenomeInfoDb_1.34.9  IRanges_2.32.0        S4Vectors_0.36.2
## [13] BiocGenerics_0.44.0  ggpplot2_3.4.2
```

```

##
## loaded via a namespace (and not attached):
## [1] MatrixGenerics_1.10.0      Biobase_2.58.0
## [3] tidyR_1.3.0                carData_3.0-5
## [5] highr_0.10                 BSgenome_1.66.3
## [7] GenomeInfoDbData_1.2.9    cellranger_1.1.0
## [9] Rsamtools_2.14.0           yaml_2.3.7
## [11] pillar_1.9.0               backports_1.4.1
## [13] lattice_0.20-45          glue_1.6.2
## [15] digest_0.6.31             polyclip_1.10-4
## [17] XVector_0.38.0            ggsignif_0.6.4
## [19] colorspace_2.1-0          htmltools_0.5.4
## [21] Matrix_1.5-3              XML_3.99-0.14
## [23] pkgconfig_2.0.3           broom_1.0.4
## [25] zlibbioc_1.44.0           purrr_1.0.1
## [27] scales_1.2.1              BiocParallel_1.32.6
## [29] generics_0.1.3             farver_2.1.1
## [31] car_3.1-2                 ggpubr_0.6.0
## [33] withr_2.5.0               SummarizedExperiment_1.28.0
## [35] cli_3.6.0                 magrittr_2.0.3
## [37] crayon_1.5.2              evaluate_0.21
## [39] fansi_1.0.4                rstatix_0.7.2
## [41] tools_4.2.3                BiocIO_1.8.0
## [43] lifecycle_1.0.3            matrixStats_0.63.0
## [45] munsell_0.5.0              DelayedArray_0.23.2
## [47] Biostrings_2.66.0          compiler_4.2.3
## [49] rlang_1.1.0                grid_4.2.3
## [51] RCurl_1.98-1.12           rstudioapi_0.14
## [53] rjson_0.2.21               bitops_1.0-7
## [55] labeling_0.4.2             rmarkdown_2.22
## [57] restfulr_0.0.15            gtable_0.3.3
## [59] codetools_0.2-19           abind_1.4-5
## [61] R6_2.5.1                  GenomicAlignments_1.34.1
## [63] knitr_1.43                 fastmap_1.1.1
## [65] utf8_1.2.3                 polylabelr_0.2.0
## [67] parallel_4.2.3              Rcpp_1.0.10
## [69] vctrs_0.6.2                tidyselect_1.2.0
## [71] xfun_0.39

```