

find_MMsat4

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Setup

```
setwd("D:/Krueger_Lab/Publications/miR181_paper/Figure2/MMsat4")
```

packages

```
library(AnnotationHub)
```

```
## 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: BiocFileCache
```

```
## Loading required package: dbplyr
```

```
library(dplyr)
```

```
##
```

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

```
## The following objects are masked from 'package:dbplyr':
```

```
##
```

```
##      ident, sql
```

```
## 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(ggplot2)
library(ggpubr)
library(rtracklayer)

## Loading required package: GenomicRanges
## Loading required package: stats4
## Loading required package: S4Vectors
##
## Attaching package: 'S4Vectors'
## The following objects are masked from 'package:dplyr':
##
## first, rename
## The following objects are masked from 'package:base':
##
## expand.grid, I, unname
## Loading required package: IRanges
##
## Attaching package: 'IRanges'
## The following objects are masked from 'package:dplyr':
##
## collapse, desc, slice
## The following object is masked from 'package:grDevices':
##
## windows
## Loading required package: GenomeInfoDb
##
## Attaching package: 'rtracklayer'
## The following object is masked from 'package:AnnotationHub':
##
## hubUrl
```

data

```
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")

#target data
tject <- readRDS("D:/Krueger_Lab/Publications/miR181_paper/Figure1/mir181_binding_sites__venn_types/mir181_binding_sites__venn_types.rds")
names(tject) <- 1:length(tject$geneName)
tframe <- as.data.frame(tject)
head(tframe)
```

##	seqnames	start	end	width	strand	scoreSum	scoreMean	scoreMax
## 1	chr1	6245651	6245657	7	+	9.52553	4.762765	6.00678
## 2	chr1	6248341	6248347	7	+	92.68921	23.172303	48.76900
## 3	chr1	6248857	6248863	7	+	14.07133	7.035665	7.04425
## 4	chr1	6248918	6248924	7	+	38.91451	12.971503	20.65080
## 5	chr1	7170481	7170487	7	+	66.92218	13.384436	25.84490
## 6	chr1	9899605	9899611	7	+	25.15963	6.289907	8.61019
##	geneType	geneName	geneID	region	BS_ID	mir_IP		
## 1	protein_coding	Rb1cc1	ENSMUSG00000025907	cds	5	mmu-miR-181a-5p		
## 2	protein_coding	Rb1cc1	ENSMUSG00000025907	cds	8	mmu-miR-181a-5p		
## 3	protein_coding	Rb1cc1	ENSMUSG00000025907	cds	10	mmu-miR-181a-5p		
## 4	protein_coding	Rb1cc1	ENSMUSG00000025907	cds	11	mmu-miR-181a-5p		
## 5	protein_coding	Pcmdt1	ENSMUSG00000051285	utr3	19	mmu-miR-181a-5p		
## 6	protein_coding	Sgk3	ENSMUSG00000025915	utr3	23	mmu-miR-181a-5p		
##	n_mir181	n_mir181a	n_mir181b	n_mir181c	n_mir181d	set	WT	KO
## 1	1	1	0	0	0	ago_bs_mir181_chi	1	1
## 2	5	5	0	0	0	ago_bs_mir181_chi	1	1
## 3	6	6	0	0	0	ago_bs_mir181_chi	1	0
## 4	6	6	0	0	0	ago_bs_mir181_chi	1	1
## 5	4	4	0	0	0	ago_bs_mir181_chi	1	1
## 6	1	1	0	0	0	ago_bs_mir181_chi	NA	NA
##	geneID.2	geneName.1	region.1	counts.bs.1_KO	counts.bs.2_KO			
## 1	ENSMUSG00000025907	Rb1cc1	cds	4	3			
## 2	ENSMUSG00000025907	Rb1cc1	cds	28	32			
## 3	ENSMUSG00000025907	Rb1cc1	cds	13	11			
## 4	ENSMUSG00000025907	Rb1cc1	cds	15	15			
## 5	ENSMUSG00000051285	Pcmdt1	utr3	12	22			
## 6	<NA>	<NA>	<NA>	NA	NA			
##	counts.bs.3_KO	counts.bs.4_WT	counts.bs.5_WT	counts.bs.6_WT				
## 1	3	3	10	3				
## 2	27	46	41	20				
## 3	4	22	13	12				
## 4	10	33	20	18				
## 5	14	16	20	9				
## 6	NA	NA	NA	NA				
##	geneID.1	counts.bg.1_KO	counts.bg.2_KO	counts.bg.3_KO				
## 1	ENSMUSG00000025907	1609	1973	1250				
## 2	ENSMUSG00000025907	1609	1973	1250				
## 3	ENSMUSG00000025907	1609	1973	1250				
## 4	ENSMUSG00000025907	1609	1973	1250				
## 5	ENSMUSG00000051285	1355	1706	1064				
## 6	<NA>	NA	NA	NA				
##	counts.bg.4_WT	counts.bg.5_WT	counts.bg.6_WT	resBs.baseMean				
## 1	2638	2231	1352	92.10645				
## 2	2638	2231	1352	281.53271				
## 3	2638	2231	1352	145.51107				
## 4	2638	2231	1352	186.74162				
## 5	1654	1348	755	151.36245				
## 6	NA	NA	NA	NA				
##	resBs.log2FoldChange	resBs.lfcSE	resBs.stat	resBs.pvalue	resBs.padj			
## 1	-0.1093039	0.5923673	0.03419066	0.8533018	0.9652601			
## 2	0.2749428	0.2351157	1.35874137	0.2437557	0.6729889			
## 3	-0.1805519	0.3623758	0.25017050	0.6169550	0.8961239			
## 4	-0.2606282	0.3062717	0.73169661	0.3923338	0.7868678			

```

## 5          0.1466485    0.3122905 0.22052922    0.6386370 0.9013566
## 6          NA          NA          NA          NA          NA
##   resBg.baseMean resBg.log2FoldChange resBg.lfcSE resBg.stat resBg.pvalue
## 1          NA          NA          NA          NA          NA
## 2          NA          NA          NA          NA          NA
## 3          NA          NA          NA          NA          NA
## 4          NA          NA          NA          NA          NA
## 5          NA          NA          NA          NA          NA
## 6          NA          NA          NA          NA          NA
##   resBg.padj tpm.counts.bg.1_KO tpm.counts.bg.2_KO tpm.counts.bg.3_KO
## 1          NA          133.7259          117.9980          129.8669
## 2          NA          133.7259          117.9980          129.8669
## 3          NA          133.7259          117.9980          129.8669
## 4          NA          133.7259          117.9980          129.8669
## 5          NA          248.6210          225.2505          244.0445
## 6          NA          NA          NA          NA
##   tpm.counts.bg.4_WT tpm.counts.bg.5_WT tpm.counts.bg.6_WT
## 1          139.8635          146.2855          163.5360
## 2          139.8635          146.2855          163.5360
## 3          139.8635          146.2855          163.5360
## 4          139.8635          146.2855          163.5360
## 5          193.5994          195.1330          201.6149
## 6          NA          NA          NA
##   BS_ID.1 tpm_support_KO tpm_support_WT tpm_supported down
## 1 ENSMUSG00000025907.bs5          3          3          TRUE FALSE
## 2 ENSMUSG00000025907.bs8          3          3          TRUE FALSE
## 3 ENSMUSG00000025907.bs10         3          3          TRUE FALSE
## 4 ENSMUSG00000025907.bs11         3          3          TRUE FALSE
## 5 ENSMUSG00000051285.bs4          3          3          TRUE FALSE
## 6          <NA>          NA          NA          NA    NA

```

#colours

```

farbeneg <- "#b4b4b4"
farbe1 <- "#0073C2FF"
farbe2 <- "#EFC000FF"
farbe3 <- "#CD534CFF"
farbe4 <- "#7AA6DCFF"
farbe5 <- "#868686FF"
farbe6 <- "#003C67FF"
farbe7 <- "#8F7700FF"
farbe8 <- "#3B3B3BFF"
farbe9 <- "#A73030FF"
farbe10 <- "#4A6990FF"
farbe11 <- "#FF6F00FF"
farbe12 <- "#C71000FF"
farbe13 <- "#008EA0FF"
farbe14 <- "#8A4198FF"
farbe15 <- "#5A9599FF"
farbe16 <- "#FF6348FF"

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

```

Get annotation

```
# ah = AnnotationHub()
# query(ah, c("RepeatMasker", "Mus musculus"))
# repeat_masker <- ah[["AH99012"]]

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

## GRanges object with 1693 ranges and 11 metadata columns:
##
##           seqnames           ranges strand |   swScore   milliDiv
##           <Rle>           <IRanges> <Rle> | <integer> <numeric>
##      [1]         chr1    75624925-75625061   + |       347       293
##      [2]         chr1    75625261-75625377   + |       228       292
##      [3]         chr1    75625502-75625561   + |       257       233
##      [4]         chr1 116745797-116745936   + |       357       314
##      [5]         chr1 116745987-116746488   + |       600       228
##      ...         ...         ...         ... |       ...       ...
## [1689] chr9_KB469738_fix      24254-24454   - |       304       289
## [1690] chr9_KB469738_fix      24588-24803   - |       440       281
## [1691] chr9_KB469738_fix      25005-25142   - |       399       270
## [1692] chr9_KB469738_fix      25257-25488   - |       389       275
## [1693] chrY_JH792832_fix      349767-349817   + |       230       180
##
##           milliDel   milliIns   genoLeft   repName   repClass   repFamily
##           <numeric> <numeric> <integer> <character> <character> <character>
##      [1]          29          29 -119846910   MMSAT4   Satellite   Satellite
##      [2]          34          34 -119846594   MMSAT4   Satellite   Satellite
##      [3]           0           0 -119846410   MMSAT4   Satellite   Satellite
##      [4]           7           0 -78726035   MMSAT4   Satellite   Satellite
##      [5]          48          22 -78725483   MMSAT4   Satellite   Satellite
##      ...         ...         ...         ...         ...         ...
## [1689]          24          16 -186187   MMSAT4   Satellite   Satellite
## [1690]           0           0 -185838   MMSAT4   Satellite   Satellite
## [1691]           7           7 -185499   MMSAT4   Satellite   Satellite
## [1692]          21          21 -185153   MMSAT4   Satellite   Satellite
## [1693]           0          20 -194372   MMSAT4   Satellite   Satellite
##
##           repStart   repEnd   repLeft
##           <integer> <integer> <integer>
##      [1]          32         168         0
##      [2]          32         148        -20
##      [3]          31          90        -78
##      [4]          27         167         -1
##      [5]           1         514         0
##      ...         ...         ...         ...
## [1689]           0         202          1
## [1690]           0         216          1
## [1691]           0         168         31
## [1692]           0         232          1
## [1693]         115         164         -4
## -----
## seqinfo: 239 sequences (1 circular) from mm10 genome
```

find overlaps

```
# same strand
MMSAT4 <- repeat_masker[repeat_masker$repName == "MMSAT4"]

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

# opposite strand
antiMMSAT4 <- MMSAT4
strand(antiMMSAT4) <- ifelse(strand(MMSAT4) == '+', '-', '+')

antiOLgenes <- as.data.frame(subsetByOverlaps(gff23, antiMMSAT4))

dim(OLgenes)

## [1] 3806 28
dim(antiOLgenes)

## [1] 140 28
RNA$MMSat4 <- "No_MMsat4"
RNA$MMSat4[RNA$gene_symbol %in% OLgenes$gene_name] <- "MMsat4"
RNA$MMSat4[RNA$gene_symbol %in% antiOLgenes$gene_name] <- "anti-MMsat4"
table(RNA$MMSat4)

##
## anti-MMsat4      MMsat4   No_MMsat4
##           12         238       13051

RPF$MMSat4 <- "No_MMsat4"
RPF$MMSat4[RPF$gene_symbol %in% OLgenes$gene_name] <- "MMsat4"
RPF$MMSat4[RPF$gene_symbol %in% antiOLgenes$gene_name] <- "anti-MMsat4"
table(RPF$MMSat4)

##
## anti-MMsat4      MMsat4   No_MMsat4
##           12         225       11132
```

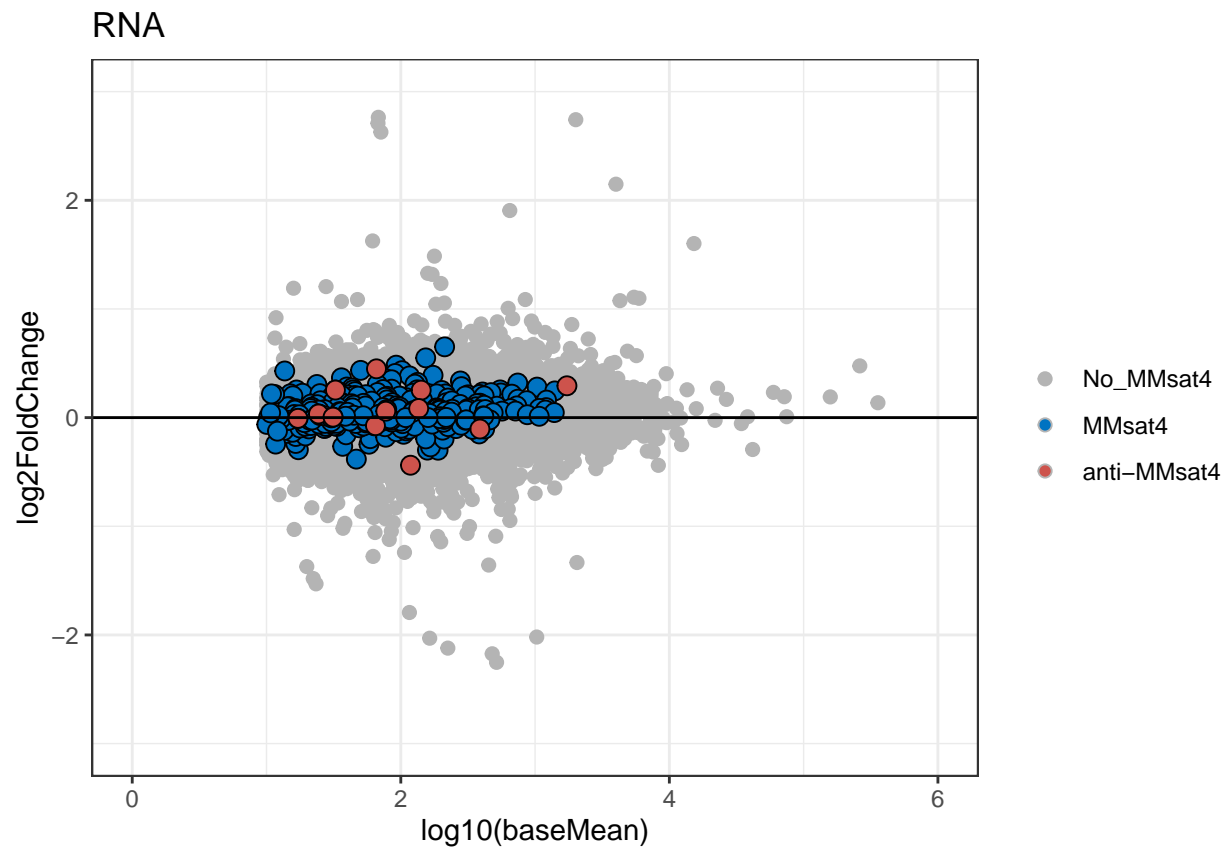
plot into MA plots

```
#RNA
RNAMA <- ggplot(RNA, aes(x=log10(baseMean), y=log2FoldChange, fill=factor(MMsat4, levels = c("No_MMsat4", "MMsat4", "anti-MMsat4")))) +
  geom_point(shape=21, size=2, colour=farbeneg) +
  scale_fill_manual(values = c(farbeneg, farbe1, farbe3)) +
  coord_cartesian(ylim = c(-3,3), xlim = c(0,6)) +
  geom_point(data=RNA[RNA$gene_symbol %in% OLgenes$gene_name,], aes(x=log10(baseMean), y=log2FoldChange)) +
  geom_point(data=RNA[RNA$gene_symbol %in% antiOLgenes$gene_name,], aes(x=log10(baseMean), y=log2FoldChange)) +
  geom_hline(yintercept = 0, colour= "black") +
  theme_bw() +
  theme(legend.title = element_blank()) +
  ggtitle("RNA")

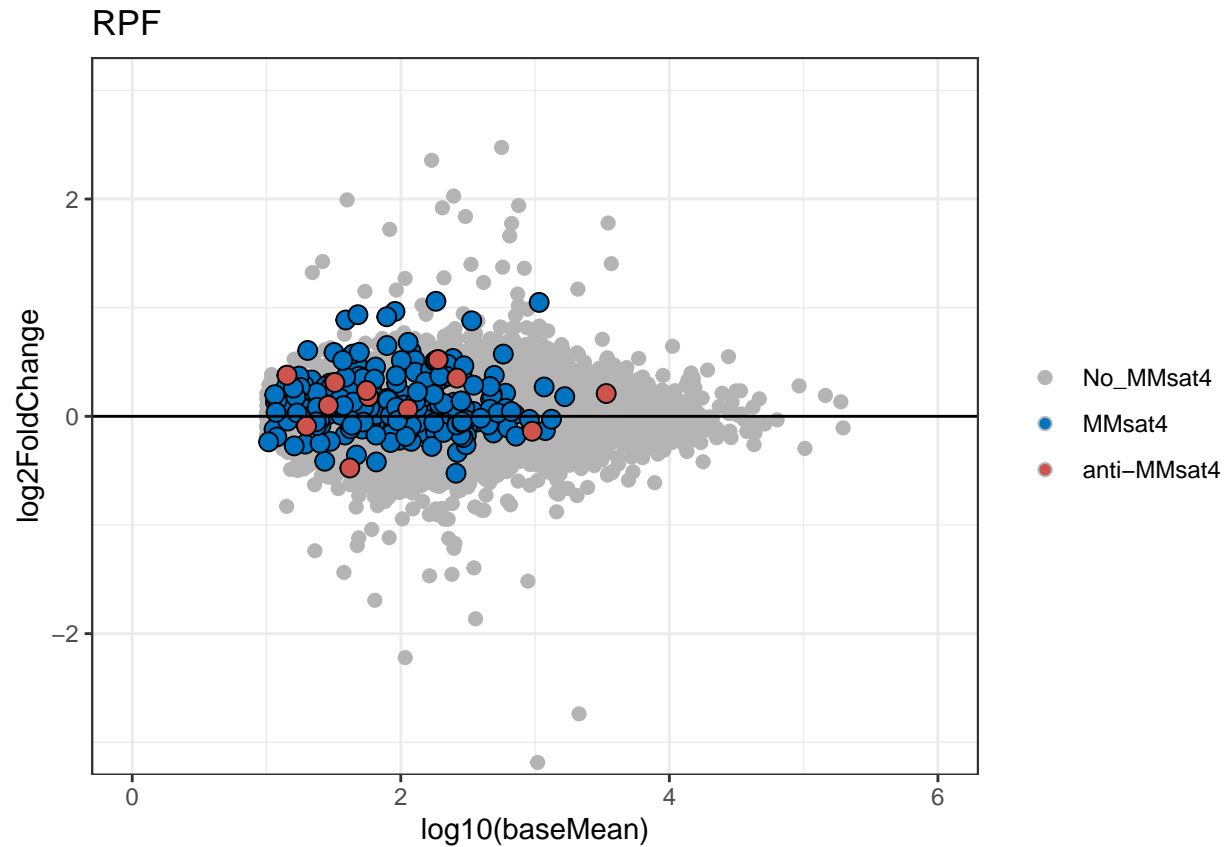
#RPF
```

```
RPFMA <- ggplot(RPF, aes(x=log10(baseMean), y=log2FoldChange, fill=factor(MMsat4, levels = c("No_MMsat4", "MMsat4", "anti-MMsat4")), shape=21, size=2, colour=farbeneg) +
  scale_fill_manual(values = c(farbeneg, farbe1, farbe3))+
  coord_cartesian(ylim = c(-3,3), xlim = c(0,6))+
  geom_point(data=RPF[RPF$gene_symbol %in% OLgenes$gene_name,], aes(x=log10(baseMean), y=log2FoldChange), fill="black", colour="black")+
  geom_point(data=RPF[RPF$gene_symbol %in% antiOLgenes$gene_name,], aes(x=log10(baseMean), y=log2FoldChange), fill="black", colour="black")+
  geom_hline(yintercept = 0, colour= "black") +
  theme_bw() +
  theme(legend.title = element_blank()) +
  ggtitle("RPF")
```

RNAMA



RPFMA

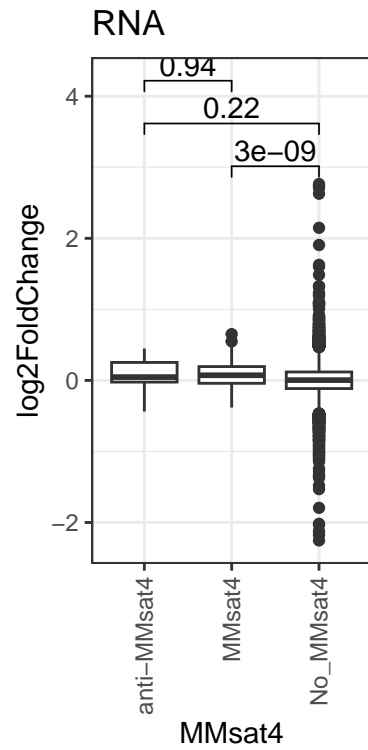


```
my_comparisons <- list( c("No_MMsat4", "MMsat4"), c("No_MMsat4", "anti-MMsat4"), c("MMsat4", "anti-MMsat4") )
```

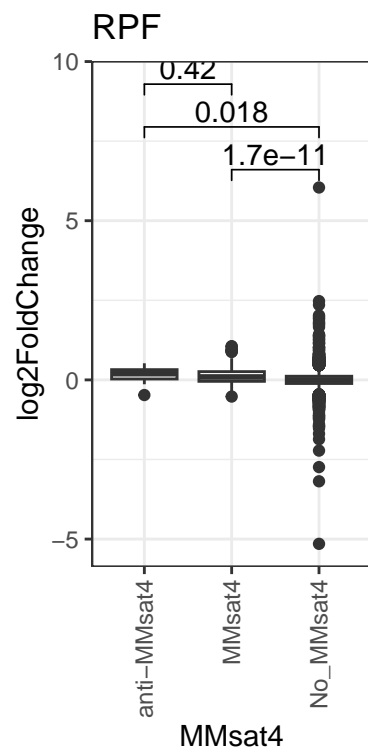
```
RNAbox <- ggplot(RNA, aes(x=MMsat4, y=log2FoldChange)) +
  geom_boxplot() +
  stat_compare_means(comparisons = my_comparisons) +
  theme_bw() +
  theme(axis.text.x = element_text(angle = 90, hjust = 1, vjust = 0.5)) +
  ggtitle("RNA")
```

```
RPFbox <- ggplot(RPF, aes(x=MMsat4, y=log2FoldChange)) +
  geom_boxplot() +
  stat_compare_means(comparisons = my_comparisons) +
  theme_bw() +
  theme(axis.text.x = element_text(angle = 90, hjust = 1, vjust = 0.5)) +
  ggtitle("RPF")
```

RNAbox



RPFbox



ecdf plot with targets vs MMsat4

#RNA

```
RNA$tvsmmsat4 <- "Non-target"
RNA$tvsmmsat4[RNA$gene_symbol %in% OLgenes$gene_name] <- "MMsat4"
RNA$tvsmmsat4[RNA$gene_symbol %in% tframe$geneName] <- "miR-181 target"
RNA$tvsmmsat4[RNA$gene_symbol %in% tframe$geneName & RNA$gene_symbol %in% OLgenes$gene_name] <- "both"
table(RNA$tvsmmsat4)
```

##

##	both	miR-181 target	MMsat4	Non-target
##	103	3441	141	9616

#RPF

```
RPF$tvsmmsat4 <- "Non-target"
RPF$tvsmmsat4[RPF$gene_symbol %in% OLgenes$gene_name] <- "MMsat4"
RPF$tvsmmsat4[RPF$gene_symbol %in% tframe$geneName] <- "miR-181 target"
RPF$tvsmmsat4[RPF$gene_symbol %in% tframe$geneName & RPF$gene_symbol %in% OLgenes$gene_name] <- "both"
table(RPF$tvsmmsat4)
```

##

##	both	miR-181 target	MMsat4	Non-target
##	100	3405	131	7733

#RNA

```
tolECDFRNA <- ggplot(RNA, aes(as.numeric(log2FoldChange), colour=factor(tvsmmsat4, levels = c("Non-target", "MMsat4", "miR-181 target", "both")))) +
  stat_ecdf(geom="step", size=1) +
  scale_colour_manual(values = c("black", farbe1, farbe3, RPFncol)) +
  coord_cartesian(xlim = c(-0.75, 0.75)) + theme_bw() +
  theme(legend.position = c(0.8, 0.35), legend.title = element_blank(),
        legend.background = element_rect(colour = "transparent", fill="transparent"),
        axis.title=element_text(size=16), plot.title = element_text(size=16, face = "bold")) +
  ggtitle("RNA")
```

Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.

i Please use `linewidth` instead.

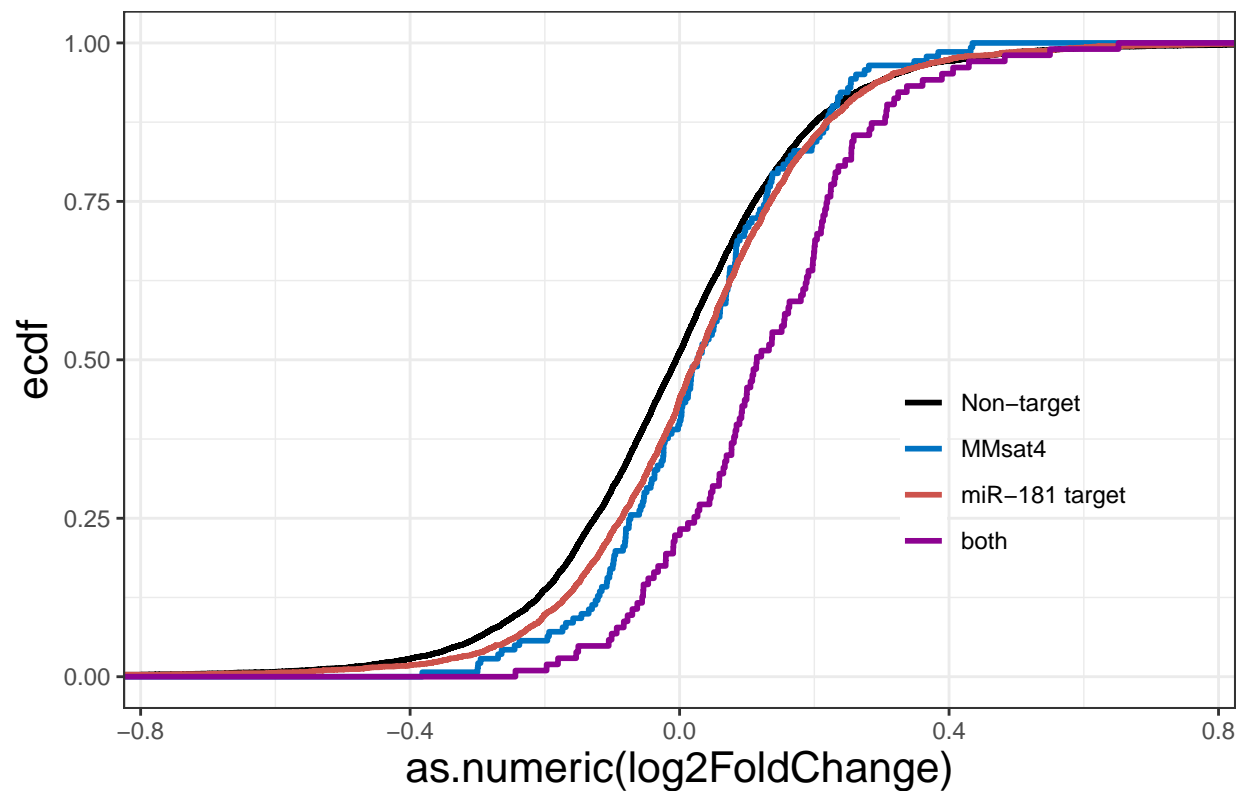
This warning is displayed once every 8 hours.

Call `lifecycle::last_lifecycle_warnings()` to see where this warning was

generated.

tolECDFRNA

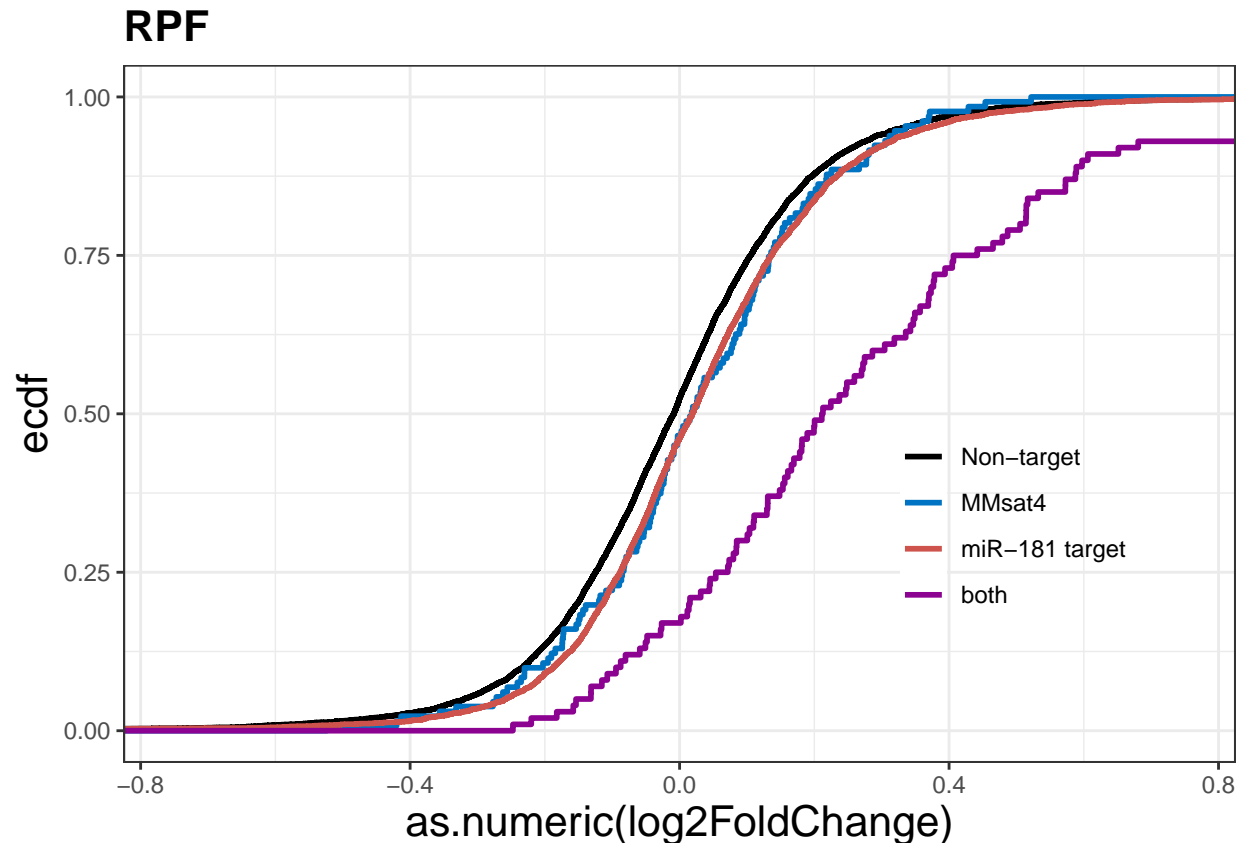
RNA



#RPF

```
tolECDFRPF <- ggplot(RPF, aes(as.numeric(log2FoldChange), colour=factor(tvsmmsat4, levels = c("Non-target", "MMsat4", "miR-181 target", "both")))) +
  stat_ecdf(geom="step", size=1) +
  scale_colour_manual(values = c("black", "blue", "red", "purple")) +
  coord_cartesian(xlim = c(-0.75, 0.75)) + theme_bw() +
  theme(legend.position = c(0.8, 0.35), legend.title = element_blank(),
        legend.background = element_rect(colour = "transparent", fill="transparent"),
        axis.title=element_text(size=16), plot.title = element_text(size=16, face = "bold")) +
  ggtitle("RPF")
```

tolECDFRPF



split by region

3'UTR and CDS

Here we took all targets (genes) that also contain a MMsat4 element and split them by 3'UTR or UTR. The location of the MMsat4 within the gene is not considered in this analysis.

```
rframe <- tframe[tframe$geneName %in% OLgenes$gene_name,]

#RNA
RNA$regMMsat4 <- "Non-target"
RNA$regMMsat4[RNA$gene_symbol %in% rframe[rframe$region == "cds","geneName"]] <- "cds"
RNA$regMMsat4[RNA$gene_symbol %in% rframe[rframe$region == "utr3","geneName"]] <- "utr3"
RNA$regMMsat4[RNA$gene_symbol %in% rframe[rframe$region == "utr3","geneName"] &
  RNA$gene_symbol %in% rframe[rframe$region == "cds","geneName"]] <- "both"

table(RNA$regMMsat4)
```

```
##
##      both      cds Non-target      utr3
##      159       51      13069       22
```

```
#RPF
RPF$regMMsat4 <- "Non-target"
RPF$regMMsat4[RPF$gene_symbol %in% rframe[rframe$region == "cds","geneName"]] <- "cds"
RPF$regMMsat4[RPF$gene_symbol %in% rframe[rframe$region == "utr3","geneName"]] <- "utr3"
RPF$regMMsat4[RPF$gene_symbol %in% rframe[rframe$region == "utr3","geneName"] &
```

```
RPF$gene_symbol %in% rframe[rframe$region == "cds","geneName"] <- "both"

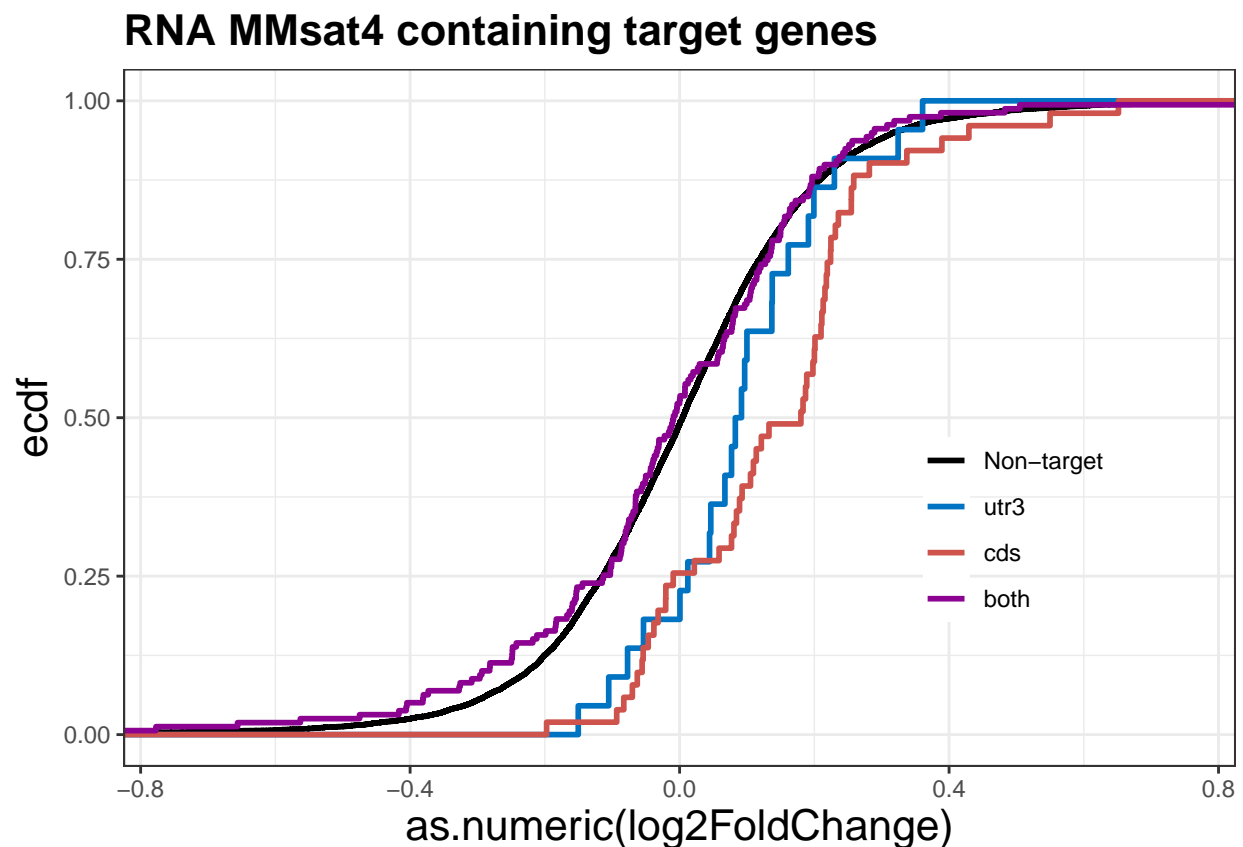
table(RPF$regMMsat4)
```

```
##
##      both      cds Non-target      utr3
##      15       49      11283       22
```

make ecdf plots with the position data

```
#RNA
posECDFRNA <- ggplot(RNA, aes(as.numeric(log2FoldChange), colour=factor(regMMsat4, levels = c("Non-target", "utr3", "cds", "both")))) +
  stat_ecdf(geom="step", size=1) +
  scale_colour_manual(values = c("black", farbe1, farbe3, RPFncol)) +
  coord_cartesian(xlim = c(-0.75, 0.75)) + theme_bw() +
  theme(legend.position = c(0.8, 0.35), legend.title = element_blank(),
        legend.background = element_rect(colour = "transparent", fill="transparent"),
        axis.title=element_text(size=16), plot.title = element_text(size=16, face = "bold")) +
  ggtitle("RNA MMsat4 containing target genes")

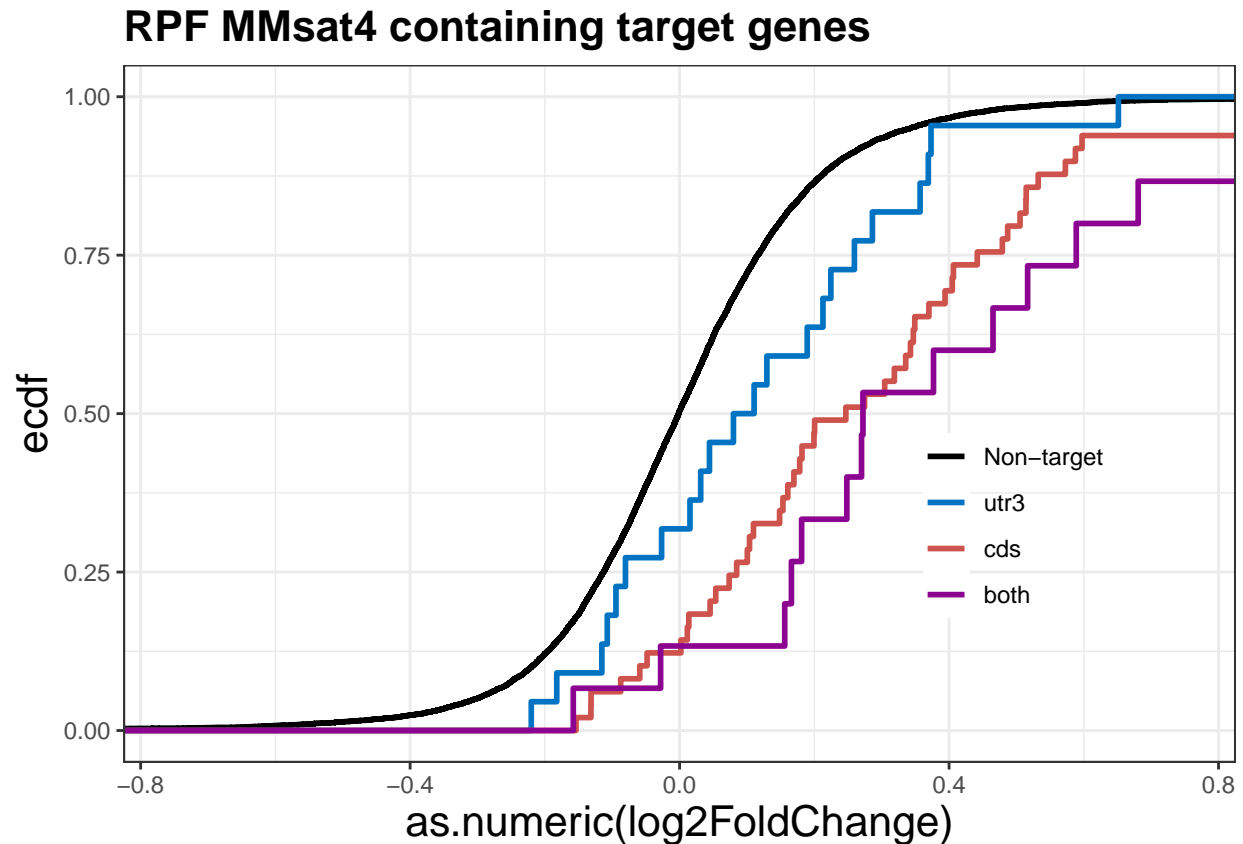
posECDFRNA
```



```
#RPF
posECDFRPF <- ggplot(RPF, aes(as.numeric(log2FoldChange), colour=factor(regMMsat4, levels = c("Non-target", "utr3", "cds", "both")))) +
  stat_ecdf(geom="step", size=1) +
  scale_colour_manual(values = c("black", farbe1, farbe3, RPFncol)) +
```

```
coord_cartesian(xlim = c(-0.75, 0.75)) + theme_bw() +
theme(legend.position = c(0.8, 0.35), legend.title = element_blank(),
      legend.background = element_rect(colour = "transparent", fill="transparent"),
      axis.title=element_text(size=16),plot.title = element_text(size=16, face = "bold")) +
ggtitle("RPF MMsat4 containing target genes")
```

posECDFRPF



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] rtracklayer_1.58.0   GenomicRanges_1.50.2 GenomeInfoDb_1.34.9
## [4] IRanges_2.32.0       S4Vectors_0.36.2     ggpubr_0.6.0
## [7] ggplot2_3.4.2        dplyr_1.1.2          AnnotationHub_3.6.0
## [10] BiocFileCache_2.6.1  dbplyr_2.3.2         BiocGenerics_0.44.0
##
## loaded via a namespace (and not attached):
## [1] bitops_1.0-7          matrixStats_0.63.0
## [3] bit64_4.0.5           filelock_1.0.2
## [5] httr_1.4.6            tools_4.2.3
## [7] backports_1.4.1       utf8_1.2.3
## [9] R6_2.5.1              DBI_1.1.3
## [11] colorspace_2.1-0      withr_2.5.0
## [13] tidyselect_1.2.0      bit_4.0.5
## [15] curl_5.0.0            compiler_4.2.3
## [17] cli_3.6.0             Biobase_2.58.0
## [19] DelayedArray_0.23.2   labeling_0.4.2
## [21] scales_1.2.1          rappdirs_0.3.3
## [23] digest_0.6.31         Rsamtools_2.14.0
## [25] rmarkdown_2.21        XVector_0.38.0
## [27] pkgconfig_2.0.3       htmltools_0.5.4
## [29] MatrixGenerics_1.10.0 highr_0.10
## [31] fastmap_1.1.1         rlang_1.1.0
## [33] rstudioapi_0.14       RSQLite_2.3.1
## [35] shiny_1.7.4           farver_2.1.1
## [37] BiocIO_1.8.0          generics_0.1.3
## [39] BiocParallel_1.32.6   car_3.1-2
## [41] RCurl_1.98-1.12       magrittr_2.0.3
## [43] GenomeInfoDbData_1.2.9 Matrix_1.5-3
## [45] Rcpp_1.0.10           munsell_0.5.0
## [47] fansi_1.0.4           abind_1.4-5
## [49] lifecycle_1.0.3       yaml_2.3.7
## [51] carData_3.0-5         SummarizedExperiment_1.28.0
## [53] zlibbioc_1.44.0       grid_4.2.3
## [55] blob_1.2.4            parallel_4.2.3
## [57] promises_1.2.0.1      crayon_1.5.2
## [59] lattice_0.20-45       Biostrings_2.66.0
## [61] KEGGREST_1.38.0       knitr_1.42
## [63] pillar_1.9.0          rjson_0.2.21
## [65] ggsignif_0.6.4        codetools_0.2-19
## [67] XML_3.99-0.14         glue_1.6.2
## [69] BiocVersion_3.16.0    evaluate_0.21
## [71] BiocManager_1.30.20   png_0.1-8
## [73] vctrs_0.6.2           httpuv_1.6.11
## [75] gtable_0.3.3          purrr_1.0.1
## [77] tidyr_1.3.0           cachem_1.0.8
## [79] xfun_0.39             mime_0.12
## [81] xtable_1.8-4          broom_1.0.4
## [83] restfulr_0.0.15       rstatix_0.7.2
## [85] later_1.3.1           tibble_3.2.1
## [87] GenomicAlignments_1.34.1 AnnotationDbi_1.60.2
## [89] memoise_2.0.1         ellipsis_0.3.2

```

```
## [91] interactiveDisplayBase_1.36.0
```