Figure2 RAPseq

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1 Sep 2024 (16:39:06)

Contents

0.1 ENV settings

```
###
# @Description: Figure2
# @Description: Adapted from https://github.com/IonutAtanasoai1/RAPseq
# @Author: LiQun
# @Email: qun.li@ki.se
# @Date: 1 Sep 2024 ( 16:39:06 )
###

rm(list = ls())
setwd("/Users/liqun/Desktop/Projects/RAPseq/0_RAPSeq/")
```

0.2 R libraries

```
library(ChIPpeakAnno)
## Loading required package: IRanges
## 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
## Loading required package: stats4
##
## Attaching package: 'S4Vectors'
## The following object is masked from 'package:utils':
##
##     findMatches
## The following objects are masked from 'package:base':
##
##     expand.grid, I, unname
## Loading required package: GenomicRanges
## Loading required package: GenomeInfoDb
## Warning: package 'GenomeInfoDb' was built under R version 4.3.3
library(Biostrings)
## Warning: package 'Biostrings' was built under R version 4.3.3
## Loading required package: XVector
##
## Attaching package: 'Biostrings'
## The following object is masked from 'package:base':
##
##     strsplit
library(edgeR)
```

```
## Loading required package: limma
##
## Attaching package: 'limma'
## The following object is masked from 'package:BiocGenerics':
##
##     plotMA
library(ggfortify)
## Loading required package: ggplot2
library(tidyverse)
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v lubridate 1.9.3     v tibble    3.2.1
## v purrr     1.0.2     v tidyr     1.3.1
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x lubridate::%within%() masks IRanges::%within%()
## x dplyr::collapse()     masks Biostrings::collapse(), IRanges::collapse()
## x dplyr::combine()      masks BiocGenerics::combine()
## x purrr::compact()      masks XVector::compact()
## x dplyr::desc()         masks IRanges::desc()
## x tidyr::expand()       masks S4Vectors::expand()
## x dplyr::filter()       masks stats::filter()
## x dplyr::first()        masks S4Vectors::first()
## x dplyr::lag()          masks stats::lag()
## x ggplot2::Position()   masks BiocGenerics::Position(), base::Position()
## x purrr::reduce()       masks GenomicRanges::reduce(), IRanges::reduce()
## x dplyr::rename()       masks S4Vectors::rename()
## x lubridate::second()   masks S4Vectors::second()
## x lubridate::second<-() masks S4Vectors::second<-()
## x dplyr::slice()        masks XVector::slice(), IRanges::slice()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become error
library(scales)
##
## Attaching package: 'scales'
##
## The following object is masked from 'package:purrr':
##
##     discard
##
## The following object is masked from 'package:readr':
##
##     col_factor
library(ggplot2)
library(dendextend)
##
## ---------------------
## Welcome to dendextend version 1.17.1
## Type citation('dendextend') for how to cite the package.
##
## Type browseVignettes(package = 'dendextend') for the package vignette.
## The github page is: https://github.com/talgalili/dendextend/
##
## Suggestions and bug-reports can be submitted at: https://github.com/talgalili/dendextend/issues
```

```
## You may ask questions at stackoverflow, use the r and dendextend tags:
##   https://stackoverflow.com/questions/tagged/dendextend
##
##  To suppress this message use:  suppressPackageStartupMessages(library(dendextend))
## ----------------------
##
##
## Attaching package: 'dendextend'
##
## The following object is masked from 'package:Biostrings':
##
##     nnodes
##
## The following object is masked from 'package:stats':
##
##     cutree
library(dichromat)
library(reshape2)
##
## Attaching package: 'reshape2'
##
## The following object is masked from 'package:tidyr':
##
##     smiths
library(dplyr)
library(stringr)
library(GenomicRanges)
library(GenomicFeatures)
## Warning: package 'GenomicFeatures' was built under R version 4.3.3
## Loading required package: AnnotationDbi
## Loading required package: Biobase
## Welcome to Bioconductor
##
##     Vignettes contain introductory material; view with
##     'browseVignettes()'. To cite Bioconductor, see
##     'citation("Biobase")', and for packages 'citation("pkgname")'.
##
##
## Attaching package: 'AnnotationDbi'
##
## The following object is masked from 'package:dplyr':
##
##     select
library(gplots)
##
## Attaching package: 'gplots'
##
## The following object is masked from 'package:IRanges':
##
##     space
##
## The following object is masked from 'package:S4Vectors':
##
```

```
##     space
##
## The following object is masked from 'package:stats':
##
##     lowess
library(clusterProfiler)
## Warning: package 'clusterProfiler' was built under R version 4.3.3
##
## clusterProfiler v4.10.1  For help: https://yulab-smu.top/biomedical-knowledge-mining-book/
##
## If you use clusterProfiler in published research, please cite:
## T Wu, E Hu, S Xu, M Chen, P Guo, Z Dai, T Feng, L Zhou, W Tang, L Zhan, X Fu, S Liu, X Bo, and G Yu.
##
## Attaching package: 'clusterProfiler'
##
## The following object is masked from 'package:AnnotationDbi':
##
##     select
##
## The following object is masked from 'package:purrr':
##
##     simplify
##
## The following object is masked from 'package:XVector':
##
##     slice
##
## The following object is masked from 'package:IRanges':
##
##     slice
##
## The following object is masked from 'package:S4Vectors':
##
##     rename
##
## The following object is masked from 'package:stats':
##
##     filter
library(org.Hs.eg.db)
##
library(org.Dr.eg.db)
##
library(tidyr)
library(gtools)
library(ggrepel)
library(ggbeeswarm)
library(ReactomePA)
## ReactomePA v1.46.0  For help: https://yulab-smu.top/biomedical-knowledge-mining-book/
##
## If you use ReactomePA in published research, please cite:
## Guangchuang Yu, Qing-Yu He. ReactomePA: an R/Bioconductor package for reactome pathway analysis and
library(VennDiagram)
## Loading required package: grid
```

```
##
## Attaching package: 'grid'
##
## The following object is masked from 'package:Biostrings':
##
##     pattern
##
## Loading required package: futile.logger
##
## Attaching package: 'futile.logger'
##
## The following object is masked from 'package:gtools':
##
##     scat
##
##
## Attaching package: 'VennDiagram'
##
## The following object is masked from 'package:dendextend':
##
##     rotate
library(LSD)
library(gridExtra)
##
## Attaching package: 'gridExtra'
##
## The following object is masked from 'package:Biobase':
##
##     combine
##
## The following object is masked from 'package:dplyr':
##
##     combine
##
## The following object is masked from 'package:BiocGenerics':
##
##     combine
library(UpSetR)
library(ggpubr)
##
## Attaching package: 'ggpubr'
##
## The following object is masked from 'package:VennDiagram':
##
##     rotate
##
## The following object is masked from 'package:dendextend':
##
##     rotate
library(GenomicScores)
##
## Attaching package: 'GenomicScores'
##
```

```
## The following object is masked from 'package:utils':
##
##     citation
library(phastCons7way.UCSC.hg38)
## Warning: replacing previous import 'utils::findMatches' by
## 'S4Vectors::findMatches' when loading 'phastCons7way.UCSC.hg38'
library(phastCons100way.UCSC.hg38)
## Warning: replacing previous import 'utils::findMatches' by
## 'S4Vectors::findMatches' when loading 'phastCons100way.UCSC.hg38'
library(corrplot)
## Warning: package 'corrplot' was built under R version 4.3.3
## corrplot 0.94 loaded
library(ggforce)
library(idr)
library(GGally)
## Registered S3 method overwritten by 'GGally':
##   method from
##   +.gg   ggplot2
library(eulerr)
## Registered S3 method overwritten by 'eulerr':
##   method    from
##   plot.venn gplots
##
## Attaching package: 'eulerr'
##
## The following object is masked from 'package:gplots':
##
##     venn
library(ggseqlogo)
library(robustbase)
## Warning: package 'robustbase' was built under R version 4.3.3
##
## Attaching package: 'robustbase'
##
## The following object is masked from 'package:Biobase':
##
##     rowMedians
library(zoo)
##
## Attaching package: 'zoo'
##
## The following objects are masked from 'package:base':
##
##     as.Date, as.Date.numeric
```

0.3 Colors settings

```
acqua_greens <- c("#04493F","#02655B", "#08756A", "#0C8074", "#179286", "#25A296", "#3EB3A7", "#5FCBC1"
acqua_blues  <- c("#02465B","#015666", "#0C6476", "#157589", "#1E8498", "#4397A8", "#4FB0C3", "#70C2D2"
greys <- c("#202020", "#404040", "#606060", "#808080", "#A0A0A0", "#C0C0C0", "#E0E0E0", "#FFFFFF")
reds <- c("#C10303", "#D83535", "#E95F5F", "#F08686", "#FAAEAE")
```

```
pinks <- c("#660000", "#990000", "#CC0000", "#FF0000", "#FF6666", "#FF9999","#FFCECE")
yellows <- c( "#9C8803", "#A59213", "#B09D1F", "#BAA82F", "#C6B441", "#D0BF53", "#DACB69", "#E4D782", "#
oranges <- c( "#A15000", "#CE7012", "#E47B12", "#F07D09", "#FF8B15", "#FFA141","#FFCC99")
```

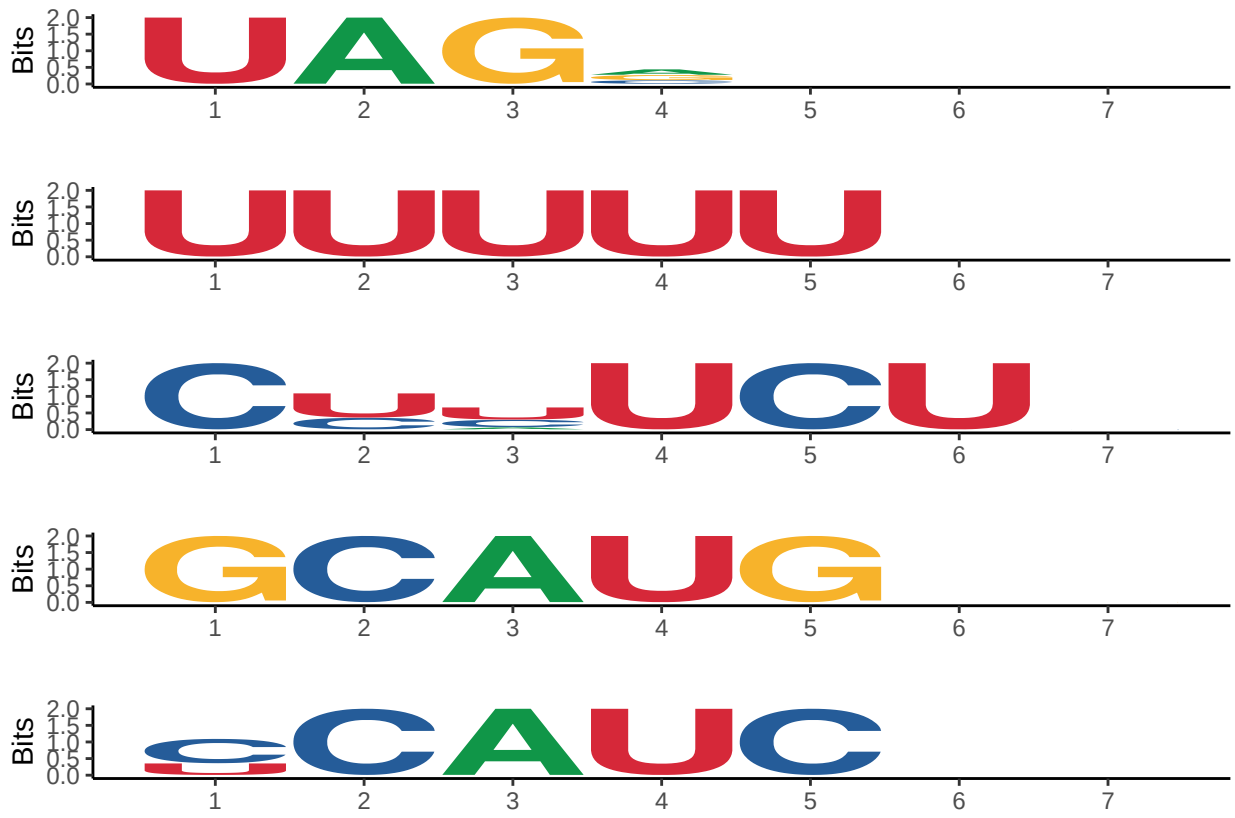
0.4 Motifs settings

```
## the following lines reconstructs the sequence motif logos from PWM published by the relative studies
## the RAP and CLIP PWM are computed by DREME with the parameters specified in the manuscript methods s
## For YBX3 in order to obtain the ACAHC motif, one background 4 mers (GAAC, masked to NNNN) needed to
## The RBFOX2 GMAUG motif is recomputed by weighing the abundance of GCAUG and GAAUG with the binding s
## de novo motif discovery was performed only for RAPseq and eCLIPseq
## in figure 2A the logos for RBNS were drawn based on the logos published on the ENCODE Project websit
```

0.4.1 eCLIP

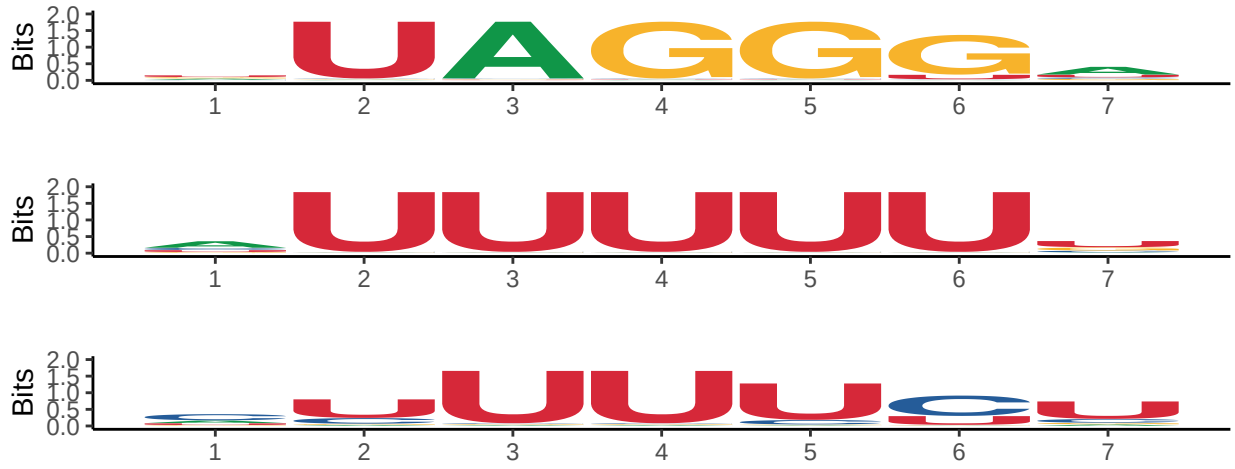
```
##########################    eCLIP-seq data   ##################
# https://www.encodeproject.org
# HNRNPA1, accession ENCFF797GSK
# HNRNPC, accession ENCFF440ROZ
# PTBP1, accession ENCFF726SQU
# RBFOX2, accession ENCFF871NYM
# YBX3, accession ENCFF185OEI

# annotated data
PATH_eCLIP_ann <- "./Data/eCLIP/annotated/"
PEAKS_eCLIP_ann <- list.files(path = PATH_eCLIP_ann)
Names_eCLIP_ann <- unlist(str_split(PEAKS_eCLIP_ann,"\\.p"))[grep("txt",unlist(str_split(PEAKS_eCLIP_an
CLIPs <- list()
for (i in 1:length(Names_eCLIP_ann)){
  CLIPs[[i]] <- as.data.frame(read.table(paste(PATH_eCLIP_ann,PEAKS_eCLIP_ann[i],sep = ""), header = T,
}
names(CLIPs) <- Names_eCLIP_ann


# PFMs
PATH_eCLIP_PFMs <- "./Data/eCLIP/PFMs/"
PEAKS_eCLIP_PFMs <- list.files(path = PATH_eCLIP_PFMs)
Names_eCLIP <- unlist(str_split(PEAKS_eCLIP_PFMs,"\\."))[grep("txt",unlist(str_split(PEAKS_eCLIP_PFMs,"
eCLIPseq <- list()

for (i in 1:length(Names_eCLIP)){
  eCLIPseq[[i]] <- t(as.data.frame(read.table(paste(PATH_eCLIP_PFMs,PEAKS_eCLIP_PFMs[i],sep = ""), stri
  rownames(eCLIPseq[[i]]) <- c("A","C","G","U")
  colnames(eCLIPseq[[i]]) <- NULL
}

names(eCLIPseq) <- Names_eCLIP
eCLIPseq$HNRNPA1 <- cbind(eCLIPseq$HNRNPA1,c(0,0,0,0),c(0,0,0,0),c(0,0,0,0))
eCLIPseq$HNRNPC <- cbind(eCLIPseq$HNRNPC,c(0,0,0,0),c(0,0,0,0))
```

```
eCLIPseq$PTBP1 <- cbind(eCLIPseq$PTBP1,c(0,0,0,0))
eCLIPseq$RBFOX2 <- cbind(eCLIPseq$RBFOX2,c(0,0,0,0),c(0,0,0,0))
eCLIPseq$YBX3 <- cbind(eCLIPseq$YBX3,c(0,0,0,0),c(0,0,0,0))

logos_eCLIPseq <- list()

for (i in 1:length(Names_eCLIP)){
  logos_eCLIPseq[[i]] <- ggplot() + geom_logo(eCLIPseq[[Names_eCLIP[i]]], font="helvetica_bold") + theme
}
## Warning: The `<scale>` argument of `guides()` cannot be `FALSE`. Use "none" instead as
## of ggplot2 3.3.4.
## i The deprecated feature was likely used in the ggseqlogo package.
##   Please report the issue at <https://github.com/omarwagih/ggseqlogo/issues>.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
names(logos_eCLIPseq) <- Names_eCLIP
eCLIP_logo <- ggarrange(logos_eCLIPseq$HNRNPA1,logos_eCLIPseq$HNRNPC,logos_eCLIPseq$PTBP1,logos_eCLIPseq
eCLIP_logo
```



0.4.2 RNA Compete

```
##########################    RNA Compete   ##################
# Ref: A compendium of RNA-binding motifs for decoding gene regulation
# Link: https://hugheslab.ccbr.utoronto.ca/supplementary-data/RNAcompete_eukarya/
# HNRNPA1: https://hugheslab.ccbr.utoronto.ca/supplementary-data/RNAcompete_eukarya/Experiment_reports/
# HNRNPC: https://hugheslab.ccbr.utoronto.ca/supplementary-data/RNAcompete_eukarya/Experiment_reports/R
# PTBP1: https://hugheslab.ccbr.utoronto.ca/supplementary-data/RNAcompete_eukarya/Experiment_reports/RN
#            https://hugheslab.ccbr.utoronto.ca/supplementary-data/RNAcompete_eukarya/Experiment_report

PATH_RNACompete <- "./Data/RNAcompete/"
PEAKS_RNACompete <- list.files(path = PATH_RNACompete)
Names_RNACompete <- unlist(str_split(PEAKS_RNACompete,"\\."))[grep("txt",unlist(str_split(PEAKS_RNACompe
RNACompete <- list()
for (i in 1:length(Names_RNACompete)){
  RNACompete[[i]] <- as.data.frame(read.table(paste(PATH_RNACompete,PEAKS_RNACompete[i],sep = ""), stri
  RNACompete[[i]] <- t(RNACompete[[i]][,-1])
}
names(RNACompete) <- Names_RNACompete

logos_plots_RNACompete <- list()
for (i in 1:length(Names_RNACompete)){
  logos_plots_RNACompete[[i]] <- ggplot() + geom_logo(RNACompete[[Names_RNACompete[i]]], font="helvetica
}
names(logos_plots_RNACompete) <- Names_RNACompete
RNA_Compete_logo <- ggarrange(logos_plots_RNACompete$HNRNPA1,logos_plots_RNACompete$HNRNPC,logos_plots_
RNA_Compete_logo
```



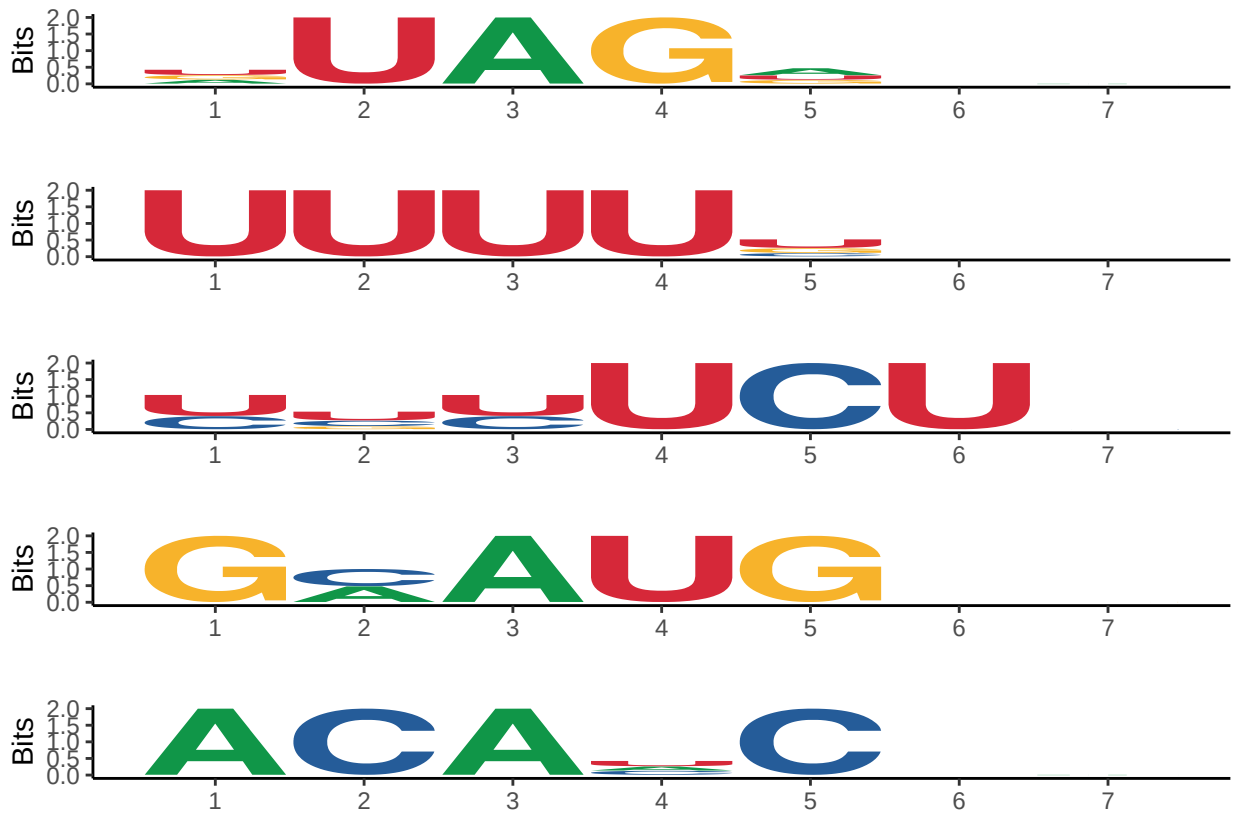
0.4.3 RBNS

```
# Ref: Sequence, Structure, and Context Preferences of Human RNA Binding Proteins
# Link: https://ars.els-cdn.com/content/image/1-s2.0-S1097276518303514-mmc4.xlsx
# Link: https://www.encodeproject.org/encore-matrix/?type=Experiment&status=released&internal_tags=ENCO
# HNRNPC: https://www.encodeproject.org/experiments/ENCSR569UIU/
#         https://www.encodeproject.org/documents/35943eb4-837d-4f96-a705-46eec6838f5d/@@download/attac
# RBFOX2: https://www.encodeproject.org/experiments/ENCSR441HLP/
#         https://www.encodeproject.org/documents/2403659a-974e-4312-900f-45d0c8e3566d/@@download/attac
```

0.4.4 RAPSeq

```
############################    RAP SEQ    ################################
PATH_RAP_ann <- "./Data/RAPseq/annotated/"
PEAKS_RAP_ann <- list.files(path = PATH_RAP_ann)
Names_RAP <- unlist(str_split(PEAKS_RAP_ann,"\\.p"))[grep("txt",unlist(str_split(PEAKS_RAP_ann,"\\.p"))
RAPs <- list()
for (i in 1:length(Names_RAP)){
  print(paste(PATH_RAP_ann,PEAKS_RAP_ann[i],sep = ""))
  RAPs[[i]] <- as.data.frame(read.table(paste(PATH_RAP_ann,PEAKS_RAP_ann[i],sep = ""), header = T, stri
}
## [1] "./Data/RAPseq/annotated/HNRNPA1.peaks.txt"
## [1] "./Data/RAPseq/annotated/HNRNPC.peaks.txt"
## [1] "./Data/RAPseq/annotated/hsHuRHUMAN.peaks.txt"
## [1] "./Data/RAPseq/annotated/HuRPTBP1.peaks.txt"
## [1] "./Data/RAPseq/annotated/IGF2BP1.peaks.txt"
## [1] "./Data/RAPseq/annotated/PTBP1.peaks.txt"
## [1] "./Data/RAPseq/annotated/RBFOX2.peaks.txt"
## [1] "./Data/RAPseq/annotated/YBX3.peaks.txt"
names(RAPs) <- Names_RAP

###   A   C   G   U   #####
#GCATG <- RAPs[["RBFOX2"]][grep("GAATG",str_sub(RAPs[["RBFOX2"]]$positive_fa,80,120),invert=T),]
GCATG <- RAPs[["RBFOX2"]][grep("GCATG",str_sub(RAPs[["RBFOX2"]]$positive_fa,80,120)),"BS"]
GCATG <- rep( "GCATG",round(sqrt(length(GCATG))*median(GCATG)) )

#GAATG <- RAPs[["RBFOX2"]][grep("GCATG",str_sub(RAPs[["RBFOX2"]]$positive_fa,80,120),invert=T),]
GAATG <- RAPs[["RBFOX2"]][grep("GAATG",str_sub(RAPs[["RBFOX2"]]$positive_fa,80,120)),"BS"]
GAATG <- rep( "GAATG",round(sqrt(length(GAATG))*median(GAATG)) )
GMATG <- c(GCATG,GAATG)
GMATG <- DNAStringSet(GMATG)
GMATG <- consensusMatrix(DNAStringSet(GMATG))[1:4,]
rownames(GMATG) <- c("A","C","G","U")
GMAUG <- GMATG
GMAUG <- cbind(GMAUG,c(0,0,0,0),c(0,0,0,0))

GMAUG_logo <- ggplot() + geom_logo(GMAUG, font="helvetica_bold") + theme_classic() + ylim(0,2)

PATH_RAP_PFMs <- "./Data/RAPseq/PFMs/"
PEAKS_RAP_PFMs <- list.files(path = PATH_RAP_PFMs)
Names_RAP_PFMs <- unlist(str_split(PEAKS_RAP_PFMs,"\\."))[grep("txt",unlist(str_split(PEAKS_RAP_PFMs,"\\
```

```
RAPseq <- list()

for (i in 1:length(Names_RAP_PFMs)){
  RAPseq[[i]] <- t(as.data.frame(read.table(paste(PATH_RAP_PFMs,PEAKS_RAP_PFMs[i],sep = ""), stringsAsFa
  rownames(RAPseq[[i]]) <- c("A","C","G","U")
  colnames(RAPseq[[i]]) <- NULL
}

names(RAPseq) <- Names_RAP_PFMs
RAPseq$HNRNPA1 <- cbind(RAPseq$HNRNPA1,c(0,0,0,0),c(0,0,0,0))
RAPseq$HNRNPC <- cbind(RAPseq$HNRNPC,c(0,0,0,0),c(0,0,0,0))
RAPseq$PTBP1 <- cbind(RAPseq$PTBP1,c(0,0,0,0))
RAPseq$YBX3 <- cbind(RAPseq$YBX3,c(0,0,0,0),c(0,0,0,0))
logos_RAPseq <- list()
for (i in 1:length(Names_RAP_PFMs)){
  logos_RAPseq[[i]] <- ggplot() + geom_logo(RAPseq[[Names_RAP_PFMs[i]]], font="helvetica_bold") + theme_
}
names(logos_RAPseq) <- Names_RAP_PFMs
RAP_logo <- ggarrange(logos_RAPseq$HNRNPA1,logos_RAPseq$HNRNPC,logos_RAPseq$PTBP1,GMAUG_logo,logos_RAPse
RAP_logo
```



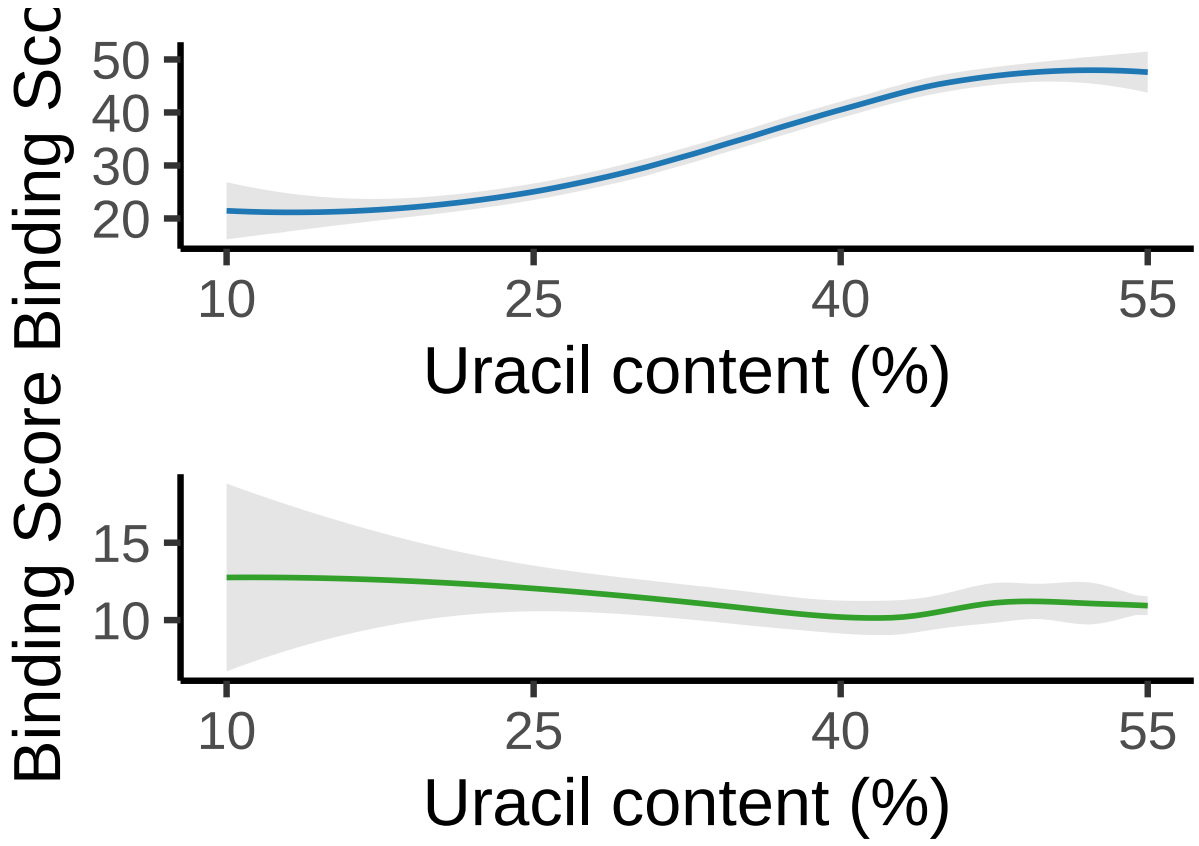
0.5 Figures settings

0.5.1 Figure 2A

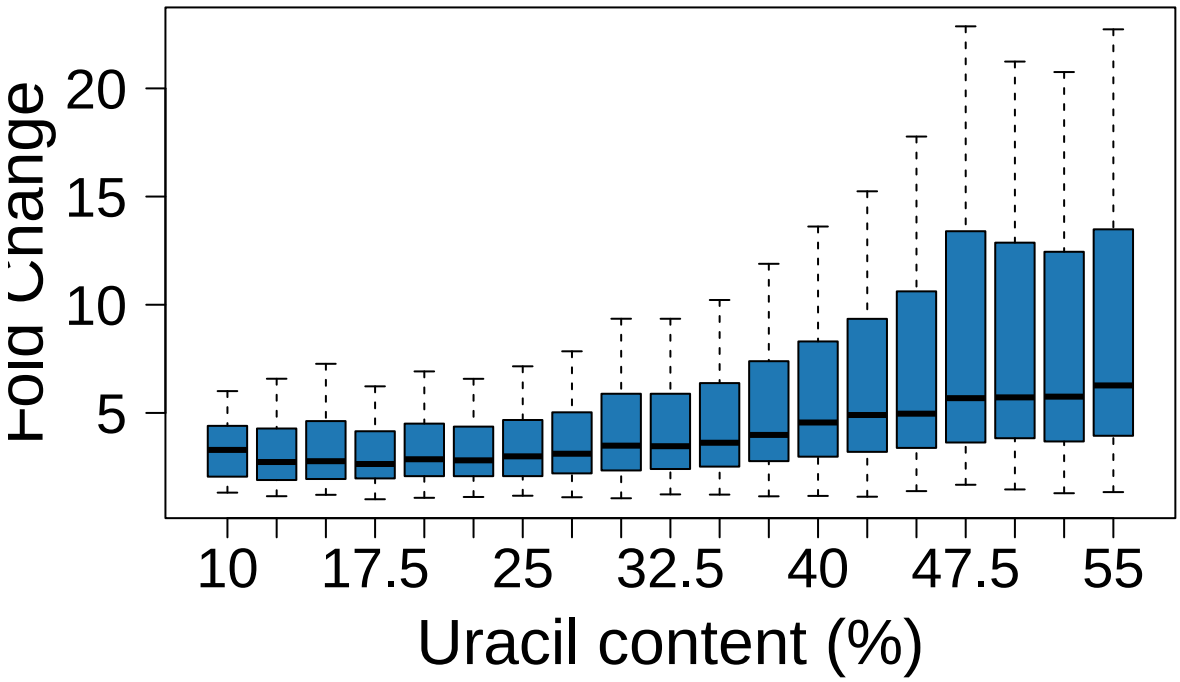
```
# RAP_logo,eCLIP_logo,RNA_Compete_logo and HTRSELEX_logo
# RBNS data were from ENCODE Project
p_motifLOGO <- ggarrange(RAP_logo,eCLIP_logo,RNA_Compete_logo,NULL, ncol=4)
ggsave(filename = "./Figure/Figure2A_motifLogo.pdf", plot = p_motifLOGO, width = 11.5, height = 7.8)
```

0.5.2 Figure 2B

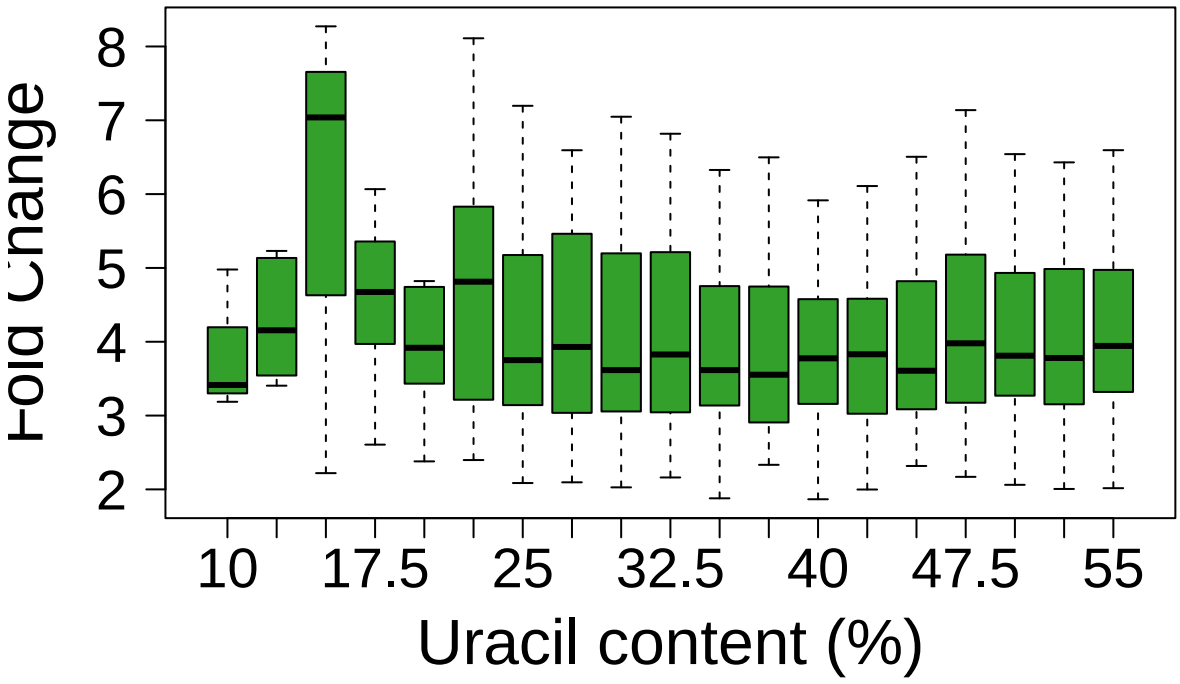
```
# uracil content
RAPs[["HNRNPC"]]$Us <- str_count(str_sub(RAPs[["HNRNPC"]]$positive_fa,80,120),"T") / (120-80)
CLIPs[["HNRNPC"]]$Us <- str_count(str_sub(CLIPs[["HNRNPC"]]$positive_fa,43,83),"T") / (83-43)

#
RAP_Us_data <- RAPs[["HNRNPC"]][,c("Us","BS","Mean_FCI")]
colnames(RAP_Us_data) <- c("Us","BS","MeanFC")
RAP_Us_data$Assay <- rep("RAP",nrow(RAP_Us_data))
CLIP_Us_data <- CLIPs[["HNRNPC"]][,c("Us","BS","Mean_FC")]
colnames(CLIP_Us_data) <- c("Us","BS","MeanFC")
CLIP_Us_data$Assay <- rep("CLIP",nrow(CLIP_Us_data))

HNRNPC_Us_data <- rbind(RAP_Us_data,CLIP_Us_data)
HNRNPC_Us_data$Us <- HNRNPC_Us_data$Us*100
HNRNPC_Us_data$Us[HNRNPC_Us_data$Us < 10] <- 10
HNRNPC_Us_data$Us[HNRNPC_Us_data$Us > 55] <- 55

fig_bindingScore_rap <- ggplot2::ggplot(data=HNRNPC_Us_data[HNRNPC_Us_data$Assay == "RAP",], aes(x=Us, y
  stat_smooth(method="loess", color="#1f78b4", fill=greys[6], level = 0.99) +
  theme_classic2(base_size = 25) +
  ylab("Binding Score") +
  xlab("Uracil content (%)") +
  scale_x_continuous(breaks = c(10,25,40,55))

fig_bindingScore_clip <- ggplot2::ggplot(data=HNRNPC_Us_data[HNRNPC_Us_data$Assay == "CLIP",], aes(x=Us
  stat_smooth(method="loess", color="#33a02c", fill=greys[6], level = 0.99) +
  theme_classic2(base_size = 25) +
  ylab("Binding Score") +
  xlab("Uracil content (%)") +
  scale_x_continuous(breaks = c(10,25,40,55))

p_bindingScore_Us <- ggarrange(fig_bindingScore_rap, fig_bindingScore_clip, ncol=1)
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
p_bindingScore_Us
```




```
ggsave(filename = "./Figure/Figure2B_BingdingScoreUracilContent_LOSSES.pdf", plot = p_bindingScore_Us, w

#pdf("./Figure/Figure2B_UracilContentBoxplot_RAP.pdf", width = 11.5, height = 7.8)
boxplot(data=HNRNPC_Us_data[HNRNPC_Us_data$Assay == "RAP",], MeanFC~Us, outline=F, range=1, notch=F, col
```




```
#dev.off()

#pdf("./Figure/Figure2B_UracilContentBoxplot_CLIP.pdf", width = 11.5, height = 7.8)
boxplot(data=HNRNPC_Us_data[HNRNPC_Us_data$Assay == "CLIP",], MeanFC~Us, outline=F, range=1, notch=F, co
```

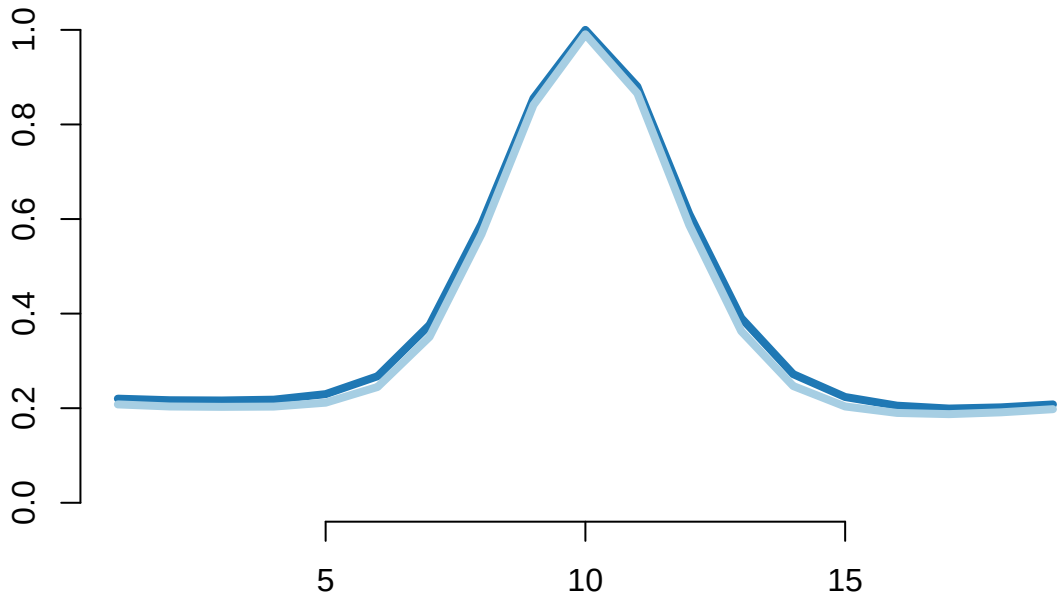


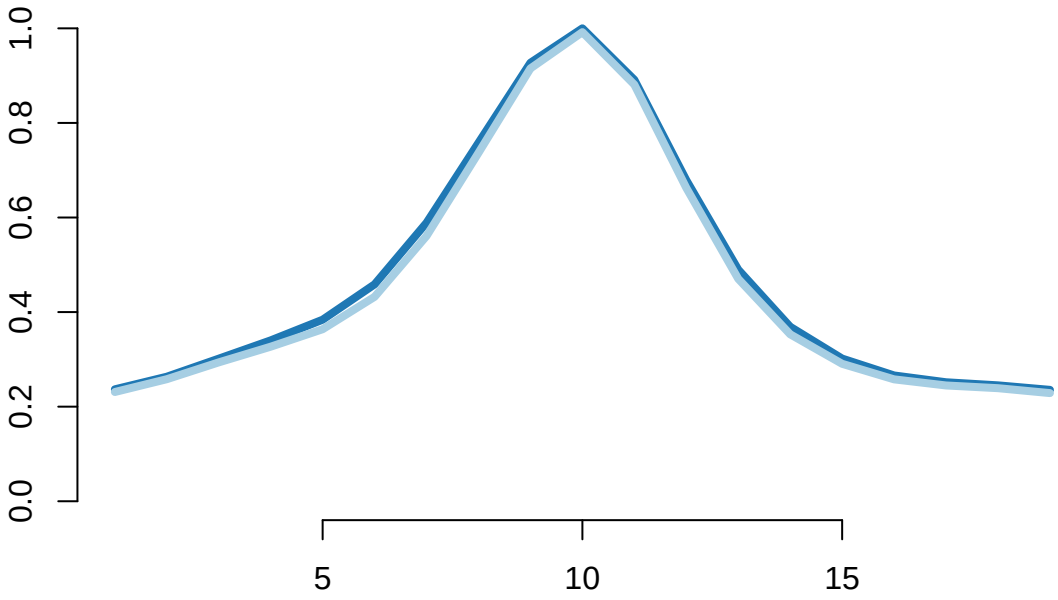

```
#dev.off()
```

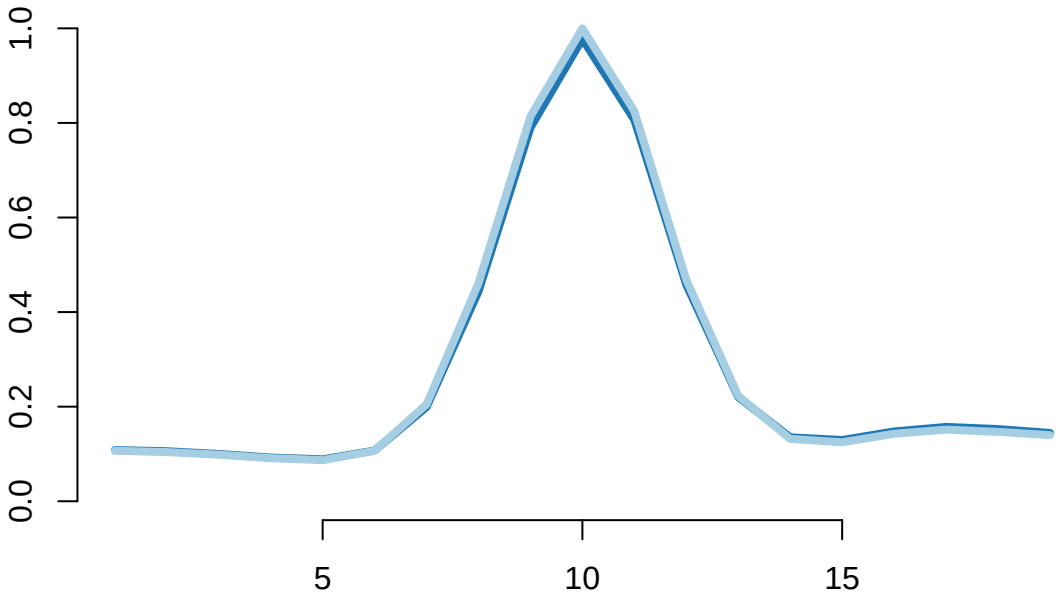
0.5.3 Figure 2C

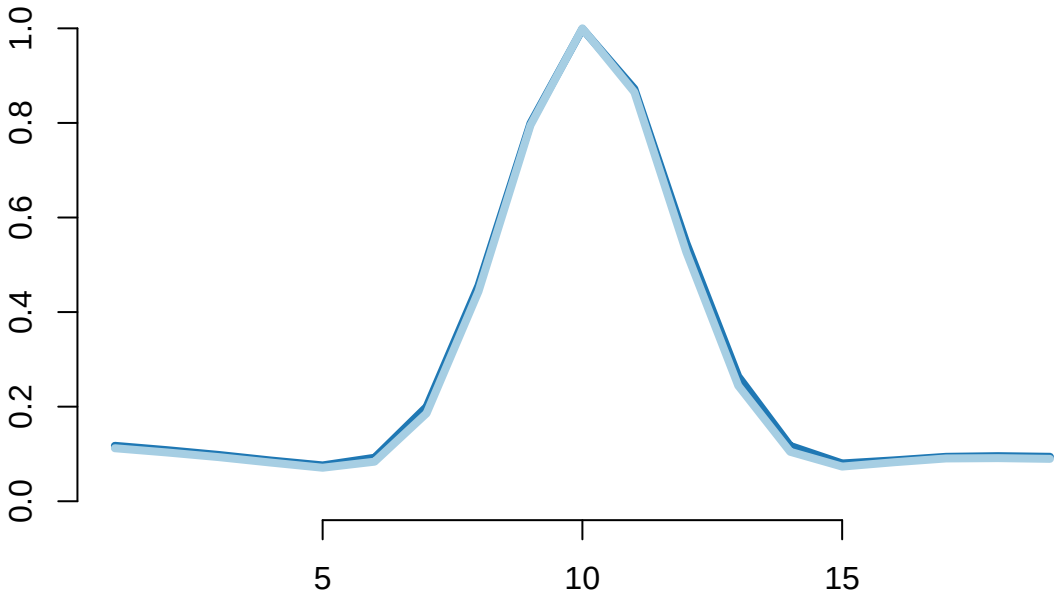
```
## DeepTools count matrices (bin size = 10nt) are read in
## DeepTools was used with the following command to generate the per nt count matrices
## computeMatrix reference-point -S rep1.bw -R rep1.bed -a 100 -b 100 -bs 10
## RAPseq
PATH_RAP_Coverage <- "./Data/RAPseq/Coverage/10nt/"
PEAKS_RAP_Coverage <- list.files(path = PATH_RAP_Coverage)
Names_RAP_Coverage <- unlist(str_split(PEAKS_RAP_Coverage,"\\.matr"))[grep("txt",unlist(str_split(PEAKS_
RAPseq_Coverage <- list()

for (i in 1:length(Names_RAP_Coverage)){
  RAPseq_Coverage[[i]] <- as.data.frame(read.table(paste(PATH_RAP_Coverage,PEAKS_RAP_Coverage[i],sep = "
}
names(RAPseq_Coverage) <- Names_RAP_Coverage

#par(mfrow=c(4,5),bty="n")
Names_protein <- c("HNRNPA1","HNRNPC","PTBP1","RBFOX2","YBX3")
# coverage normalized RPM
for (i in 1:length(Names_protein)){

  rep1_name <- paste (Names_protein[i],".rep1",sep="")
```

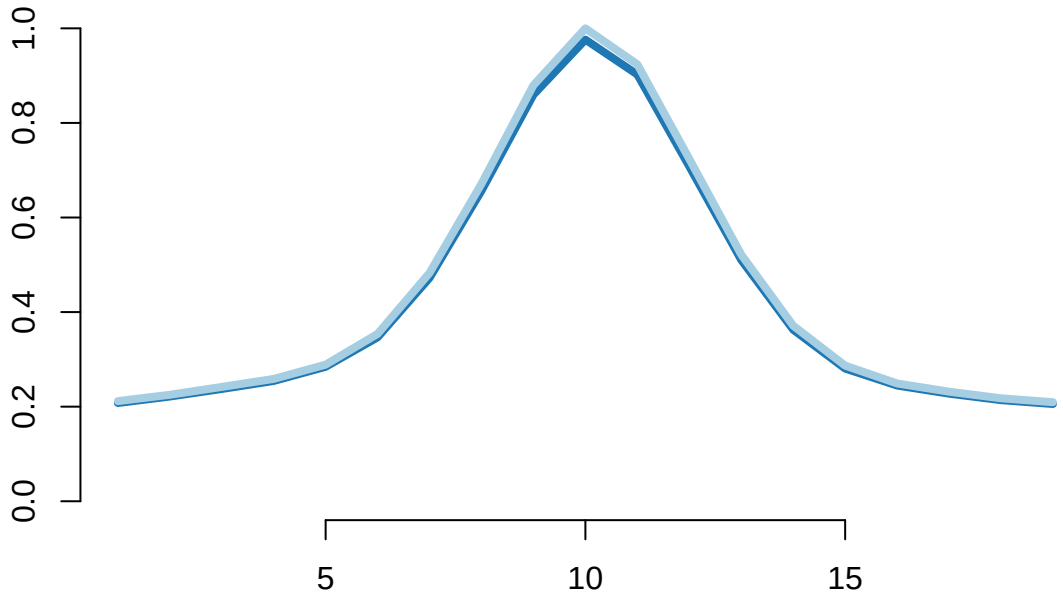
```
  rep2_name <- paste (Names_protein[i],".rep2",sep="")


  mean_rep1 <- rollapply(colMeans(as.matrix(RAPseq_Coverage[[rep1_name]])), width=2, FUN = mean)
  mean_rep2 <- rollapply(colMeans(as.matrix(RAPseq_Coverage[[rep2_name]])), width=2, FUN = mean)

  normalize_rep1 <- mean_rep1/max(c(mean_rep1,mean_rep2))
  normalize_rep2 <- mean_rep2/max(c(mean_rep1,mean_rep2))

  plot(normalize_rep1, type="l",col="#1f78b4", lwd=4, ylab=NA, xlab=NA, ylim=c(0,1), las=1, axes=FALSE)
  axis(side=1, labels=T)
  axis(side=2, labels=T)
  points(normalize_rep2,type="l",col="#a6cee3", lwd=4)
}
```



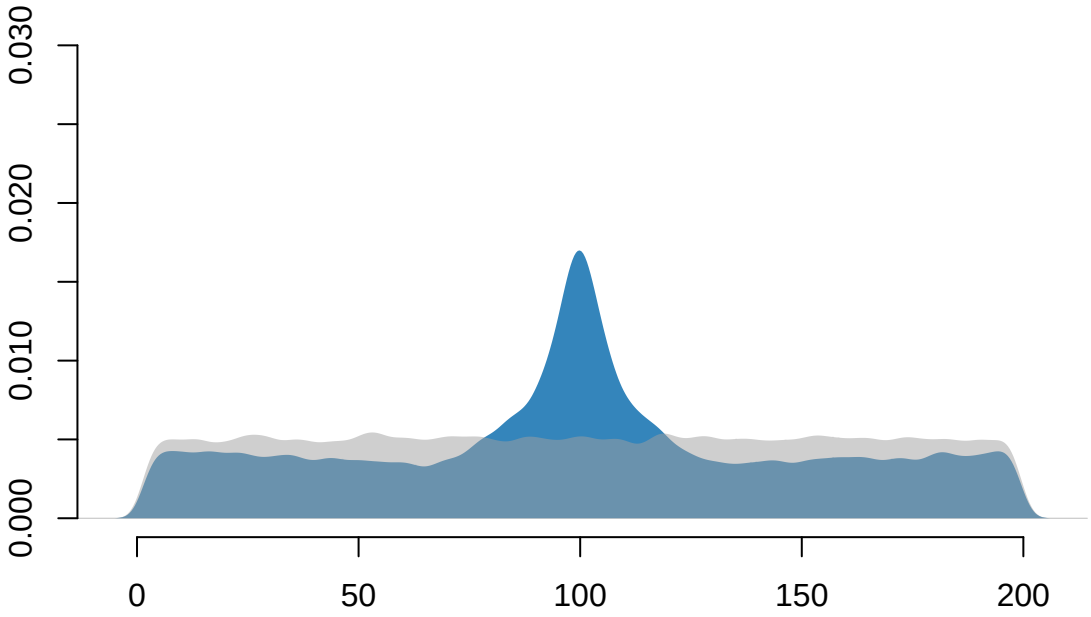

0.0
0.2
0.4
0.6
0.8
1.0
5
10
15

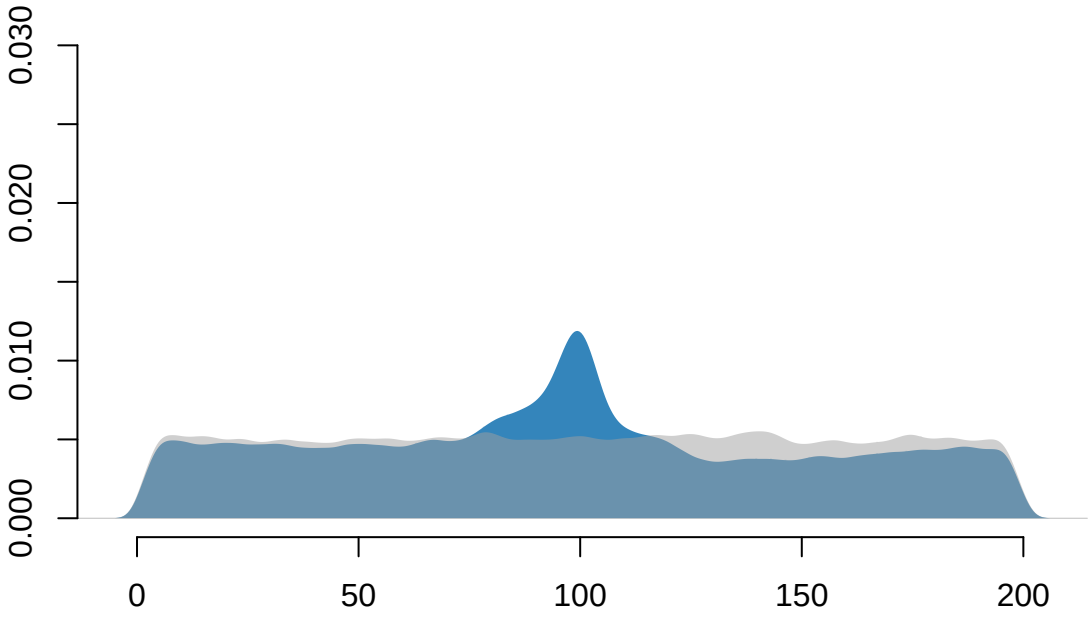

0.0
0.2
0.4
0.6
0.8
1.0
5
10
15

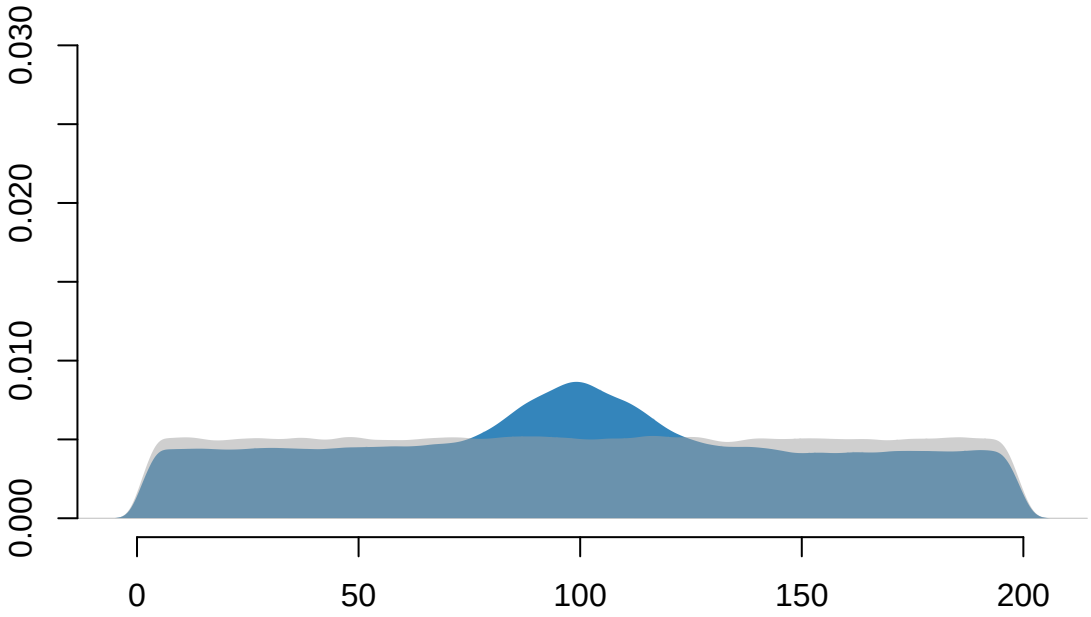

0.0
0.2
0.4
0.6
0.8
1.0
5
10
15

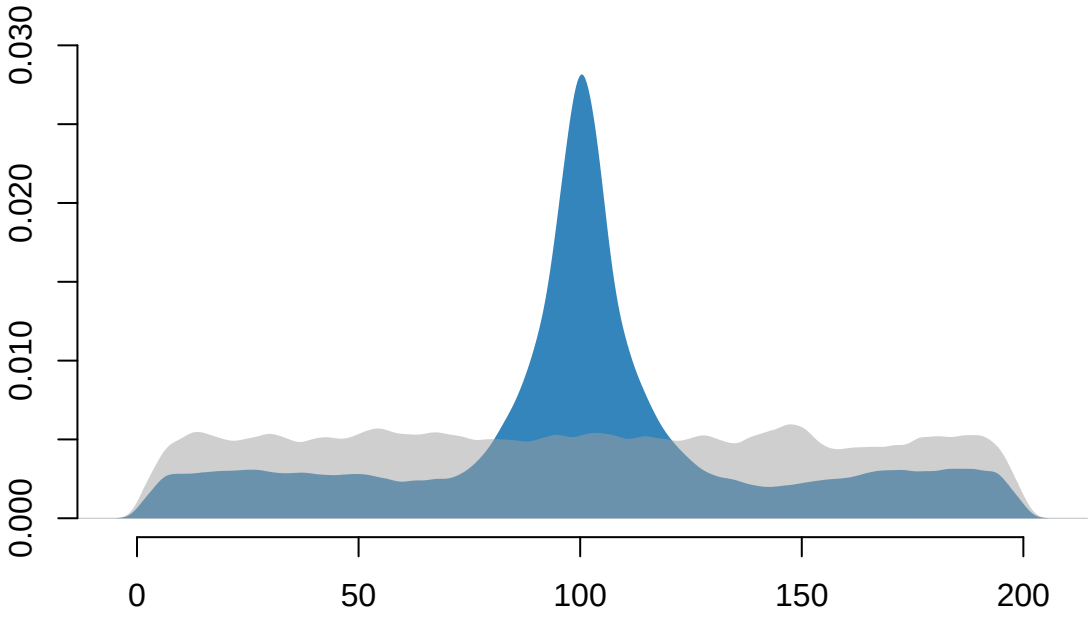


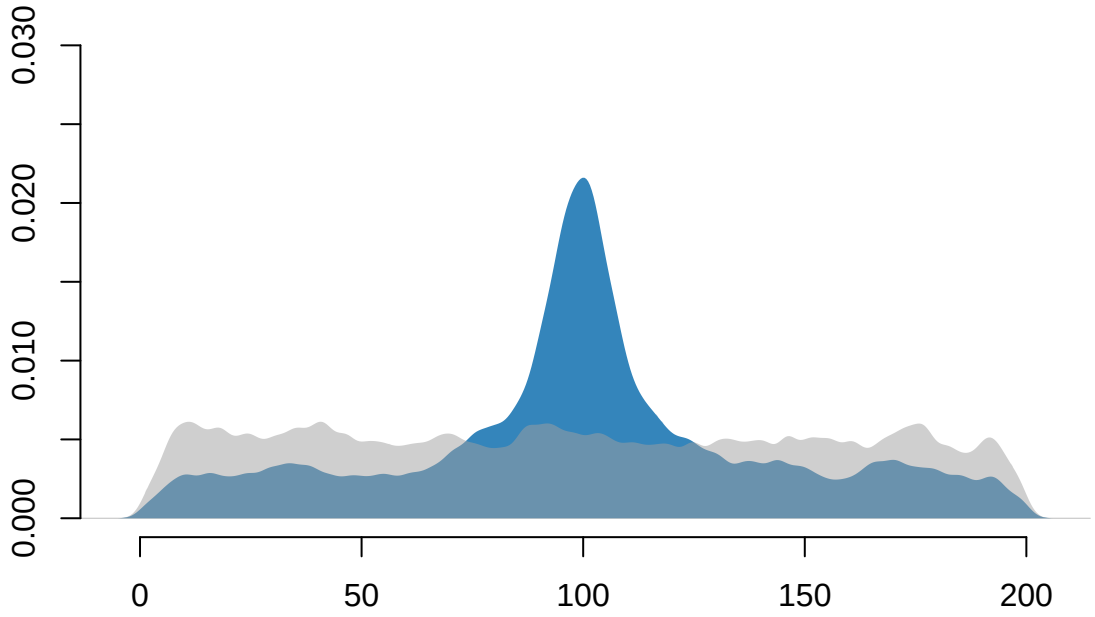

```
# motif density
RAPs_motifdensity <- RAPs
RAPs_motifdensity[["PTBP1"]]$positive_fa <- gsub("T","Y",RAPs_motifdensity[["PTBP1"]]$positive_fa)
RAPs_motifdensity[["PTBP1"]]$positive_fa <- gsub("C","Y",RAPs_motifdensity[["PTBP1"]]$positive_fa)
RAPs_motifdensity[["PTBP1"]]$negative_fa <- gsub("T","Y",RAPs_motifdensity[["PTBP1"]]$negative_fa)
RAPs_motifdensity[["PTBP1"]]$negative_fa <- gsub("C","Y",RAPs_motifdensity[["PTBP1"]]$negative_fa)

Motifs <- c("TAG","TTTT","YYYY","GCATG|GAATG","AACATC|AACAAC|AACACC")

for (i in 1:length(Names_protein)){
  signal <- density(unlist(str_locate_all(RAPs_motifdensity[[Names_protein[i]]]$positive_fa,Motifs[i])))
  noise <- density(unlist(str_locate_all(RAPs_motifdensity[[Names_protein[i]]]$negative_fa,Motifs[i])),
  plot(signal, col=NA, main=NA, xlab=NA, ylab=NA, ylim=c(0,0.03), axes=FALSE)
  axis(side=1, labels=T)
  axis(side=2, labels=T)
  polygon(signal, col=alpha("#1f78b4", 0.9),border = NA)
  polygon(noise, col=alpha("#A0A0A0", 0.5),border = NA)
}
```


0.030
0.020
0.010
0.000
0
50
100
150
200


0.030
0.020
0.010
0.000
0
50
100
150
200

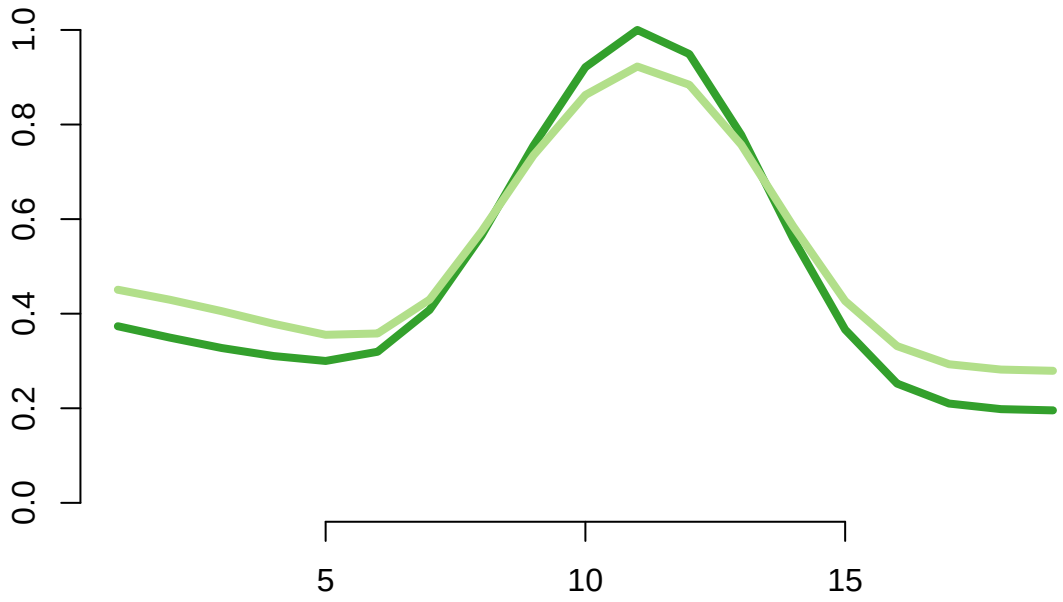

0.030
0.020
0.010
0.000
0
50
100
150
200

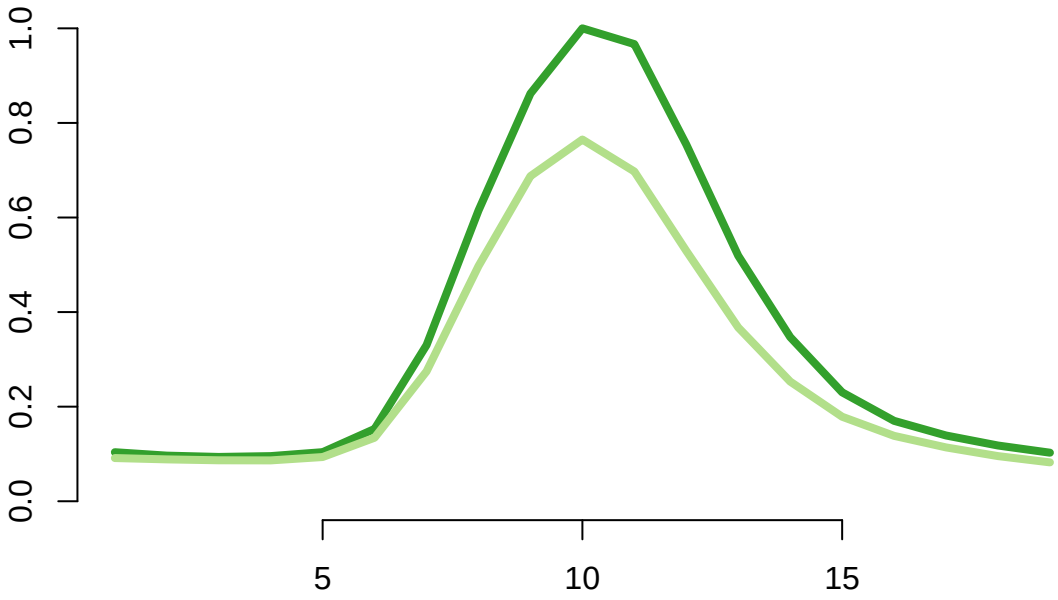

0.030
0.020
0.010
0.000
0
50
100
150
200

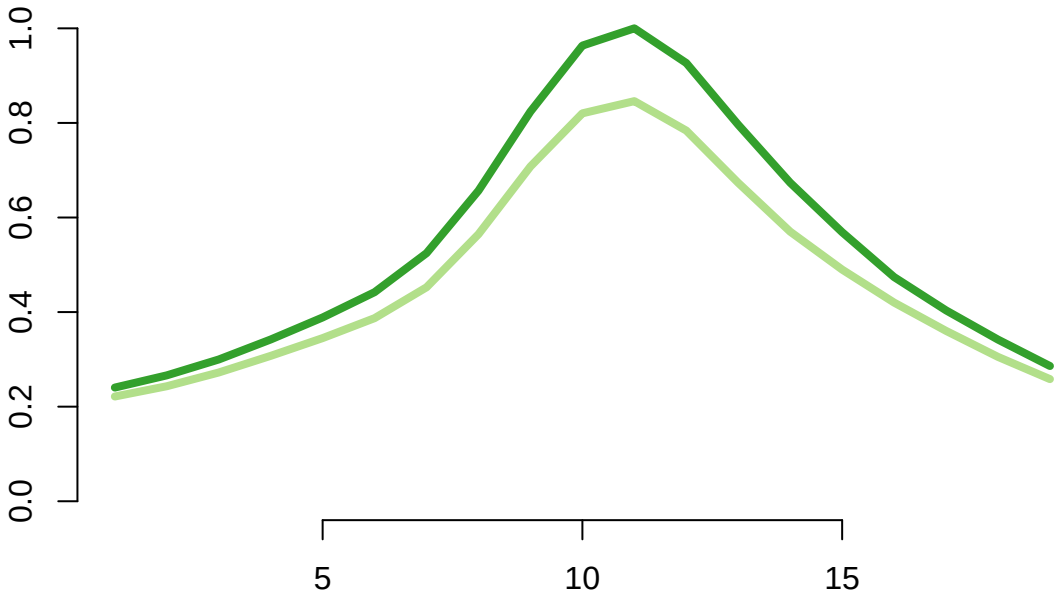


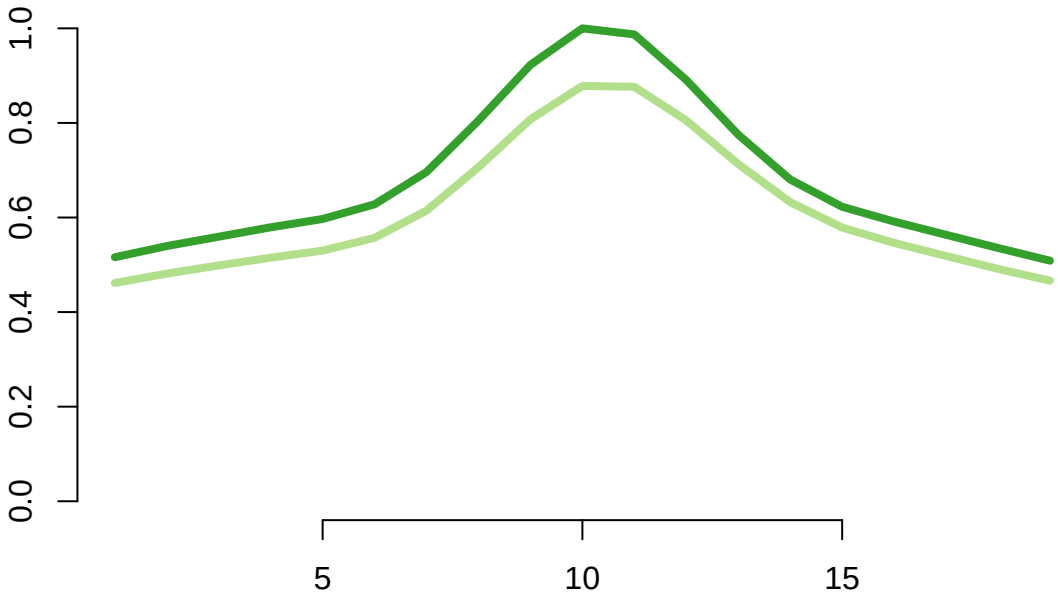

```
# eCLIP
## DeepTools count matrices (bin size = 10nt) are read in
## DeepTools was used with the following command to generate the per nt count matrices
## computeMatrix reference-point -S rep1.bw -R rep1.bed -a 100 -b 100 -bs 10
PATH_eCLIP_Coverage <- "./Data/eCLIP/Coverage/10nt/"
PEAKS_eCLIP_Coverage <- list.files(path = PATH_eCLIP_Coverage)
Names_eCLIP_Coverage <- unlist(str_split(PEAKS_eCLIP_Coverage,"\\.matr"))[grep("txt",unlist(str_split(PE
CLIPseq_Coverage <- list()
for (i in 1:length(Names_eCLIP_Coverage)){
  CLIPseq_Coverage[[i]] <- as.data.frame(read.table(paste(PATH_eCLIP_Coverage,PEAKS_eCLIP_Coverage[i],se
}
names(CLIPseq_Coverage) <- Names_eCLIP_Coverage
Names_eCLIP_Coverage <- c("HNRNPA1_eCLIP","HNRNPC_eCLIP","PTBP1_eCLIP","RBFOX2_eCLIP","YBX3_eCLIP")
# coverage normalized RPM
for (i in 1:length(Names_eCLIP_Coverage)){

  rep1_name <- paste (Names_eCLIP_Coverage[i],".rep1",sep="")
  rep2_name <- paste (Names_eCLIP_Coverage[i],".rep2",sep="")

  rep1_mean <- rollapply(colMeans(as.matrix(CLIPseq_Coverage[[rep1_name]])), width=2, FUN = mean)
  rep2_mean <- rollapply(colMeans(as.matrix(CLIPseq_Coverage[[rep2_name]])), width=2, FUN = mean)

  x <- rep1_mean/max(c(rep1_mean,rep2_mean))
  y <- rep2_mean/max(c(rep1_mean,rep2_mean))
```

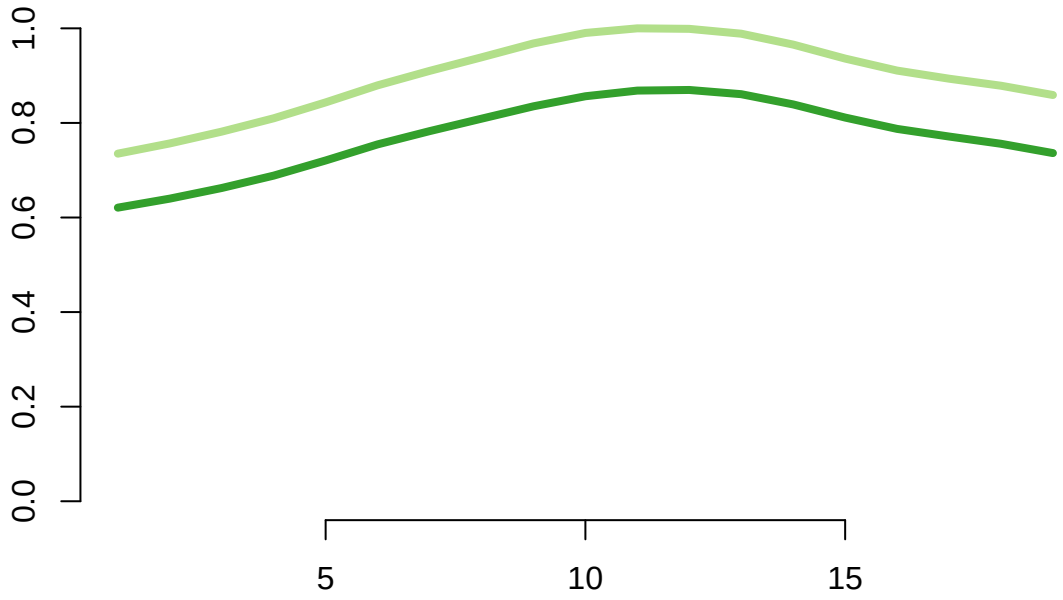
```
  plot(x,type="l",col="#33a02c", lwd=4, ylab=NA, xlab=NA, ylim=c(0,1), las=1, axes=FALSE)
  axis(side=1, labels=T)
  axis(side=2, labels=T)
  points(y,type="l",col="#b2df8a", lwd=4)
}
```



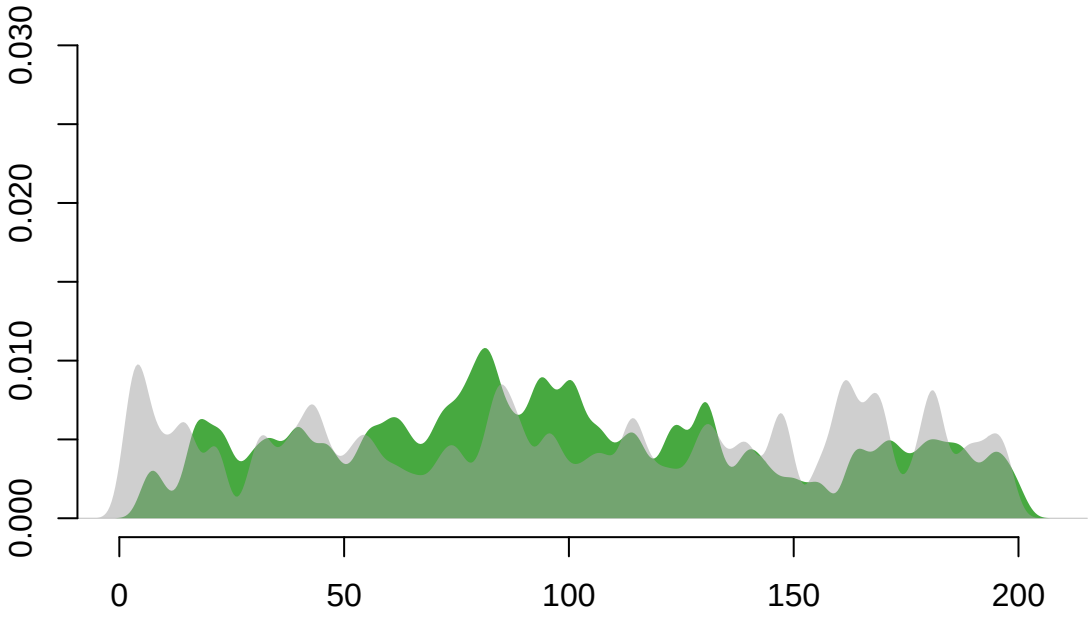

0.0
0.2
0.4
0.6
0.8
1.0
5
10
15

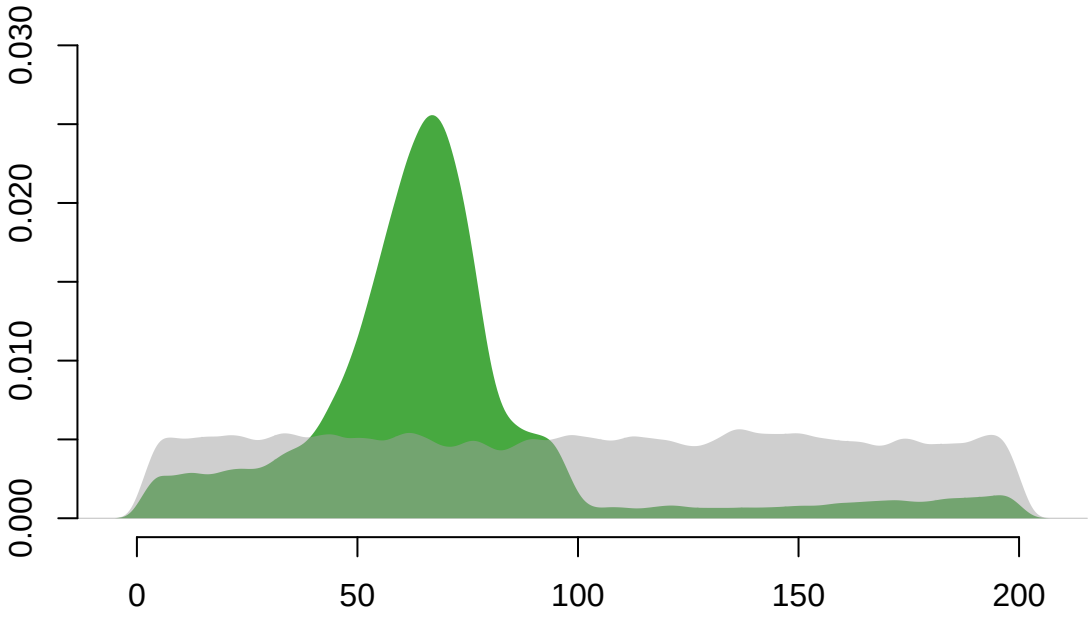

0.0
0.2
0.4
0.6
0.8
1.0
5
10
15

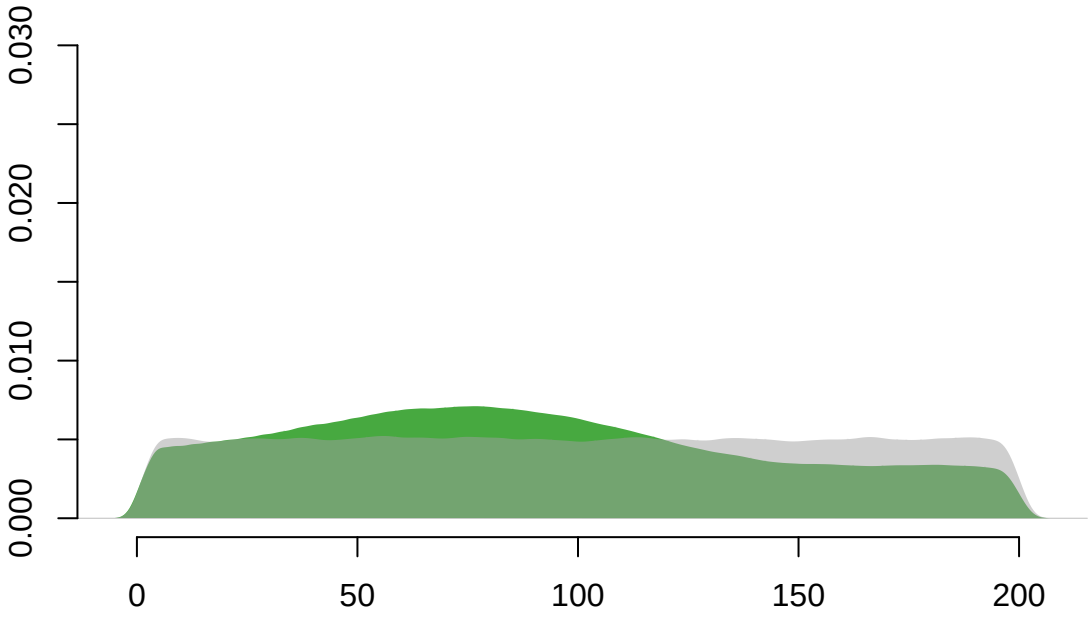

0.0
0.2
0.4
0.6
0.8
1.0
5
10
15

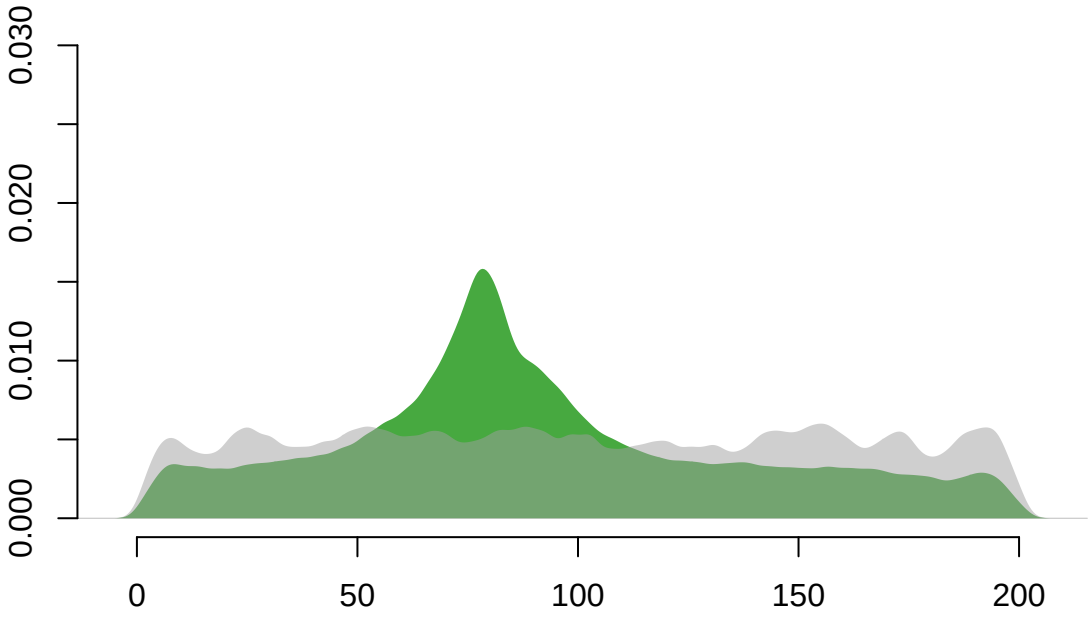


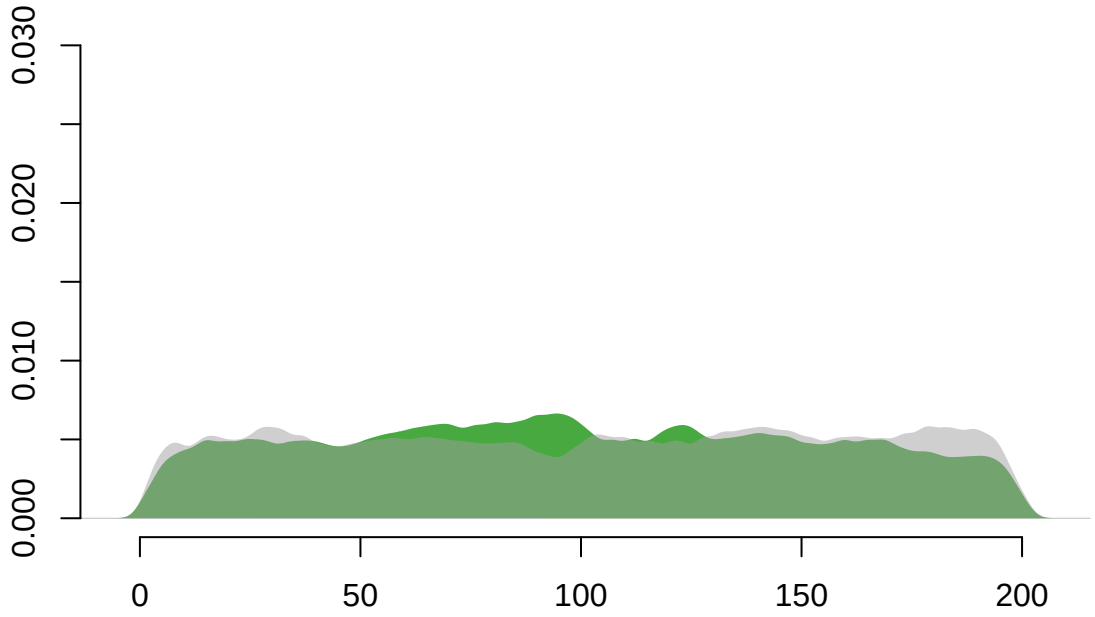

```
# motif density
CLIPs[["PTBP1"]]$positive_fa <- gsub("T","Y",CLIPs[["PTBP1"]]$positive_fa)
CLIPs[["PTBP1"]]$positive_fa <- gsub("C","Y",CLIPs[["PTBP1"]]$positive_fa)
CLIPs[["PTBP1"]]$negative_fa <- gsub("T","Y",CLIPs[["PTBP1"]]$negative_fa)
CLIPs[["PTBP1"]]$negative_fa <- gsub("C","Y",CLIPs[["PTBP1"]]$negative_fa)

Motifs <- c("TAG","TTTT","YYYY","GCATG","CCATC|TCATC")
Names_protein <- c("HNRNPA1","HNRNPC","PTBP1","RBFOX2","YBX3")
for (i in 1:length(Names_protein)){

  signal <- density(unlist(str_locate_all(CLIPs[[Names_protein[i]]]$positive_fa,Motifs[i])),bw=2)
  noise <- density(unlist(str_locate_all(CLIPs[[Names_protein[i]]]$negative_fa,Motifs[i])),bw=2)

  plot(signal, col=NA, main=NA, xlab=NA, ylab=NA, ylim=c(0,0.03), axes=FALSE)
  axis(side=1, labels=T)
  axis(side=2, labels=T)
  polygon(signal, col=alpha("#33a02c", 0.9),border = NA)
  polygon(noise, col=alpha("#A0A0A0", 0.5),border = NA)
}
```


0.030
0.020
0.010
0.000
0
50
100
150
200


0.030
0.020
0.010
0.000
0
50
100
150
200


0.030
0.020
0.010
0.000
0
50
100
150
200

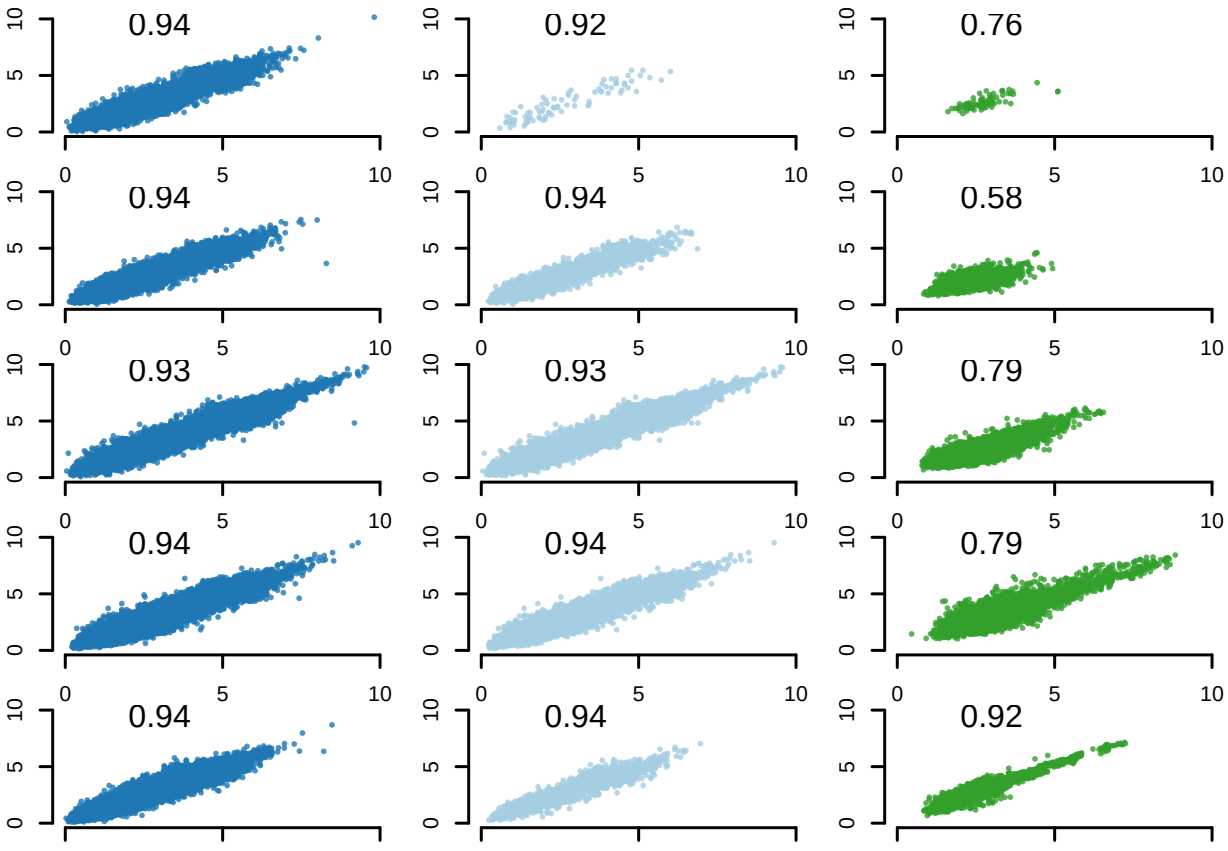

0.000
0.010
0.020
0.030
0
50
100
150
200



0.5.4 Figure 2E

```
Names_protein <- c("HNRNPA1","HNRNPC","PTBP1","RBFOX2","YBX3")

#pdf("./Figure/Figure2E_similarity.pdf", width = 11, height = 11)
par(mfrow=c(5,3), mar=c(1,2,1,1))
set.seed(123)

for(i in Names_protein){
  # RAPSeq
  raps_rep1 <- log2(RAPs[[i]]$FCH_rep1)
  raps_rep2 <- log2(RAPs[[i]]$FCH_rep2)
  plot(raps_rep1, raps_rep2, xlim=c(0,10),ylim=c(0,10), xlab=NA, ylab=NA, bty="n", xaxt="n", yaxt="n", c
  axis(1, at = c(0, 5, 10), lwd=1.5, labels = T)
  axis(2, at = c(0, 5, 10), lwd=1.5, labels = T)
  # spearman
  text_ann <- "rho ="
  raps_spearman <- round(cor(raps_rep1,raps_rep2, method = "spearman"), 2)
  text_ann <- paste(text_ann, raps_spearman,sep=" ")
  text(3,9.5,labels = raps_spearman, cex=1.5)

  # RAP sampling
  raps_sample <- RAPs[[i]][sample(1:nrow(RAPs[[i]]),(nrow(CLIPs[[i]]))),]
  raps_sample_rep1 <- log2(raps_sample$FCH_rep1)
```

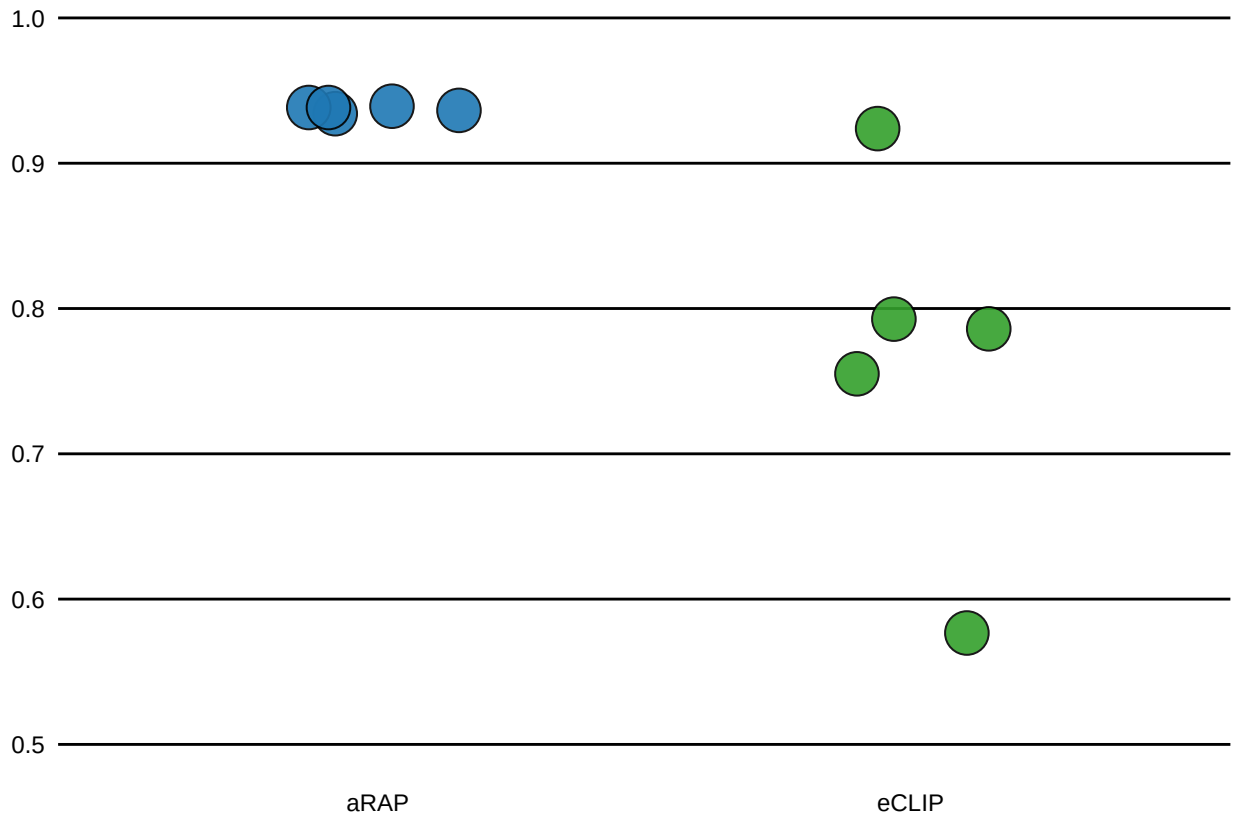
```
  raps_sample_rep2 <- log2(raps_sample$FCH_rep2)
  plot(raps_sample_rep1,raps_sample_rep2,xlim=c(0,10),ylim=c(0,10), xlab=NA, ylab=NA, bty="n", xaxt="n"
  axis(1, at = c(0, 5, 10), lwd=1.5, labels = T)
  axis(2, at = c(0, 5, 10), lwd=1.5, labels = T)
  raps_sample_spearman <- round(cor(raps_sample_rep1,raps_sample_rep2, method = "spearman"), 2)
  text_ann <- paste(text_ann, raps_sample_spearman, sep=" ")
  text(3,9.5,labels = raps_sample_spearman, cex=1.5)

  # eCLIP
  eCLIP_rep1 <- log2(CLIPs[[i]]$FC_rep1)
  eCLIP_rep2 <- log2(CLIPs[[i]]$FC_rep2)
  plot(eCLIP_rep1, eCLIP_rep2, xlim=c(0,10),ylim=c(0,10), xlab=NA, ylab=NA, bty="n", xaxt="n", yaxt="n"
  axis(1, at = c(0, 5, 10), lwd=1.5, labels = T)
  axis(2, at = c(0, 5, 10), lwd=1.5, labels = T)
  eCLIP_spearman <- round(cor(eCLIP_rep1,eCLIP_rep2, method = "spearman"), 2)
  text_ann <- paste(text_ann, eCLIP_spearman,sep=" ")
  text(3,9.5, labels = eCLIP_spearman, cex=1.5)
}
```




```
#dev.off()
```

0.5.5 Figure 2F

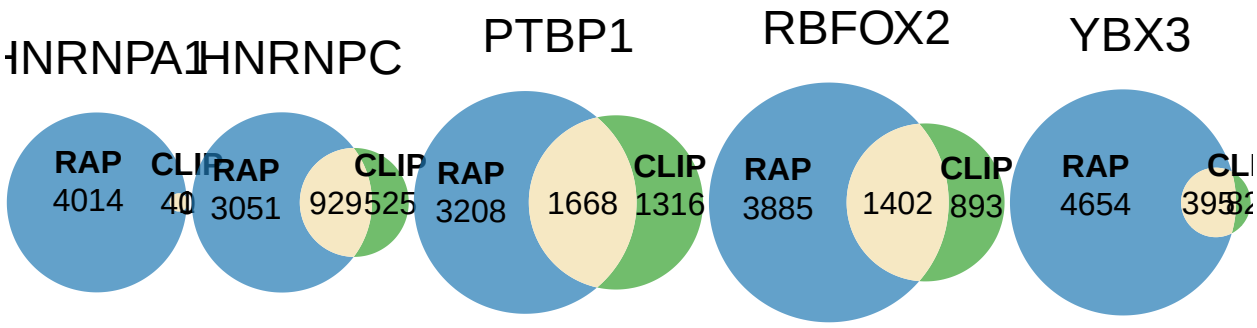
```
# spearman
RAP_spearman <- c()
CLIP_spearman <- c()
Names_protein <- c("HNRNPA1","HNRNPC","PTBP1","RBFOX2","YBX3")
for(i in Names_protein){
  raps_rep1 <- RAPs[[i]]$FCH_rep1
  raps_rep2 <- RAPs[[i]]$FCH_rep2
  RAP_spearman <- c(RAP_spearman, cor(raps_rep1, raps_rep2, method="spearman"))

  clip_rep1 <- CLIPs[[i]]$FC_rep1
  clip_rep2 <- CLIPs[[i]]$FC_rep2
  CLIP_spearman <- c(CLIP_spearman, cor(clip_rep1,clip_rep2,method="spearman"))
}

# merging
cors <- c(RAP_spearman,CLIP_spearman)
assay <- c(rep("aRAP",5),rep("eCLIP",5))

# data frame
data_cors <- data.frame(cors,assay)
data_cors$cors <- as.numeric(data_cors$cors)
data_cors$assay <- as.factor(data_cors$assay)

# plot
set.seed(1)
#pdf("./Figure/Figure2_F.pdf", width = 2.9, height = 5.3)
ggplot(data=data_cors,aes(x=assay,y=cors,fill=assay)) +
  geom_dotplot(binaxis = "y",
               stackdir='center',
               binwidth = .005,
               dotsize = 6,
               position = position_jitter(height=NULL, width = 0.15),
               alpha = 0.9
  ) +
  theme(panel.background = element_blank(),
        panel.grid.major.x = element_blank(),
        panel.grid.minor.x = element_blank(),
        panel.grid.major.y = element_line(color="black"),
        axis.ticks = element_blank(),
        axis.text = element_text(color="black"),
        legend.position = "none",
        axis.title = element_blank()
  ) +
  scale_fill_manual(values = c("#1f78b4","#33a02c") ) +
  ylim(0.5,1)
```



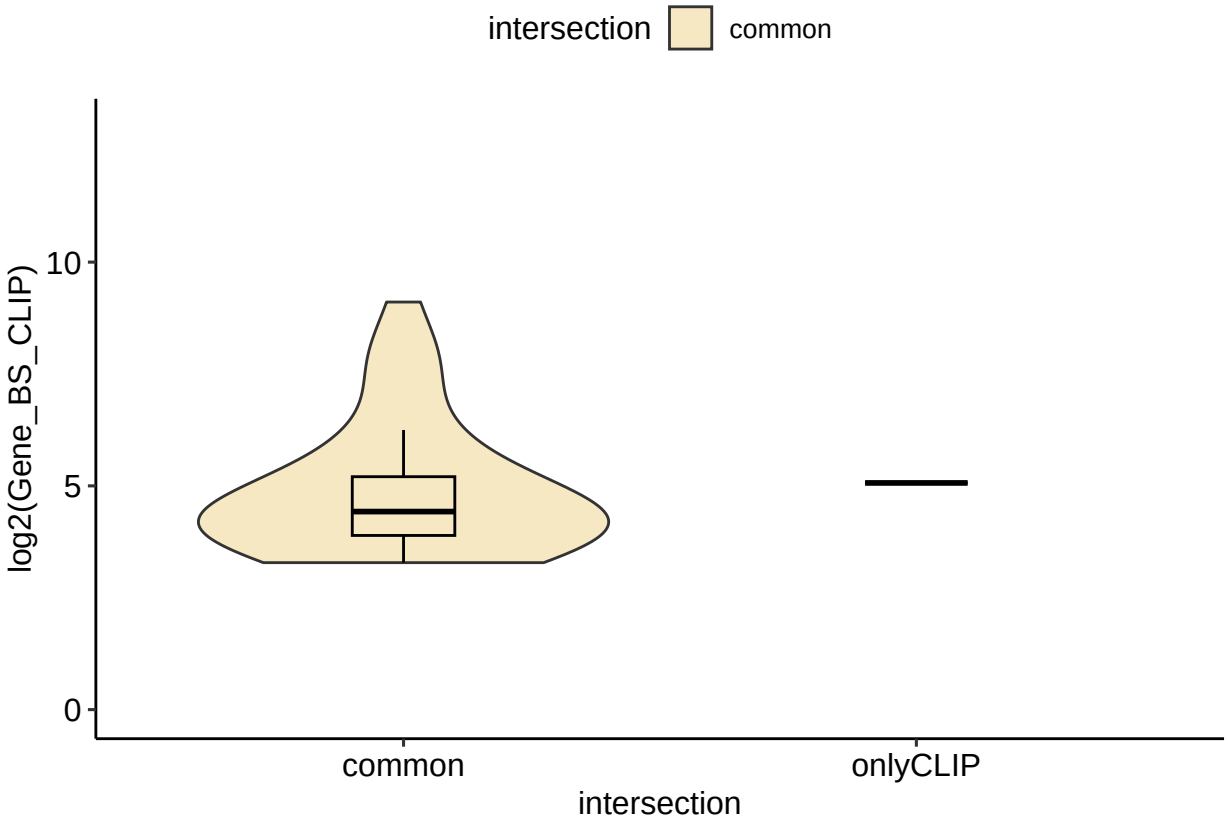

```
#dev.off()
```

0.5.6 Figure 2G

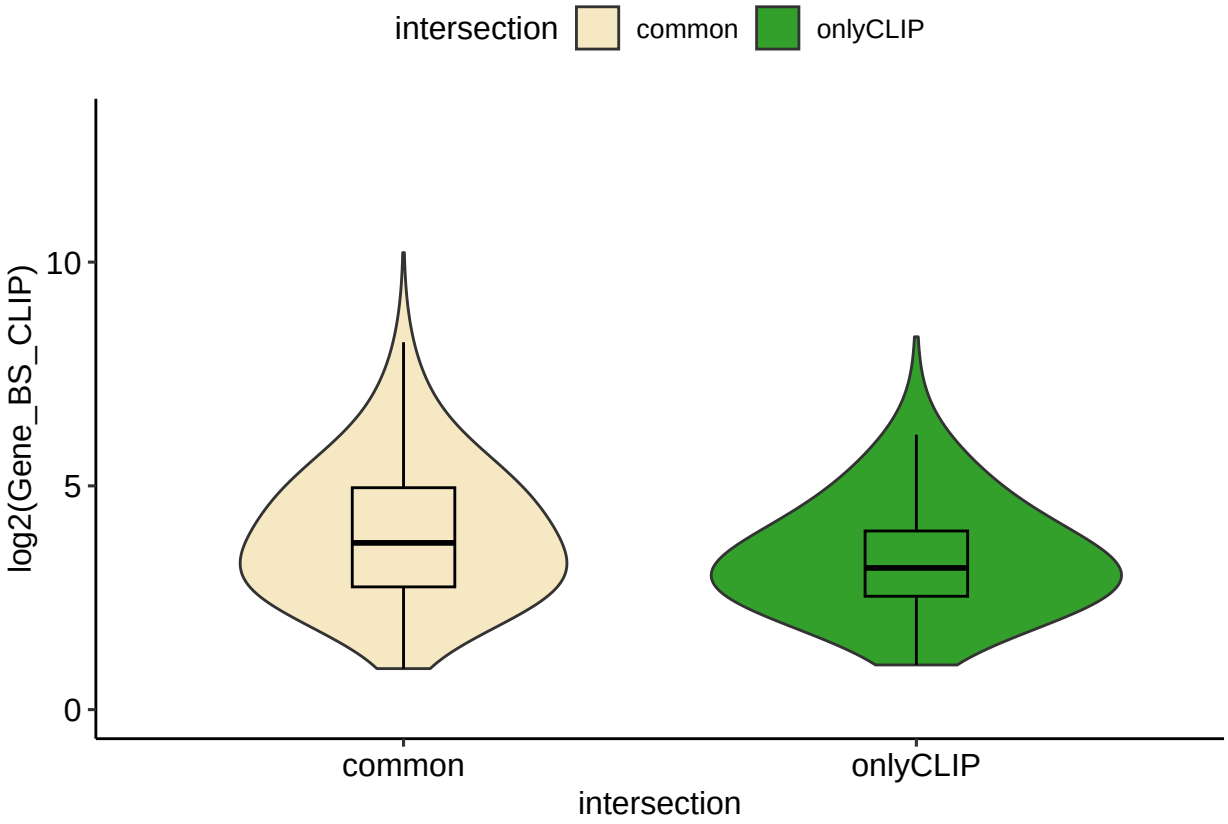
```
# left
venns <- list()
plot_area <- c()
Names_protein <- c("HNRNPA1","HNRNPC","PTBP1","RBFOX2","YBX3")
for (i in 1:length(Names_protein)){
  common_RAPs_CLIPs <- length(intersect(unique(RAPs[[Names_protein[i]]]$gene_ID),unique(CLIPs[[Names_pr
  uniq_RAP <- length(unique(RAPs[[Names_protein[i]]]$gene_ID)) - common_RAPs_CLIPs
  uniq_CLIP <- length(unique(CLIPs[[Names_protein[i]]]$gene_ID)) - common_RAPs_CLIPs
  plot_area <- c(plot_area,length(unique(RAPs[[Names_protein[i]]]$gene_ID)) + common_RAPs_CLIPs)

  v <- euler(c(RAP=uniq_RAP, CLIP=uniq_CLIP, "RAP&CLIP"=common_RAPs_CLIPs))
  venns[[i]] <- plot( v, fills=c(alpha("#1f78b4",0.7),alpha("#33a02c",0.7), "#f6e8c3"), main=Names_prot
}
#pdf("./Figure/Figure2G_Venn.pdf", width = 30, height = 12.6)
grid.arrange(grobs = venns, widths=plot_area)
```



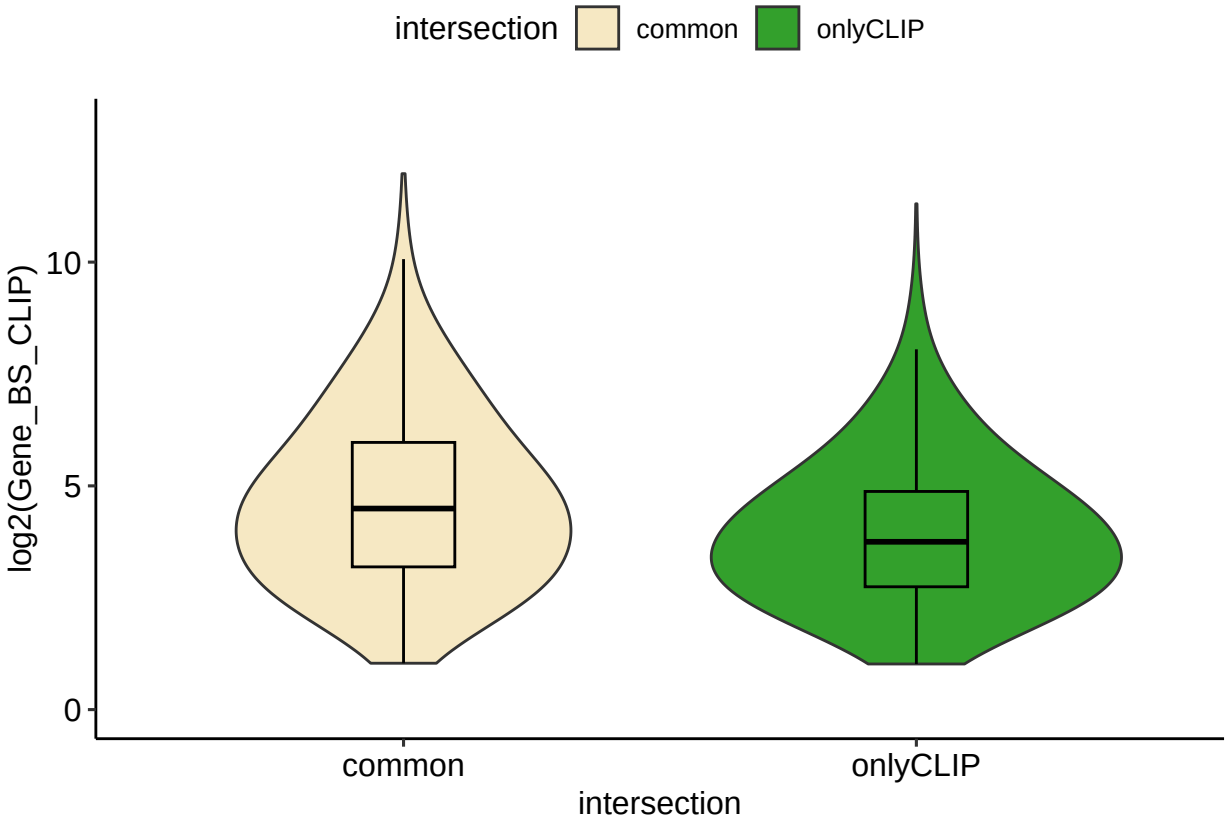

```
#dev.off()

# right
# HNRNPA1_pval
RAPs_HNRNPA1 <- unique(RAPs[["HNRNPA1"]][,c("gene_ID","Gene_BS")])
CLIPs_HNRNPA1 <- unique(CLIPs[["HNRNPA1"]][,c("gene_ID","Gene_BS_CLIP")])
RAPs_CLIPs_common_HNRNPA1 <- CLIPs_HNRNPA1[grep(paste(intersect(CLIPs_HNRNPA1$gene_ID,RAPs_HNRNPA1$gene
RAPs_CLIPs_common_HNRNPA1$intersection <- rep("common",nrow(RAPs_CLIPs_common_HNRNPA1))
CLIPs_uniq_HNRNPA1 <- CLIPs_HNRNPA1[grep(paste(setdiff(CLIPs_HNRNPA1$gene_ID,RAPs_HNRNPA1$gene_ID),colla
CLIPs_uniq_HNRNPA1$intersection <- rep("onlyCLIP",nrow(CLIPs_uniq_HNRNPA1))
CLIPS_common_uniq_HNRNPA1 <- rbind(RAPs_CLIPs_common_HNRNPA1,CLIPs_uniq_HNRNPA1)
plot_HNRNPA1 <- ggplot( data = CLIPS_common_uniq_HNRNPA1, aes( x=intersection,y=log2(Gene_BS_CLIP) ) ) +
  geom_violin(aes(fill = intersection), bw=0.85, width=0.8) +
  scale_fill_manual(values = c("#f6e8c3", "#33a02c")) +
  geom_boxplot(color="black", fill=NA, width = 0.2, outlier.shape = NA) +
  theme_pubr() +
  coord_cartesian(ylim=c(0,13))
plot_HNRNPA1
## Warning: Groups with fewer than two datapoints have been dropped.
## i Set `drop = FALSE` to consider such groups for position adjustment purposes.
```



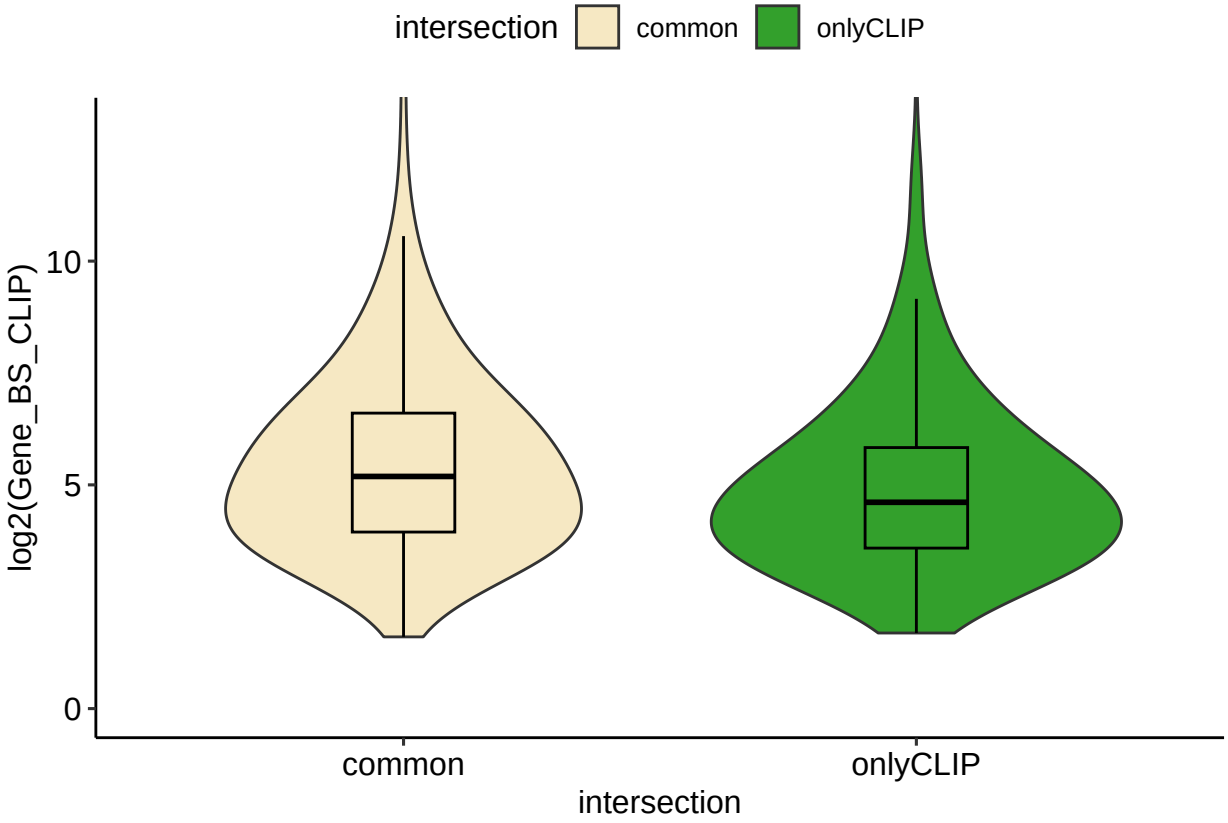

```
HNRNPA1_pval <- wilcox.test(RAPs_CLIPs_common_HNRNPA1$Gene_BS_CLIP,CLIPs_uniq_HNRNPA1$Gene_BS_CLIP, alt

# HNRNPC_pval
RAPs_HNRNPC <- unique(RAPs[["HNRNPC"]][,c("gene_ID","Gene_BS")])
CLIPs_HNRNPC <- unique(CLIPs[["HNRNPC"]][,c("gene_ID","Gene_BS_CLIP")])
RAPs_CLIPs_common_HNRNPC <- CLIPs_HNRNPC[grep(paste(intersect(CLIPs_HNRNPC$gene_ID,RAPs_HNRNPC$gene_ID)
RAPs_CLIPs_common_HNRNPC$intersection <- rep("common",nrow(RAPs_CLIPs_common_HNRNPC))
CLIPs_uniq_HNRNPC <- CLIPs_HNRNPC[grep(paste(setdiff(CLIPs_HNRNPC$gene_ID,RAPs_HNRNPC$gene_ID),collapse=
CLIPs_uniq_HNRNPC$intersection <- rep("onlyCLIP",nrow(CLIPs_uniq_HNRNPC))
CLIPS_common_uniq_HNRNPC <- rbind(RAPs_CLIPs_common_HNRNPC,CLIPs_uniq_HNRNPC)
plot_HNRNPC <- ggplot( data = CLIPS_common_uniq_HNRNPC, aes( x=intersection,y=log2(Gene_BS_CLIP) ) ) +
  geom_violin(aes(fill = intersection), bw=0.85, width=0.8) +
  scale_fill_manual(values = c("#f6e8c3", "#33a02c")) +
  geom_boxplot(color="black", fill=NA, width = 0.2, outlier.shape = NA) +
  theme_pubr() +
  coord_cartesian(ylim=c(0,13))
plot_HNRNPC
```



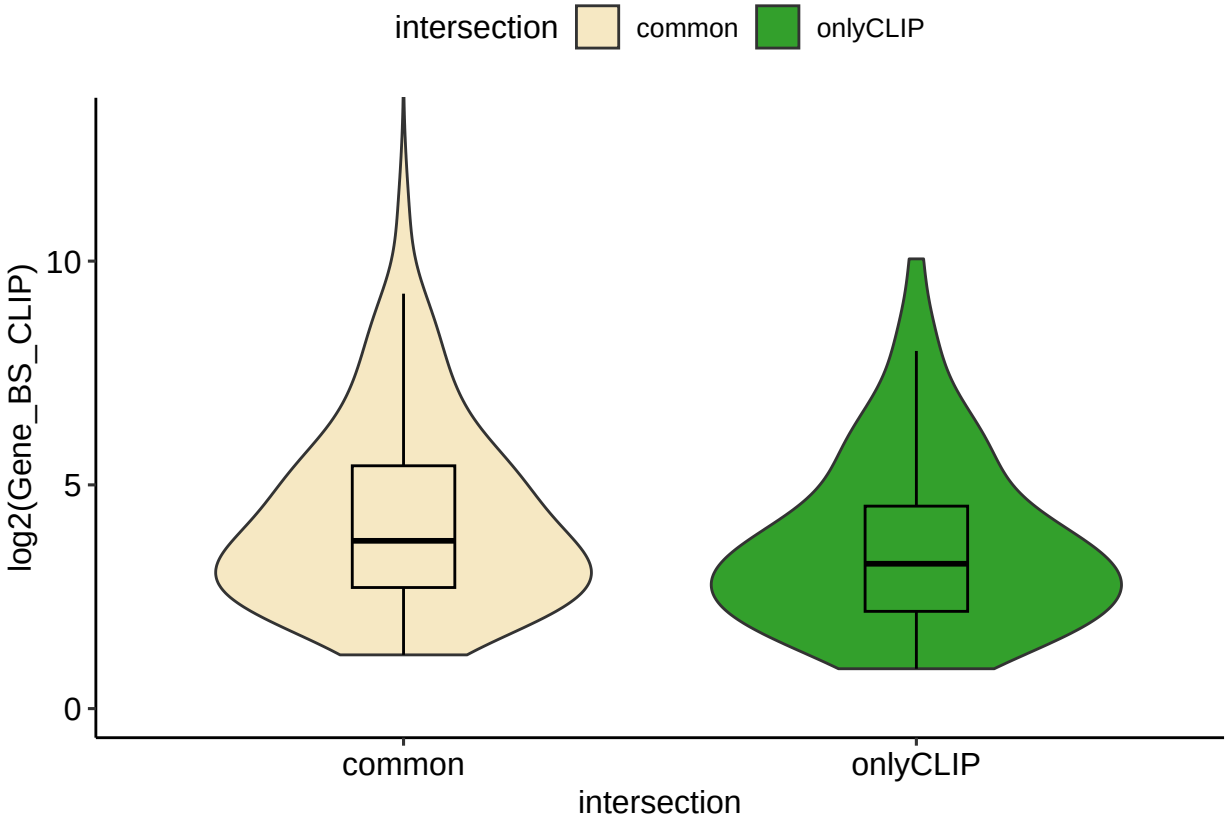

```
HNRNPC_pval <- wilcox.test(RAPs_CLIPs_common_HNRNPC$Gene_BS_CLIP,CLIPs_uniq_HNRNPC$Gene_BS_CLIP, alterna

# PTBP1_pval
RAPs_PTBP1 <- unique(RAPs[["PTBP1"]][,c("gene_ID","Gene_BS")])
CLIPs_PTBP1 <- unique(CLIPs[["PTBP1"]][,c("gene_ID","Gene_BS_CLIP")])
RAPs_CLIPs_common_PTBP1 <- CLIPs_PTBP1[grep(paste(intersect(CLIPs_PTBP1$gene_ID,RAPs_PTBP1$gene_ID),col
RAPs_CLIPs_common_PTBP1$intersection <- rep("common",nrow(RAPs_CLIPs_common_PTBP1))
CLIPs_uniq_PTBP1 <- CLIPs_PTBP1[grep(paste(setdiff(CLIPs_PTBP1$gene_ID,RAPs_PTBP1$gene_ID),collapse="|"
CLIPs_uniq_PTBP1$intersection <- rep("onlyCLIP",nrow(CLIPs_uniq_PTBP1))
CLIPS_common_uniq_PTBP1 <- rbind(RAPs_CLIPs_common_PTBP1,CLIPs_uniq_PTBP1)
plot_PTBP1 <- ggplot( data = CLIPS_common_uniq_PTBP1, aes( x=intersection,y=log2(Gene_BS_CLIP) ) ) +
  geom_violin(aes(fill = intersection), bw=0.85, width=0.8) +
  scale_fill_manual(values = c("#f6e8c3", "#33a02c")) +
  geom_boxplot(color="black", fill=NA, width = 0.2, outlier.shape = NA) +
  theme_pubr() +
  coord_cartesian(ylim=c(0,13))
plot_PTBP1
```




```
PTBP1_pval <- wilcox.test(RAPs_CLIPs_common_PTBP1$Gene_BS_CLIP,CLIPs_uniq_PTBP1$Gene_BS_CLIP, alternati

# RBFOX2_pval
RAPs_RBFOX2 <- unique(RAPs[["RBFOX2"]][,c("gene_ID","Gene_BS")])
CLIPs_RBFOX2 <- unique(CLIPs[["RBFOX2"]][,c("gene_ID","Gene_BS_CLIP")])
RAPs_CLIPs_common_RBFOX2 <- CLIPs_RBFOX2[grep(paste(intersect(CLIPs_RBFOX2$gene_ID,RAPs_RBFOX2$gene_ID)
RAPs_CLIPs_common_RBFOX2$intersection <- rep("common",nrow(RAPs_CLIPs_common_RBFOX2))
CLIPs_uniq_RBFOX2 <- CLIPs_RBFOX2[grep(paste(setdiff(CLIPs_RBFOX2$gene_ID,RAPs_RBFOX2$gene_ID),collapse=
CLIPs_uniq_RBFOX2$intersection <- rep("onlyCLIP",nrow(CLIPs_uniq_RBFOX2))
CLIPS_common_uniq_RBFOX2 <- rbind(RAPs_CLIPs_common_RBFOX2,CLIPs_uniq_RBFOX2)
plot_RBFOX2 <- ggplot( data = CLIPS_common_uniq_RBFOX2, aes( x=intersection,y=log2(Gene_BS_CLIP) ) ) +
  geom_violin(aes(fill = intersection), bw=0.85, width=0.8) +
  scale_fill_manual(values = c("#f6e8c3", "#33a02c")) +
  geom_boxplot(color="black", fill=NA, width = 0.2, outlier.shape = NA) +
  theme_pubr() +
  coord_cartesian(ylim=c(0,13))
plot_RBFOX2
```



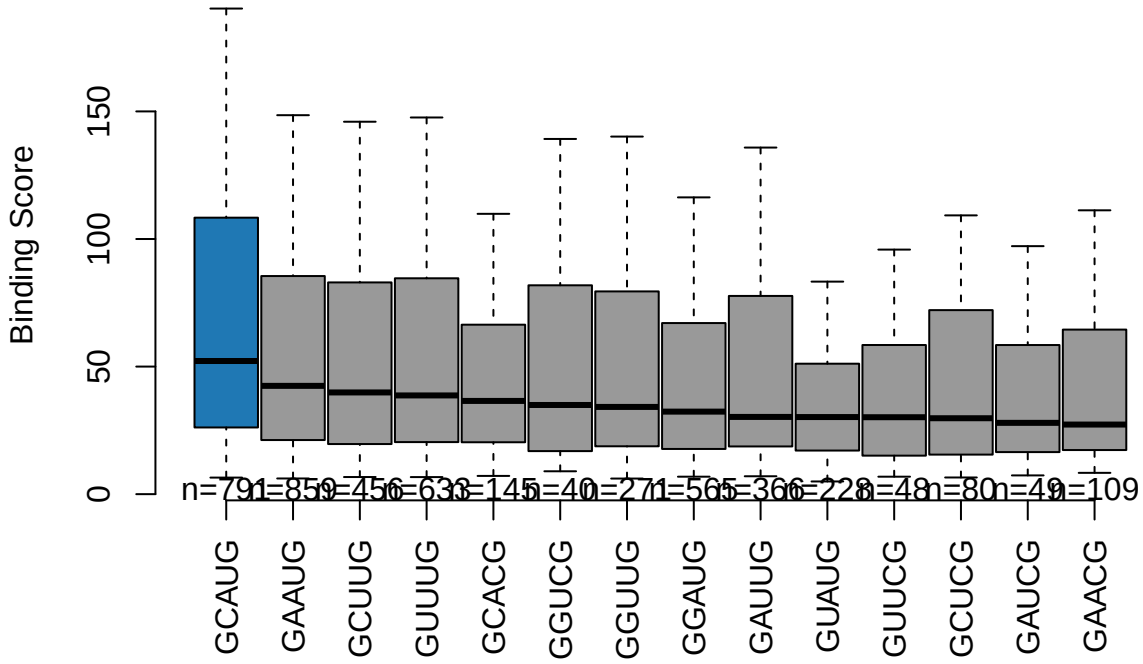

```
RBFOX2_pval <- wilcox.test(RAPs_CLIPs_common_RBFOX2$Gene_BS_CLIP,CLIPs_uniq_RBFOX2$Gene_BS_CLIP, alterna

# YBX3_pval
RAPs_YBX3 <- unique(RAPs[["YBX3"]][,c("gene_ID","Gene_BS")])
CLIPs_YBX3 <- unique(CLIPs[["YBX3"]][,c("gene_ID","Gene_BS_CLIP")])
RAPs_CLIPs_common_YBX3 <- CLIPs_YBX3[grep(paste(intersect(CLIPs_YBX3$gene_ID,RAPs_YBX3$gene_ID),collaps
RAPs_CLIPs_common_YBX3$intersection <- rep("common",nrow(RAPs_CLIPs_common_YBX3))
CLIPs_uniq_YBX3 <- CLIPs_YBX3[grep(paste(setdiff(CLIPs_YBX3$gene_ID,RAPs_YBX3$gene_ID),collapse="|"),CL
CLIPs_uniq_YBX3$intersection <- rep("onlyCLIP",nrow(CLIPs_uniq_YBX3))
CLIPS_common_uniq_YBX3 <- rbind(RAPs_CLIPs_common_YBX3,CLIPs_uniq_YBX3)
plot_YBX3 <- ggplot( data = CLIPS_common_uniq_YBX3, aes( x=intersection,y=log2(Gene_BS_CLIP) ) ) +
  geom_violin(aes(fill = intersection), bw=0.85, width=0.8) +
  scale_fill_manual(values = c("#f6e8c3", "#33a02c")) +
  geom_boxplot(color="black", fill=NA, width = 0.2, outlier.shape = NA) +
  theme_pubr() +
  coord_cartesian(ylim=c(0,13))
plot_YBX3
```




```
YBX3_pval <- wilcox.test(RAPs_CLIPs_common_YBX3$Gene_BS_CLIP,CLIPs_uniq_YBX3$Gene_BS_CLIP, alternative =

# all
print("Wilcoxon rank sum test p values")
## [1] "Wilcoxon rank sum test p values"
print(paste("HNRNPA1",HNRNPA1_pval, sep=" "))
## [1] "HNRNPA1 0.731707317073171"
print(paste("HNRNPC",HNRNPC_pval,sep=" "))
## [1] "HNRNPC 2.89503670453362e-11"
print(paste("PTBP1",PTBP1_pval,sep=" "))
## [1] "PTBP1 5.50574629210848e-26"
print(paste("RBFOX2",RBFOX2_pval,sep=" "))
## [1] "RBFOX2 6.83842013493099e-13"
print(paste("YBX3",YBX3_pval,sep=" "))
## [1] "YBX3 0.00225799395930255"

p_figure_violin_2G <- ggarrange(plot_HNRNPA1,plot_HNRNPC,plot_PTBP1,plot_RBFOX2,plot_YBX3,nrow=5, commo
## Warning: Groups with fewer than two datapoints have been dropped.
## i Set `drop = FALSE` to consider such groups for position adjustment purposes.
## Groups with fewer than two datapoints have been dropped.
## i Set `drop = FALSE` to consider such groups for position adjustment purposes.
ggsave(filename = "./Figure/Figure2G_Violin.pdf", plot = p_figure_violin_2G, width = 4.7, height = 12.6
```

0.5.7 Figure S2B

```
GNWYG <- c("GCATG","GAATG","GGATG","GTTTG","GCTTG","GATTG","GGTTG","GAACG","GCACG","GTATG","GATCG","GCT
GNWYG_scores <- list()
medians <- c()
for (i in 1:length(GNWYG)){
  RAPs_GNWYG <- RAPs[["RBFOX2"]][grep(GNWYG[i],str_sub(RAPs[["RBFOX2"]]$positive_fa,50,150)),]
  GNWYG_subset <- GNWYG[grep(GNWYG[i],GNWYG,invert=T)]
  GNWYG_scores[[i]] <- RAPs_GNWYG[grep(paste(GNWYG_subset,collapse = "|"),str_sub(RAPs_GNWYG$positive_fa
  medians <- c(medians,median(GNWYG_scores[[i]]))
}

GNWYG <- gsub("T","U",GNWYG)
names(GNWYG_scores) <- GNWYG

#pdf("./Figure/Figure2/FigureS2B.pdf", width = 11, height = 7)
par(bty="n")
boxplot2(GNWYG_scores[order(-medians)], outline=F, horizontal=F, las=3, ylab="Binding Score", range=1, c
```



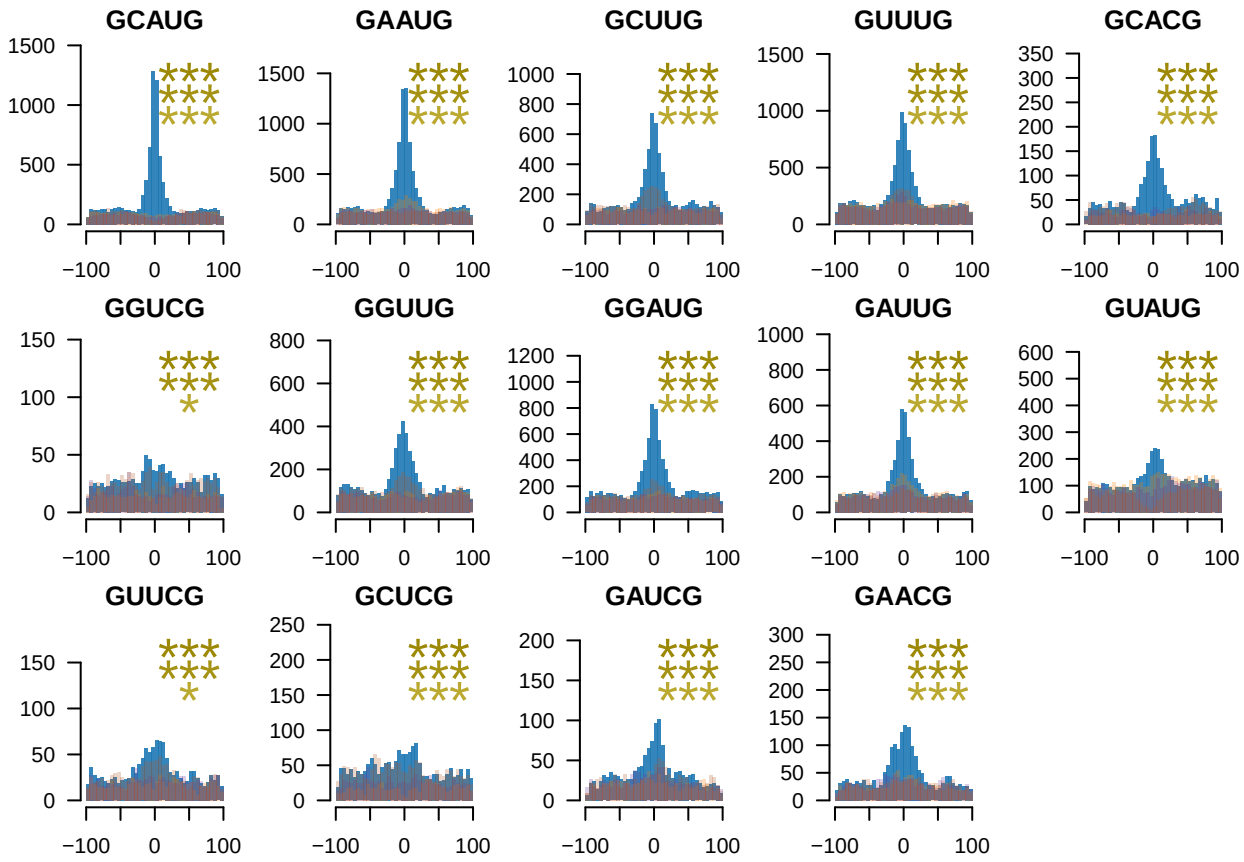

```
#dev.off()

GCAUG <- GNWYG_scores$GCAUG
GNWYG_scores <- GNWYG_scores[-1]
```

```
for (i in names(GNWYG_scores)){
  anno_text_0 <- paste("GCAUG vs",i)
  test_compare <- wilcox.test(GCAUG,GNWYG_scores[[i]], alternative = "greater")$p.value
  anno_text <- paste("P-value =", test_compare)
  anno_text <- paste(anno_text_0,anno_text,sep=" ")
  print(anno_text)
}
## [1] "GCAUG vs GAAUG P-value = 9.38213587417563e-05"
## [1] "GCAUG vs GGAUG P-value = 8.7513673404477e-15"
## [1] "GCAUG vs GUUUG P-value = 6.72701490669523e-06"
## [1] "GCAUG vs GCUUG P-value = 2.26751767631132e-05"
## [1] "GCAUG vs GAUUG P-value = 1.80794177652017e-09"
## [1] "GCAUG vs GGUUG P-value = 2.42211552289614e-06"
## [1] "GCAUG vs GAACG P-value = 1.12624213658034e-06"
## [1] "GCAUG vs GCACG P-value = 0.000118438890142496"
## [1] "GCAUG vs GUAUG P-value = 1.65144861681473e-13"
## [1] "GCAUG vs GAUCG P-value = 0.000109909237762615"
## [1] "GCAUG vs GCUCG P-value = 2.27699137994817e-05"
## [1] "GCAUG vs GUUCG P-value = 0.000228605484824889"
## [1] "GCAUG vs GGUCG P-value = 0.0406718691302042"
```

0.5.8 Figure S2C

```
GNWYG <- c("GCATG","GAATG","GGATG","GTTTG","GCTTG","GATTG","GGTTG","GAACG","GCACG","GTATG","GATCG","GCT
GNWYG <- GNWYG[order(-medians)]

#pdf("./Figure/Figure2/FigureS2C.pdf", width = 10, height = 8)
par(mfrow=c(3,5), mar=c(2,3.5,2,0.5))

for (i in GNWYG){
  ymax <- round(nrow(RAPs[["RBFOX2"]][grep(i,str_sub(RAPs[["RBFOX2"]]$positive_fa,50,150)),]) / 2)

  hist(unlist(str_locate_all(RAPs[["RBFOX2"]]$positive_fa,i))-100, breaks=40, main=gsub("T","U",i), ylab
  axis(side = 1, at = c(-100,-50,0,50,100), labels = c("-100",NA,"0",NA,"100"))
  x <- nrow(RAPs[["RBFOX2"]][grep(i,str_sub(RAPs[["RBFOX2"]]$positive_fa,80,120)),])
  n <- nrow(RAPs[["RBFOX2"]][grep(i,RAPs[["RBFOX2"]]$positive_fa),])

  hist(unlist(str_locate_all(RAPs[["HNRNPA1"]]$positive_fa,i))-100, breaks=40, type="l",col=alpha("#ff7
  n_neg <- nrow(RAPs[["HNRNPA1"]][grep(i,RAPs[["HNRNPA1"]]$positive_fa),])
  x_neg <- nrow(RAPs[["HNRNPA1"]][grep(i,str_sub(RAPs[["HNRNPA1"]]$positive_fa,80,120)),])
  p <- x_neg / n_neg
  bt <- binom.test(x,n,p, alternative = "greater")
  btp <- bt$p.value
  if ( btp <= 0.001 ) {
    to_add <- "***"
  } else if ( btp <= 0.01 ) {
    to_add <- "**"
  } else if ( btp <= 0.05 ) {
    to_add <- "*"
  } else {
    to_add <- "n.s."
  }
```

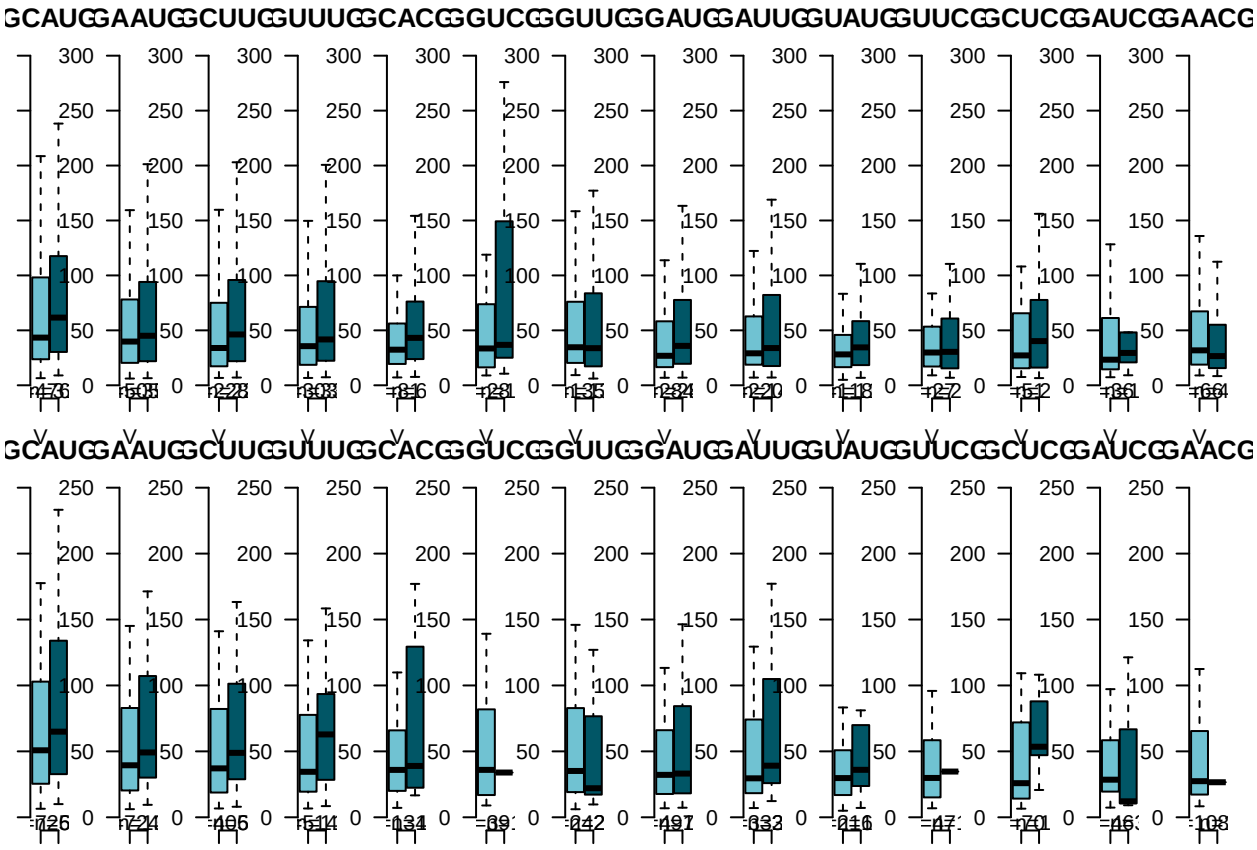
```
  text(50,ymax/10*9,labels = to_add, cex=2.5, col = yellows[1])



  hist(unlist(str_locate_all(RAPs[["HNRNPC"]]$positive_fa,i))-100, breaks=40, type="l",col=alpha("#6a3d9
  n_neg <- nrow(RAPs[["HNRNPC"]][grep(i,RAPs[["HNRNPC"]]$positive_fa),])
  x_neg <- nrow(RAPs[["HNRNPC"]][grep(i,str_sub(RAPs[["HNRNPC"]]$positive_fa,80,120)),])
  p <- x_neg / n_neg
  bt <- binom.test(x,n,p, alternative = "greater")
  btp <- bt$p.value
  if ( btp <= 0.001 ) {
    to_add <- "***"
  } else if ( btp <= 0.01 ) {
    to_add <- "**"
  } else if ( btp <= 0.05 ) {
    to_add <- "*"
  } else {
    to_add <- "n.s."
  }
  text(50,ymax/10*7.75,labels = to_add, cex=2.5, col = yellows[2])



  hist(unlist(str_locate_all(RAPs[["PTBP1"]]$positive_fa,i))-100, breaks=40, type="l",col=alpha("#b15928
  n_neg <- nrow(RAPs[["PTBP1"]][grep(i,RAPs[["PTBP1"]]$positive_fa),])
  x_neg <- nrow(RAPs[["PTBP1"]][grep(i,str_sub(RAPs[["PTBP1"]]$positive_fa,80,120)),])
  p <- x_neg / n_neg
  bt <- binom.test(x,n,p, alternative = "greater")
  btp <- bt$p.value
  if ( btp <= 0.001 ) {
    to_add <- "***"
  } else if ( btp <= 0.01 ) {
    to_add <- "**"
  } else if ( btp <= 0.05 ) {
    to_add <- "*"
  } else {
    to_add <- "n.s."
  }
  text(50,ymax/10*6.5,labels = to_add, cex=2.5, col = yellows[4])

}

#dev.off()
```



0.5.9 Figure S2D

```
GNWYG <- c("GCATG","GAATG","GGATG","GTTTG","GCTTG","GATTG","GGTTG","GAACG","GCACG","GTATG","GATCG","GCT
GNWYG <- GNWYG[order(-medians)]

#pdf("./Figure/Figure2/FigureS2D.pdf", width = 18, height = 5.3)
par(mar=c(1,1,2,1),mfrow=c(2,14),bty="n")

for (i in GNWYG){
  RAPs_GNWYG <- RAPs[["RBFOX2"]][grep(i,str_sub(RAPs[["RBFOX2"]]$positive_fa,50,150)),]
  GNWYG_subset <- GNWYG[grep(i,GNWYG,invert=T)]
  RAPs_GNWYG <- RAPs_GNWYG[grep(paste(GNWYG_subset,collapse = "|"),str_sub(RAPs_GNWYG$positive_fa,50,15
  aaa <- paste("T",i,sep="")
  TGNWYG <- RAPs_GNWYG[grep(aaa,str_sub(RAPs_GNWYG$positive_fa,50,150)),]$BS
  VGNWYG <- RAPs_GNWYG[grep(aaa,str_sub(RAPs_GNWYG$positive_fa,50,150), invert = T),]$BS
  NGNWYG <- list(VGNWYG, TGNWYG)
  names(NGNWYG) <- c("V","U")
  boxplot2(NGNWYG, outline=F, ylab=NA, main=gsub("T","U",i), cex.lab=2, las=1, boxwex=0.95,ylim=c(0,300
}

for (i in GNWYG){
  RAPs_GNWYG <- RAPs[["RBFOX2"]][grep(i,str_sub(RAPs[["RBFOX2"]]$positive_fa,50,150)),]
  GNWYG_subset <- GNWYG[grep(i,GNWYG,invert=T)]
  RAPs_GNWYG <- RAPs_GNWYG[grep(paste(GNWYG_subset,collapse = "|"),str_sub(RAPs_GNWYG$positive_fa,50,15
```

```
  RAPs_GNWYG$GNWYG_subset <- str_count(str_sub(RAPs_GNWYG$positive_fa,50,150),i)
  RAPs_GNWYG$GNWYG_subset[RAPs_GNWYG$GNWYG_subset>2] <- 2
  RAPs_GNWYG$GNWYG_subset <- factor(as.character(RAPs_GNWYG$GNWYG_subset),levels=c("1","2"))
  boxplot2(data=RAPs_GNWYG,BS~GNWYG_subset, outline=F, ylab=NA,main=gsub("T","U",i), cex.lab=2, las=1, l
}
```



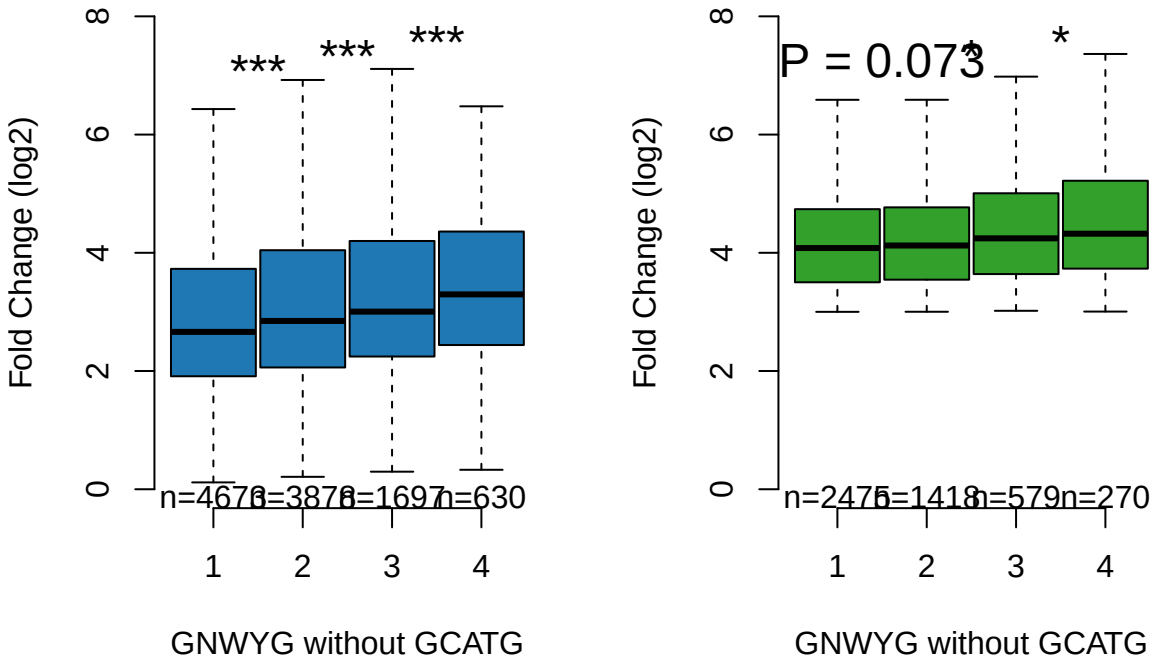

```
#dev.off()
```

0.5.10 Figure S2E

```
## the following lines exclude canonical GCAUG as part of the GNWYG to demonstrate that GNWYG acts indi
#pdf("./Figure/Figure2/FigureS2E.pdf", width = 8, height = 5)
par(mfrow=c(1,2),bty="n")
GNWYG <- c("GAATG","GGATG","GTTTG","GCTTG","GATTG","GGTTG","GAACG","GCACG","GTATG","GATCG","GCTCG","GTT

RAPs_GNWYG_count <- str_count(str_sub(RAPs[["RBFOX2"]]$positive_fa,50,150),paste(GNWYG,collapse="|"))
RAPs_GNWYG_Mean_FCI <- log2(RAPs[["RBFOX2"]][RAPs_GNWYG_count>0,"Mean_FCI"])

RAPs_GNWYG_count[RAPs_GNWYG_count>4] <- 4
RAPs_GNWYG_count <- RAPs_GNWYG_count[RAPs_GNWYG_count>0]
boxplot2(RAPs_GNWYG_Mean_FCI~RAPs_GNWYG_count,outline=F,boxwex=0.95, ylab="Fold Change (log2)", ylim=c(
```

```
x <- RAPs_GNWYG_Mean_FCI[RAPs_GNWYG_count == 1]
y <- RAPs_GNWYG_Mean_FCI[RAPs_GNWYG_count == 2]
rst <- t.test(x,y,alternative = "less")$p.value
if ( rst <= 0.001 ) {
  to_add <- "***"
} else if ( rst <= 0.01 ) {
  to_add <- "**"
} else if ( rst <= 0.05 ) {
  to_add <- "*"
} else {
  a <- "P ="
  b <- round(rst,3)
  to_add <- paste(a,b,sep=" ")
}
text(1.5,7.25,labels = to_add, cex=1.5)

x <- RAPs_GNWYG_Mean_FCI[RAPs_GNWYG_count == 2]
y <- RAPs_GNWYG_Mean_FCI[RAPs_GNWYG_count == 3]
rst <- t.test(x,y,alternative = "less")$p.value
if ( rst <= 0.001 ) {
  to_add <- "***"
} else if ( rst <= 0.01 ) {
  to_add <- "**"
} else if ( rst <= 0.05 ) {
  to_add <- "*"
} else {
  a <- "P ="
  b <- round(rst,3)
  to_add <- paste(a,b,sep=" ")
}
text(2.5,7.5,labels = to_add, cex=1.5)

x <- RAPs_GNWYG_Mean_FCI[RAPs_GNWYG_count == 3]
y <- RAPs_GNWYG_Mean_FCI[RAPs_GNWYG_count == 4]
rst <- t.test(x,y,alternative = "less")$p.value
if ( rst <= 0.001 ) {
  to_add <- "***"
} else if ( rst <= 0.01 ) {
  to_add <- "**"
} else if ( rst <= 0.05 ) {
  to_add <- "*"
} else {
  a <- "P ="
  b <- round(rst,3)
  to_add <- paste(a,b,sep=" ")
}
text(3.5,7.75,labels = to_add, cex=1.5)

CLIPs_GNWYG_count <- str_count(str_sub(CLIPs[["RBFOX2"]]$positive_fa,20,120),paste(GNWYG,collapse="|"))
CLIPs_GNWYG_MeanFC <- CLIPs[["RBFOX2"]][CLIPs_GNWYG_count>0,"MeanFC"]
CLIPs_GNWYG_count[CLIPs_GNWYG_count>4] <- 4
CLIPs_GNWYG_count <- CLIPs_GNWYG_count[CLIPs_GNWYG_count>0]
boxplot2(CLIPs_GNWYG_MeanFC~CLIPs_GNWYG_count,outline=F,boxwex=0.95, ylab="Fold Change (log2)", ylim=c(
```

```
x <- CLIPs_GNWYG_MeanFC[CLIPs_GNWYG_count == 1]
y <- CLIPs_GNWYG_MeanFC[CLIPs_GNWYG_count == 2]
rst <- t.test(x,y,alternative = "less")$p.value
if ( rst <= 0.001 ) {
  to_add <- "***"
} else if ( rst <= 0.01 ) {
  to_add <- "**"
} else if ( rst <= 0.05 ) {
  to_add <- "*"
} else {
  a <- "P ="
  b <- round(rst,3)
  to_add <- paste(a,b,sep=" ")
}
text(1.5,7.25,labels = to_add, cex=1.5)

x <- CLIPs_GNWYG_MeanFC[CLIPs_GNWYG_count == 2]
y <- CLIPs_GNWYG_MeanFC[CLIPs_GNWYG_count == 3]
rst <- t.test(x,y,alternative = "less")$p.value
if ( rst <= 0.001 ) {
  to_add <- "***"
} else if ( rst <= 0.01 ) {
  to_add <- "**"
} else if ( rst <= 0.05 ) {
  to_add <- "*"
} else {
  a <- "P ="
  b <- round(rst,3)
  to_add <- paste(a,b,sep=" ")
}
text(2.5,7.5,labels = to_add, cex=1.5)

x <- CLIPs_GNWYG_MeanFC[CLIPs_GNWYG_count == 3]
y <- CLIPs_GNWYG_MeanFC[CLIPs_GNWYG_count == 4]
rst <- t.test(x,y,alternative = "less")$p.value
if ( rst <= 0.001 ) {
  to_add <- "***"
} else if ( rst <= 0.01 ) {
  to_add <- "**"
} else if ( rst <= 0.05 ) {
  to_add <- "*"
} else {
  a <- "P ="
  b <- round(rst,3)
  to_add <- paste(a,b,sep=" ")
}
text(3.5,7.75,labels = to_add, cex=1.5)
```




```
#dev.off()
```

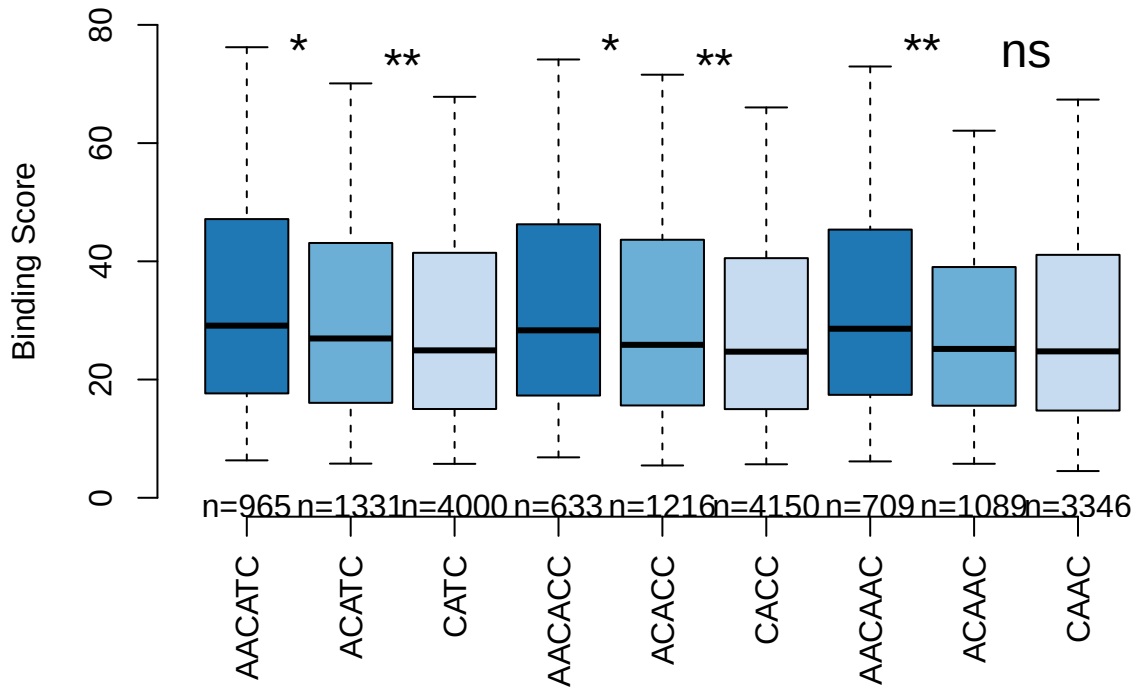
0.5.11 Figure S2F

```
AACAHC <- c("AACATC","AACACC","AACAAC")
ACAHC <- c("ACATC","ACACC","ACAAC")
CAHC <- c("CATC","CACC","CAAC")

AACAHC_scores <- list()
for (i in 1:3){
  RAPs_AACAHC <- RAPs[["YBX3"]][grep(AACAHC[i],str_sub(RAPs[["YBX3"]]$positive_fa,50,150)),]
  RAPs_AACAHC_target <- CAHC[-i]
  AACAHC_scores[[i]] <- RAPs_AACAHC[grep(paste(RAPs_AACAHC_target,collapse = "|"),str_sub(RAPs_AACAHC$po
  AACAHC_scores[[i]] <- RAPs_AACAHC$BS
}
names(AACAHC_scores) <- AACAHC

ACAHC_scores <- list()
for (i in 1:3){
  RAPs_ACAHC <- RAPs[["YBX3"]][grep(AACAHC[i],str_sub(RAPs[["YBX3"]]$positive_fa,50,150), invert=T),]
  RAPs_ACAHC <- RAPs_ACAHC[grep(ACAHC[i],str_sub(RAPs_ACAHC$positive_fa,50,150)),]
  RAPs_ACAHC_target <- CAHC[-i]
  ACAHC_scores[[i]] <- RAPs_ACAHC[grep(paste(RAPs_ACAHC_target,collapse = "|"),str_sub(RAPs_ACAHC$positi
```

```
  ACAHC_scores[[i]] <- RAPs_ACAHC$BS
}
names(ACAHC_scores) <- ACAHC


CAHC_scores <- list()
for (i in 1:3){
  RAPs_CAHC <- RAPs[["YBX3"]][grep(AACAHC[i],str_sub(RAPs[["YBX3"]]$positive_fa,50,150), invert=T),]
  RAPs_CAHC <- RAPs_CAHC[grep(ACAHC[i],str_sub(RAPs_CAHC$positive_fa,50,150), invert=T),]
  RAPs_CAHC <- RAPs_CAHC[grep(CAHC[i],str_sub(RAPs_CAHC$positive_fa,50,150)),]
  RAPs_CAHC_target <- CAHC[-i]
  CAHC_scores[[i]] <- RAPs_CAHC[grep(paste(RAPs_CAHC_target,collapse = "|"),str_sub(RAPs_CAHC$positive_
  CAHC_scores[[i]] <- RAPs_CAHC$BS
}
names(CAHC_scores) <- CAHC

ALL_CAHCs_scores <- c(AACAHC_scores[1],ACAHC_scores[1],CAHC_scores[1], AACAHC_scores[2],ACAHC_scores[2]



#pdf("./Figure/Figure2/FigureS2F.pdf", width = 8, height = 5)
par(bty="n")

boxplot2(ALL_CAHCs_scores,outline=F, range=1, col= c("#1f78b4", "#6baed6", "#c6dbef"), las=3, ylim=c(0,8

x <- ALL_CAHCs_scores$AACATC
y <- ALL_CAHCs_scores$ACATC
rst <- t.test(x,y,alternative = "greater")$p.value
if ( rst <= 0.001 ) {
  to_add <- "***"
} else if ( rst <= 0.01 ) {
  to_add <- "**"
} else if ( rst <= 0.05 ) {
  to_add <- "*"
} else {
  to_add <- "ns"
}
text(1.5,77.5,labels = to_add, cex=1.5)

x <- ALL_CAHCs_scores$ACATC
y <- ALL_CAHCs_scores$CATC
rst <- t.test(x,y,alternative = "greater")$p.value
if ( rst <= 0.001 ) {
  to_add <- "***"
} else if ( rst <= 0.01 ) {
  to_add <- "**"
} else if ( rst <= 0.05 ) {
  to_add <- "*"
} else {
  to_add <- "ns"
}
text(2.5,75,labels = to_add, cex=1.5)
```

```
x <- ALL_CAHCs_scores$AACACC
y <- ALL_CAHCs_scores$ACACC
rst <- t.test(x,y,alternative = "greater")$p.value
if ( rst <= 0.001 ) {
  to_add <- "***"
} else if ( rst <= 0.01 ) {
  to_add <- "**"
} else if ( rst <= 0.05 ) {
  to_add <- "*"
} else {
  to_add <- "ns"
}
text(4.5,77.5,labels = to_add, cex=1.5)

x <- ALL_CAHCs_scores$ACACC
y <- ALL_CAHCs_scores$CACC
rst <- t.test(x,y,alternative = "greater")$p.value
if ( rst <= 0.001 ) {
  to_add <- "***"
} else if ( rst <= 0.01 ) {
  to_add <- "**"
} else if ( rst <= 0.05 ) {
  to_add <- "*"
} else {
  to_add <- "ns"
}
text(5.5,75,labels = to_add, cex=1.5)

x <- ALL_CAHCs_scores$AACAAC
y <- ALL_CAHCs_scores$ACAAC
rst <- t.test(x,y,alternative = "greater")$p.value
if ( rst <= 0.001 ) {
  to_add <- "***"
} else if ( rst <= 0.01 ) {
  to_add <- "**"
} else if ( rst <= 0.05 ) {
  to_add <- "*"
} else {
  to_add <- "ns"
}
text(7.5,77.5,labels = to_add, cex=1.5)

x <- ALL_CAHCs_scores$ACAAC
y <- ALL_CAHCs_scores$CAAC
rst <- t.test(x,y,alternative = "greater")$p.value
if ( rst <= 0.001 ) {
  to_add <- "***"
} else if ( rst <= 0.01 ) {
  to_add <- "**"
} else if ( rst <= 0.05 ) {
  to_add <- "*"
} else {
```

```
  to_add <- "ns"
}
text(8.5,75,labels = to_add, cex=1.5)
```

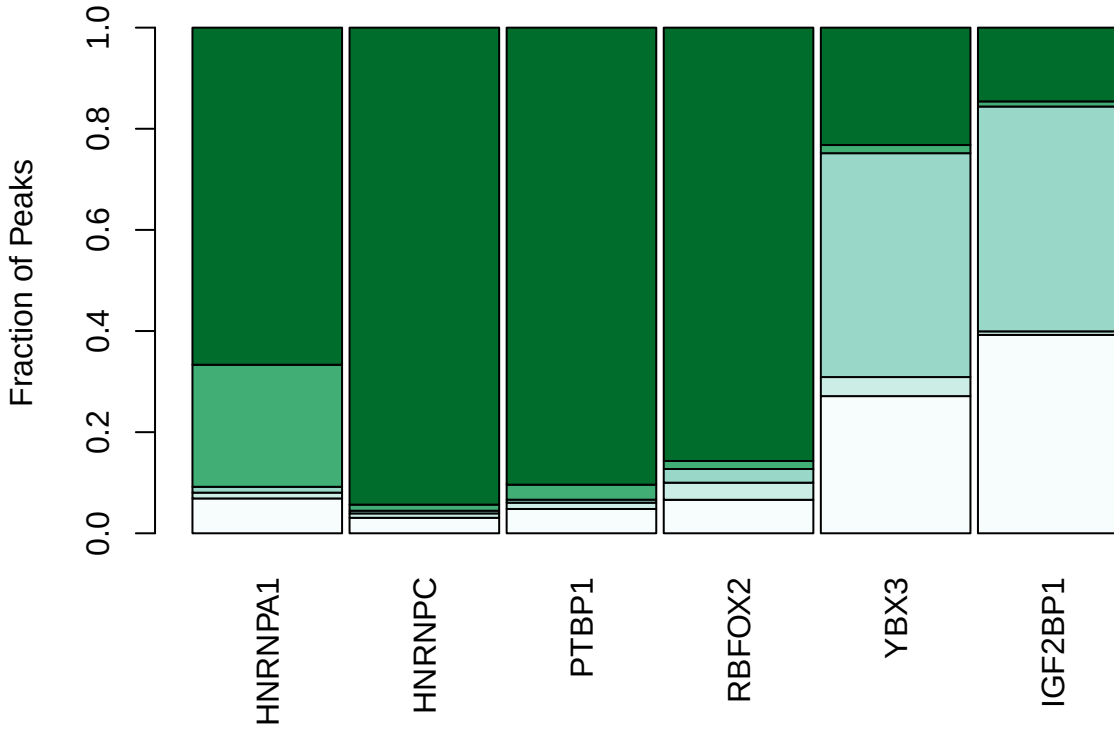



```
#dev.off()
```

0.5.12 Figure S2G

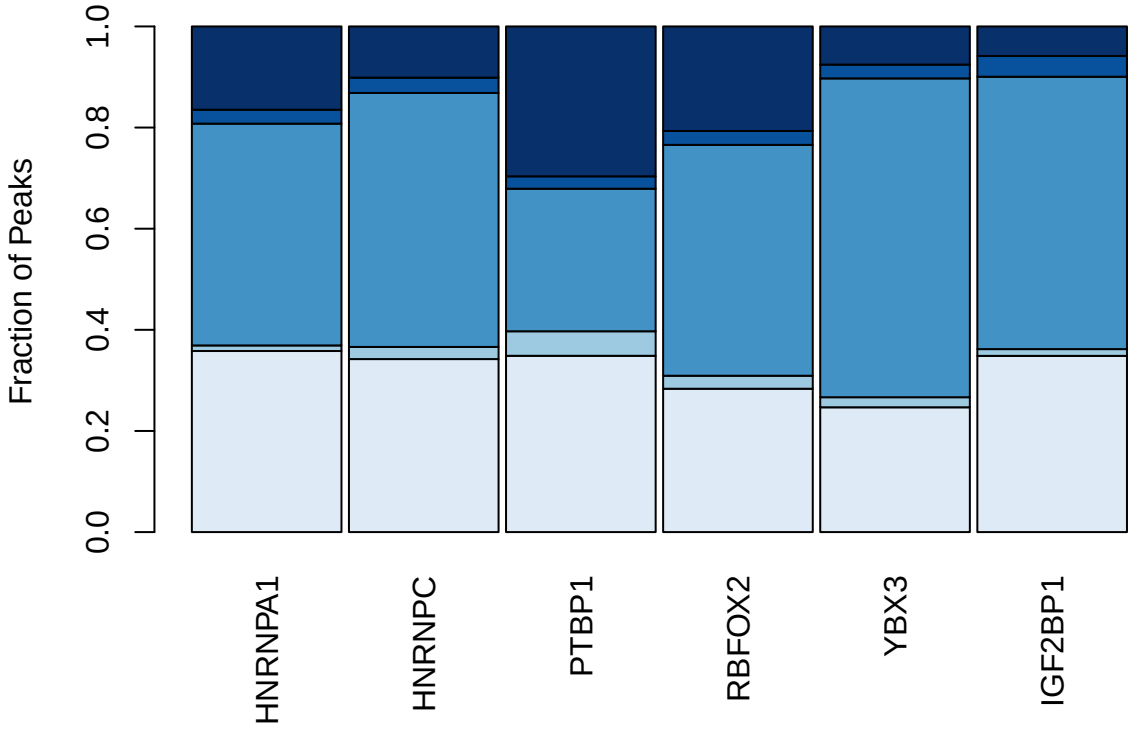
```
Names_protein <- c("HNRNPA1","HNRNPC","PTBP1","RBFOX2","YBX3","IGF2BP1")

# CLIPs
CLIPs_RBFOX2_feature_count <- table(CLIPs[["RBFOX2"]][,"feature"])

for (i in Names_protein){
  CLIPs_RBFOX2_feature_tmp <- table(CLIPs[[i]][,"feature"])/nrow(CLIPs[[i]])
  CLIPs_RBFOX2_feature_count <- rbind(CLIPs_RBFOX2_feature_count,CLIPs_RBFOX2_feature_tmp)
}
CLIPs_RBFOX2_feature_count <- CLIPs_RBFOX2_feature_count[-1,]
CLIPs_RBFOX2_feature_count <- t(CLIPs_RBFOX2_feature_count)
colnames(CLIPs_RBFOX2_feature_count) <- Names_protein
```

```
# RAPs
RAPs_RBFOX2_feature_count <- table(RAPs[["RBFOX2"]][,"feature"])
for (i in Names_protein){
  print(i)
  RAPs_RBFOX2_feature_tmp <- table(RAPs[[i]][,"feature"])/nrow(RAPs[[i]])
  RAPs_RBFOX2_feature_count <- rbind(RAPs_RBFOX2_feature_count,RAPs_RBFOX2_feature_tmp)
}
## [1] "HNRNPA1"
## [1] "HNRNPC"
## [1] "PTBP1"
## [1] "RBFOX2"
## [1] "YBX3"
## [1] "IGF2BP1"
RAPs_RBFOX2_feature_count <- RAPs_RBFOX2_feature_count[-1,]
RAPs_RBFOX2_feature_count <- t(RAPs_RBFOX2_feature_count)
colnames(RAPs_RBFOX2_feature_count) <- Names_protein

barplot(CLIPs_RBFOX2_feature_count, col=c("#f7fcfd", "#ccece6", "#99d8c9", "#41ae76", "#006d2c"), las=3
```

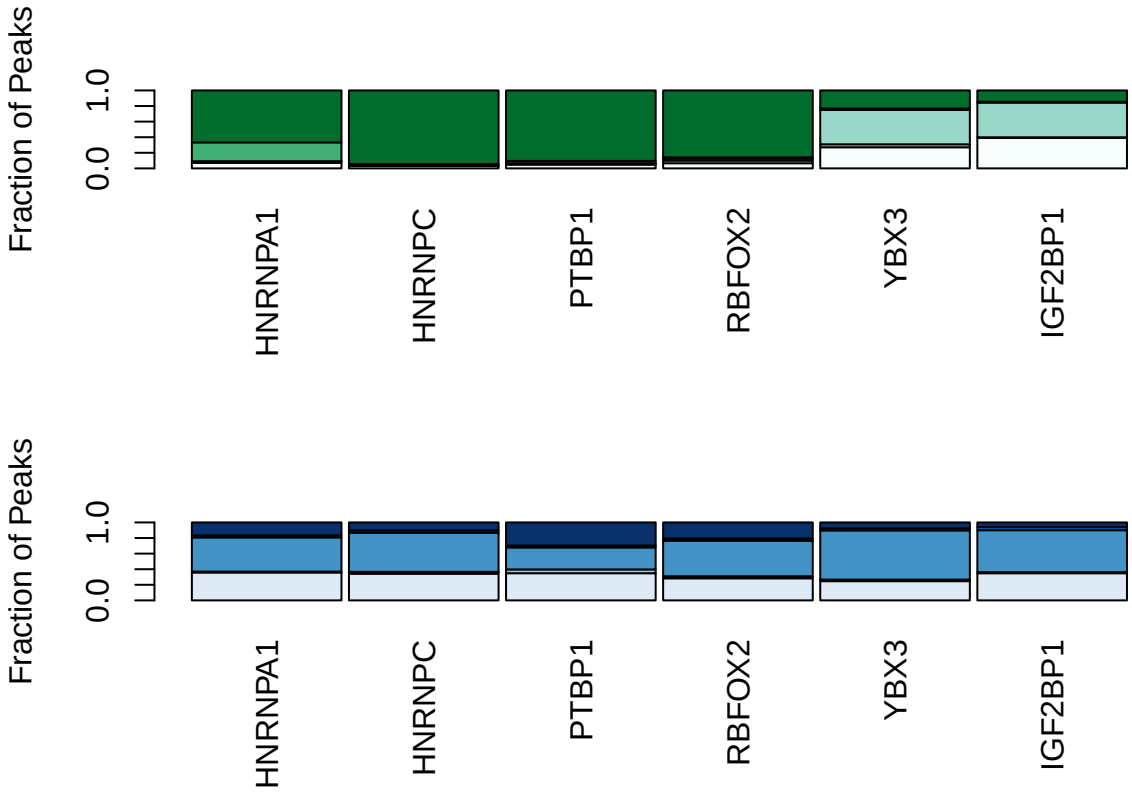


0.5.12.1 include exon

```
barplot(RAPs_RBFOX2_feature_count, col=c("#deebf7","#9ecae1", "#4292c6","#08519c","#08306b"), las=3, sp
```



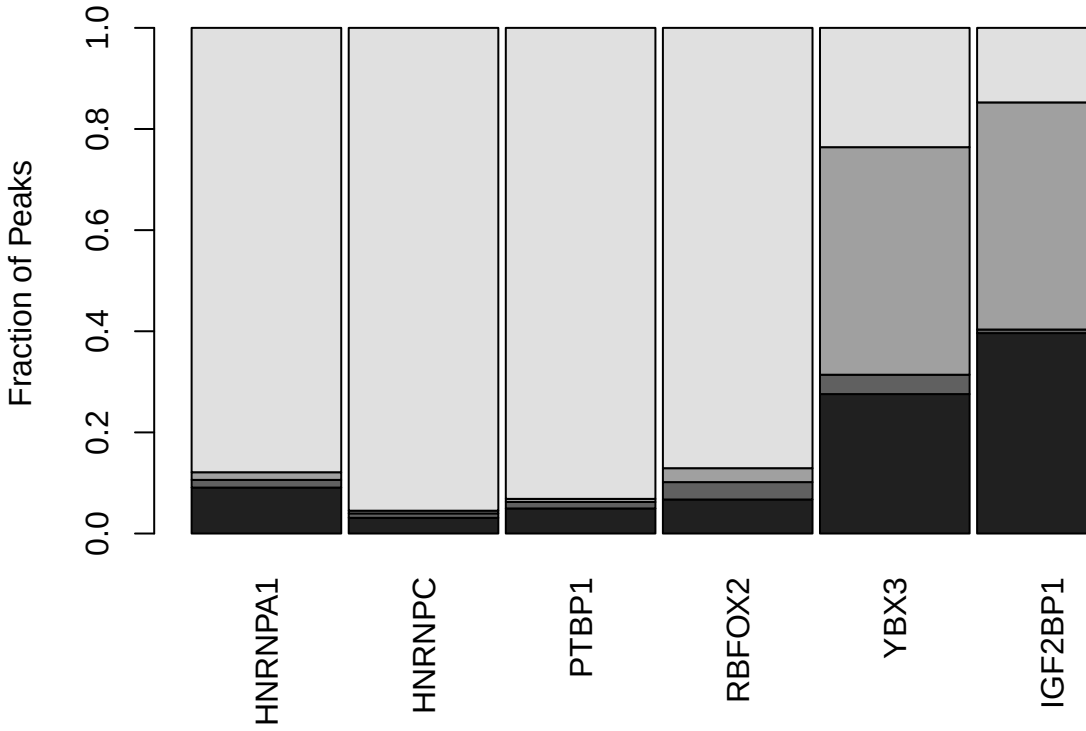

```
#pdf("./Figure/Figure2/FigureS2G.pdf", width = 13.9, height = 13.7)
par(mfrow=c(2,1))
barplot(CLIPs_RBFOX2_feature_count, col=c("#f7fcfd", "#ccece6", "#99d8c9", "#41ae76", "#006d2c"), las=3
barplot(RAPs_RBFOX2_feature_count, col=c("#deebf7","#9ecae1", "#4292c6","#08519c","#08306b"), las=3, spa
```




```
#dev.off()
```

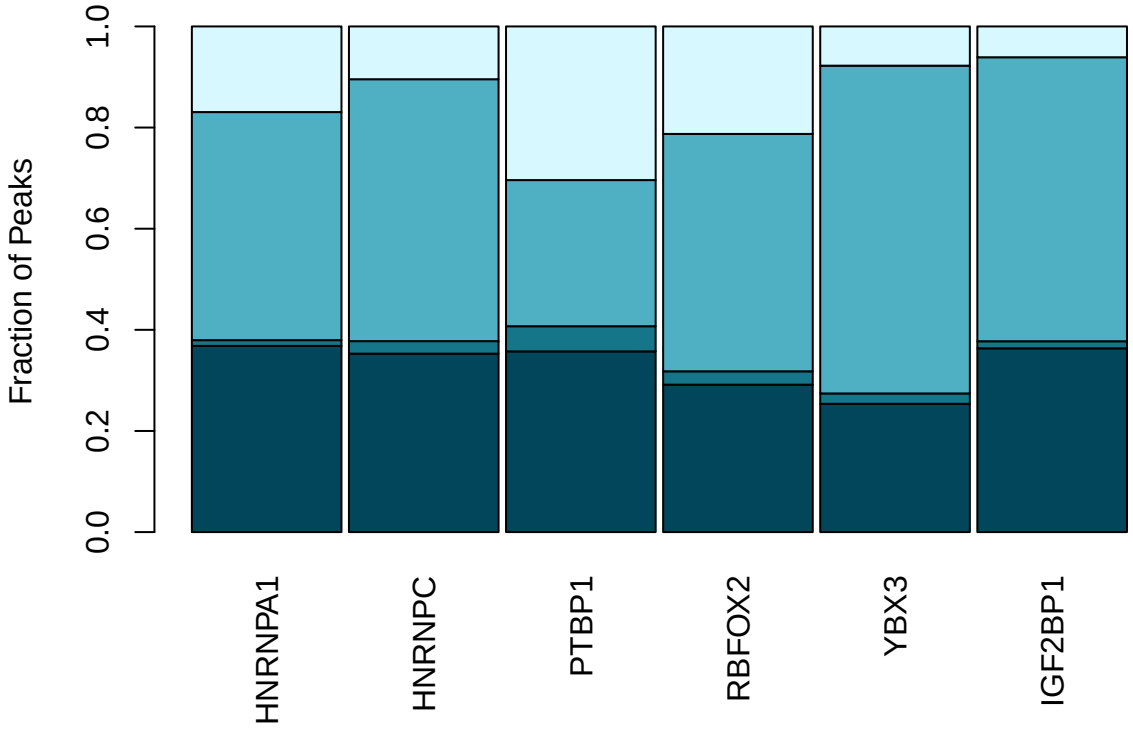
```
Names_protein <- c("HNRNPA1","HNRNPC","PTBP1","RBFOX2","YBX3","IGF2BP1")

# CLIPs
CLIPs_RBFOX2_feature_count <- table(CLIPs[["RBFOX2"]][CLIPs[["RBFOX2"]]$feature != "exon","feature"])

for (i in Names_protein){
  CLIPs_RBFOX2_feature_tmp <- table(CLIPs[[i]][CLIPs[[i]]$feature != "exon","feature"])/nrow(CLIPs[[i]]
  CLIPs_RBFOX2_feature_count <- rbind(CLIPs_RBFOX2_feature_count,CLIPs_RBFOX2_feature_tmp)
}
CLIPs_RBFOX2_feature_count <- CLIPs_RBFOX2_feature_count[-1,]
CLIPs_RBFOX2_feature_count <- t(CLIPs_RBFOX2_feature_count)
colnames(CLIPs_RBFOX2_feature_count) <- Names_protein

# RAPs
RAPs_RBFOX2_feature_count <- table(RAPs[["RBFOX2"]][RAPs[["RBFOX2"]]$feature != "exon","feature"])
for (i in Names_protein){
  print(i)
  RAPs_RBFOX2_feature_tmp <- table(RAPs[[i]][RAPs[[i]]$feature != "exon","feature"])/nrow(RAPs[[i]][RAP
  RAPs_RBFOX2_feature_count <- rbind(RAPs_RBFOX2_feature_count,RAPs_RBFOX2_feature_tmp)
}
## [1] "HNRNPA1"
```

```
## [1] "HNRNPC"
## [1] "PTBP1"
## [1] "RBFOX2"
## [1] "YBX3"
## [1] "IGF2BP1"
RAPs_RBFOX2_feature_count <- RAPs_RBFOX2_feature_count[-1,]
RAPs_RBFOX2_feature_count <- t(RAPs_RBFOX2_feature_count)
colnames(RAPs_RBFOX2_feature_count) <- Names_protein

barplot(CLIPs_RBFOX2_feature_count, col=greys[c(1,3,5,7)], las=3, space=0.05, ylab="Fraction of Peaks")
```

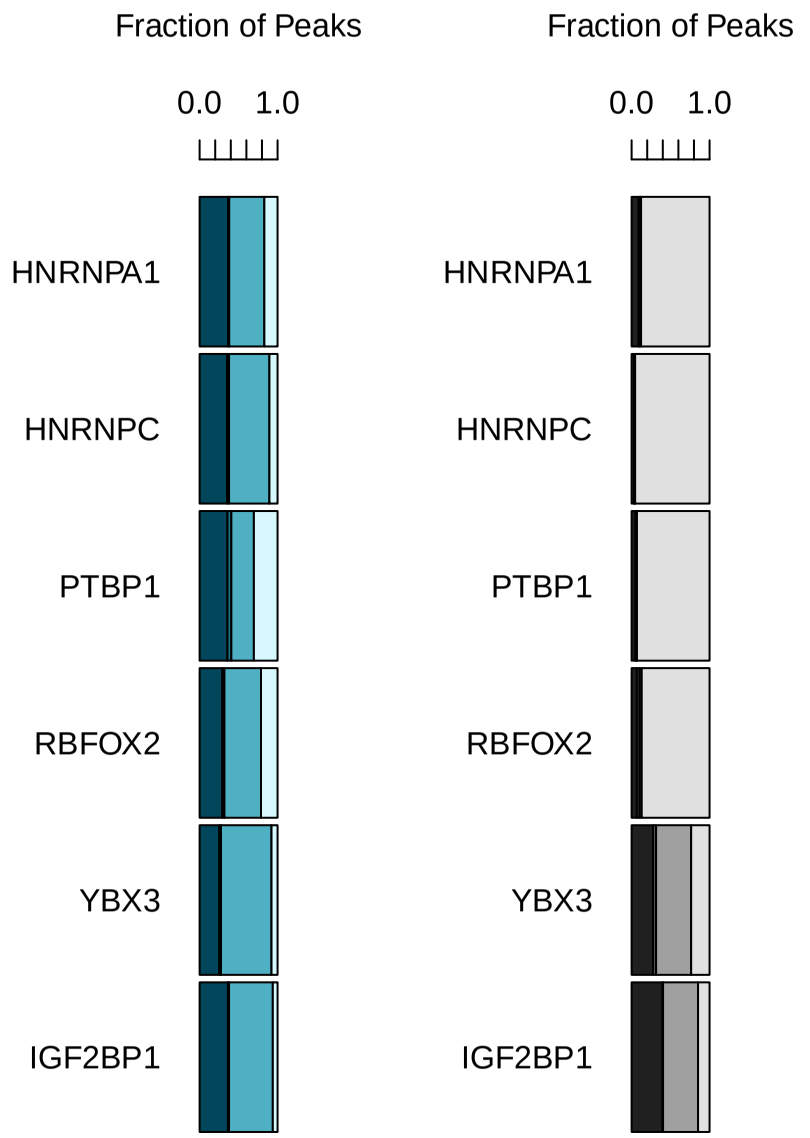


0.5.12.2 exclude exome

```
barplot(RAPs_RBFOX2_feature_count, col=acqua_blues[c(1,4,7,11)], las=3, space=0.05, ylab="Fraction of P
```




```
par(mfrow=c(2,1))
barplot(CLIPs_RBFOX2_feature_count, col=greys[c(1,3,5,7)], las=3, space=0.05, ylab="Fraction of Peaks")
barplot(RAPs_RBFOX2_feature_count, col=acqua_blues[c(1,4,7,11)], las=3, space=0.05, ylab="Fraction of P
```


Fraction of Peaks
0.0
1.0
HNRNPA1
HNRNPC
PTBP1
RBFOX2
YBX3
IGF2BP1
Fraction of Peaks
0.0
1.0
HNRNPA1
HNRNPC
PTBP1
RBFOX2
YBX3
IGF2BP1