Gviz_fig1

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setup

directory

```r
setwd("D:/Krueger_Lab/Publications/miR181_paper/Figure1/Genome_tracks")
```

packages

```r
library(Gviz)
```

```
## Loading required package: S4Vectors

## 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

##
## 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: GenomicRanges

## Loading required package: GenomeInfoDb

## Loading required package: grid
```

```
library(GenomicRanges)
library(rtracklayer)
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(plyranges)
```

```
##
## Attaching package: 'plyranges'

## The following objects are masked from 'package:dplyr':
##
##     between, n, n_distinct

## The following object is masked from 'package:IRanges':
##
##     slice

## The following object is masked from 'package:stats':
##
##     filter
```

Import data

```r
# diferential results
diffres <- rtracklayer::import(con = "D:/Krueger_Lab/miReCLIP/Mirco/DifferentialBinding/BsDifferentialR

# non enriched non chimeric
IPKOminus <- import.bw("D:/Krueger_Lab/miReCLIP/Melina/pipe_output_22_02_14/pipe_output_22_02_14/non-chi
IPKOplus <- import.bw("D:/Krueger_Lab/miReCLIP/Melina/pipe_output_22_02_14/pipe_output_22_02_14/non-chi
IPWTminus <- import.bw("D:/Krueger_Lab/miReCLIP/Melina/pipe_output_22_02_14/pipe_output_22_02_14/non-chi
IPWTplus <- import.bw("D:/Krueger_Lab/miReCLIP/Melina/pipe_output_22_02_14/pipe_output_22_02_14/non-chi

# enriched chimeric
IP181chimWTminus <- import.bw("D:/Krueger_Lab/miReCLIP/Melina/pipe_output_22_02_14/pipe_output_22_02_14,
IP181chimWTplus <- import.bw("D:/Krueger_Lab/miReCLIP/Melina/pipe_output_22_02_14/pipe_output_22_02_14/
```

setting regions

Use this panel to change the coordinates in all following plots

```r
scoord = 20405350
ecoord = 20406237
tchr = "chr13"
clim = 10
```

Zfp36l1: chr12 80107716-80108070 Zfp36l2: chr17 84184290-84184345 Cblb: chr16:52171980-52172133 elmo1: chr13:20405350-20406237

Tracks

Annotation track

```r
gatrack <- GenomeAxisTrack()
```

pureclip (merged)

Always just activate or inactivate the strand that actually contains data

```r
# -

# #KO minus
# KOm <- as.data.frame(IPKOminus)
# KOm <- KOm[KOm$seqnames == tchr & KOm$start >= scoord & KOm$end <= ecoord,]
# KOm$seqnames <- as.character(KOm$seqnames)
# KOm <- makeGRangesFromDataFrame(KOm, keep.extra.columns = T)
#
# KOmT <- DataTrack(KOm, name="KO-", ylim = c(0,clim))
#
#
# #WT minus
# WTm <- as.data.frame(IPWTminus)
# WTm <- WTm[WTm$seqnames == tchr & WTm$start >= scoord & WTm$end <= ecoord,]
# WTm$seqnames <- as.character(WTm$seqnames)
# WTm <- makeGRangesFromDataFrame(WTm, keep.extra.columns = T)
#
```

```r
# WTmT <- DataTrack(WTm, name="WT-", ylim = c(0,clim))

# +

#KO plus
KOp <- as.data.frame(IPKOplus)
KOp <- KOp[KOp$seqnames == tchr & KOp$start >= scoord & KOp$end <= ecoord,]
KOp$seqnames <- as.character(KOp$seqnames)
KOp <- makeGRangesFromDataFrame(KOp, keep.extra.columns = T)

KOpT <- DataTrack(KOp, name="KO+", ylim = c(0,clim))

#WT plus
WTp <- as.data.frame(IPWTplus)
WTp <- WTp[WTp$seqnames == tchr & WTp$start >= scoord & WTp$end <= ecoord,]
WTp$seqnames <- as.character(WTp$seqnames)
WTp <- makeGRangesFromDataFrame(WTp, keep.extra.columns = T)

WTpT <- DataTrack(WTp, name="WT+", ylim = c(0,clim))
```

chimeric reads

```r
#minus
# chim181m <- as.data.frame(IP181chimWTminus)
# chim181m <- chim181m[chim181m$seqnames == tchr & chim181m$start >= scoord & chim181m$end <= ecoord,]
# chim181m$seqnames <- as.character(chim181m$seqnames)
# chim181m <- makeGRangesFromDataFrame(chim181m, keep.extra.columns = T)
#
# chim181mT <- DataTrack(chim181m, name="WT181rich-", ylim = c(0,clim))

#plus
chim181p <- as.data.frame(IP181chimWTplus)
chim181p <- chim181p[chim181p$seqnames == tchr & chim181p$start >= scoord & chim181p$end <= ecoord,]
chim181p$seqnames <- as.character(chim181p$seqnames)
chim181p <- makeGRangesFromDataFrame(chim181p, keep.extra.columns = T)

chim181pT <- DataTrack(chim181p, name="WT181rich-", ylim = c(0,clim))
```

differential binding

```r
diffresf <- diffres %>% filter(seqnames == tchr)

diffresT <- AnnotationTrack(diffresf, name = "dBS", id=diffresf$name)
```
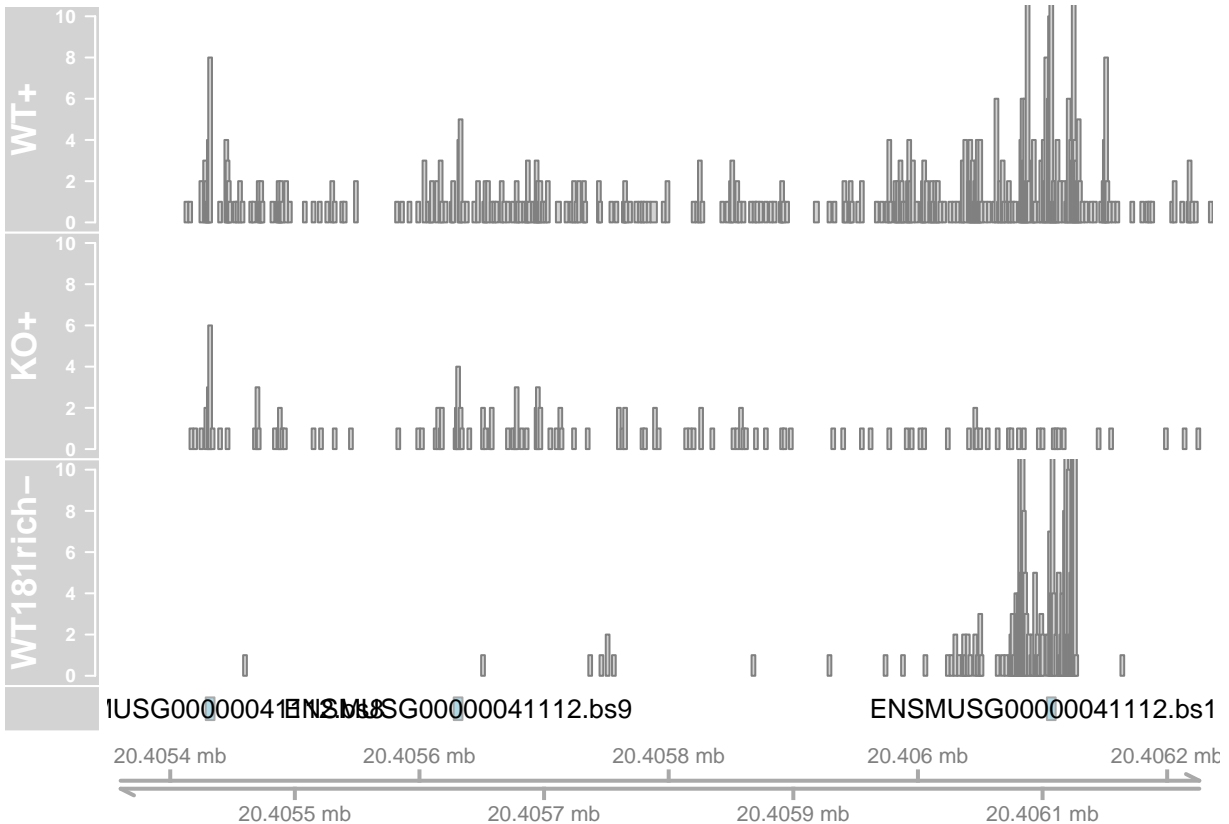
plot

```r
plotTracks(list(WTpT, KOpT, chim181pT, diffresT,  gatrack), from = scoord, to= ecoord, type="histogram"
           fontsize.feature=10, fontcolor.feature = "black")
```

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] grid      stats4    stats     graphics  grDevices utils     datasets
## [8] methods   base
##
## other attached packages:
## [1] plyranges_1.18.0    dplyr_1.1.1         rtracklayer_1.58.0
## [4] Gviz_1.42.1         GenomicRanges_1.50.2 GenomeInfoDb_1.34.9
## [7] IRanges_2.32.0      S4Vectors_0.36.2    BiocGenerics_0.44.0
##
## loaded via a namespace (and not attached):
```

```
##   [1] ProtGenerics_1.30.0      bitops_1.0-7
##   [3] matrixStats_0.63.0       bit64_4.0.5
##   [5] filelock_1.0.2           RColorBrewer_1.1-3
##   [7] progress_1.2.2           httr_1.4.5
##   [9] tools_4.2.3              backports_1.4.1
##  [11] utf8_1.2.3               R6_2.5.1
##  [13] rpart_4.1.19             lazyeval_0.2.2
##  [15] Hmisc_5.0-1              DBI_1.1.3
##  [17] colorspace_2.1-0         nnet_7.3-18
##  [19] tidyselect_1.2.0         gridExtra_2.3
##  [21] prettyunits_1.1.1        bit_4.0.5
##  [23] curl_5.0.0               compiler_4.2.3
##  [25] cli_3.6.0                Biobase_2.58.0
##  [27] htmlTable_2.4.1          xml2_1.3.3
##  [29] DelayedArray_0.23.2      scales_1.2.1
##  [31] checkmate_2.1.0          rappdirs_0.3.3
##  [33] stringr_1.5.0            digest_0.6.31
##  [35] Rsamtools_2.14.0         foreign_0.8-84
##  [37] rmarkdown_2.21           XVector_0.38.0
##  [39] jpeg_0.1-10              dichromat_2.0-0.1
##  [41] base64enc_0.1-3          pkgconfig_2.0.3
##  [43] htmltools_0.5.4          MatrixGenerics_1.10.0
##  [45] highr_0.10               ensembldb_2.22.0
##  [47] dbplyr_2.3.2             fastmap_1.1.1
##  [49] BSgenome_1.66.3          htmlwidgets_1.6.2
##  [51] rlang_1.1.0              rstudioapi_0.14
##  [53] RSQLite_2.3.1            BiocIO_1.8.0
##  [55] generics_0.1.3           BiocParallel_1.32.6
##  [57] VariantAnnotation_1.44.1 RCurl_1.98-1.12
##  [59] magrittr_2.0.3           GenomeInfoDbData_1.2.9
##  [61] Formula_1.2-5            interp_1.1-4
##  [63] Matrix_1.5-3             Rcpp_1.0.10
##  [65] munsell_0.5.0            fansi_1.0.4
##  [67] lifecycle_1.0.3          stringi_1.7.12
##  [69] yaml_2.3.7               SummarizedExperiment_1.28.0
##  [71] zlibbioc_1.44.0          BiocFileCache_2.6.1
##  [73] blob_1.2.4               parallel_4.2.3
##  [75] crayon_1.5.2             deldir_1.0-6
##  [77] lattice_0.20-45          Biostrings_2.66.0
##  [79] GenomicFeatures_1.50.4   hms_1.1.3
##  [81] KEGGREST_1.38.0          knitr_1.42
##  [83] pillar_1.9.0             rjson_0.2.21
##  [85] codetools_0.2-19         biomaRt_2.54.1
##  [87] XML_3.99-0.14            glue_1.6.2
##  [89] evaluate_0.20            latticeExtra_0.6-30
##  [91] biovizBase_1.46.0        data.table_1.14.8
##  [93] png_0.1-8                vctrs_0.6.1
##  [95] gtable_0.3.3             cachem_1.0.7
##  [97] ggplot2_3.4.2            xfun_0.37
##  [99] AnnotationFilter_1.22.0  restfulr_0.0.15
## [101] tibble_3.2.1             GenomicAlignments_1.34.1
## [103] AnnotationDbi_1.60.2     memoise_2.0.1
## [105] cluster_2.1.4
```