

Gviz_fig1

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setup

directory

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

packages

```
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
library(BSgenome.Mmusculus.UCSC.mm10)

## Loading required package: BSgenome
## Loading required package: Biostrings

```

```
## Loading required package: XVector
##
## Attaching package: 'Biostrings'
## The following object is masked from 'package:grid':
##
##     pattern
## The following object is masked from 'package:base':
##
##     strsplit
```

Import data

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

# non enriched non chimeric
IPK0minus <- import.bw("D:/Krueger_Lab/miReCLIP/Melina/pipe_output_22_02_14/pipe_output_22_02_14/non-ch
IPK0plus <- 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-ch
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

```
scoord = 140652591
ecoord = 140652785
tchr = "chr6"
clim = 30
```

Zfp36l1: chr12 80107716-80108070 Zfp36l2: chr17 84184290-84184345 Cblb: chr16:52171980-52172133 elmo1:
chr13:20405350-20406237 srsf11: chr3:158,010,824-158,012,135 Aebp2: chr6:140652591-140652785 # Tracks

Annotation track

```
# genome axis
gatrack <- GenomeAxisTrack()

# gene track-----this is not working yet
# data(cpgIslands)
# class(cpgIslands)
# ## [1] "GRanges"
# ## attr(,"package")
# ## [1] "GenomicRanges"
# chr <- as.character(unique(seqnames(cpgIslands)))
# gen <- genome(cpgIslands)
# atrack <- AnnotationTrack(cpgIslands, name = "CpG")
#
```

```

# data(geneModels)
#
# gff <- import.gff3("D:/Krueger_Lab/Ribo_Profiling/run15112022M23/ref_genome/gencode.vM23.annotation.g
#
# gffloc <- as.data.frame(gff)
#
# gffloc <- gffloc[gffloc$seqnames==tchr,]
#
# grtrack <- GeneRegionTrack(gffloc, genome = "mm10", chromosome = tchr,
#                             name = "Gene")
#
# grtrack <- GeneRegionTrack(geneModels, genome = BSgenome.Mmusculus.UCSC.mm10, chromosome = tchr,
#                             name = "foo")

```

pureclip (merged)

Always just activate or inactivate the strand that actually contains data

```

# -

# #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)
#
# WtmT <- DataTrack(Wtm, name="WT-", ylim = c(0,clim))

# +

#KO plus
KOp <- as.data.frame(IPKOpplus)
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

```
#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))
```

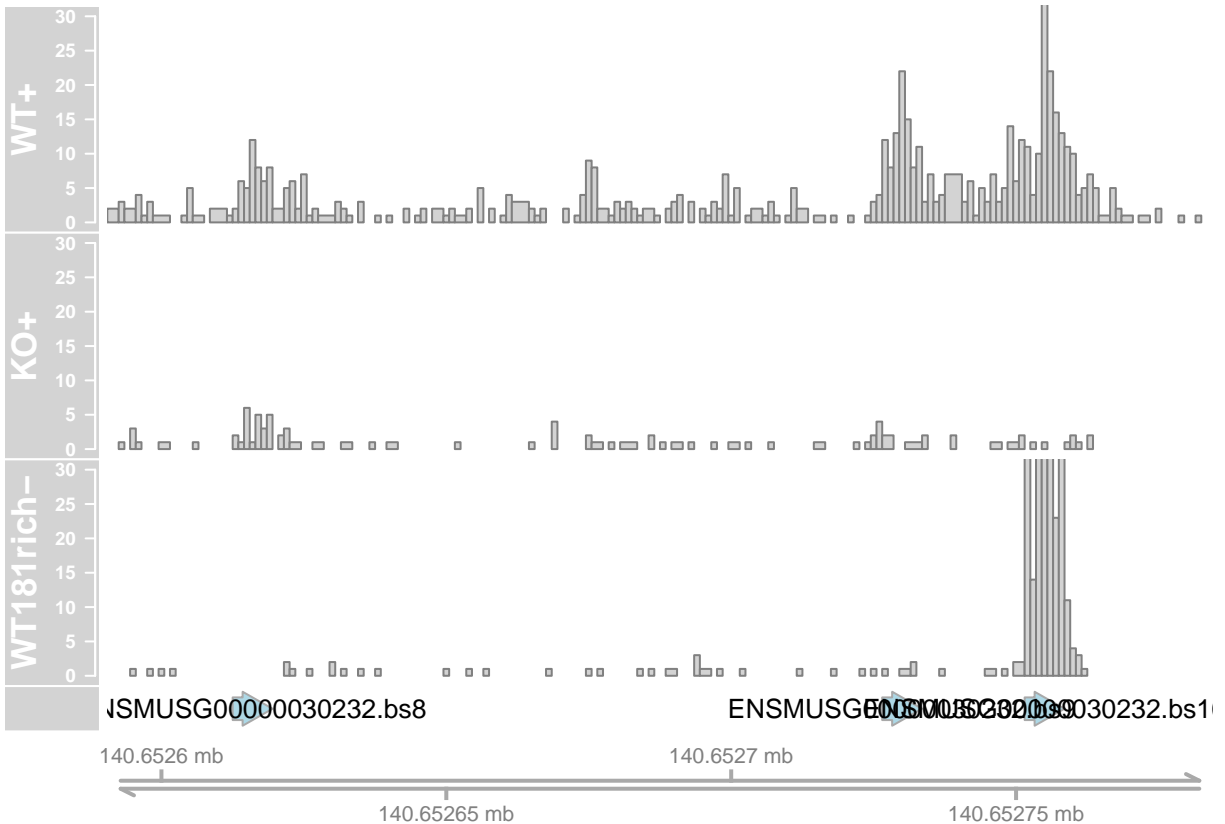
differential binding

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

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

plot

```
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] BSgenome.Mmusculus.UCSC.mm10_1.4.3 BSgenome_1.66.3
## [3] Biostrings_2.66.0                  XVector_0.38.0
## [5] plyranges_1.18.0                    dplyr_1.1.1
## [7] rtracklayer_1.58.0                  Gviz_1.42.1
## [9] GenomicRanges_1.50.2                GenomeInfoDb_1.34.9
```

```

## [11] IRanges_2.32.0                S4Vectors_0.36.2
## [13] 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                http_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                jpeg_0.1-10
## [39] dichromat_2.0-0.1             base64enc_0.1-3
## [41] pkgconfig_2.0.3               htmltools_0.5.4
## [43] MatrixGenerics_1.10.0          highr_0.10
## [45] ensembledb_2.22.0             dbplyr_2.3.2
## [47] fastmap_1.1.1                 htmlwidgets_1.6.2
## [49] rlang_1.1.0                   rstudioapi_0.14
## [51] RSQLite_2.3.1                 BiocIO_1.8.0
## [53] generics_0.1.3                BiocParallel_1.32.6
## [55] VariantAnnotation_1.44.1       RCurl_1.98-1.12
## [57] magrittr_2.0.3                GenomeInfoDbData_1.2.9
## [59] Formula_1.2-5                 interp_1.1-4
## [61] Matrix_1.5-3                  Rcpp_1.0.10
## [63] munsell_0.5.0                 fansi_1.0.4
## [65] lifecycle_1.0.3               stringi_1.7.12
## [67] yaml_2.3.7                    SummarizedExperiment_1.28.0
## [69] zlibbioc_1.44.0               BiocFileCache_2.6.1
## [71] blob_1.2.4                    parallel_4.2.3
## [73] crayon_1.5.2                  deldir_1.0-6
## [75] lattice_0.20-45               GenomicFeatures_1.50.4
## [77] hms_1.1.3                     KEGGREST_1.38.0
## [79] knitr_1.42                     pillar_1.9.0
## [81] rjson_0.2.21                  codetools_0.2-19
## [83] biomaRt_2.54.1                XML_3.99-0.14
## [85] glue_1.6.2                     evaluate_0.20
## [87] latticeExtra_0.6-30           biovizBase_1.46.0
## [89] data.table_1.14.8             png_0.1-8
## [91] vctrs_0.6.1                   gtable_0.3.3
## [93] cachem_1.0.7                  ggplot2_3.4.2
## [95] xfun_0.37                     AnnotationFilter_1.22.0
## [97] restfulr_0.0.15               tibble_3.2.1
## [99] GenomicAlignments_1.34.1      AnnotationDbi_1.60.2

```

[101] memoise_2.0.1

cluster_2.1.4