

# Package ‘VplotR’

January 3, 2025

**Type** Package

**Title** Set of tools to make V-plots and compute footprint profiles

**Version** 1.16.0

**Date** 2021-11-21

**Encoding** UTF-8

**Description** The pattern of digestion and protection from DNA nucleases such as DNase I, micrococcal nuclease, and Tn5 transposase can be used to infer the location of associated proteins. This package contains useful functions to analyze patterns of paired-end sequencing fragment density. VplotR facilitates the generation of V-plots and footprint profiles over single or aggregated genomic loci of interest.

**URL** <https://github.com/js2264/VplotR>

**BugReports** <https://github.com/js2264/VplotR/issues>

**Depends** R (>= 4.0), GenomicRanges, IRanges, ggplot2

**Imports** cowplot, magrittr, GenomeInfoDb, GenomicAlignments, RColorBrewer, zoo, Rsamtools, S4Vectors, parallel, reshape2, methods, graphics, stats

**Suggests** GenomicFeatures, TxDb.Scerevisiae.UCSC.sacCer3.sgdGene, testthat, covr, knitr, rmarkdown, pkgdown

**VignetteBuilder** knitr

**biocViews** NucleosomePositioning, Coverage, Sequencing, BiologicalQuestion, ATACSeq, Alignment

**License** GPL (>= 3)

**RoxygenNote** 7.2.3

**git\_url** <https://git.bioconductor.org/packages/VplotR>

**git\_branch** RELEASE\_3\_20

**git\_last\_commit** cdb105d

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.20

**Date/Publication** 2025-01-02

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---

ABF1\_sacCer3

*ABF1\_sacCer3*

---

### Description

Genomic loci with a REB1 binding motifs according to <http://jaspar.genereg.net/api/v1/matrix/MA0265.1.jaspar>. PWM and scanning done with TFBSTools.

### Usage

```
data(ABF1_sacCer3)
```

### Format

An object of class "GRanges".

## References

Rossi, Lai & Pugh 2018 Genome Research

## Examples

```
data(ABF1_sacCer3)
ABF1_sacCer3
```

---

alignToTSS

*A function to re-align a GRanges object to TSSs*

---

## Description

This function re-aligns ranges (typically regulatory elements) to a set of coordinates, either the TSS column or the TSS.fwd and TSS.rev columns. If none are found, the function assumes the ranges are promoters and that the end or the ranges are the TSSs.

## Usage

```
alignToTSS(granges, upstream = 0, downstream = 1)
```

## Arguments

granges	A stranded GRanges object with a TSS column or TSS.rev and TSS.fwd columns
upstream	How many bases upstream of the TSS should the GRanges object be extended by? [Default: 0]
downstream	How many bases downstream of the TSS should the GRanges object be extended by? [Default: 1]

## Value

GRanges aligned to the TSS column or to TSS.rev and TSS.fwd columns, and extended by upstream/downstream bp.

## Examples

```
data(ce11_proms)
ce11_proms
alignToTSS(ce11_proms)
```

---

ATAC\_ce11\_Serizay2020 ATAC\_ce11\_Serizay2020

---

### Description

A sample of ATAC-seq fragments from individual worm tissues (Serizay et al. 2020, "Tissue-specific profiling reveals distinctive regulatory architectures for ubiquitous, germline and somatic genes", BiorXiv)

### Usage

```
data(ATAC_ce11_Serizay2020)
```

### Format

An object of class "list".

### Examples

```
data(ATAC_ce11_Serizay2020)  
ATAC_ce11_Serizay2020
```

---

bam\_test

*bam\_test*

---

### Description

A .bam file sample

### Usage

```
data(bam_test)
```

### Format

An object of class "GRanges".

### Examples

```
data(bam_test)  
bam_test
```

---

`ce11_all_REs`*ce11\_all\_REs*

---

**Description**

Regulatory elements annotated in *C. elegans* (ce11) according to Serizay et al. 2020, "Tissue-specific profiling reveals distinctive regulatory architectures for ubiquitous, germline and somatic genes", BiorXiv.

**Usage**

```
data(ce11_all_REs)
```

**Format**

GRanges

**Source**

[BiorXiv](#)

**References**

Serizay et al. 2020, "Tissue-specific profiling reveals distinctive regulatory architectures for ubiquitous, germline and somatic genes", BiorXiv. ([DOI](#))

**Examples**

```
data(ce11_all_REs)
table(ce11_all_REs$regulatory_class)
table(ce11_all_REs$which.tissues)
```

---

`ce11_proms`*ce11\_proms*

---

**Description**

Promoters annotated in *C. elegans* (ce11) according to Serizay et al. 2020, "Tissue-specific profiling reveals distinctive regulatory architectures for ubiquitous, germline and somatic genes", BiorXiv.

**Usage**

```
data(ce11_proms)
```

**Format**

An object of class "GRanges".

**Source**

[BiorXiv](#)

**References**

Serizay et al. 2020, "Tissue-specific profiling reveals distinctive regulatory architectures for ubiquitous, germline and somatic genes", BiorXiv. (DOI)

**Examples**

```
data(ce11_proms)
table(ce11_proms$which.tissues)
```

---

```
computeNucleosomeEnrichmentOverBackground
Internal function
```

---

**Description**

A function to compute nucleosome enrichment of a Vmat

**Usage**

```
computeNucleosomeEnrichmentOverBackground(
  Vmat,
  background = NULL,
  plus1_nuc_only = FALSE,
  minus1_nuc = list(c(xmin = -150, xmax = -70), c(ymin = 165, ymax = 260)),
  minus1_nuc_neg = list(c(xmin = -150, xmax = -70), c(ymin = 60, ymax = 145)),
  plus1_nuc = list(c(xmin = 70, xmax = 150), c(ymin = 165, ymax = 260)),
  plus1_nuc_neg = list(c(xmin = 70, xmax = 150), c(ymin = 50, ymax = 145)),
  ...
)
```

**Arguments**

Vmat	A Vmat computed by nucleosomeEnrichment function
background	a background Vmat
plus1_nuc_only	Boolean Should compute nucleosome enrichment only for +1 nucleosome?
minus1_nuc	list where the -1 nucleosome is located
minus1_nuc_neg	where the background of the -1 nucleosome is located
plus1_nuc	where the +1 nucleosome is located
plus1_nuc_neg	where the background of the +1 nucleosome is located
...	additional parameters

**Value**

list

---

 computeVmat

*A function to compute Vplot matrix*


---

### Description

This function computes the underlying matrix shown as a heatmap in Vplots. For each pair of coordinates (x: distance from fragment midpoint to center of GRanges of interest; y: fragment size), the function computes how many fragments there are.

### Usage

```
computeVmat(
  bam_granges,
  granges,
  cores = 1,
  xlims = c(-250, 250),
  ylims = c(50, 300)
)
```

### Arguments

bam_granges	GRanges, paired-end fragments
granges	GRanges, regions to map the fragments onto
cores	Integer, nb of threads to parallelize fragments subsetting
xlims	The x limits of the computed Vmat
ylims	The y limits of the computed Vmat

### Value

A table object

### Examples

```
data(bam_test)
data(ce11_all_REs)
Vmat <- computeVmat(bam_test, ce11_all_REs)
dim(Vmat)
Vmat[seq(1,5), seq(1,10)]
```

---

 CTCF\_hg38

*CTCF\_hg38*


---

### Description

high-score CTCF binding motifs, obtained from JASPAR

### Usage

```
data(CTCF_hg38)
```

**Format**

An object of class "GRanges".

**Examples**

```
data(CTCF_hg38)
CTCF_hg38
```

---

deconvolveBidirectionalPromoters

*A function to duplicate bi-directional GRanges*

---

**Description**

This function splits bi-directional ranges into + and - stranded ranges. It duplicates the ranges which are '\*'.

**Usage**

```
deconvolveBidirectionalPromoters(granges)
```

**Arguments**

granges            A stranded GRanges object

**Value**

GRanges with only '+' and '-' strands. GRanges with '\*' strand have been duplicated and split into forward and reverse strands.

**Examples**

```
data(ce11_all_REs)
library(GenomicRanges)
proms <- ce11_all_REs[grepl('prom', ce11_all_REs$regulatory_class)]
proms
table(strand(proms))
proms <- deconvolveBidirectionalPromoters(proms)
proms
table(strand(proms))
```



---

getCuts	<i>Internal function</i>
---------	--------------------------

---

**Description**

Function to extract cuts (i.e. extremities) of fragments stored as GRanges.

**Usage**

```
getCuts(gr)
```

**Arguments**

gr	GRanges Paired-end fragments used to extract their extremities
----	--

**Value**

GRanges

---

getFragmentsDistribution
--------------------------

*A function to compute sizes distribution for paired-end fragments*

---

**Description**

This function takes fragments and compute the distribution of their sizes over a set or multiple sets of GRanges.

**Usage**

```
getFragmentsDistribution(
  fragments,
  granges_list = NULL,
  extend_granges = c(-500, 500),
  limits = c(0, 600),
  roll = 3,
  cores = 1
)
```

**Arguments**

fragments	GRanges object containing paired-end fragments. See importPEBamFiles for more details on how to create such object.
granges_list	GRanges, can be a list of different sets of GRanges.
extend_granges	numeric vector of length 2, how the GRanges should be extended.
limits	numeric vector of length 2, only consider fragments within this window of sizes.
roll	Integer, apply a moving average of this size
cores	Integer, number of threads used to compute fragment size distribution

**Value**

A list of tbl, one for each .bam file.

**Examples**

```
data(bam_test)
data(ce11_proms)
df <- getFragmentsDistribution(
  bam_test,
  ce11_proms,
  extend_granges = c(-500, 500)
)
head(df)
which.max(df$y)
```

---

importPEBamFiles

*A function to import paired end bam files as GRanges*


---

**Description**

This function takes bam file paths and read them into GRanges objects. Note: Can be quite lengthy for .bam files with 5+ millions fragments.

**Usage**

```
importPEBamFiles(
  files,
  genome = NULL,
  where = NULL,
  max_insert_size = 1000,
  shift_ATAC_fragments = FALSE,
  cores = 10,
  verbose = TRUE
)
```

**Arguments**

files	character vector, each element of the vector is the path of an individual .bam file.
genome	character, genome ID (e.g. "sacCer3", "ce11", "dm6", "mm10" or "hg38").
where	GRanges, only import the fragments mapping to the input GRanges (can fasten the import process a lot).
max_insert_size	Integer, filter out fragments larger than this size.
shift_ATAC_fragments	Boolean, if the fragments come from ATAC-seq, one might want to shift the extremities by +5 / -4 bp.
cores	Integer, number of cores to use when indexing bam files
verbose	Boolean

**Value**

A GRanges object containing fragments from the input .bam file.

**Examples**

```
bamfile <- system.file("extdata", "ex1.bam", package = "Rsamtools")
fragments <- importPEBamFiles(
  bamfile,
  shift_ATAC_fragments = TRUE
)
fragments
```

---

MNase\_sacCer3\_Henikoff2011

*MNase\_sacCer3\_Henikoff2011*

---

**Description**

A sample of MNase-seq fragments from yeast (Henikoff et al. 2011, "Epigenome characterization at single base-pair resolution", PNAS)

**Usage**

```
data(MNase_sacCer3_Henikoff2011)
```

**Format**

An object of class "GRanges".

**Examples**

```
data(MNase_sacCer3_Henikoff2011)
MNase_sacCer3_Henikoff2011
```

---

MNase\_sacCer3\_Henikoff2011\_subset

*MNase\_sacCer3\_Henikoff2011\_subset*

---

**Description**

A sample of fragments from multiple MNase-seq experiments performed in yeast (Henikoff et al. 2011, "Epigenome characterization at single base-pair resolution", PNAS), mapping over chrXV:186,400-187,400.

**Usage**

```
data(MNase_sacCer3_Henikoff2011_subset)
```

**Format**

An object of class "GRanges".

**Examples**

```
data(MNase_sacCer3_Henikoff2011_subset)
MNase_sacCer3_Henikoff2011_subset
```

---

normalizeVmat	<i>A function to normalized a Vmat</i>
---------------	--

---

**Description**

This function normalizes a Vmat. Several different approaches have been implemented to normalize the Vmats.

**Usage**

```
normalizeVmat(
  Vmat,
  bam_granges,
  granges,
  normFun = c("zscore"),
  s = 0.99,
  roll = 1,
  verbose = TRUE
)
```

**Arguments**

Vmat	A Vmat, usually output of computeVmat
bam_granges	GRanges, the paired-end fragments
granges	GRanges, the regions to map the fragments onto
normFun	character. A Vmat should be scaled either by: <ul style="list-style-type: none"> <li>• 'libdepth+nloci', e.g. the library depth and the number of loci used to compute the Vmat;</li> <li>• zscore, if relative patterns of fragment density are more important than density per se;</li> <li>• Alternatively, the Vmat can be scaled to a chosen quantile ('quantile') or to the max Vmat value ('max').</li> </ul>
s	A float indicating which quantile to use if 'quantile' normalization is chosen
roll	integer, to use as the window to smooth the Vmat rows by rolling mean.
verbose	Boolean

**Value**

A normalized Vmat object

**Examples**

```

data(bam_test)
data(ce11_all_REs)
Vmat <- computeVmat(bam_test, ce11_all_REs)
Vmat <- normalizeVmat(
  Vmat,
  bam_test,
  ce11_all_REs,
  normFun = c('libdepth+nloci')
)

```

---

nucleosomeEnrichment *A function to compute nucleosome enrichment over a set of GRanges*

---

**Description**

A function to compute nucleosome enrichment over a set of GRanges

**Usage**

```
nucleosomeEnrichment(x, ...)
```

**Arguments**

x	a GRanges or Vmat
...	additional parameters

**Value**

list

**Examples**

```

data(bam_test)
data(ce11_proms)
n <- nucleosomeEnrichment(bam_test, ce11_proms)
n$fisher_test
n$plot

```

---

nucleosomeEnrichment.GRanges

*A function to compute nucleosome enrichment over a set of GRanges*

---

**Description**

A function to compute nucleosome enrichment over a set of GRanges

**Usage**

```

## S3 method for class 'GRanges'
nucleosomeEnrichment(x, granges, plus1_nuc_only = FALSE, verbose = TRUE, ...)

```

**Arguments**

x	GRanges, paired-end fragments
granges	GRanges, loci to map the fragments onto
plus1_nuc_only	Boolean, should compute nucleosome enrichment only for +1 nucleosome?
verbose	Boolean
...	additional parameters

**Value**

list

**Examples**

```
data(bam_test)
data(ce11_proms)
n <- nucleosomeEnrichment(bam_test, ce11_proms)
n$fisher_test
n$plot
```

---

nucleosomeEnrichment.Vmat

*A function to compute nucleosome enrichment over a Vmat*

---

**Description**

A function to compute nucleosome enrichment over a Vmat

**Usage**

```
## S3 method for class 'Vmat'
nucleosomeEnrichment(x, background, plus1_nuc_only = FALSE, ...)
```

**Arguments**

x	a computed Vmat. Should be un-normalized.
background	a background Vmat. Should be un-normalized.
plus1_nuc_only	Boolean, should compute nucleosome enrichment only for +1 nucleosome?
...	additional parameters

**Value**

list

**Examples**

```

data(bam_test)
data(ce11_proms)
V <- plotVmat(
  bam_test,
  ce11_proms,
  normFun = '',
  return_Vmat = TRUE
)
V_bg <- plotVmat(
  bam_test,
  sampleGRanges(ce11_proms),
  normFun = '',
  return_Vmat = TRUE
)
n <- nucleosomeEnrichment(V, V_bg)
n$fisher_test
n$plot

```

---

plotFootprint

*A function to plot footprint of paired-end data at given loci*


---

**Description**

This function takes paired-end fragments, extract the "cuts" (i.e. extremities) and plot the footprint profile over a set of GRanges.

**Usage**

```

plotFootprint(
  frags,
  targets,
  split_strand = FALSE,
  plot_central = TRUE,
  xlim = c(-75, 75),
  bin = 1,
  verbose = 1
)

```

**Arguments**

frags	GRanges, the paired-end fragments
targets	GRanges, the loci to map the fragments onto
split_strand	Boolean, should the + and - strand be splitted?
plot_central	plot grey rectangle over the loci
xlim	numeric vector of length 2, the x limits of the computed Vmat
bin	Integer, bin used to smooth the footprint profile
verbose	Integer

**Value**

A footprint ggplot

**Examples**

```
data(bam_test)
data(ce11_proms)
plotFootprint(bam_test, ce11_proms)
```

---

plotProfile

*A function to generate a Vplot along chromosome coordinates*

---

**Description**

The paired-end fragments overlapping a locus of interest (e.g., binding sites, provided in the ‘loci’ argument) are shown in red while the remaining fragments mapping to the genomic window are displayed in black. Marginal curves are also plotted on the side of the distribution plot. They highlight the smoothed distribution of the position of paired-end fragment midpoints (top) or of the paired-end fragment length (right)

**Usage**

```
plotProfile(
  fragments,
  window = loc,
  loci = NULL,
  annots = NULL,
  min = 50,
  max = 200,
  alpha = 0.5,
  size = 1,
  with_densities = TRUE,
  verbose = TRUE
)
```

**Arguments**

fragments	GRanges
window	character, chromosome location
loci	GRanges, optional genomic locus. Fragments overlapping this locus will be in red.
annots	GRanges, optional gene annotations
min	integer, minimum fragment size
max	integer, maximum fragment size
alpha	float, transparency value
size	float, dot size
with_densities	Boolean, should the densities be plotted?
verbose	Boolean



**Value**

A ggplot

**Examples**

```
data(bam_test)
data(ce11_proms)
V <- plotProfile(
  bam_test,
  'chrI:10000-12000',
  loci = ce11_proms,
  min = 80,
  max = 200
)
```

---

plotVmat

*A function to generate a Vplot*

---

**Description**

See individual methods for further detail

**Usage**

```
plotVmat(x, ...)
```

**Arguments**

x	GRanges or list or Vmat
...	additional parameters

**Value**

A Vmat ggplot

**Examples**

```
data(bam_test)
data(ce11_proms)
V <- plotVmat(
  bam_test,
  ce11_proms,
  normFun = 'libdepth+nloci'
)
```

---

plotVmat.default      *A function to plot a computed Vmat*

---

### Description

The default plotVmat method generates a ggplot representing a heatmap of fragment density.

### Usage

```
## Default S3 method:
plotVmat(
  x,
  hm = 90,
  colors = COLORSCALE_VMAT,
  breaks = NULL,
  xlim = c(-250, 250),
  ylim = c(50, 300),
  main = "",
  xlab = "Distance from center of elements",
  ylab = "Fragment length",
  key = "Score",
  ...
)
```

### Arguments

x	A computed Vmat (ideally, should be normalized)
hm	Integer, should be between 0 and 100. Used to automatically scale the range of colors (best to keep between 90 and 100)
colors	a vector of colors
breaks	a vector of breaks. length(breaks) == length(colors) + 1
xlim	vector of two integers, x limits
ylim	vector of two integers, y limits
main	character, title of the plot
xlab	character, x-axis label
ylab	character, y-axis label
key	character, legend label
...	additional parameters

### Value

A Vmat ggplot

**Examples**

```

data(bam_test)
data(ce11_proms)
V <- plotVmat(
  bam_test,
  ce11_proms,
  normFun = 'libdepth+nloci',
  return_Vmat = TRUE
)
plotVmat(V)

```

---

plotVmat.GRanges      *A function to compute (and plot) a Vmat*

---

**Description**

The plotVmat.GRanges() method computes and normalizes a Vmat before passing it to plotVmat.Vmat() method.

**Usage**

```

## S3 method for class 'GRanges'
plotVmat(
  x,
  granges,
  xlims = c(-250, 250),
  ylims = c(50, 300),
  normFun = "",
  s = 0.95,
  roll = 3,
  cores = 1,
  return_Vmat = FALSE,
  verbose = 1,
  ...
)

```

**Arguments**

x	GRanges, paired-end fragments
granges	GRanges, loci to map the fragments onto
xlims	x limits of the computed Vmat
ylims	y limits of the computed Vmat
normFun	character. A Vmat should be scaled either by: <ul style="list-style-type: none"> <li>• 'libdepth+nloci', e.g. the library depth and the number of loci used to compute the Vmat;</li> <li>• zscore, if relative patterns of fragment density are more important than density per se;</li> <li>• Alternatively, the Vmat can be scaled to a chosen quantile ('quantile') or to the max Vmat value ('max').</li> </ul>

s	A float indicating which quantile to use if 'quantile' normalization is chosen
roll	integer, to use as the window to smooth the Vmat rows by rolling mean.
cores	Integer, number of threads to parallelize fragments subsetting
return_Vmat	Boolean, should the function return the computed Vmat rather than the plot?
verbose	Boolean
...	additional parameters

**Value**

A Vmat ggplot

**Examples**

```
data(bam_test)
data(ce11_proms)
V <- plotVmat(
  bam_test,
  ce11_proms,
  normFun = 'libdepth+nloci',
  roll = 5
)
```

---

plotVmat.list

*A function to compute (and plot) several Vmats.*

---

**Description**

The plotVmat.GRanges() method computes and normalizes multiple Vmats before passing them to plotVmat.VmatList() method.

**Usage**

```
## S3 method for class 'list'
plotVmat(
  x,
  cores = 1,
  cores_subsetting = 1,
  nrow = NULL,
  ncol = NULL,
  xlims = c(-250, 250),
  ylims = c(50, 300),
  normFun = "libdepth+nloci",
  s = 0.95,
  roll = 3,
  return_Vmat = FALSE,
  verbose = 1,
  ...
)
```

**Arguments**

x	list	Each element of the list should be a list containing paired-end fragments and GRanges of interest.
cores	Integer	number of cores to parallelize the plots
cores_subsetting	Integer	number of threads to parallelize fragments subsetting
nrow	Integer	how many rows in facet?
ncol	Integer	how many cols in facet?
xlims	x limits	of the computed Vmat
ylims	y limits	of the computed Vmat
normFun	character	A Vmat should be scaled either by: <ul style="list-style-type: none"> <li>• 'libdepth+nloci', e.g. the library depth and the number of loci used to compute the Vmat;</li> <li>• zscore, if relative patterns of fragment density are more important than density per se;</li> <li>• Alternatively, the Vmat can be scaled to a chosen quantile ('quantile') or to the max Vmat value ('max').</li> </ul>
s	A float	indicating which quantile to use if 'quantile' normalization is chosen
roll	integer	to use as the window to smooth the Vmat rows by rolling mean.
return_Vmat	Boolean	should the function return the computed Vmat rather than the plot?
verbose	Boolean	
...	additional	parameters

**Value**

A list of Vmat ggplots

**Examples**

```

data(bam_test)
data(ce11_proms)
list_params <- list(
  'germline' = list(
    bam_test,
    ce11_proms[ce11_proms$which.tissues == 'Germline']
  ),
  'muscle' = list(
    bam_test,
    ce11_proms[ce11_proms$which.tissues == 'Muscle']
  )
)
V <- plotVmat(
  list_params,
  normFun = 'libdepth+nloci',
  roll = 5
)

```

---

plotVmat.Vmat      *A function to plot a computed Vmat*

---

### Description

The plotVmat.Vmat() method forwards the Vmat to plotVmat.default().

### Usage

```
## S3 method for class 'Vmat'
plotVmat(x, ...)
```

### Arguments

x                    A computed Vmat (ideally, should be normalized)  
 ...                  additional parameters

### Value

A Vmat ggplot

### Examples

```
data(bam_test)
data(ce11_proms)
V <- plotVmat(
  bam_test,
  ce11_proms,
  normFun = 'libdepth+nloci',
  return_Vmat = TRUE
)
plotVmat(V)
```

---

plotVmat.VmatList      *A function to plot a computed VmatList*

---

### Description

The plotVmat.VmatList() method forwards the Vmat to plotVmat.default().

### Usage

```
## S3 method for class 'VmatList'
plotVmat(x, nrow = NULL, ncol = NULL, dir = "v", ...)
```

### Arguments

x                    A VmatList (output of plotVmat.list())  
 nrow                Integer, how many rows in facet?  
 ncol                Integer, how many cols in facet?  
 dir                  str, direction of facets?  
 ...                  additional parameters

**Value**

A Vmat ggplot

**Examples**

```
data(bam_test)
data(ce11_proms)
list_params <- list(
  'germline' = list(
    bam_test,
    ce11_proms[ce11_proms$which.tissues == 'Germline']
  ),
  'muscle' = list(
    bam_test,
    ce11_proms[ce11_proms$which.tissues == 'Muscle']
  )
)
V <- plotVmat(
  list_params,
  normFun = 'libdepth+nloci',
  roll = 5
)
```

---

REB1\_sacCer3

*REB1\_sacCer3*

---

**Description**

Genomic loci with a REB1 binding motifs according to <http://jaspar.genereg.net/api/v1/matrix/MA0363.1.jaspar>. PWM and scanning done with TFBSTools.

**Usage**

```
data(REB1_sacCer3)
```

**Format**

An object of class "GRanges".

**References**

Rossi, Lai & Pugh 2018 Genome Research

**Examples**

```
data(REB1_sacCer3)
REB1_sacCer3
```

---

sampleGRanges      *A function to sample GRanges from GRanges*

---

### Description

This function takes a given GRanges and returns another GRanges object. The new GRanges has the same number of ranges and the same chromosome, width and strand distributions than the original GRanges.

### Usage

```
sampleGRanges(  
  x,  
  n = NULL,  
  width = NULL,  
  exclude = FALSE,  
  avoid_overlap = FALSE  
)
```

### Arguments

x	GRanges object
n	Integer, number of sampled GRanges
width	Integer, width of sampled GRanges
exclude	Boolean, should the original GRanges be excluded?
avoid_overlap	Boolean, should the sampled GRanges not be overlapping?

### Value

A GRanges object of length n

### Examples

```
data(ce11_proms)  
sampleGRanges(ce11_proms, 100)
```

---

sampleGRanges.GRanges      *A function to sample GRanges within GRanges*

---

### Description

This function takes a given GRanges and returns another GRanges object. The new GRanges has the same number of ranges and the same chromosome, width and strand distributions than the original GRanges.



**Usage**

```
## S3 method for class 'GRanges'
sampleGRanges(
  x,
  n = NULL,
  width = NULL,
  exclude = FALSE,
  avoid_overlap = FALSE
)
```

**Arguments**

x	GRanges object
n	Integer, number of sampled GRanges
width	Integer, width of sampled GRanges
exclude	Boolean, should the original GRanges be excluded?
avoid_overlap	Boolean, should the sampled GRanges not be overlapping?

**Value**

A GRanges object of length n

**Examples**

```
data(ce11_proms)
sampleGRanges(ce11_proms, 100)
```

---

shiftATACGranges	<i>A function to shift GRanges fragments by 5/-4. This is useful when dealing with fragments coming from ATAC-seq.</i>
------------------	--

---

**Description**

A function to shift GRanges fragments by 5/-4. This is useful when dealing with fragments coming from ATAC-seq.

**Usage**

```
shiftATACGranges(g, pos_shift = 4, neg_shift = 5)
```

**Arguments**

g	GRanges of ATAC-seq fragments
pos_shift	Integer. How many bases should fragments on direct strand be shifted by?
neg_shift	Integer. How many bases should fragments on negative strand be shifted by?

**Value**

A GRanges object containing fragments from the input .bam file.

**Examples**

```
data(bam_test)
shiftATACGranges(bam_test)
```

---

shuffleVmat	<i>A function to shuffle a Vmat</i>
-------------	-------------------------------------

---

**Description**

This function works on a Vmat (the output of computeVmat()). It shuffles the matrix to randomize the fragment densities.

**Usage**

```
shuffleVmat(Vmat)
```

**Arguments**

Vmat                    A Vmat, usually output of computeVmat

**Value**

A shuffled Vmat object

**Examples**

```
data(bam_test)
data(ce11_all_REs)
Vmat <- computeVmat(bam_test, ce11_all_REs)
Vmat <- shuffleVmat(Vmat)
```

---

theme_ggplot2	<i>Personal ggplot2 theming function, adapted from roboto-condensed at <a href="https://github.com/hrbrmstr/hrbrthemes/">https://github.com/hrbrmstr/hrbrthemes/</a></i>
---------------	--

---

**Description**

Personal ggplot2 theming function, adapted from roboto-condensed at <https://github.com/hrbrmstr/hrbrthemes/>

**Usage**

```
theme_ggplot2(
  grid = TRUE,
  border = TRUE,
  base_family = "",
  base_size = 8,
  plot_title_family = base_family,
  plot_title_size = 12,
  plot_title_face = "plain",
  plot_title_margin = 5,
```

```

  subtitle_size = 11,
  subtitle_face = "plain",
  subtitle_margin = 5,
  strip_text_family = base_family,
  strip_text_size = 10,
  strip_text_face = "bold",
  caption_size = 9,
  caption_face = "plain",
  caption_margin = 3,
  axis_text_size = base_size,
  axis_title_family = base_family,
  axis_title_size = 9,
  axis_title_face = "plain",
  axis_title_just = "rt",
  panel_spacing = grid::unit(2, "lines"),
  grid_col = "#cccccc",
  plot_margin = margin(12, 12, 12, 12),
  axis_col = "#cccccc",
  axis = FALSE,
  ticks = FALSE
)

```

### Arguments

grid	panel grid ('TRUE', 'FALSE', or a combination of 'X', 'x', 'Y', 'y')
border	border if 'TRUE' add border
base_family, base_size	base font family and size
plot_title_family, plot_title_face	plot title family, face
plot_title_size, plot_title_margin	plot title size and margin
subtitle_face, subtitle_size	plot subtitle family, face and size
subtitle_margin	plot subtitle margin bottom (single numeric value)
strip_text_family, strip_text_face, strip_text_size	facet label font family, face and size
caption_face, caption_size, caption_margin	plot caption family, face, size and margin
axis_text_size	font size of axis text
axis_title_family, axis_title_face, axis_title_size	axis title font family, face and size
axis_title_just	axis title font justificationk one of '[blmrt]'
panel_spacing	panel spacing (use 'unit()')
grid_col	grid color
plot_margin	plot margin (specify with [ggplot2::margin])
axis_col	axis color
axis	add x or y axes? 'TRUE', 'FALSE', "'xy'"
ticks	ticks if 'TRUE' add ticks

**Value**

theme A ggplot theme

**Examples**

```
library(ggplot2)

ggplot(mtcars, aes(mpg, wt)) +
  geom_point() +
  labs(x="Fuel efficiency (mpg)", y="Weight (tons)",
       title="Seminal ggplot2 scatterplot example") +
  theme_ggplot2()
```

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