Package ‘MEDIPSData’

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Title Example data for MEDIPS and QSEA packages
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Description Example data for MEDIPS and QSEA packages, consisting of chromosome 22 MeDIP and control/Input sample data. Additionally, the package contains MeDIP seq data from 3 NSCLC samples and adjacent normal tissue (chr 20-22). All data has been aligned to human genome hg19.
License GPL (>= 2)
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</table>
Description

This is a list of GRanges objects, which contain genomic annotations for hg19 reference, obtained from UCSC table browser.

Usage

```
data(annotation)
```

Examples

```
## Not run:
data(annotation)
library(GenomicRanges)
names(ROIs)
ROIs$'gene body'
names(tfbs)

## End(Not run)
```

Description

This is a CpG coupling set generated by the MEDIPS package based on the human chromosome 22 (hg19) and with a window size of 100bp.

Usage

```
data(CS)
```
DE_Input

control data set from definitive endoderm

Description

This is a MEDIPS SET object created from Input-seq control data derived from definitive endoderm as presented by Chavez et al. 2010. The parameter settings are: BSgenome= "BSgenome.Hsapiens.UCSC.hg19" extend= 300 shift= 0 uniq= T ws= 100 chr.select= "chr22"

Usage

data(DE_Input)

References


DE_MeDIP

Concatenated set of three MeDIP-seq data sets (replicates) from definitive endoderm

Description

This is a concatenated set of three MEDIPS SET objects created from MeDIP-seq data derived from definitive endoderm as presented by Chavez et al. 2010. The parameter settings are: BSgenome= "BSgenome.Hsapiens.UCSC.hg19" extend= 300 shift= 0 uniq= T ws= 100 chr.select= "chr22"
Usage

data(DE_MeDIP)

References


Examples

```r
## Not run:
data(DE_MeDIP)
library(MEDIPS)
DE_MeDIP

## End(Not run)
```

hESCs_Input

control data set from human embryonic stem cells

Description

This is a MEDIPS SET object created from Input-seq control data derived from human embryonic stem cells as presented by Chavez et al. 2010. The parameter settings are: BSgenome= "BSgenome.Hsapiens.UCSC.hg19" extend= 300 shift= 0 uniq= T ws= 100 chr.select= "chr22"

Usage

data(hESCs_Input)

References


Examples

```r
## Not run:
data(hESCs_Input)
library(MEDIPS)
hESCs_Input

## End(Not run)
```
hESCs_MeDIP

**hESCs_MeDIP**  
*Concatenated set of three MeDIP-seq data sets (replicates) from human embryonic stem cells*

**Description**

This is a concatenated set of three MEDIPS SET objects created from MeDIP-seq data derived from human embryonic stem cells as presented by Chavez et al. 2010. The parameter settings are: BSgenome= "BSgenome.Hsapiens.UCSC.hg19" extend= 300 shift= 0 uniq= T ws= 100 chr.select= "chr22"

**Usage**

`data(hESCs_MeDIP)`

**References**


**Examples**

```r
## Not run:
data(hESCs_MeDIP)
library(MEDIPS)
hESCs_MeDIP
## End(Not run)
```

---

**mart_gene**

*An annotation object generated by accessing biomaRt using the MEDIPS.getAnnotation function of the MEDIPS package.*

**Description**

This is an annotation object generated by accessing biomaRt using the MEDIPS.getAnnotation function of the MEDIPS package: mart_gene = MEDIPS.getAnnotation(mart="ensembl", dataset=c("hsapiens_gene_ensembl"), annotation=c("GENE"), chr=22) The annotation object contains genomic coordinates of human genes on chromosome 22.

**Usage**

`data(mart_gene)`
Examples

```
## Not run:
data(mart_gene)
data(resultTable)
library(MEDIPS)
resultTable = MEDIPS.setAnnotation(regions=resultTable, annotation=mart_gene)

## End(Not run)
```

### NSCLC_dataset

**QSEA MeDIP-seq lung cancer example dataset**

**Description**

This is a qsea set object `qseaSet` and a qsa glm object `qseaGLM` `qseaSet` contains MeDIP seq data from NSCLC samples and adjacent normal. `qseaGLM` contains test statistics for the comparison of tumor and normal samples.

**Usage**

```r
data(annotation)
```

**Examples**

```
## Not run:
data(NSCLC_dataset)
library(qsea)
qseaSet
qseaGLM

## End(Not run)
```

### resultTable

**A result table as returned by the MEDIPS.meth function of the MEDIPS package**

**Description**

This is a result table as returned by the MEDIPS.meth function using the following command:

```r
mr.edgeR = MEDIPS.meth(MSet1=hESCs, MSet2=DE, CSet=CS, ISet1=hESCs.Input, ISet2=DE.Input, p.adj="bonferroni", diff.method="edgeR", prob.method="poisson", CNV=F, MeDIP=T) where hESCs, DE, and CS are data objects included in this data package.
```

**Usage**

```r
data(resultTable)
```
samplesNSCLC

Examples

```r
## Not run:
data(resultTable)
library(MEDIPS)
mr.edgeR.s = MEDIPS.selectSig(results=mr.edgeR, p.value=0.05, adj=T, ratio=NULL, bg.counts=NULL, CNV=F)
mr.edgeR.s

## End(Not run)
```

samplesNSCLC | QSEA lung cancer MeDIP seq sample table

Description

This data set contains a sample table describing the samples of the QSEA lung cancer MeDIP seq example data.

Usage

```r
data(samplesNSCLC)
```

Examples

```r
## Not run:
data(samplesNSCLC)
samplesNSCLC

## End(Not run)
```

tcga_luad_lusc_450kmeth

Lung cancer calibration data

Description

Calibration data for the lung cancer MeDIP seq example data, taken from TCGA LUAD and LUSC studies.

Usage

```r
data(CS)
```

Examples

```r
## Not run:
data(tcga_luad_lusc_450kmeth)
tcga_luad_lusc_450kmeth

## End(Not run)
```
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