

# Package ‘MEDIPSData’

December 24, 2024

**Type** Package

**Title** Example data for MEDIPS and QSEA packages

**Version** 1.43.0

**Depends** R (>= 2.15.0)

**Date** 2021-11-21

**Author** Lukas Chavez

**Maintainer** Lukas Chavez <lchavez@liai.org>

**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)

**LazyLoad** yes

**biocViews** ExperimentData, Genome, SequencingData

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

**git\_branch** devel

**git\_last\_commit** 13378c9

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

**Repository** Bioconductor 3.21

**Date/Publication** 2024-12-24

## Contents

annotation . . . . .	2
CS . . . . .	2
DE_Input . . . . .	3
DE_MeDIP . . . . .	3
hESCs_Input . . . . .	4
hESCs_MeDIP . . . . .	5

mart_gene . . . . .	5
NSCLC_dataset . . . . .	6
resultTable . . . . .	6
samplesNSCLC . . . . .	7
tcga_luad_lusc_450kmeth . . . . .	7
<b>Index</b>	<b>8</b>

---

annotation	<i>QSEA example annotation</i>
------------	--------------------------------

---

### Description

This is a list of GRange 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)
```

---

CS	<i>COUPLING SET</i>
----	---------------------

---

### 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)
```

**Examples**

```
## Not run:  
data(CS)  
library(MEDIPS)  
CS  
  
## End(Not run)
```

---

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**

Chavez, L., Jozefczuk, J., Grimm, C., Dietrich, J., Timmermann, B., Herwig, R., Adjaye, J. (2010): Computational analysis of genome-wide DNA methylation during the differentiation of human embryonic stem cells along the endodermal lineage, *Genome Research*. 20(10):1441-50

**Examples**

```
## Not run:  
data(DE_Input)  
library(MEDIPS)  
DE_Input  
  
## End(Not run)
```

---

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**

Chavez, L., Jozefczuk, J., Grimm, C., Dietrich, J., Timmermann, B., Herwig, R., Adjaye, J. (2010): Computational analysis of genome-wide DNA methylation during the differentiation of human embryonic stem cells along the endodermal lineage, *Genome Research*. 20(10):1441-50

**Examples**

```
## 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**

Chavez, L., Jozefczuk, J., Grimm, C., Dietrich, J., Timmermann, B., Herwig, R., Adjaye, J. (2010): Computational analysis of genome-wide DNA methylation during the differentiation of human embryonic stem cells along the endodermal lineage, *Genome Research*. 20(10):1441-50

**Examples**

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

---

hESCs_MeDIP	<i>Concatenated set of three MeDIP-seq data sets (replicates) from human embryonic stem cells</i>
-------------	---

---

### 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

Chavez, L., Jozefczuk, J., Grimm, C., Dietrich, J., Timmermann, B., Herwig, R., Adjaye, J. (2010): Computational analysis of genome-wide DNA methylation during the differentiation of human embryonic stem cells along the endodermal lineage, *Genome Research*. 20(10):1441-50

### Examples

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

## End(Not run)
```

---

mart_gene	<i>An annotation object generated by accessing biomaRt using the MEDIPS.getAnnotation function of the MEDIPS package.</i>
-----------	---

---

### 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	<i>QSEA MeDIP-seq lung cancer example dataset</i>
---------------	---

---

**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**

```
data(annotation)
```

**Examples**

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

## End(Not run)
```

---

resultTable	<i>A result table as returned by the MEDIPS.meth function of the MEDIPS package</i>
-------------	---

---

**Description**

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

```
data(resultTable)
```

**Examples**

```
## 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**

```
data(samplesNSCLC)
```

**Examples**

```
## 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**

```
data(CS)
```

**Examples**

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

## End(Not run)
```

# Index

## \* datasets

- annotation, [2](#)
- CS, [2](#)
- DE\_Input, [3](#)
- DE\_MeDIP, [3](#)
- hESCs\_Input, [4](#)
- hESCs\_MeDIP, [5](#)
- mart\_gene, [5](#)
- NSCLC\_dataset, [6](#)
- resultTable, [6](#)
- samplesNSCLC, [7](#)
- tcga\_luad\_lusc\_450kmeth, [7](#)

annotation, [2](#)

CS, [2](#)

DE\_Input, [3](#)

DE\_MeDIP, [3](#)

hESCs\_Input, [4](#)

hESCs\_MeDIP, [5](#)

mart\_gene, [5](#)

NSCLC\_dataset, [6](#)

resultTable, [6](#)

samplesNSCLC, [7](#)

tcga\_luad\_lusc\_450kmeth, [7](#)