

# Package ‘MEDIPSData’

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**Type** Package

**Title** Example data for the MEDIPS package.

**Version** 0.99.5

**Depends** R (>= 2.15.0)

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**Author** Lukas Chavez

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

**Description** Data for the MEDIPS package, consisting of chromosome 22 MeDIP and control/Input sample data from DNA methylation analysis of human embryonic stem cells and mapped to the human genome hg19 using bowtie.

**License** GPL (>= 2)

**LazyLoad** yes

**biocViews** ExperimentData, ChIPseq, DNAMethylation,DifferentialExpression, HighThroughputSequencing, Methyleseq,Preprocessing, QualityControl, Sequencing, Software,Visualization

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CS	<i>COUPLING SET</i>
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**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)
```

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DE_Input	<i>control data set from definitive endoderm</i>
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**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)
```

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DE_MeDIP	<i>Concatenated set of three MeDIP-seq data sets (replicates) from definitive endoderm</i>
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**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)
```

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hESCs_Input	<i>control data set from human embryonic stem cells</i>
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**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)
```

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hESCs\_MeDIP

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

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**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)
```

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

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

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