# Package 'mCSEAdata'

**Type** Package

**Title** Data package for mCSEA package

**Version** 1.26.0

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**Description** Data objects necessary to some mCSEA package functions.
There are also example data objects to illustrate mCSEA package functionality.

**Depends** R (>= 3.5)

**Imports** GenomicRanges

**Suggests** BiocStyle, knitr, rmarkdown

**VignetteBuilder** knitr

**biocViews** Homo_sapiens_Data, MethylationArrayData, MicroarrayData,
ExperimentData

**License** GPL-2

**Encoding** UTF-8

**LazyData** true

**LazyDataCompression** xz

**git_url** https://git.bioconductor.org/packages/mCSEAdata

**git_branch** RELEASE_3_20

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mCSEAdata-package     *Data and examples for mCSEA package*

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**Description**

Association files between Illumina's 450K and EPIC microarrays probes and promoters, CpG Islands and gene bodies. Annotation for the previous microarrays' probes. There are also sample data from EPIC platform and expression microarrays to test mCSEA functions and a necessary object for mCSEAPlot function.

**Author(s)**

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**Examples**

```
data(mcseadata)
data(bandTable)
```

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bandTable     *Human chromosomes information*

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**Description**

bandTable contains chromosomes band information and centromer location. It is used by mCSEAPlot() function to plot the chromosome track.

**Usage**

```
data(bandTable)
```

**Format**

data.frame

**Source**

Obtained with Gviz's IdeogramTrack() function.

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mcseadata                    *Data and examples for mCSEA package*

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**Description**

Association files between Illumina's 450K and EPIC microarrays probes and promoters, CpG Islands and gene bodies. There are also sample data from EPIC platform to test mCSEA functions and annotation for 450K and EPIC probes.

**Usage**

```
data(mcseadata)
```

**Format**

matrix (`betaTest` and `exprTest`), data.frame (`phenoTest`), list (`assocPromoters450k`, `assocPromotersEPIC`, `assocGenes450k`, `assocGenesEPIC`, `assocCGI450k` and `assocCGIEPIC`) and GRanges (`annot450K` and `annotEPIC`)

**Source**

`betaTest` and `phenoTest` are simulated data. `exprTest` was obtained from leukemiasEset package. `annot450K` and `annotEPIC` were constructed with minfi package. `assocPromoters450k`, `assocPromotersEPIC`, `assocGenes450k`, `assocGenesEPIC`, `assocCGI450k` and `assocCGIEPIC` were constructed from IlluminaHumanMethylation450kanno.ilmn12.hg19 and IlluminaHumanMethylationEPICanno.ilm10b2.hg19 packages annotation data.

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