Package ‘DMRcatedata’

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Type Package

Title Data Package for DMRcate package

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Description This package contains 7 data objects supporting functionality and examples of the Bioconductor package DMRcate.

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Depends R (>= 3.2.2), GenomicRanges

Suggests knitr

biocViews ExperimentData, SNPData

VignetteBuilder knitr

NeedsCompilation no

R topics documented:

`DMRcatedata-package` *Dataset to use with the DMRcate Pipeline*

Description

SNP annotation, cross-hybridising probes and sample 450k data

Author(s)

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Examples

```
data(dmrcatedata)
```

`dmrcatedata` *Accompanying data package for DMRcate*

Description

SNP and Gencode annotation, cross-hybridising probes and sample 450K and simulated WGBS data

Usage

```
data(dmrcatedata)
```

Format

matrix (`myBetas`), factor (`crosshyb`) and data.frame (`illuminaSNPs`)

Source

`myBetas` sourced from The Cancer Genome Atlas (TCGA) data repository, colon and rectal adenocarcinoma; `illuminaSNPs` sourced from `http://supportres.illumina.com/documents/myillumina/88bab663-307c-444a-848e-0ed6c338ee4d/humanmethylation450_15017482_v.1.2.snpupdate.table.v3.txt`, accessed February 2014; `crosshyb` sourced from `http://www.sickkids.ca/MS-Office-Files/Research/WeksbergLab/48639-non-specific-probes-Illumina450k.xlsx`, accessed February 2014; `tx.hg19`, `tx.hg38` and `tx.mm10` sourced from `ftp://ftp.ensembl.org`, accessed July 2015

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