

Package ‘DMRcatedata’

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Type Package

Title Data Package for DMRcate package

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Description This package contains 8 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	1
dmrcatedata	2

Index	3
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DMRcatedata-package *Dataset to use with the DMRcate Pipeline*

Description

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

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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; snpsall sourced from <http://genomebiology.biomedcentral.com/articles/10.1186/s13059-016-1066-1>, accessed October 2016, http://supportres.illumina.com/documents/myillumina/88bab663-307c-444a-848e-0ed6c338ee4d/humanmethylation450_15017482_v.1.2.snupdate.table.v3.txt, accessed February 2014; crosshyb sourced from <http://genomebiology.biomedcentral.com/articles/10.1186/s13059-016-1066-1>, accessed October 2016, <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

Index

*Topic **datasets**

dmrcatedata, [2](#)

DMRcatedata-package, [1](#)

DMRcatedata (DMRcatedata-package), [1](#)

dmrcatedata, [2](#)

DMRcatedata-package, [1](#)