

Package ‘DMRcatedata’

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Type Package

Title Data Package for DMRcate package

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Description This package contains 3 data objects supporting functionality and examples of DMRcate

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Depends R (>= 3.0.2)

biocViews 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 and sample 450k data

Author(s)

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Examples

```
data(dmrcatedata)
```

dmrcatedata

Accompanying data package for DMRcate

Description

SNP annotation, cross-hybridising probes and sample 450k 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

Index

*Topic **datasets**

dmrcatedata, [2](#)

DMRcatedata-package, [1](#)

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

dmrcatedata, [2](#)

DMRcatedata-package, [1](#)