

# Package ‘DMRcatedata’

April 8, 2015

**Type** Package

**Title** Data Package for DMRcate package

**Version** 1.1.1

**Date** 2013-20-12

**Author** Tim Peters

**Maintainer** Tim Peters <Tim.Peters@csiro.au>

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

**License** GPL-3

**Depends** R (>= 3.0.2)

**biocViews** IlluminaChip

**VignetteBuilder** knitr

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

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## Description

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

## Author(s)

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Maintainer: Tim Peters<Tim.Peters@csiro.au>

**Examples**

```
data(dmrcatedata)
```

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dmrcatedata

*Accompanying data package for DMRcate*

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**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](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

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