

# Package ‘DMRcatedata’

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**Type** Package

**Title** Data Package for DMRcate

**Version** 2.2.1

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**Description** This package contains 9 data objects supporting functionality and examples of the Bioconductor package DMRcate.

**License** GPL-3

**Depends** R (>= 3.6), ExperimentHub

**Imports** GenomicFeatures, Gviz, readxl, plyr, rtracklayer,  
IlluminaHumanMethylation450kanno.ilmn12.hg19,  
IlluminaHumanMethylationEPICanno.ilm10b4.hg19

**LazyData** true

**Suggests** knitr

**biocViews** ExperimentHub, ExperimentData, SNPData, Homo\_sapiens\_Data,  
Mus\_musculus\_Data, SequencingData, MicroarrayData, Genome

**VignetteBuilder** knitr

**git\_url** <https://git.bioconductor.org/packages/DMRcatedata>

**git\_branch** RELEASE\_3\_10

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

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**Description**

SNP annotation, cross-hybridising probes, XY probes, and gene annotation for hg19, hg38 and mm10

**Author(s)**

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**Examples**

```
data(crosshyb)
data(snpsall)
data(hg19.grt)
data(hg19.generanges)
```

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crosshyb     *Potentially cross-hybridising Illumina probes*

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**Description**

This is a character vector of Illumina probes whose probe sequence promiscuously aligns to non-target sections of the genome with a matching of 47bp or higher.

**Usage**

```
data(crosshyb)
```

**Format**

character

**Source**

[https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059\\_2016\\_1066\\_MOESM2\\_ESM.csv](https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM2_ESM.csv) (accessed September 2019) [https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059\\_2016\\_1066\\_MOESM3\\_ESM.csv](https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM3_ESM.csv) (accessed September 2019) <http://www.sickkids.ca/MS-Office-Files/Research/WeksbergLab/48639-non-specific-probes-Illumina450k.xlsx> (accessed September 2019)

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hg19.generanges	<i>Start and stop positions of all genes in hg19</i>
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**Description**

This data set gives the genomic intervals of all gene regions in the Ensembl Release 75 of hg19.

**Usage**

```
data(hg19.generanges)
```

**Format**

A GRanges object with 55773 intervals.

**Source**

[ftp://ftp.ensembl.org/pub/release-75/gtf/homo\\_sapiens/Homo\\_sapiens.GRCh37.75.gtf.gz](ftp://ftp.ensembl.org/pub/release-75/gtf/homo_sapiens/Homo_sapiens.GRCh37.75.gtf.gz)

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hg19.grt	<i>GeneRegionTrack for hg19</i>
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**Description**

This is a GeneRegionTrack formulated from TxDb.Hsapiens.UCSC.hg19.knownGene.

**Usage**

```
data(hg19.grt)
```

**Format**

GeneRegionTrack

---

hg38.generanges	<i>Start and stop positions of all genes in hg38</i>
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**Description**

This data set gives the genomic intervals of all gene regions in the Ensembl Release 96 of hg38.

**Usage**

```
data(hg38.generanges)
```

**Format**

A GRanges object with 57316 intervals.

**Source**

[ftp://ftp.ensembl.org/pub/release-96/gtf/homo\\_sapiens/Homo\\_sapiens.GRCh38.96.chr.gtf.gz](ftp://ftp.ensembl.org/pub/release-96/gtf/homo_sapiens/Homo_sapiens.GRCh38.96.chr.gtf.gz)

---

hg38.grt	<i>GeneRegionTrack for hg38</i>
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**Description**

This is a GeneRegionTrack formulated from TxDb.Hsapiens.UCSC.hg38.knownGene.

**Usage**

```
data(hg38.grt)
```

**Format**

GeneRegionTrack

---

mm10.generanges	<i>Start and stop positions of all genes in mm10</i>
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**Description**

This data set gives the genomic intervals of all gene regions in the Ensembl Release 96 of mm10.

**Usage**

```
data(mm10.generanges)
```

**Format**

A GRanges object with 55341 intervals.

**Source**

[ftp://ftp.ensembl.org/pub/release-96/gtf/mus\\_musculus/Mus\\_musculus.GRCm38.96.chr.gtf.gz](ftp://ftp.ensembl.org/pub/release-96/gtf/mus_musculus/Mus_musculus.GRCm38.96.chr.gtf.gz)

---

mm10.grt	<i>GeneRegionTrack for mm10</i>
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---

**Description**

This is a GeneRegionTrack formulated from TxDb.Mmusculus.UCSC.mm10.knownGene.

**Usage**

```
data(mm10.grt)
```

**Format**

GeneRegionTrack

---

`snpsall`*SNP information for Illumina probes*

---

**Description**

This is a data.frame of Illumina probes whose target CpG lies on or near a known SNP. SNP ID, distance and minor allele frequency are all reported here.

**Usage**

```
data(snpsall)
```

**Format**

```
data.frame
```

**Source**

[https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059\\_2016\\_1066\\_MOESM4\\_ESM.csv](https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM4_ESM.csv) (accessed September 2019) [https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059\\_2016\\_1066\\_MOESM5\\_ESM.csv](https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM5_ESM.csv) (accessed September 2019) [https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059\\_2016\\_1066\\_MOESM6\\_ESM.csv](https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM6_ESM.csv) (accessed September 2019) <http://www.sickkids.ca/MS-Office-Files/Research/WeksbergLab/48640-polymorphic-CpGs-Illumina.xlsx> (accessed September 2019)

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`XY.probes`*Sex chromosome Illumina probes*

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**Description**

This is a character vector of Illumina probes whose target CpG site is on a sex chromosome.

**Usage**

```
data(XY.probes)
```

**Format**

```
character
```

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