

# Package ‘DMRcatedata’

May 15, 2025

**Type** Package

**Title** Data Package for DMRcate

**Version** 2.26.0

**Date** 2024-08-03

**Author** Tim Peters

**Maintainer** Tim Peters <t.peters@garvan.org.au>

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

**License** GPL-3

**Depends** R (>= 4.0), 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\_21

**git\_last\_commit** 383a0a9

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.21

**Date/Publication** 2025-05-15

## Contents

DMRcatedata-package . . . . .	2
ALLbetas . . . . .	2

crosshyb . . . . .	3
epicv2snps . . . . .	3
hg19.geranges . . . . .	4
hg19.grt . . . . .	4
hg38.geranges . . . . .	5
hg38.grt . . . . .	5
mm10.geranges . . . . .	6
mm10.grt . . . . .	6
snpsall . . . . .	7
XY.probes . . . . .	7

<b>Index</b>	<b>8</b>
--------------	----------

---

DMRcatedata-package	<i>Dataset to use with the DMRcate pipeline</i>
---------------------	---

---

### Description

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

### Author(s)

Tim Peters, Immunogenomics Laboratory, Garvan Institute of Medical Research

Maintainer: Tim Peters<t.peters@garvan.org.au>

### Examples

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

---

ALLbetas	<i>EPICv2 beta values for DMR calling</i>
----------	---

---

### Description

Matrix of EPICv2 beta values from Noguera-Castells et al. (2023) consisting of five B cell acute lymphoblastic leukaemia (BALL) and five T cell acute lymphoblastic leukaemia (TALL) samples for DMR calling.

### Usage

```
data(ALLbetas)
```

**Format**

data.frame

**Source**

[https://ftp.ncbi.nlm.nih.gov/geo/series/GSE222nnn/GSE222919/suppl/GSE222919\\_processed\\_data.txt.gz](https://ftp.ncbi.nlm.nih.gov/geo/series/GSE222nnn/GSE222919/suppl/GSE222919_processed_data.txt.gz)

---

crosshyb

*Potentially cross-hybridising Illumina probes*

---

**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)

---

epicv2snps

*SNP information for EPICv2 Illumina probes*

---

**Description**

This is a data.frame of Illumina probes from EPICv2 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%2Fs12864-024-10027-5/MediaObjects/12864\\_2024\\_10027\\_MOESM4\\_ESM.csv](https://static-content.springer.com/esm/art%3A10.1186%2Fs12864-024-10027-5/MediaObjects/12864_2024_10027_MOESM4_ESM.csv)

---

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

---

**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 57773 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)

---

hg19.grt	<i>GeneRegionTrack for hg19</i>
----------	---------------------------------

---

**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>
-----------------	--

---

**Description**

This data set gives the genomic intervals of all gene regions in the Ensembl Release 102 of hg38.

**Usage**

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

**Format**

A GRanges object with 60616 intervals.

**Source**

[ftp://ftp.ensembl.org/pub/release-102/gtf/homo\\_sapiens/Homo\\_sapiens.GRCh38.102.chr.gtf.gz](ftp://ftp.ensembl.org/pub/release-102/gtf/homo_sapiens/Homo_sapiens.GRCh38.102.chr.gtf.gz)

---

hg38.grt	<i>GeneRegionTrack for hg38</i>
----------	---------------------------------

---

**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>
-----------------	--

---

**Description**

This data set gives the genomic intervals of all gene regions in the Ensembl Release 102 of mm10.

**Usage**

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

**Format**

A GRanges object with 55401 intervals.

**Source**

```
ftp://ftp.ensembl.org/pub/release-96/gtf/mus_musculus/Mus_musculus.GRCm38.102.chr.gtf.gz
```

---

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

---

**Description**

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

**Usage**

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

**Format**

GeneRegionTrack

---

`snpsall`*SNP information for EPICv1 and 450K Illumina probes*

---

**Description**

This is a data.frame of Illumina probes from EPICv1 and 450K 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)

---

`XY.probes`*Sex chromosome Illumina probes*

---

**Description**

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

**Usage**

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

**Format**

```
character
```

# Index

## \* datasets

- ALLbetas, [2](#)
- crosshyb, [3](#)
- DMRcatedata-package, [2](#)
- epicv2snps, [3](#)
- hg19.geranges, [4](#)
- hg19.grt, [4](#)
- hg38.geranges, [5](#)
- hg38.grt, [5](#)
- mm10.geranges, [6](#)
- mm10.grt, [6](#)
- snpsall, [7](#)
- XY.probes, [7](#)

ALLbetas, [2](#)

crosshyb, [3](#)

DMRcatedata (DMRcatedata-package), [2](#)  
DMRcatedata-package, [2](#)

epicv2snps, [3](#)

hg19.geranges, [4](#)  
hg19.grt, [4](#)  
hg38.geranges, [5](#)  
hg38.grt, [5](#)

mm10.geranges, [6](#)  
mm10.grt, [6](#)

snpsall, [7](#)

XY.probes, [7](#)