Package ‘DMRcatedata’

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Type Package
Title Data Package for DMRcate
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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 (>= 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
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**ALLbetas**

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

**Description**

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

**Author(s)**

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**Examples**

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

---

**ALLbetas**  
*EPICv2 beta values for DMR calling*

**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**

```r
data(ALLbetas)
```
crosshyb

Format
data.frame

Source

---

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

---

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

hg19.generanges  Start and stop positions of all genes in hg19

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

hg19.grt  GeneRegionTrack for hg19

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

Usage
data(hg19.grt)

Format
GeneRegionTrack
hg38.generanges  

Start and stop positions of all genes in hg38

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

```
```

---

hg38.grt  

GeneRegionTrack for hg38

Description

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

Usage

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

Format

GeneRegionTrack
**mm10.generanges**

Start and stop positions of all genes in mm10

**Description**

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

**Usage**

```r
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

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**mm10.grt**

GeneRegionTrack for mm10

**Description**

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

**Usage**

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

**Format**

GeneRegionTrack
**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**

```r
data(snpsall)
```

**Format**

`data.frame`

**Source**


---

**XY.probes**

**Description**

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

**Usage**

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

**Format**

`character`
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