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
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Contents

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

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

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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)
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
**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**


---

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

**Format**  
A GRanges object with 55401 intervals.

**Source**  

---

**mm10.grt**  
*GeneRegionTrack for mm10*

**Description**  
This is a GeneRegionTrack formulated from TxDb.Mmuscus.UCSC.mm10.knownGene.

**Usage**  
`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
data(snpsall)

Format
data.frame

Source

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.generanges, 4
  hg19.grt, 4
  hg38.generanges, 5
  hg38.grt, 5
  mm10.generanges, 6
  mm10.grt, 6
  snpsall, 7
  XY.probes, 7

ALLbetas, 2

crosshyb, 3

DMRcatedata (DMRcatedata-package), 2
DMRcatedata-package, 2

epicv2snps, 3

hg19.generanges, 4
hg19.grt, 4
hg38.generanges, 5
hg38.grt, 5

mm10.generanges, 6
mm10.grt, 6

snpsall, 7

XY.probes, 7