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
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R topics documented:

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

**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**

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**

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

<table>
<thead>
<tr>
<th>Format</th>
<th>data.frame</th>
</tr>
</thead>
</table>

**Description**

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

**Usage**

data(hg19.generanges)

### hg19.grt

GeneRegionTrack for hg19

<table>
<thead>
<tr>
<th>Format</th>
<th>GeneRegionTrack</th>
</tr>
</thead>
</table>

**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**

`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.Mmuculus.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**


**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.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