Package ‘DMRcatedata’

May 2, 2024

Type Package
Title Data Package for DMRcate
Version 2.22.0
Date 2024-08-03
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Description This package contains 9 data objects supporting functionality and examples of the Bio-conductor 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_19
git_last_commit 709b821
git_last_commit_date 2024-04-30
Repository Bioconductor 3.19
Date/Publication 2024-05-02

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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)

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**


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<tr>
<th>crosshyb</th>
<th>Potentially cross-hybridising Illumina probes</th>
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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**


epicv2snps

**SNP information for EPICv2 Illumina probes**

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<th>SNP information for EPICv2 Illumina probes</th>
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**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**

```r
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**

```r
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
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

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**


---

**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
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