

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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DMRcatedata-package	<i>Dataset to use with the DMRcate pipeline</i>
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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.geranges)
```

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

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 (accessed September 2019) 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

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

ftp://ftp.ensembl.org/pub/release-75/gtf/homo_sapiens/Homo_sapiens.GRCh37.75.gtf.gz

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	<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

hg38.grt	<i>GeneRegionTrack for hg38</i>
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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>
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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 (accessed September 2019) 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 (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

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