Package 'DMRcatedata'

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Type Package

Title Data Package for DMRcate

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Author Tim Peters

Maintainer Tim Peters <t.peters@garvan.org.au>

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` *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)

Tim Peters, Immunogenomics Laboratory, Garvan Institute of Medical Research

Maintainer: Tim Peters<t.peters@garvan.org.au>

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)
```

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 *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

ftp://ftp.ensembl.org/pub/release-102/gtf/homo_sapiens/Homo_sapiens.GRCh38.102.chr.gtf.gz

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

mm10.grt *GeneRegionTrack for mm10*

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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