Package ‘CLLmethylation’

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Title Methylation data of primary CLL samples in PACE project

Version 1.26.0

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Description The package includes DNA methylation data for the primary Chronic Lymphocytic Leukemia samples included in the Primary Blood Cancer Encyclopedia (PACE) project. Raw data from the 450k DNA methylation arrays is stored in the European Genome-Phenome Archive (EGA) under accession number EGAS0000100174.
For more information concerning the project please refer to the paper ``Drug-perturbation-based stratification of blood cancer'' by Dietrich S, Oles M, Lu J et al., J. Clin. Invest. (2018) and R/Bioconductor package BloodCancerMultiOmics2017.

Depends R (>= 3.5.0)

Encoding UTF-8

VignetteBuilder knitr

Imports SummarizedExperiment, ExperimentHub

Suggests BiocStyle, ggplot2, knitr, rmarkdown

License LGPL

biocViews ExperimentData, DiseaseModel, CancerData, LeukemiaCancerData

LazyData true

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Contents

`meth` *DNA methylation data*

Description

The data was produced with the use of either 450k or 850k methylation arrays. Preprocessing of raw IDAT files was made using minfi R/Bioconductor package version 1.19.16. Intensities were normalized using the functional normalization algorithm. CpG sites containing SNPs inside the probe body were removed. Data is a subset of CpG sites present in 450k methylation arrays.

Format

`"RangedSummarizedExperiment"` object with Features 435155 and Samples 196.

Author(s)

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Examples

```
library("SummarizedExperiment")
library("ExperimentHub")
eh = ExperimentHub()
meth = eh[["EH1071"]]
colData(meth)
assay(meth)[1:5,1:5]
head(rowData(meth))
```

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