

Package ‘TCGAMethylation450k’

October 16, 2021

Type Package

Title The Cancer Genome Atlas Illumina 450k methylation example data

Version 1.28.0

Date 2011-10-21

Author Sean Davis

Maintainer Sean Davis <sdavis2@mail.nih.gov>

Description The Cancer Genome Atlas (TCGA) is applying genomics technologies to over 20 different types of cancer. This package contains a small set of 450k array data in idat format.

License GPL-2

biocViews Genome, CancerData, MethylationArrayData

git_url <https://git.bioconductor.org/packages/TCGAMethylation450k>

git_branch RELEASE_3_13

git_last_commit 6e29401

git_last_commit_date 2021-05-19

Date/Publication 2021-10-16

R topics documented:

TCGAMethylation450k-package 1

Index 3

TCGAMethylation450k-package

The Cancer Genome Atlas Illumina 450k methylation example data

Description

The Cancer Genome Atlas (TCGA) is applying genomics technologies to over 20 different types of cancer. This package contains a small set of 450k array data in idat format.

Data are included in this package in extdata/idat. A typical way of accessing these data would be to use the methylumi package methylumIDAT function.

Details

Package: TCGAMethylation450k
Type: Package
License: GPL-2

Author(s)

Sean Davis

Maintainer: Sean Davis <sdavis2@mail.nih.gov>

References

<http://cancergenome.nih.gov/>

See Also

[methyumi](#)

Index

* **package**

TCGAMethylation450k-package, [1](#)

methylumi, [2](#)

TCGAMethylation450k

(TCGAMethylation450k-package),

[1](#)

TCGAMethylation450k-package, [1](#)