

# Package ‘TCGAMethylation450k’

April 14, 2020

**Type** Package

**Title** The Cancer Genome Atlas Illumina 450k methylation example data

**Version** 1.22.0

**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\_10

**git\_last\_commit** caa470d

**git\_last\_commit\_date** 2019-10-29

**Date/Publication** 2020-04-14

## 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

\*Topic **package**

TCGMethylation450k-package, [1](#)

methylumi, [2](#)

TCGMethylation450k

(TCGMethylation450k-package),

[1](#)

TCGMethylation450k-package, [1](#)