

# Package ‘RTCGA.methylation’

March 21, 2019

**Type** Package

**Title** Methylation datasets from The Cancer Genome Atlas Project

**Version** 1.10.0

**Date** 2015-12-23

**Description** Package provides methylation (humanmethylation27) datasets from The Cancer Genome Atlas Project for all available cohorts types from <http://gdac.broadinstitute.org/>. Data format is explained here <https://wiki.nci.nih.gov/display/TCGA/DNA+methylation> Data from 2015-11-01 snapshot.

**License** GPL-2

**LazyData** TRUE

**Repository** Bioconductor

**BugReports** <https://github.com/RTCGA/RTCGA/issues>

**Depends** R (>= 3.3.0), RTCGA

**Suggests** knitr

**biocViews** AnnotationData

**VignetteBuilder** knitr

**NeedsCompilation** no

**RoxygenNote** 5.0.1

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**git\_url** <https://git.bioconductor.org/packages/RTCGA.methylation>

**git\_branch** RELEASE\_3\_8

**git\_last\_commit** 2e72951

**git\_last\_commit\_date** 2018-10-30

**Date/Publication** 2019-03-21

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methylation

*Methylation datasets from TCGA project*

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## Description

Package provides methylation (humanmethylation27) datasets from The Cancer Genome Atlas Project for all cohorts types from <http://gdac.broadinstitute.org/>. Data were downloaded using [RTCGA-package](#) and contain snapshots for the date: 2015-11-01. The process is described here: <http://rtcga.github.io/RTCGA/>. Use cases, examples and information about datasets in **RTCGA.data** family can be found here: `browseVignettes("RTCGA")`. Methylation data format is explained here <https://wiki.nci.nih.gov/display/TCGA/DNA+methylation>. Converting **RTCGA.methylation** datasets from `data.frames` to Bioconductor classes is explained here [convertTCGA](#).

## Usage

BRCA.methylation

COAD.methylation

COADREAD.methylation

GBM.methylation

GBMLGG.methylation

KIPAN.methylation

KIRC.methylation

KIRP.methylation

LAML.methylation

LUAD.methylation

LUSC.methylation

OV.methylation2

OV.methylation1

READ.methylation

STAD.methylation

STES.methylation

UCEC.methylation

**Details**

```
browseVignettes("RTCGA")
```

**Value**

Data frames with methylation data.

**Source**

<http://gdac.broadinstitute.org/>

**Examples**

```
## Not run:  
browseVignettes("RTCGA")  
  
## End(Not run)
```

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