

Package ‘RTCGA.miRNASeq’

November 20, 2025

Type Package

Title miRNASeq datasets from The Cancer Genome Atlas Project

Version 1.38.0

Date 2015-12-03

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Description Package provides miRNASeq 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/miRNASeq#miRNASeq-DataOverview> Data from 2015-11-01 snapshot.

License GPL-2

LazyData TRUE

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

Depends R (>= 3.3.0), RTCGA

Suggests knitr, rmarkdown

biocViews AnnotationData

VignetteBuilder knitr

NeedsCompilation no

RoxygenNote 7.1.1

git_url <https://git.bioconductor.org/packages/RTCGA.miRNASeq>

git_branch RELEASE_3_22

git_last_commit bb4e69b

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2025-11-20

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miRNASeq*miRNASeq datasets from TCGA project*

Description

Package provides miRNASeq 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")`. miRNASeq data format is explained here <https://wiki.nci.nih.gov/display/TCGA/miRNASeq#miRNASeq-DataOverview>. There is one extra column "machine" in each dataset which describes a machine that produced dataset. It can be: Illumina Genome Analyzer, Illumina HiSeq 2000 or both. Converting **RTCGA.miRNASeq** datasets from `data.frames` to Bioconductor classes is explained here [convertTCGA](#).

Usage

`ACC.miRNASeq``BLCA.miRNASeq``BRCA.miRNASeq``CESC.miRNASeq``CHOL.miRNASeq``COAD.miRNASeq``COADREAD.miRNASeq``DLBC.miRNASeq``ESCA.miRNASeq``FPPP.miRNASeq``GBM.miRNASeq``GBMLGG.miRNASeq``HNSC.miRNASeq``KICH.miRNASeq``KIPAN.miRNASeq``KIRC.miRNASeq``KIRP.miRNASeq`

LAML.miRNASeq

LGG.miRNASeq

LIHC.miRNASeq

LUAD.miRNASeq

LUSC.miRNASeq

MESO.miRNASeq

OV.miRNASeq

PAAD.miRNASeq

PCPG.miRNASeq

PRAD.miRNASeq

READ.miRNASeq

SARC.miRNASeq

SKCM.miRNASeq

STAD.miRNASeq

STES.miRNASeq

TGCT.miRNASeq

THCA.miRNASeq

THYM.miRNASeq

UCEC.miRNASeq

UCS.miRNASeq

UVM.miRNASeq

Details

`browseVignettes("RTCGA")`

Value

Data frames with miRNASeq data.

Source

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

Examples

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

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