

Package ‘RTCGA.miRNASeq’

September 11, 2025

Type Package

Title miRNASeq datasets from The Cancer Genome Atlas Project

Version 1.37.0

Date 2015-12-03

Author Witold Chodor <witoldchodor@gmail.com>

Maintainer Marcin Kosinski <m.p.kosinski@gmail.com>

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 devel

git_last_commit b259962

git_last_commit_date 2025-04-15

Repository Bioconductor 3.22

Date/Publication 2025-09-11

Contents

miRNASeq	2
Index	5

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)
```

Index

* **datasets**miRNASeq, [2](#)

ACC.miRNASeq (miRNASeq), 2

[illegible]

BLCA.miRNASeq (miRNASeq), 2

BRCA.miRNASeq (miRNASeq), 2

CESC.miRNASeq (miRNASeq), 2

CHOL.miRNASeq (miRNASeq), 2

COAD.miRNASeq (miRNASeq), 2

COADREAD.miRNASeq (miRNASeq), 2

convertTCGA, 2

DLBC.miRNASeq (miRNASeq), 2

ESCA.miRNASeq (miRNASeq), 2

FPPP.miRNASeq (miRNASeq), [2](#)

GBM.miRNASeq (miRNASeq), 2

GBMLGG.miRNASeq (miRNASeq), 2

HNSC.miRNASeq (miRNASeq), 2

KICH.miRNASeq (miRNASeq), 2

KIPAN.miRNASeq (miRNASeq), 2

KIRC.miRNASeq (miRNASeq), [2](#)

KIRP.miRNASeq (miRNASeq), 2

LAML.miRNASeq (miRNASeq), 2

LGG.miRNASeq (miRNASeq), [2](#)

LIHC.miRNASeq (miRNASeq), [2](#)

LUAD.miRNASeq (miRNASeq), 2

LUSC.miRNASeq (miRNASeq), 2

MESO.miRNASeq (miRNASeq), [2](#)

miRNASeq, 2

OV.miRNASeq (miRNASeq), 2

PAAD.miRNASeq (miRNASeq), 2

PCPG.miRNASeq (miRNASeq), 2

PRAD.miRNASeq (miRNASeq), 2

READ.miRNASeq (miRNASeq), 2

RTCGA-package, [2](#)

SARC.miRNASeq (miRNASeq), 2

CSKIPRNASeq,SeqLMiRNASeq,COAD.miRNASeq,COADREAD.miRNASeq

STAD.miRNASeq (miRNASeq), 2

```
STES.miRNASeq(miRNASeq), 2
```

TGCT.miRNASeq (miRNASeq), 2

THCA.miRNASeq (miRNASeq), 2

THYM.miRNASeq (miRNASeq), 2

UCEC.miRNASeq (miRNASeq), 2

UCS.miRNASeq (miRNASeq), 2

UVM.miRNASeq (miRNASeq), 2