

# Package ‘RTCGA.miRNASeq’

July 2, 2024

**Type** Package

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

**Version** 1.32.0

**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\_19

**git\_last\_commit** 2dfa1bd

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.19

**Date/Publication** 2024-07-02

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miRNASeq

*miRNASeq datasets from TCGA project*

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### 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://rtcg.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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## \* datasets

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