

# Package ‘RTCGA.miRNASeq’

July 29, 2025

**Type** Package

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

**Version** 1.36.0

**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** RELEASE\_3\_21

**git\_last\_commit** d189b24

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.21

**Date/Publication** 2025-07-29

## 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](#)

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, RCTCGA-package, SARC.miRNASeq, SKCM.miRNASeq, STAD.miRNASeq, STES.miRNASeq, TGCT.miRNASeq, THCA.miRNASeq, THYM.miRNASeq, UCEC.miRNASeq, UCS.miRNASeq, UVM.miRNASeq, [2](#)

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](#)

RCTCGA-package, [2](#)

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

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

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](#)