

Package ‘RTCGA.miRNASeq’

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Type Package

Title miRNASeq datasets from The Cancer Genome Atlas Project

Version 1.35.0

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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 devel

git_last_commit eb001af

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Repository Bioconductor 3.21

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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://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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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, miRNASeq, OV.miRNASeq, PAAD.miRNASeq, PCPG.miRNASeq, PRAD.miRNASeq, RCTGA-package, SARC.miRNASeq, SKCM.miRNASeq, STAD.miRNASeq, STES.miRNASeq, TGCT.miRNASeq, THCA.miRNASeq, THYM.miRNASeq, UCEC.miRNASeq, UCS.miRNASeq, UVM.miRNASeq

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