Package ‘RTCGA.miRNASeq’

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Type Package

Title miRNASeq datasets from The Cancer Genome Atlas Project

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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

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Contents

`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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