

Package ‘microRNAome’

October 14, 2018

Version 1.2.0

Date 2017-11-14

Title SummarizedExperiment for the microRNAome project

Description This package provides a SummarizedExperiment object of read counts for microRNAs across tissues, cell-types, and cancer cell-lines. The read count matrix was prepared and provided by the author of the study: Towards the human cellular microRNAome.

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Depends R (>= 3.4), SummarizedExperiment

Suggests BiocGenerics, RUnit

biocViews ExperimentData, CellCulture, CancerData, SequencingData, RNASeqData, miRNAData

License GPL (>= 2)

git_url <https://git.bioconductor.org/packages/microRNAome>

git_branch RELEASE_3_7

git_last_commit ab7922e

git_last_commit_date 2018-04-30

Date/Publication 2018-10-14

R topics documented:

microRNAome	2
Index	3

microRNAome

MicroRNAome Data

Description

Read counts per miRNA for the microRNAome collection of RNA-Seq experiments

Usage

```
data("microRNAome")
```

Format

SummarizedExperiment

Details

New small RNA-seq data from 39 primary cells obtained by culture, flow cytometry or centrifugation were augmented with Sequence Read Archive (SRA) small RNA-seq read data from 496 samples with over 1 million microRNA reads, and the data from FANTOM5 and the Hemmrich-Stanisak lab. All samples were processed through miRge (Baras et al. 2015), which uses modified microRNA libraries and multiple Bowtie steps for optimal alignments on multiplexed runs.

Source

Read count matrix prepared and provided by authors of the study

References

Matthew N McCall, Min-Sik Kim, Mohammed Adil, Arun H Patil, Yin Lu, Christopher J Mitchell, Pamela Leal-Rojas, Jinchong Xu, Manoj Kumar, Valina L Dawson, Ted M Dawson, Alexander S Baras, Avi Z Rosenberg, Dan E Arking, Kathleen H Burns, Akhilesh Pandey, Marc Halushka (2017). Toward the human cellular microRNAome. *Genome Research*. 27(10):1769-1781.

Examples

```
data(microRNAome)
## the microRNAome SummarizedExperiment object contains only one matrix
## in the assays field: a matrix of miRNA counts
names(assays(microRNAome))
assays(microRNAome)$counts[1:3,1:3]
```

Index

*Topic **datasets**

microRNAome, [2](#)

microRNAome, [2](#)