Package 'microRNAome'

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Version 1.0.0

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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)

NeedsCompilation no

R topics documented:

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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. These were primary cell cultures, immortalized/cancer cell lines or normal tissues. 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. From an initial 2546 microRNAs across 535 samples, we retained the 2131 microRNAs with non-zero expression in at least 5 samples and the 528 samples that were of acceptable quality.

Source

Read count matrix prepared and provided by authors of the study

References

Towards the human cellular microRNAome 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. doi: https://doi.org/10.1101/120394

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]
```

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