Package ‘microRNAome’

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Version 1.35.0

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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)

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Repository Bioconductor 3.24

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Contents

`microRNAome` *MicroRNAome Data*

Description

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

Usage

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

Format

SummarizedExperiment

Details

Small RNA-seq data on 2406 samples from the Sequence Read Archive (SRA) processed using the miRge3 pipeline.

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.\ \ Patil AH, Baran A, Brehm ZP, McCall MN, Halushka MK. A curated human cellular microRNAome based on 196 primary cell types. Gigascience. 2022 Aug 25;11:giac083. doi: 10.1093/gigascience/giac083.

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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