

# Package ‘microRNAome’

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**Version** 1.29.0

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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.

**Author** Matthew N. McCall <mccallm@gmail.com>, Marc K. Halushka <mhalush1@jhmi.edu>, Arun H. Patil <arun26feb@gmail.com>

**Maintainer** Matthew N. McCall <mccallm@gmail.com>

**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>

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microRNAome

*MicroRNAome Data*

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### 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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\* **datasets**

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