

# Package ‘microRNAome’

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**Version** 1.8.0

**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\_10

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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**

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]
```

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\*Topic **datasets**

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