

Package ‘EpiMix.data’

February 26, 2026

Title Data for the EpiMix package

Version 1.12.0

Description Supporting data for the EpiMix R package.

It include:

- HM450_lncRNA_probes.rda
- HM450_miRNA_probes.rda
- EPIC_lncRNA_probes.rda
- EPIC_miRNA_probes.rda
- EpigenomeMap.rda
- LUAD.sample.annotation
- TCGA_BatchData
- MET.data
- mRNA.data
- microRNA.data
- lncRNA.data
- Sample_EpiMixResults_lncRNA
- Sample_EpiMixResults_miRNA
- Sample_EpiMixResults_Regular
- Sample_EpiMixResults_Enhancer
- lncRNA expression data of tumors from TCGA that are stored in the ExperimentHub.

License GPL-3

Encoding UTF-8

Depends R (>= 4.2.0), ExperimentHub (>= 0.99.6)

Suggests rmarkdown, knitr

biocViews ExperimentData, ExperimentHub, Genome, RNASeqData,
ExpressionData

NeedsCompilation no

RoxygenNote 7.2.3

VignetteBuilder knitr

BugReports <https://github.com/gevaertlab/EpiMix/issues>

git_url <https://git.bioconductor.org/packages/EpiMix.data>

git_branch RELEASE_3_22

git_last_commit 581330e

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2026-02-26

Author Yuanning Zheng [aut, cre]

Maintainer Yuanning Zheng <eric2021@stanford.edu>

Contents

EPIC_lncRNA_probes	2
EPIC_miRNA_probes	3
EpigenomeMap	3
HM450_lncRNA_probes	4
HM450_miRNA_probes	4
lncRNA.data	5
LUAD.sample.annotation	5
MET.data	6
microRNA.data	6
mRNA.data	7
Sample_EpiMixResults_Enhancer	7
Sample_EpiMixResults_lncRNA	8
Sample_EpiMixResults_miRNA	8
Sample_EpiMixResults_Regular	9
TCGA_BatchData	9
Index	10

EPIC_lncRNA_probes	<i>A character vector that maps CpG probes to lncRNA genes. The vectors names are genes and the values are CpG probes</i>
--------------------	---

Description

A character vector that maps CpG probes to lncRNA genes. The vectors names are genes and the values are CpG probes

Usage

```
EPIC_lncRNA_probes
```

Format

A character vector with 205645 elements

Examples

```
## Not run:
data("EPIC_lncRNA_probes")

## End(Not run)
```

EPIC_miRNA_probes	<i>A dataframe that maps CpG probes genes to microRNA genes. The vectors names are genes and the values are CpG probes</i>
-------------------	--

Description

A dataframe that maps CpG probes genes to microRNA genes. The vectors names are genes and the values are CpG probes

Usage

```
EPIC_miRNA_probes
```

Format

A dataframe with 23,907 rows and 4 columns

Examples

```
## Not run:  
data("EPIC_miRNA_probes")  
  
## End(Not run)
```

EpigenomeMap	<i>A list that map epigenome groups to epigenome IDs</i>
--------------	--

Description

The data were generated from the RoadmapEpigenomic project (Nature, PMID: 25693563, figure 2).

Usage

```
EpigenomeMap
```

Format

A list with 17 elements. The names are epigenome/tissue groups and the values are epigenome IDs for specific cells.

Examples

```
## Not run:  
data("EpigenomeMap")  
  
## End(Not run)
```

HM450_lncRNA_probes *A character vector that maps CpG probes to lncRNA genes. The vectors names are genes and the values are CpG probes*

Description

A character vector that maps CpG probes to lncRNA genes. The vectors names are genes and the values are CpG probes

Usage

```
HM450_lncRNA_probes
```

Format

A character vector with 108202 elements

Examples

```
## Not run:  
data("HM450_lncRNA_probes")  
  
## End(Not run)
```

HM450_miRNA_probes *A dataframe that maps CpG probes genes to microRNA genes.*

Description

A dataframe that maps CpG probes genes to microRNA genes.

Usage

```
HM450_miRNA_probes
```

Format

A dataframe with 17,495 rows and 4 columns

Examples

```
## Not run:  
data("HM450_miRNA_probes")  
  
## End(Not run)
```

`lncRNA.data`*Toy lncRNA expression dataset for demonstration purpose.*

Description

This is a subset of lncRNA expression data from TCGA-LUAD, used for testing the program.

Usage`lncRNA.data`**Format**

a matrix

Examples

```
## Not run:  
data("lncRNA.data")  
  
## End(Not run)
```

`LUAD.sample.annotation`*toy dataset for sample annotation*

Description

a dataframe with two columns: the first column is the patient identifier, and the second column is the sample annotation

Usage`LUAD.sample.annotation`**Format**

a dataframe

Examples

```
## Not run:  
data("LUAD.sample.annotation")  
  
## End(Not run)
```

MET.data

Toy DNA methylation dataset for demonstration purpose.

Description

This is a subset of DNA methylation data from TCGA-LUAD, used for testing the program.

Usage

MET.data

Format

a matrix

Examples

```
## Not run:  
data("MET.data")  
  
## End(Not run)
```

microRNA.data

Toy microRNA expression dataset for demonstration purpose.

Description

This is a subset of microRNA expression data from TCGA-LUAD, used for testing the program.

Usage

microRNA.data

Format

a matrix

Examples

```
## Not run:  
data("microRNA.data")  
  
## End(Not run)
```

`mRNA.data`*Toy gene expression dataset for demonstration purpose.*

Description

This is a subset of gene expression data from TCGA-LUAD, used for testing the program.

Usage`mRNA.data`**Format**

a matrix

Examples

```
## Not run:  
data("mRNA.data")  
  
## End(Not run)
```

`Sample_EpiMixResults_Enhancer`*toy dataset for EpiMix output with Enhancer mode*

Description

a list object returned from EpiMix

Usage`Sample_EpiMixResults_Enhancer`**Format**

a list

Examples

```
## Not run:  
data("Sample_EpiMixResults_Enhancer")  
  
## End(Not run)
```

Sample_EpiMixResults_lncRNA

toy dataset for EpiMix output with lncRNA mode

Description

a list object returned from EpiMix

Usage

```
Sample_EpiMixResults_lncRNA
```

Format

a list

Examples

```
## Not run:  
data("Sample_EpiMixResults_lncRNA")  
  
## End(Not run)
```

Sample_EpiMixResults_miRNA

toy dataset for EpiMix output with miRNA mode

Description

a list object returned from EpiMix

Usage

```
Sample_EpiMixResults_miRNA
```

Format

a list

Examples

```
## Not run:  
data("Sample_EpiMixResults_miRNA")  
  
## End(Not run)
```

Sample_EpiMixResults_Regular
toy dataset for EpiMix output with Regular mode

Description

a list object returned from EpiMix

Usage

```
Sample_EpiMixResults_Regular
```

Format

a list

Examples

```
## Not run:  
data("Sample_EpiMixResults_Regular")  
  
## End(Not run)
```

TCGA_BatchData *A dataframe with the batch information of TCGA patient.*

Description

a dataframe with two columns: the first column is the patient identifier, and the second column is the technical batch

Usage

```
TCGA_BatchData
```

Format

a dataframe

Examples

```
## Not run:  
data("TCGA_BatchData")  
  
## End(Not run)
```

Index

* internal

- EPIC_lncRNA_probes, [2](#)
- EPIC_miRNA_probes, [3](#)
- EpigenomeMap, [3](#)
- HM450_lncRNA_probes, [4](#)
- HM450_miRNA_probes, [4](#)
- lncRNA.data, [5](#)
- LUAD.sample.annotation, [5](#)
- MET.data, [6](#)
- microRNA.data, [6](#)
- mRNA.data, [7](#)
- Sample_EpiMixResults_Enhancer, [7](#)
- Sample_EpiMixResults_lncRNA, [8](#)
- Sample_EpiMixResults_miRNA, [8](#)
- Sample_EpiMixResults_Regular, [9](#)
- TCGA_BatchData, [9](#)

- EPIC_lncRNA_probes, [2](#)
- EPIC_miRNA_probes, [3](#)
- EpigenomeMap, [3](#)

- HM450_lncRNA_probes, [4](#)
- HM450_miRNA_probes, [4](#)

- lncRNA.data, [5](#)
- LUAD.sample.annotation, [5](#)

- MET.data, [6](#)
- microRNA.data, [6](#)
- mRNA.data, [7](#)

- Sample_EpiMixResults_Enhancer, [7](#)
- Sample_EpiMixResults_lncRNA, [8](#)
- Sample_EpiMixResults_miRNA, [8](#)
- Sample_EpiMixResults_Regular, [9](#)

- TCGA_BatchData, [9](#)