

# Package ‘EpiMix.data’

February 5, 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** 2026-02-05  
**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         |
| <b>Index</b>                            | <b>10</b> |

---

|                    |                                                                                                                           |
|--------------------|---------------------------------------------------------------------------------------------------------------------------|
| 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 | <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

```
HM450_lncRNA_probes
```

### Format

A character vector with 108202 elements

### Examples

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

## End(Not run)
```

---

|                    |                                                                  |
|--------------------|------------------------------------------------------------------|
| HM450_miRNA_probes | <i>A dataframe that maps CpG probes genes to microRNA genes.</i> |
|--------------------|------------------------------------------------------------------|

---

### 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](#)