

# Package ‘EpiMix.data’

May 21, 2024

**Title** Data for the EpiMix package

**Version** 1.6.0

**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>

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## 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>

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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>
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### 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>
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---

**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>
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**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