# Package ‘EpiMix.data’

May 7, 2026

**Title** Data for the EpiMix package

**Version** 1.15.0

**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** devel

**git_last_commit** 3c653e6

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**Repository** Bioconductor 3.24

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# Contents

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

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

---

### 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` *A list that map epigenome groups to epigenome IDs*

---

### 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 micoRNA 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