

# Package ‘minfiDataEPIC’

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**Version** 1.35.0

**Title** Example data for the Illumina Methylation EPIC array

**Description**

Data from 3 technical replicates of the cell line GM12878 from the EPIC methylation array.

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**License** Artistic-2.0

**Depends** R (>= 3.3), minfi (>= 1.21.2),  
IlluminaHumanMethylationEPICmanifest,  
IlluminaHumanMethylationEPICanno.ilm10b2.hg19

**LazyData** yes

**biocViews** Homo\_sapiens\_Data, MethylationArrayData, MicroarrayData

**NeedsCompilation** no

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## Contents

|                     |          |
|---------------------|----------|
| MsetEPIC . . . . .  | 2        |
| RGsetEPIC . . . . . | 2        |
| <b>Index</b>        | <b>4</b> |

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|----------|-----------------------------------------------------------------------------------------------|
| MsetEPIC | <i>An example dataset for Illumina's Human Methylation EPIC dataset, after preprocessing.</i> |
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**Description**

This contains the raw data for 3 technical replicates of the cell line GM12878 from the Illumina's Human Methylation EPIC platform. The data has been preprocessed with preprocessRaw.

**Usage**

```
data(MsetEPIC)
```

**Format**

An object of class "MethylSet"

**Details**

Scripts for creating the object is found in the scripts directory of the package and extdata contains the IDAT files. The data has been preprocessed using preprocessRaw.

**See Also**

[MethylSet](#) for the class definition, [preprocessRaw](#) for the preprocessing function, [RGsetEPIC](#) for the companion raw data.

**Examples**

```
data(MsetEPIC)
pData(MsetEPIC)
```

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|           |                                                                               |
|-----------|-------------------------------------------------------------------------------|
| RGsetEPIC | <i>An example dataset for the Illumina's Human Methylation EPIC platform.</i> |
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**Description**

This contains the raw data for 3 technical replicates of the cell line GM12878 from the Illumina's Human Methylation EPIC platform.

**Usage**

```
data(RGsetEPIC)
```

**Format**

An object of class "RGChannelSet"

**Details**

Scripts for creating the object is found in the `scripts` directory of the package and `extdata` contains the IDAT files.

**See Also**

[RGChannelSet](#) for the class definition, [MsetEPIC](#) for the comparion preprocessed data.

**Examples**

```
data(RGsetEPIC)
pData(RGsetEPIC)
```

# Index

## \* **datasets**

MsetEPIC, [2](#)

RGsetEPIC, [2](#)

MethylSet, [2](#)

MsetEPIC, [2](#), [3](#)

preprocessRaw, [2](#)

RGChannelSet, [3](#)

RGsetEPIC, [2](#), [2](#)