

# Package ‘ARRmData’

February 18, 2025

**Version** 1.43.0

**Title** Example dataset for normalization of Illumina 450k Methylation data

**Description** Raw Beta values from 36 samples across 3 groups from Illumina 450k methylation arrays

**Author** Jean-Philippe Fortin, Celia M.T. Greenwood, Aurelie Labbe

**Maintainer** Jean-Philippe Fortin <jfortin@jhsph.edu>

**License** Artistic-2.0

**Depends** R (>= 3.0.0)

**biocViews** ExperimentData, MethylationArrayData

**git\_url** <https://git.bioconductor.org/packages/ARRmData>

**git\_branch** devel

**git\_last\_commit** 2b2b55f

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.21

**Date/Publication** 2025-02-18

## Contents

betaMatrix . . . . .	2
greenControlMatrix . . . . .	2
redControlMatrix . . . . .	3
sampleNames . . . . .	4

<b>Index</b>	<b>5</b>
--------------	----------

---

`betaMatrix`*Example of a matrix of Beta values from the Illumina 450k array*

---

**Description**

The matrix contains the Beta values of a set of 36 samples from the Illumina Infinium Human-Methylation 450k array

**Usage**

```
data(betaMatrix)
```

**Format**

A data frame with 485577 observations (rows) and 36 samples (columns)

**Details**

Column names correspond to the sample names (of the form 5621146025\_R06C02)

**See Also**

[normalizeARRm](#) for normalization of the Beta values, [greenControlMatrix](#) and [redControlMatrix](#) for the associated negative control probe data.

**Examples**

```
data(betaMatrix)
```

---

`greenControlMatrix`*Example of a matrix containing the green negative control probes from the Illumina 450k array*

---

**Description**

The matrix contains the raw intensities of 600 negative control probes measured in the green channel for 36 samples from the Illumina Infinium HumanMethylation 450k array

**Usage**

```
data(greenControlMatrix)
```

**Format**

A data frame with 600 observations (rows) and 36 samples (columns)

**Details**

Column names correspond to the sample names (of the form 5621146023\_R01C01). These samples correspond to those of [betaMatrix](#).

**See Also**

[getBackground](#) to obtain background information, [redControlMatrix](#) for the equivalent negative control probes in the red channel

**Examples**

```
data(greenControlMatrix)
```

---

redControlMatrix	<i>Example of a matrix containing the red negative control probes from the Illumina 450k array</i>
------------------	--

---

**Description**

The matrix contains the raw intensities of 600 negative control probes measured in the red channel for 36 samples from the Illumina Infinium HumanMethylation 450k array

**Usage**

```
data(redControlMatrix)
```

**Format**

A data frame with 600 observations (rows) and 36 samples (columns)

**Details**

Column names correspond to the sample names (of the form 5621146023\_R01C01). These samples correspond to those of [betaMatrix](#)

**See Also**

[getBackground](#) to obtain background information, [greenControlMatrix](#) for the equivalent negative control probes in the green channel

**Examples**

```
data(redControlMatrix)
```

---

`sampleNames`*An example of sample names for the Illumina 450k array*

---

**Description**

Sample names for a dataset containing 36 samples from the Illumina Infinium HumanMethylation 450k array.

**Usage**

```
data(sampleNames)
```

**Format**

A character vector

**Details**

Names are of the form 5621146023\_R01C01. These sample names correspond to the names of the samples in [betaMatrix](#)

**See Also**

[getDesignInfo](#) to obtain design information,

**Examples**

```
data(sampleNames)
```

# Index

## \* datasets

- betaMatrix, 2
- greenControlMatrix, 2
- redControlMatrix, 3
- sampleNames, 4

betaMatrix, 2, 3, 4

getBackground, 3  
getDesignInfo, 4  
greenControlMatrix, 2, 2, 3

normalizeARRm, 2

redControlMatrix, 2, 3, 3

sampleNames, 4