

# Package ‘miRcompData’

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**Version** 1.39.0

**Date** 2015-09-25

**Title** Data used in the miRcomp package

**Description** Raw amplification data from a large microRNA mixture / dilution study. These data are used by the miRcomp package to assess the performance of methods that estimate expression from the amplification curves.

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**Depends** R (>= 3.2),

**Imports** utils

**License** GPL-3 | file LICENSE

**biocViews** ExperimentData, ExpressionData, qPCRData, Homo\_sapiens\_Data

**NeedsCompilation** no

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

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## Contents

|                       |   |
|-----------------------|---|
| miRcompData . . . . . | 2 |
| Index                 | 3 |

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`miRcompData`*Data used in the miRcomp package.*

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**Description**

Raw amplification data from a large miRNA mixture / dilution study. These data are used by the miRcomp package to assess the performance of methods that estimate expression from the amplification curves.

**Usage**

```
data(miRcompData)
```

**Format**

A data.frame with 9 elements.

|            |                                                   |
|------------|---------------------------------------------------|
| Barcode    | unique identifier for each multi-well plate       |
| Well       | unique identifier for each well in a plate        |
| SampleID   | name given to each sample                         |
| FeatureSet | either "A" or "B" denoting the two feature groups |
| TargetName | target miRNA name                                 |
| Cycle      | PCR cycle of the amplification                    |
| Rn         | fluorescence signal                               |
| dRn        | background-subtracted fluorescence signal         |
| NumCycle   | total number of PCR cycles performed              |

**Examples**

```
data(miRcompData)
```

# Index

## \* **datasets**

miRcompData, [2](#)

miRcompData, [2](#)