

# Package ‘miRcompData’

April 23, 2026

**Version** 1.41.0

**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.

**Author** Matthew N. McCall <mccallm@gmail.com>

**Maintainer** Matthew N. McCall <mccallm@gmail.com>

**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>

**git\_branch** devel

**git\_last\_commit** d087ded

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.24

**Date/Publication** 2026-04-23

## Contents

miRcompData . . . . .	2
<b>Index</b>	<b>3</b>

---

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

---

**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](#)