

# Package ‘SpikeInSubset’

June 11, 2026

**Title** Part of Affymetrix's Spike-In Experiment Data

**Version** 1.53.0

**Author** Rafael Irizarry <rafa@ds.dfci.harvard.edu> and Zhijin Wu

**Maintainer** Robert D Shear <rshear@ds.dfci.harvard.edu>

**URL** <https://bioconductor.org/packages/SpikeInSubset>

**BugReports** <https://github.com/rafalab/SpikeInSubset/issues>

## Description

Includes probe-level and expression data for the HGU133 and HGU95 spike-in experiments

**License** LGPL

**Depends** R (>= 2.4.0), Biobase (>= 2.5.5), affy (>= 1.23.4)

**biocViews** ExperimentData, MicroarrayData

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

**git\_branch** devel

**git\_last\_commit** 5f6a18a

**git\_last\_commit\_date** 2026-04-28

**Repository** Bioconductor 3.24

**Date/Publication** 2026-06-11

## Contents

|                                |          |
|--------------------------------|----------|
| hgu133a.spikein.xhyb . . . . . | 2        |
| SpikeIn . . . . .              | 2        |
| <b>Index</b>                   | <b>4</b> |

hgu133a.spikein.xhyb *Cross hybridizers*

---

### Description

Probe Sets likely to crosshybridize to spiked-in probesets in the Affymetrix HGU133A spike in

This object is list. Each component of the list contains probeset names of possible crosshybridizers. The sequences of each spiked-in clone were collected and blasted against all HG-U133A target sequences. Target sequences are the ~600bp regions from which probes were selected. Thresholds of 100, 150 and 200bp were used and define the three components of the list.

### Usage

```
data(hgu133a.spikein.xhyb)
```

### Format

A list

### Source

Simon Cawley <simon\_cawley@affymetrix.com>

---

SpikeIn *Subset of Affymetrix SpikeIn Experiment Data*

---

### Description

Probe-level and pre-processed data for six arrays (two triplicates) from the HGU95 and HGU133 SpikeIn experiments.

### Usage

```
data(spikein95)
data(rma95)
data(mas95)
```

```
data(spikein133)
data(rma133)
data(mas133)
```

### Format

SpikeIn is [ProbeSet](#) containing the \$PMS\$ and \$MMS\$ intensities for a gene spiked in at different concentrations. Use pData to see the concentrations.

**Source**

spikein95 and spikein133 are instances of [ProbeSet](#) with the probe-level data for six arrays (two triplicates) from the HGU95 and HGU133 SpikeIn experiments respectively. rma95 and rma133 contain the data pre-processed with RMA. mas95 and mas133 contain the data pre-processed with mas5 (expression and present/absent calls). The calls are in objects called pacalls95 and pacalls133.

For more information see Irizarry, R.A., et al. NAR (2003) <http://www.biostat.jhsph.edu/~ririzarr/papers/index.html>

# Index

## \* datasets

hgu133a.spikein.xhyb, [2](#)  
SpikeIn, [2](#)

hgu133a.spikein.xhyb, [2](#)

mas133 (SpikeIn), [2](#)  
mas95 (SpikeIn), [2](#)

pacalls133 (SpikeIn), [2](#)  
pacalls95 (SpikeIn), [2](#)  
ProbeSet, [2](#), [3](#)

rma133 (SpikeIn), [2](#)  
rma95 (SpikeIn), [2](#)

SpikeIn, [2](#)  
spikein133 (SpikeIn), [2](#)  
spikein95 (SpikeIn), [2](#)