Package ‘SpikeInSubset’

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Title Part of Affymetrix's Spike-In Experiment Data

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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

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

biocViews ExperimentData, MicroarrayData

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Contents

`hgu133a.spikein.xhyb` *Cross hybridizers*

Description

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

This objact 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-proecssed 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 PM and MM intensities for a gene spiked in at different concentrations. Use `pData` to see the cosntrations.

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 preprocessed 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`

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