Package 'lumiBarnes'

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Type Package

Title Barnes Benchmark Illumina Tissues Titration Data

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Description The Barnes benchmark dataset can be used to evaluate the algorithms for Illumina microarrays. It measured a titration series of two human tissues, blood and placenta, and includes six samples with the titration ratio of blood and placenta as 100:0, 95:5, 75:25, 50:50, 25:75 and 0:100. The samples were hybridized on HumanRef-8 BeadChip (Illumina, Inc) in duplicate. The data is loaded as an LumiBatch Object (see documents in the lumi package).

License LGPL

Depends R (>= 2.0), Biobase (>= 2.5.5), lumi (>= 1.1.0)

biocViews ExperimentData, Tissue, MicroarrayData, ChipOnChipData

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lumiBarnes *Barnes Benchmark Illumina Tissues Titration Data*

Description

The Barnes data set measured a titration series of two human tissues, blood and placenta. It includes six samples with the titration ratio of blood and placenta as 100:0, 95:5, 75:25, 50:50, 25:75 and 0:100. The samples were hybridized on HumanRef-8 BeadChip (Illumina, Inc) in duplicate. See (Barnes, et al., 2005) for details. The data is saved as a LumiBatch object and should be use together with lumi package.

Because the Barnes data utilized the pre-released version of HumanRef-8 version 1 BeadChip, some probes on the chip do not exist in the public released HumanRef-8 version 1 BeadChip. For annotation consistence, these probes was removed in the lumiBarnes package. For the interested users, the raw data can be downloaded from the paper companion website: http://www.bioinformatics.ubc.ca/pavlidis/lab/platformCom

Usage

```
data(lumiBarnes)
```

Format

lumiBarnes is a LumiBatch-class object.

Source

Barnes, M., Freudenberg, J., Thompson, S., Aronow, B. and Pavlidis, P. (2005) Ex-perimental comparison and cross-validation of the Affymetrix and Illumina gene expression analysis platforms, Nucleic Acids Res, 33, 5914-5923.

Examples

```
data(lumiBarnes)
lumiBarnes
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