Package 'ffpeExampleData'

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Type Package

Title Illumina DASL example microarray data

Version 1.50.0

Date 2011-11-15

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Description A subset of GSE17565 (April et al. 2009) containing 32 FFPE samples of Burkitts Lymphoma and Breast Adenocarcinoma, with a dilution series in technical duplicate.

Depends R (>= 2.10.0), lumi

Suggests genefilter, affy

biocViews Tissue, Genome, MicroarrayData, TissueMicroarrayData, GEO

License GPL (>2)

LazyLoad yes

git_url https://git.bioconductor.org/packages/ffpeExampleData

git_branch RELEASE_3_23

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Repository Bioconductor 3.23

Date/Publication 2026-10-08

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`ffpeExampleData-package` *Illumina DASL example microarray data ~~ package title ~~*

Description

A subset of GSE17565 (April et al. 2009) containing 32 FFPE samples of Burkitts Lymphoma and Breast Adenocarcinoma, with a dilution series in technical duplicate.

Details

Package:	ffpeExampleData
Type:	Package
Version:	1.0.0
Date:	2011-11-17
License:	GPL (>2)

Downloaded from the GEO URL:

http://www.ncbi.nlm.nih.gov/projects/geo/query/acc.cgi?acc=GSE17565 .

Raw data were obtained from the supplemental file GSE17565_nonorm_nobkgd.txt.gz, and inserted into a lumibatch object using the lumi:lumiR command. The metadata from GEO are also curated for ease of use.

Some analyses of this dataset are done in the ffpe Bioconductor package.

Author(s)

Levi Waldron <lwaldron@hsph.harvard.edu>

References

April C, Klotzle B, Royce T, Wickham-Garcia E et al. Whole-genome gene expression profiling of formalin-fixed, paraffin-embedded tissue samples. PLoS One 2009 Dec 3;4(12):e8162. PMID: 19997620

Data from accession ID GSE17565 of the Gene Expression Omnibus

Examples

```
library(lumi)
data(lumibatch.GSE17565)
meta.data <- pData(lumibatch.GSE17565)
expression.data <- exprs(lumibatch.GSE17565)
summary(meta.data)
boxplot(log2(expression.data))
```

lumibatch.GSE17565 *Illumina DASL expression data from FFPE tissues.*

Description

This lumibatch object contains raw expression data for 32 FFPE samples of Burkitts Lymphoma and Breast Adenocarcinoma, with dilution series and technical duplicates. From the original study by April et al. (2009). Sample metadata includes input RNA concentration, cell type, and replicate #.

Usage

```
data(lumibatch.GSE17565)
```

Format

Formal class 'LumiBatch' [package "lumi"]

Details

Downloaded from the GEO URL:

http://www.ncbi.nlm.nih.gov/projects/geo/query/acc.cgi?acc=GSE17565 .

Raw data were obtained from the supplemental file GSE17565_nonorm_nobkgd.txt.gz, and inserted into a lumibatch object using the lumi:lumiR command.

Source

April C, Klotzle B, Royce T, Wickham-Garcia E et al. Whole-genome gene expression profiling of formalin-fixed, paraffin-embedded tissue samples. PLoS One 2009 Dec 3;4(12):e8162. PMID: 19997620

Data from accession ID GSE17565 of the Gene Expression Omnibus

Examples

```
data(lumibatch.GSE17565)
meta.data <- pData(lumibatch.GSE17565)
expression.data <- exprs(lumibatch.GSE17565)
```

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