Package ‘MM2Sdata’

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Type Package

Title Gene Expression Datasets for the 'MM2S' Package

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Description Gene Expression datasets for the 'MM2S' package. Contains normalized expression data for Human Medulloblastoma ('GSE37418') as well as Mouse Medulloblastoma models ('GSE36594'). Deena Gendoo et al. (2015) <doi:10.1016/j.ygeno.2015.05.002>.

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Depends R (>= 2.10), Biobase

Suggests knitr

VignetteBuilder knitr

biocViews MM2S, ExperimentData,ExpressionData, MicroarrayData

RoxygenNote 6.1.1

NeedsCompilation no

Repository CRAN

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R topics documented:

`GSE36594Expr` *Normalized gene expression data for Mouse MB samples (from GSE36594).*

Description

Gene expression for 20 GTML Medulloblastoma mouse samples, normalized using expresso and BrainArray CDFs (see references for details).

PLEASE NOTE: The full processed GSE36594 dataset, which contains 56 samples, can be accessed from the following locations: https://github.com/DGendoo/MM2Sdata http://www.pmgenomics.ca/bhklab/software/mm2s

Usage

```
data(GSE36594Expr)
```

Value

Data and annotations are organized in a ExpressionSet of the package Biobase.

`pData`	phenoData containing mouse sample genotype and origin
`exprs`	ExpressionSet with 23783 EntrezIds and 20 samples
`fData`	List of 23783 EntrezIds

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE36594

References

Gendoo, D. M., Smirnov, P., Lupien, M. & Haibe-Kains, B. Personalized diagnosis of medulloblastoma subtypes across patients and model systems. Genomics, doi:10.1016/j.ygeno.2015.05.002 (2015)

Manuscript URL: http://www.sciencedirect.com/science/article/pii/S0888754315000774

Examples

```
data(GSE36594Expr)

# To install from github, please run the following commands in your R terminal:
# library(Biobase)
# library(devtools)
# install_github(repo="DGendoo/MM2Sdata")
# data(GSE36594Expr)
```

`GSE37418Expr` *Normalized gene expression data for Human MB (GSE37418).*

Description

Gene expression for 10 primary Medulloblastoma human samples, normalized using expresso and BrainArray CDFs (see references for details).

PLEASE NOTE: The full processed GSE37418 dataset, which contains 76 samples, can be accessed from the following locations: https://github.com/DGendoo/MM2Sdata http://www.pmgenomics.ca/bhklab/software/mm2s

Usage

```
data(GSE37418Expr)
```

Value

Data and annotations are organized in a ExpressionSet of the package Biobase.

`pData`	phenoData containing human sample MB subgroup (obtained from GEOquery of the GSE37418)
`exprs`	ExpressionSet with 19764 EntrezIds and 10 samples
`fData`	List of 19764 EntrezIds

Source

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE37418

References

Gendoo, D. M., Smirnov, P., Lupien, M. & Haibe-Kains, B. Personalized diagnosis of medulloblastoma subtypes across patients and model systems. Genomics, doi:10.1016/j.ygeno.2015.05.002 (2015)

Manuscript URL: http://www.sciencedirect.com/science/article/pii/S0888754315000774

Examples

```
data(GSE37418Expr)

# To install from github, please run the following commands in your R terminal:
# library(Biobase)
# library(devtools)
# install_github(repo="DGendoo/MM2Sdata")
# data(GSE37418Expr)
```

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