Package 'MM2Sdata'

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>.

License GPL-3

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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Contents

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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