

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](https://doi.org/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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GSE36594Expr	<i>Normalized gene expression data for Mouse MB samples (from GSE36594).</i>
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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`.

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

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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