

Package ‘PREDAsampledata’

April 14, 2020

Title expression and copy number data on clear cell renal carcinoma samples

Version 0.26.0

Author I. Cifola et al. in Cristina Battaglia Lab, University of Milan

Description Sample data for PREDA package. (annotations objects synchronized with GeneAnnot custom CDFs version 2.2.0)

Depends R (>= 2.10.0), methods, PREDA, Biobase, affy, annotate

Suggests hgu133plus2.db, hgu133plus2cdf

Maintainer Francesco Ferrari <francesco.ferrari@ifom.eu>

License Artistic-2.0

biocViews ExperimentData, Tissue, CancerData, KidneyCancerData, MicroarrayData, TissueMicroarrayData, ArrayExpress

git_url <https://git.bioconductor.org/packages/PREDAsampledata>

git_branch RELEASE_3_10

git_last_commit 1cd16bd

git_last_commit_date 2019-10-29

Date/Publication 2020-04-14

R topics documented:

AffybatchRCC	2
ExpressionSetRCC	2
GEanalysisResults	3
SODEGIRCnanalysisResults	4
SODEGIRCNDataForPREDA	4
SODEGIRGEanalysisResults	5
SODEGIRGEDataForPREDA	6
Index	7

`AffybatchRCC`*AffyBatch object for clear cell renal carcinoma (RCC) sample dataset*

Description

An AffyBatch object containing raw data from clear cell renal carcinoma (RCC) dataset CEL files

Usage

```
data(AffybatchRCC)
```

Details

The sample gene expression dataset includes 12 samples of clear cell renal carcinoma and 11 samples from normal kidney tissue.

Source

ArrayExpress dataset E-TABM-282

References

Ingrid Cifola, Roberta Spinelli, Luca Beltrame, Clelia Peano, Ester Fasoli, Stefano Ferrero, Silvano Bosari, Stefano Signorini, Francesco Rocco, Roberto Perego, Vanessa Proserpio, Francesca Raimondo, Paolo Mocarrelli, and Cristina Battaglia. Genomewide screening of copy number alterations and loh events in renal cell carcinomas and integration with gene expression profile. *Mol Cancer*, 7:6, 2008.

Examples

```
data(AffybatchRCC)
AffybatchRCC
```

`ExpressionSetRCC`*ExpressionSet object for clear cell renal carcinoma (RCC) sample dataset*

Description

An ExpressionSet object containing justRMA preprocessed data for clear cell renal carcinoma (RCC) dataset, using standard Affymetrix CDF

Usage

```
data(ExpressionSetRCC)
```

Details

The sample gene expression dataset includes 12 samples of clear cell renal carcinoma and 11 samples from normal kidney tissue.

Source

ArrayExpress dataset E-TABM-282

References

Ingrid Cifola, Roberta Spinelli, Luca Beltrame, Clelia Peano, Ester Fasoli, Stefano Ferrero, Silvano Bosari, Stefano Signorini, Francesco Rocco, Roberto Perego, Vanessa Proserpio, Francesca Raimondo, Paolo Mocarrelli, and Cristina Battaglia. Genomewide screening of copy number alterations and loh events in renal cell carcinomas and integration with gene expression profile. *Mol Cancer*, 7:6, 2008.

Examples

```
data(ExpressionSetRCC)
ExpressionSetRCC
```

GEanalysisResults

RCC gene expression sample dataset - PREDA analysis results

Description

PREDA analysis results of RCC gene expression sample dataset. The PREDA analysis was focused on the detection of differentially expressed genomic regions in tumor samples compared to normal kidney cells.

Usage

```
data(GEanalysisResults)
```

Source

ArrayExpress dataset E-TABM-282

References

<http://www.xlab.unimo.it/PREDA>

Examples

```
data(GEanalysisResults)
str(GEanalysisResults)
```

SOEGIRCNanalysisResults

SOEGIR analysis results on Copy Number data

Description

PREDAResults object containing SOEGIR analysis results on Copy Number data

Usage

```
data(SOEGIRCNanalysisResults)
```

Details

See also vignette from PREDA package

Source

Copy number data data were obtained from ArrayExpress datasets E-TABM-283/E-TABM-284

References

<http://www.xlab.unimo.it/PREDA> <http://www.xlab.unimo.it/SOEGIR>

Silvio Bicciato, Roberta Spinelli, Mattia Zampieri, Eleonora Mangano, Francesco Ferrari, Luca Beltrame, Ingrid Cifola, Clelia Peano, Aldo Solari, and Cristina Battaglia. A computational procedure to identify significant overlap of differentially expressed and genomic imbalanced regions in cancer datasets. *Nucleic Acids Res*, 37(15):5057-70, August 2009.

Examples

```
data(SOEGIRCNanalysisResults)
str(SOEGIRCNanalysisResults)
```

SOEGIRCNDataForPREDA *Copy Number input data for PREDA analysis*

Description

DataForPREDA object containing Copy Number input data for PREDA analysis

Usage

```
data(SOEGIRCNDataForPREDA)
```

Details

See also vignette from PREDA package

Source

Copy number data data were obtained from ArrayExpress datasets E-TABM-283/E-TABM-284

References

<http://www.xlab.unimo.it/PREDA> <http://www.xlab.unimo.it/SODEGIR>

Silvio Bicciato, Roberta Spinelli, Mattia Zampieri, Eleonora Mangano, Francesco Ferrari, Luca Beltrame, Ingrid Cifola, Clelia Peano, Aldo Solari, and Cristina Battaglia. A computational procedure to identify significant overlap of differentially expressed and genomic imbalanced regions in cancer datasets. *Nucleic Acids Res*, 37(15):5057-70, August 2009.

Examples

```
data(SODEGIRCNDDataForPREDA)
str(SODEGIRCNDDataForPREDA)
```

SODEGIRGEanalysisResults

SODEGIR analysis results on Gene Expression data

Description

PREDADataAndResults object containing SODEGIR analysis results on Gene Expression data

Usage

```
data(SODEGIRGEanalysisResults)
```

Details

See also vignette from PREDA package

Source

ArrayExpress dataset E-TABM-282

References

<http://www.xlab.unimo.it/PREDA> <http://www.xlab.unimo.it/SODEGIR>

Silvio Bicciato, Roberta Spinelli, Mattia Zampieri, Eleonora Mangano, Francesco Ferrari, Luca Beltrame, Ingrid Cifola, Clelia Peano, Aldo Solari, and Cristina Battaglia. A computational procedure to identify significant overlap of differentially expressed and genomic imbalanced regions in cancer datasets. *Nucleic Acids Res*, 37(15):5057-70, August 2009.

Examples

```
data(SODEGIRGEanalysisResults)
str(SODEGIRGEanalysisResults)
```

SODEGIRGEDataForPREDA *Gene Expression input data for PREDA analysis*

Description

DataForPREDA object containing Gene Expression input data for PREDA analysis

Usage

```
data(SODEGIRGEDataForPREDA)
```

Details

See also vignette from PREDA package

Source

ArrayExpress dataset E-TABM-282

References

<http://www.xlab.unimo.it/PREDA> <http://www.xlab.unimo.it/SODEGIR>

Silvio Bicciato, Roberta Spinelli, Mattia Zampieri, Eleonora Mangano, Francesco Ferrari, Luca Beltrame, Ingrid Cifola, Clelia Peano, Aldo Solari, and Cristina Battaglia. A computational procedure to identify significant overlap of differentially expressed and genomic imbalanced regions in cancer datasets. *Nucleic Acids Res*, 37(15):5057-70, August 2009.

Examples

```
data(SODEGIRGEDataForPREDA)  
str(SODEGIRGEDataForPREDA)
```

Index

*Topic **datasets**

- AffybatchRCC, [2](#)
- ExpressionSetRCC, [2](#)
- GEanalysisResults, [3](#)
- SODEGIRCNanalysisResults, [4](#)
- SODEGIRCNDataForPREDA, [4](#)
- SODEGIRGEanalysisResults, [5](#)
- SODEGIRGEDataForPREDA, [6](#)

AffybatchRCC, [2](#)

ExpressionSetRCC, [2](#)

GEanalysisResults, [3](#)

SODEGIRCNanalysisResults, [4](#)

SODEGIRCNDataForPREDA, [4](#)

SODEGIRGEanalysisResults, [5](#)

SODEGIRGEDataForPREDA, [6](#)