Package 'kidpack'

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Title DKFZ kidney package

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Depends R (>= 2.6.0), Biobase (>= 2.5.5)

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Description kidney microarray data

License GPL-2

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`eset` *renal cell cancer expression data*

Description

renal cell cancer expression data

Usage

```
data("eset")
data("esetSpot")
data("cloneanno")
```

Format

`eset` is an object of type `ExpressionSet`. Samples (columns of the expression matrix) correspond to renal cell cancer samples from 74 patients with kidney tumors. Probes (rows of the expression matrix) correspond to different cDNA clones.

`cloneanno` is a data frame with 4224 rows, one for each clone. Its columns are: `plate`, `SrcRow`, `SrcCol`, `imageid`, `AccNumber`, `spot1`, `spot2`, `description`, `vendor`

The arrays that were used to measure these data contained two features for each reporter (clone), and `esetSpot` is the data *before* averaging over the two features per reporter. Spots 4225:8448 are the duplicates of spots 1:4224.

Source

Holger Sueltmann, DKFZ. Also available from ArrayExpress, Accession number E-DKFZ-1.

The data import fro Genepix files and Excel tables, and the preprocessing is described in the files preproc.Rnw and preproc.pdf in the `scripts` subdirectory of the package. Please refer to these for details!

References

Gene expression in kidney cancer is associated with novel tumor subtypes, cytogenetic abnormalities and metastasis formation. Holger Sueltmann, Anja von Heydebreck, Wolfgang Huber, Ruprecht Kuner, Andreas Buness, Markus Vogt, Bastian Gunawan, Martin Vingron, Laszlo Fuezesi, and Annemarie Poustka. Submitted.

See Also

`qua`

Examples

```
data(eset)
eset
data(cloneanno)
cloneanno[1,]

## see also the vignette
```

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qua *renal cell cancer raw data*

Description

renal cell cancer raw data

Usage

```
data(qua)
data(spotanno)
data(hybanno)
```

Format

qua is an 8704x4x175 array. Its first dimension are the spots (probes) on the arrays, its second dimension are four different spot statistics (fg.green, bg.green, fg.red, bg.red), its third dimension are the 175 different arrays.

spotanno is a data frame with 8704 rows, one for each spot. Its columns are: Block, Row, Column, AccNumber, Name, SrcPlt, SrcRow, SrcCol, vendor, ImageID, probe. The column spotanno$probe is of class numeric, with values from 1 to 4224, referring to the rows of cloneanno.

hybanno is a data frame with 175 rows, one for each array. Its columns are: filename, patientid, slideid. The column patientid is of class character, refering to the patients in pData(eset).

Source

Holger Sueltmann, DKFZ. Also available from ArrayExpress, Accession number E-DKFZ-1.

The data import fro Genepix files and Excel tables, and the preprocessing is described in the files preproc.Rnw and preproc.pdf in the scripts subdirectory of the package. Please refer to these for details!

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See Also

eset

Examples

```
data(qua)
qua[1,,1]
data(spotanno)
spotanno[1,]
data(hybanno)
hybanno[1,]

## see also the vignette
```

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