

Package ‘PRECISIONDATA’

June 15, 2016

Type Package

Title Datasets for the PaiREd miCrona sImulation on Study desIgn for
mOlecular classification (PRECISION) Package

Version 0.1

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Description Different versions of a unique pair of Agilent microRNA microar-
ray datasets that can be used for the PRECISION package.

License GPL (>= 2)

Depends R (>= 3.0.2)

Suggests rmarkdown, knitr

LazyData TRUE

RoxygenNote 5.0.1

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noba.bench.log2	<i>The uniformly-handled probe-level dataset, before preprocessing</i>
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Description

The uniformly-handled (benchmark) probe-level dataset, with control probes removed. The expressions are on a log2 scale without background adjustment. The sample IDs (the column names) ending with "E" or "V" are used to indicate whether a sample is endometrial or ovarian tumor sample. There are 96 endometrial and 96 ovarian tumor samples.

Usage

noba.bench.log2

Format

A data matrix with 53880 rows (probes) and 192 columns (samples).

References

<http://clincancerres.aacrjournals.org/content/20/13/3371.long>

noba.bench.log2.p10	<i>The uniformly-handled probe-level dataset, 10 probes for each unique probe</i>
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Description

The uniformly-handled probe-level dataset with 10 probes for each unique probe. It is truncated from the uniformly-handled probe-level dataset (noba.bench.log2.p10), by keeping only the first 10 probes for each unique probe.

Usage

noba.bench.log2.p10

Format

A data matrix with 35230 rows (probes) and 192 columns (samples).

noba.bench.log2.p10.psl	<i>The uniformly-handled probe-set-level dataset</i>
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Description

The uniformly-handled probe-set-level dataset. It is probe-set summarized from the uniformly-handled probe-level dataset with 10 probes for each unique probe (noba.bench.log2.p10), using median.

Usage

noba.bench.log2.p10.psl

Format

A data matrix with 3523 rows (probes) and 192 columns (samples).

noba.test.log2*The non-uniformly-handled probe-level dataset, before preprocessing*

Description

The non-uniformly-handled (test) probe-level dataset, with control probes removed. The expressions are on a log2 scale without background adjustment. The sample IDs (the column names) ending with "E" or "V" are used to indicate whether a sample is endometrial or ovarian tumor sample. There are 96 endometrial and 96 ovarian tumor samples.

Usage

noba.test.log2

Format

A data matrix with 53880 rows (probes) and 192 columns (samples).

References

<http://clincancerres.aacrjournals.org/content/20/13/3371.long>

noba.test.log2.p10*The non-uniformly-handled probe-level dataset, 10 probes for each unique probe*

Description

The non-uniformly-handled probe-level dataset with 10 probes for each unique probe. It is truncated from the non-uniformly-handled probe-level dataset (noba.test.log2.p10), by keeping only the first 10 probes for each unique probe.

Usage

noba.test.log2.p10

Format

A data matrix with 35230 rows (probes) and 192 columns (samples).

noba.test.log2.p10.psl

The non-uniformly-handled probe-set-level dataset

Description

The non-uniformly-handled probe-set-level dataset. It is probe-set summarized from the non-uniformly-handled probe-level dataset with 10 probes for each unique probe (noba.test.log2.p10), using median.

Usage

noba.test.log2.p10.psl

Format

A data matrix with 3523 rows (probes) and 192 columns (samples).

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