

Package ‘ChAMPdata’

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Type Package

Title Data Packages for ChAMP package

Version 0.99.6

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Description More about what it does (maybe more than one line)

License GPL-3

Depends R (>= 3.0.1)

biocViews ExpressionData, IlluminaChip

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ChAMPdata-package *Data Packages to use with the ChAMP Chip Analysis Methylation Pipeline*

Description

This includes three data packages. ProbeInfoALL.lv includes annotation for the 450k array as required by the BMIQ normalization. probe.features includes probe annotations for the 450k array as included in the saved results files for the MVP and DMR functions. testDataSet includes loaded and filtered (for detection) p-value of 6 arrays for the 450k array along with an accompanying samples sheet. This can be used to test the package. In addition, the raw IDAT files for these 6 arrays are available and can be accessed using system.file().

Details

Package: ChAMPdata
 Type: Package
 Version: 0.99.5
 Date: 2013-10-07
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Two of the three packages are used internally by the ChAMP package. The testDataSet can be used to test the package.

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Examples

```
data(probeInfoALL.lv)
data(probe.features)
data(testDataSet)
```

probe.features *HumanMethylation450 probe annotations.*

Description

This file includes the annotation for each probe on the 450k array

Usage

```
data(probe.features)
```

Examples

```
data(probe.features)
```

probeInfoALL.lv	<i>Probe Info Data for use with the BMIQ normalization.</i>
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Description

The probe details are formatted here for the BMIQ function.

Usage

```
data(probeInfoALL.lv)
```

Format

The format is: List of 5 \$ typeC : num [1:485577] 1 1 1 1 1 1 1 1 1 ... \$ Design : num [1:485577] 2 2 2 2 2 2 2 2 2 1 ... \$ GeneGroup: int [1:485577] 1 NA 5 NA 6 6 4 1 NA 2 ... \$ CGI : num [1:485577] 1 0 0 1 0 1 1 1 1 1 ... \$ probeID : chr [1:485577] "cg00000029" "cg00000108" "cg00000109" "cg00000165" ...

Examples

```
data(probeInfoALL.lv)
```

testDataSet	<i>Test dataset.</i>
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Description

This dataset is available to test ChAMP functions.

Usage

```
data(testDataSet)
```

Format

The format is: List of 6 \$ mset :Formal class 'MethylSet' [package "minfi"] with 8 slots \$ rgSet :Formal class 'RGChannelSet' [package "minfi"] with 7 slots \$ pd :'data.frame': 6 obs. of 9 variables: ..\$ Sample_Name ..\$ Sample_Well ..\$ Sample_Plate ..\$ Sample_Group ..\$ Pool_ID ..\$ Array ..\$ Slide ..\$ Basename \$ intensity \$ beta \$ detP

Examples

```
data(testDataSet)
```

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