

# Package ‘OMICsPCAdata’

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**Type** Package

**Title** Supporting data for package OMICsPCA

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**Version** 1.28.0

**Depends** R (>= 3.5.0), MultiAssayExperiment

**Suggests** knitr, kableExtra, rmarkdown

**biocViews** RepositoryData, TechnologyData, ChIPSeqData, SequencingData,  
ExpressionData, ENCODE

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**Description** Supporting data for package OMICsPCA

**License** GPL-3

**Encoding** UTF-8

**VignetteBuilder** knitr

**LazyData** TRUE

**git\_url** <https://git.bioconductor.org/packages/OMICsPCAdata>

**git\_branch** RELEASE\_3\_22

**git\_last\_commit** 5613be2

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clustered_data	<i>cluster object</i>
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### Description

a matrix containing cluster information

### Usage

```
data("clustered_data")
```

### Format

The format is: num [1:300, 1:5] 3.37 -5.26 2.07 2.32 1.94 ... - attr(\*, "dimnames")=List of 2 ..\$ : chr [1:300] "ENST00000456433.1;ENST00000443722.1;ENST00000444457.1;ENST00000498530.1;ENST00000420236.1;ENST00000423207.2" "ENST00000429514.2;ENST00000263893.6;ENST00000492639.1;ENST00000495272.1;ENST00000487884.1" ... ..\$ : chr [1:5] "Dim.1" "Dim.2" "Dim.3" "Dim.4" ...

### Examples

```
data(clustered_data)
## maybe str(clustered_data) ; plot(clustered_data) ...
```

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groupinfo_ext	<i>An out put of create_group</i>
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### Description

An output of create\_group()

### Usage

```
data("groupinfo_ext")
```

### Format

A data frame with 28770 observations on the following variable.

group a factor with levels IntE NE RE WE

### Examples

```
data(groupinfo_ext)
## maybe str(groupinfo_ext) ; plot(groupinfo_ext) ...
```

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multi\_assay

*Example data sets*


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**Description**

Histone modification ChIP-seq and CAGE data

**Usage**

```
data("multi_assay")
```

**Format**

The datasets included in multi\_assay are: 1) Histone modification ChIP-seq peaks of H2az, H3k9ac and H3k4me1. Each of these three datasets are in dataframe format, where the rows correspond to the TSSs and the columns correspond to various cell lines/tissues etc. Each value represents ChIP-seq peak intensity.

2) TSS expression data, measured by CAGE is also in data frame format and the row and column specification is same as the ChIP-seq data. Each value represents an normalized expression value (tpm).

**Source**

The Histone modification are collected from : [https://www.encodeproject.org/matrix/?type=Experiment&assay\\_title=ChIP-seq&target.investigated\\_as=broad+histone+mark](https://www.encodeproject.org/matrix/?type=Experiment&assay_title=ChIP-seq&target.investigated_as=broad+histone+mark) The DNaseI hypersensitivity (DHS) datasets are collected from : [http://ftp.ebi.ac.uk/pub/databases/ensembl/encode/integration\\_data\\_jan2011/byDataType/openchrom/ja](http://ftp.ebi.ac.uk/pub/databases/ensembl/encode/integration_data_jan2011/byDataType/openchrom/ja)

The Histone and DHS files are downloaded as bigbed(.bb) format and converted to bed(.bed) format

The CAGE datasets are collected from : [https://www.encodeproject.org/search/?type=Experiment&assay\\_slms=Transcript](https://www.encodeproject.org/search/?type=Experiment&assay_slms=Transcript)

**Examples**

```
data(multi_assay)
## maybe str(multi_assay) ; plot(multi_assay) ...
```

---

transcript\_details

*details of GENCODE(v 17) TSSs*


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**Description**

details of GENCODE(v 17) TSSs

**Usage**

```
data("transcript_details")
```

**Format**

A data frame with 194871 observations on the following 8 variables.

**Examples**

```
data(transcript_details)
## maybe str(transcript_details) ; plot(transcript_details) ...
```

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