

Package ‘COPDSexualDimorphism.data’

January 19, 2022

Type Package

Title Data to support sexually dimorphic and COPD differential analysis for gene expression and methylation.

Version 1.30.0

Date 2013-10-14

Author J Fah Sathirapongsasuti

Maintainer J Fah Sathirapongsasuti <fah@cs.stanford.edu>

Description Datasets to support COPDSexualDimorphism Package.

License LGPL-2.1

LazyLoad yes

biocViews ExperimentData, Tissue, COPDData

git_url <https://git.bioconductor.org/packages/COPDSexualDimorphism.data>

git_branch RELEASE_3_14

git_last_commit 27b2d2e

git_last_commit_date 2021-10-26

Date/Publication 2022-01-19

R topics documented:

COPDSexualDimorphism-package	2
lgrc.expr	2

Index	4
--------------	----------

COPDSexualDimorphism-package

Data for Sexual Dimorphic and COPD Differential Analysis

Description

Data package to accompany the Package COPDSexualDimorphism.

Details

Package: COPDSexualDimorphism.data
Type: Package
Version: 1.0
Date: 2013-10-14
License: LGPL-2.1

Along with the method package COPDSexualDimorphism, this data package is to accompany the paper "Integrative Genomics of Sexual Dimorphism in COPD" by Sathirapongsasuti et al.

Author(s)

J Fah Sathirapongsasuti

Maintainer: J Fah Sathirapongsasuti <fah@cs.stanford.edu>

References

Sathirapongsasuti JF, Glass K, Huttenhower C, Quackenbush J, DeMeo DL. Integrative Genomics of Sexual Dimorphism in COPD. (In Prep).

www.lung-genomics.org

Examples

```
data(lgrc.expr.meta)
data(lgrc.expr)
data(lgrc.genes)
```

Description

Gene expression and methylation data from the Lung Genomics Research Consortium. These are from whole lungs of patients with and without COPD. Preprocessing, normalization, batch effect correction, and quality control steps are described in Sathirapongsasuti et al. Three types of data are available: gene expression (`lgrc.expr` and `lgrc.expr.meta`), methylation (`lgrc.methp`), and eQTL (`lgrc.eqtl`). `lgrc.genes` are the information about genes in `lgrc.expr` as given by BiomaRt. The data frame `eqtl` is a result of eQTL analysis of cis SNPs within 100kb upstream and 10kb downstream of the SDCD genes. It is the full list of eQTL results and are to be filtered further through `sdcd.core` function as shown in the vignette.

Usage

```
data(lgrc.expr)
```

Format

```
The format is: num [1:14557, 1:229] 10.45 1.88 12 9.02 8.81 ... - attr(*, "dimnames")=List of 2 ..$ :  
chr [1:14557] "ENSG00000000003" "ENSG00000000005" "ENSG00000000419" "ENSG00000000457"  
... ..$ : chr [1:229] "LT001098RU_COPD" "LT001796RU_CTRL" "LT005419RU_COPD" "LT007392RU_COPD"  
...
```

Source

www.lung-genomics.org

References

Sathirapongsasuti JF, Glass K, Huttenhower C, Quackenbush J, DeMeo DL. Integrative Genomics of Sexual Dimorphism in COPD. (In Prep).

Examples

```
data(lgrc.meta)  
head(meta)
```

```
data(lgrc.expr)  
data(lgrc.expr.meta)  
dim(expr)  
dim(expr.meta)  
head(expr.meta)
```

```
data(lgrc.methp)  
dim(methp)
```

```
data(lgrc.eqtl)  
dim(eqtl)
```

Index

- * **COPD**
 - COPDSexualDimorphism-package, [2](#)
- * **SDCD**
 - COPDSexualDimorphism-package, [2](#)
- * **datasets**
 - lgrc.expr, [2](#)
- * **package**
 - COPDSexualDimorphism-package, [2](#)
- * **sexual dimorphism**
 - COPDSexualDimorphism-package, [2](#)

COPDSexualDimorphism
(COPDSexualDimorphism-package),
[2](#)

COPDSexualDimorphism-package, [2](#)

eqtl (lgrc.expr), [2](#)
expr (lgrc.expr), [2](#)

lgrc.eqtl (lgrc.expr), [2](#)
lgrc.expr, [2](#)
lgrc.genes (lgrc.expr), [2](#)
lgrc.meta (lgrc.expr), [2](#)
lgrc.methp (lgrc.expr), [2](#)

meta (lgrc.expr), [2](#)
methp (lgrc.expr), [2](#)