

Package ‘COPDSexualDimorphism.data’

February 12, 2026

Type Package

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

Version 1.46.0

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_22

git_last_commit 572b6d3

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2026-02-12

Contents

COPDSexualDimorphism-package	1
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)
```

lgrc.expr

Gene Expression and Methylation Data from the LGRC

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] "ENSG000000000003" "ENSG000000000005" "ENSG000000000419" "ENSG000000000457"\$: 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, [1](#)
- * **SDCD**
 - COPDSexualDimorphism-package, [1](#)
- * **datasets**
 - lgrc.expr, [2](#)
- * **package**
 - COPDSexualDimorphism-package, [1](#)
- * **sexual dimorphism**
 - COPDSexualDimorphism-package, [1](#)

COPDSexualDimorphism
(COPDSexualDimorphism-package),
[1](#)

COPDSexualDimorphism-package, [1](#)

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](#)