

# Package ‘COPDSexualDimorphism.data’

March 29, 2021

**Type** Package

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

**Version** 1.26.0

**Date** 2013-10-14

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**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\_12

**git\_last\_commit** c093858

**git\_last\_commit\_date** 2020-10-27

**Date/Publication** 2021-03-29

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COPDSexualDimorphism-package

*Data for Sexual Dimorphic and COPD Differential Analysis*

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## 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](http://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*

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### 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](http://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)
```

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