

Package ‘Single.mTEC.Transcriptomes’

November 13, 2025

Type Package

Title Single Cell Transcriptome Data and Analysis of Mouse mTEC cells

Version 1.39.0

Date 2025-07-28

Author Alejandro Reyes

Maintainer Alejandro Reyes <alejandro.reyes.ds@gmail.com>

Description This data package contains the code used to analyse the single-cell RNA-seq and the bulk ATAC-seq data from the manuscript titled: Single-cell transcriptome analysis reveals coordinated ectopic-gene expression patterns in medullary thymic epithelial cells. This paper was published in Nature Immunology 16,933-941(2015). The data objects provided in this package has been pre-processed: the raw data files can be downloaded from ArrayExpress under the accession identifiers E-MTAB-3346 and E-MTAB-3624. The vignette of this data package provides a documented and reproducible workflow that includes the code that was used to generate each statistic and figure from the manuscript.

License LGPL

biocViews ExperimentData

VignetteBuilder knitr

Depends R (>= 3.5.0)

Suggests DESeq2, GenomicRanges, GenomicFeatures, genefilter, statmod, gdata, RColorBrewer, ggplot2, gplots, cluster, clue, grid, gridExtra, ggbio, Gviz, geneplotter, matrixStats, pheatmap, BiocStyle, knitr, BiocParallel

RoxygenNote 5.0.1

NeedsCompilation no

git_url <https://git.bioconductor.org/packages/Single.mTEC.Transcriptomes>

git_branch devel

git_last_commit 6831d50

git_last_commit_date 2025-10-29

Repository Bioconductor 3.23

Date/Publication 2025-11-13

Contents

Single.mTec.Transcriptomes-package	2
aireDependentSansom	3
biotype	3
biotypesHuman	3
cealCoexpression	4
corMatsNoMarker	4
deGenesNone	5
deGenesSansom	5
dxdATAC	5
fantom	6
geneNames	6
geneNamesHuman	6
geneRanges	7
mTECdx	7
muc1Coexpression	7
nomarkerCellsClustering	8
percentsGG	8
permutationResults	8
scLVM_output	9
tras	9
Index	10

Single.mTec.Transcriptomes-package
Single-cell transcriptome data of medullary thymic epithelial cells

Description

This document contains all the code used to analyse the single-cell RNA-seq and the bulk ATAC-seq data from the manuscript by Brennecke et al, 2015. The purpose of this package is to provide full reproducibility of the results presented in the manuscript. This package provides a documented and reproducible workflow of the code that was used to generate each number and figure from the manuscript.

References

Brennecke et al. Single-cell transcriptome analysis reveals coordinated ectopic gene-expression patterns in medullary thymic epithelial cells. Nature Immunology 16,933-941 (2015)

aireDependentSansom	<i>List of Aire-dependent genes</i>
---------------------	-------------------------------------

Description

A character vector of ensembl gene identifiers defined by Sansom et al, 2014. This list was downloaded from the supplementary material of the manuscript.

Usage

```
data(aireDependentSansom)
```

References

Sansom et al. Population and single-cell genomics reveal the Aire dependency, relief from Polycomb silencing, and distribution of self-antigen expression in thymic epithelia. *Genome Res.* 24, 1918–1931 (2014).

biotype	<i>Mouse biotypes</i>
---------	-----------------------

Description

A character vector defining biotype for each mouse ensembl gene identifier. Biotypes were queried using **biomaRt**.

Usage

```
data(biotypes)
```

biotypesHuman	<i>Human biotypes</i>
---------------	-----------------------

Description

A character vector defining biotype for each human ensembl gene identifier. Biotypes were queried using **biomaRt**.

Usage

```
data(biotypesHuman)
```

cea1Coexpression	<i>Cea1 co-expression group data</i>
------------------	--------------------------------------

Description

A data frame containing information about the Cea1 co-expression group defined in Pinto et al, 2013.

Usage

```
data(cea1Coexpression)
```

References

Pinto et al. Overlapping gene coexpression patterns in human medullary thymic epithelial cells generate self-antigen diversity. Proc. Natl. Acad. Sci. U.S.A. 110, E3497–3505, (2013).

corMatsNoMarker	<i>Gene-gene correlation network</i>
-----------------	--------------------------------------

Description

A matrix containing the gene-gene Spearman correlation across single unselected cells.

A matrix containing the gene-gene Spearman correlation across single unselected cells, using the data from Sansom et al, 2014.

Usage

```
data(corMatsNoMarker)
```

```
data(corMatsSansom)
```

References

Sansom et al. Population and single-cell genomics reveal the Aire dependency, relief from Polycomb silencing, and distribution of self-antigen expression in thymic epithelia. Genome Res. 24, 1918–1931 (2014).

deGenesNone	<i>Highly variable genes.</i>
-------------	-------------------------------

Description

List of highly variable genes according to the method by Brennecke et al, 2013.

Usage

```
data(deGenesNone)
```

References

Brennecke et al. Accounting for technical noise in single-cell RNA-seq experiments. Nat. Methods. 10, 1093-1095 (2013).

deGenesSansom	<i>Highly variable genes from Sansom et al.</i>
---------------	---

Description

List of highly variable genes according to the method by Brennecke et al, 2013, using the data by Sansom et al.

Usage

```
data(deGenesSansom)
```

References

Brennecke et al. Accounting for technical noise in single-cell RNA-seq experiments. Nat. Methods. 10, 1093-1095 (2013). Sansom et al. Population and single-cell genomics reveal the Aire dependency, relief from Polycomb silencing, and distribution of self-antigen expression in thymic epithelia. Genome Res. 24, 1918–1931 (2014).

dxdATAC	<i>ATAC-seq summarized counts.</i>
---------	------------------------------------

Description

DESeqDataSet object summarizing the ATAC-seq data presented in the manuscript. This object contains the read counts of each sample over a window of 4Kb around transcription start sites.

Usage

```
data(dxdATAC)
```

fantom	<i>FANTOM dataset</i>
--------	-----------------------

Description

DESeqDataSet object of the read counts from selected tissues from the FANTOM dataset.

Usage

```
data(fantom)
```

References

Forrest et al. A promoter-level mammalian expression atlas. 24, 1918–1931. (2014).

geneNames	<i>Mouse gene names</i>
-----------	-------------------------

Description

Character vector of mouse gene names. The gene names were queried using **biomaRt**.

Usage

```
data(geneNames)
```

geneNamesHuman	<i>Human gene names</i>
----------------	-------------------------

Description

Character vector of human gene names. The gene names were queried using **biomaRt**.

Usage

```
data(geneNamesHuman)
```

geneRanges	<i>Genomic range coordinates.</i>
------------	-----------------------------------

Description

GenomicRanges object containing the coordinate ranges of mouse protein coding genes used in the manuscript.

Usage

```
data(geneRanges)
```

mTECdx	<i>Count data from the single-mTEC data.</i>
--------	--

Description

DESeqDataSet object containing the read counts from the single-cell RNA-seq dataset generated by Brennecke et al, 2015.

Usage

```
data(mTECdx)
```

References

Brennecke et al. Single-cell transcriptome analysis reveals coordinated ectopic gene-expression patterns in medullary thymic epithelial cells. Nature Immunology 16,933-941 (2015)

muc1Coexpression	<i>Muc1 co-expression group data</i>
------------------	--------------------------------------

Description

A data frame containing information about the Muc1 co-expression group defined in Pinto et al, 2013.

Usage

```
data(muc1Coexpression)
```

References

Pinto et al. Overlapping gene coexpression patterns in human medullary thymic epithelial cells generate self-antigen diversity. Proc. Natl. Acad. Sci. U.S.A. 110, E3497–3505, (2013).

`nomarkerCellsClustering`*Clustering results*

Description

List containing the results from the clustering analysis from Figure 2 from the manuscript.

Usage

```
data(nomarkerCellsClustering)
```

`percentsGG`*Mapping statistics*

Description

Data frame containing the mapping statistics from the single-cell RNA-seq data.

Usage

```
data(percentsGG)
```

`permutationResults`*Permutation results*

Description

Result from the gene permutations from Figure 5 from the manuscript.

Usage

```
data(permutationResults)
```

scLVM_output	<i>Output from scLVM</i>
--------------	--------------------------

Description

Objects containing the output scLVM on the single-mTEC RNA-seq data.

Usage

```
data(scLVM_output)
```

References

Buettner et al. Computational analysis of cell-to-cell heterogeneity in single-cell RNA-sequencing data reveals hidden subpopulations of cells. Nat. Biotechnol. 2015.

tras	<i>Tissue restricted antigens lists.</i>
------	--

Description

Data frame containing the TRA classification from Pinto et al, 2013.

Usage

```
data(tras)
```

Index

* datasets

- aireDependentSansom, [3](#)
- biotype, [3](#)
- biotypesHuman, [3](#)
- cea1Coexpression, [4](#)
- corMatsNoMarker, [4](#)
- deGenesNone, [5](#)
- deGenesSansom, [5](#)
- dxdATAC, [5](#)
- fantom, [6](#)
- geneNames, [6](#)
- geneNamesHuman, [6](#)
- geneRanges, [7](#)
- mTECdxd, [7](#)
- muc1Coexpression, [7](#)
- nomarkerCellsClustering, [8](#)
- percentsGG, [8](#)
- permsAllClusters (permutationResults), [8](#)
- permutationResults, [8](#)
- realAllClusters (permutationResults), [8](#)
- scLVM_output, [9](#)
- Single.mTec.Transcriptomes-package, [2](#)
- tras, [9](#)
- vars (scLVM_output), [9](#)
- Ycorr (scLVM_output), [9](#)

- aireDependentSansom, [3](#)
- beta (scLVM_output), [9](#)
- beta0 (scLVM_output), [9](#)
- biotype, [3](#)
- biotypesHuman, [3](#)
- cea1Coexpression, [4](#)
- corMatsNoMarker, [4](#)
- corMatSp (corMatsNoMarker), [4](#)
- corMatSpNoMarker (corMatsNoMarker), [4](#)
- deGenesNone, [5](#)
- deGenesSansom, [5](#)
- dxd (mTECdxd), [7](#)
- dxdATAC, [5](#)
- dxdFANTOM (fantom), [6](#)
- fantom, [6](#)