

# Package ‘Single.mTEC.Transcriptomes’

November 6, 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** 2025-11-06

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         |
| mTECdxd . . . . .                            | 7         |
| muc1Coexpression . . . . .                   | 7         |
| nomarkerCellsClustering . . . . .            | 8         |
| percentsGG . . . . .                         | 8         |
| permutationResults . . . . .                 | 8         |
| scLVM_output . . . . .                       | 9         |
| tras . . . . .                               | 9         |
| <b>Index</b>                                 | <b>10</b> |

---

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 | <i>Clustering results</i> |
|-------------------------|---------------------------|

---

**Description**

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

**Usage**

data(nomarkerCellsClustering)

---

|            |                           |
|------------|---------------------------|
| percentsGG | <i>Mapping statistics</i> |
|------------|---------------------------|

---

**Description**

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

**Usage**

data(percentsGG)

---

|                    |                            |
|--------------------|----------------------------|
| permutationResults | <i>Permutation results</i> |
|--------------------|----------------------------|

---

**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](#)