# Package ‘Single.mTEC.Transcriptomes’

May 28, 2026

**Type** Package

**Title** Single Cell Transcriptome Data and Analysis of Mouse mTEC cells

**Version** 1.41.0

**Date** 2025-07-28

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**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** f51e1ab

**git_last_commit_date** 2026-04-28

**Repository** Bioconductor 3.24

**Date/Publication** 2026-05-28

# Contents

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

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### 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)

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`aireDependentSansom` *List of Aire-dependent genes*

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## 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` *Mouse biotypes*

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## Description

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

## Usage

```
data(biotypes)
```

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`biotypesHuman` *Human biotypes*

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## Description

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

## Usage

```
data(biotypesHuman)
```

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## `cea1Coexpression` *Cea1 co-expression group data*

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### 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).

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## `corMatsNoMarker` *Gene-gene correlation network*

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### 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).

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## `deGenesNone` *Highly variable genes.*

---

### 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).

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## `deGenesSansom` *Highly variable genes from Sansom et al.*

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### Description

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

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## `dxdATAC` *ATAC-seq summarized counts.*

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### 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)
```

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`fantom` *FANTOM dataset*

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### 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` *Mouse gene names*

---

### Description

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

### Usage

```
data(geneNames)
```

---

`geneNamesHuman` *Human gene names*

---

### Description

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

### Usage

```
data(geneNamesHuman)
```

---

`geneRanges` *Genomic range coordinates.*

---

### Description

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

### Usage

```
data(geneRanges)
```

---

`mTECdxd` *Count data from the single-mTEC data.*

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### Description

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

### Usage

```
data(mTECdxd)
```

### 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)

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`muc1Coexpression` *Muc1 co-expression group data*

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### 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).

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`nomarkerCellsClustering`
*Clustering results*

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### 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` *Output from scLVM*

### 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` *Tissue restricted antigens lists.*

### Description

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

### Usage

```
data(tras)
```

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