

Package ‘scTHI.data’

June 25, 2024

Type Package

Title The package contains examples of single cell data used in vignettes and examples of the scTHI package; data contain both tumor cells and immune cells from public dataset of glioma

Version 1.17.0

Description Data for the vignette and tutorial of the package scTHI.

License GPL-2

Depends R (>= 4.0)

Encoding UTF-8

LazyData false

RoxygenNote 6.1.1.9000

biocViews ExperimentData, SingleCellData

git_url <https://git.bioconductor.org/packages/scTHI.data>

git_branch devel

git_last_commit b6a98fd

git_last_commit_date 2024-04-30

Repository Bioconductor 3.20

Date/Publication 2024-06-25

Author Francesca Pia Caruso [aut],
Michele Ceccarelli [aut, cre]

Maintainer Michele Ceccarelli <m.ceccarelli@gmail.com>

Contents

| | |
|----------------------------|----------|
| H3K27 | 2 |
| H3K27.meta | 2 |
| MGH45 | 3 |
| MGH45.annotation | 3 |
| scExample | 4 |
| Index | 5 |

H3K27

Example expression matrix for scTHI.

Description

A 21673 x 527 matrix patient PatientBCH836 form Filbin, M. G., Tirosh, I., Hovestadt, V., Shaw, M. L., Escalante, L. E., Mathewson, N. D., ... & Haberler, C. (2018). Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. *Science*, 360(6386), 331-335. H3K27

Usage

H3K27

Format

An object of class `matrix` with 21673 rows and 527 columns.

H3K27.meta

Annotation for the H3K27 e expression matrix for scTHI.

Description

A dataframe 527x9 for the matrix of patient PatientBCH836 form Filbin, M. G., Tirosh, I., Hovestadt, V., Shaw, M. L., Escalante, L. E., Mathewson, N. D., ... & Haberler, C. (2018). Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. *Science*, 360(6386), 331-335. H3K27.annotation

Usage

H3K27.meta

Format

An object of class `data.frame` with 527 rows and 9 columns.

| | |
|-------|---|
| MGH45 | <i>Example expression matrix for scTHI.</i> |
|-------|---|

Description

A 17584 x 608 matrix patient PatientBCH836 form Venteicher AS, Tirosh I, Hebert C, Yizhak K et al. Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. Science 2017 Mar 31;355(6332) MGH45

Usage

MGH45

Format

An object of class `matrix` with 17584 rows and 608 columns.

| | |
|------------------|--|
| MGH45.annotation | <i>Annotation for Example expression matrix for scTHI.</i> |
|------------------|--|

Description

A 608 x 2 dataframe with the annotation for the MGH4 matrix Venteicher AS, Tirosh I, Hebert C, Yizhak K et al. Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. Science 2017 Mar 31;355(6332) MGH45.annotation

Usage

MGH45.annotation

Format

An object of class `data.frame` with 608 rows and 2 columns.

`scExample`*Example expression matrix for scTHI.*

Description

A 2000 x 100 matrix from the wiki manual to showcase the use of scTHI `scExample`

Usage

```
scExample
```

Format

An object of class `matrix` with 2000 rows and 100 columns.

Index

* datasets

H3K27, [2](#)

H3K27.meta, [2](#)

MGH45, [3](#)

MGH45.annotation, [3](#)

scExample, [4](#)

H3K27, [2](#)

H3K27.meta, [2](#)

MGH45, [3](#)

MGH45.annotation, [3](#)

scExample, [4](#)