Package ‘tissueTreg’

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Title TWGBS and RNA-seq data from tissue T regulatory cells from mice

Version 1.6.0

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Description The package provides ready to use epigenomes (obtained from TWGBS) and transcriptomes (RNA-seq) from various tissues as obtained in the study (Delacher and Imbusch 2017, PMID: 28783152).
Regulatory T cells (Treg cells) perform two distinct functions: they maintain self-tolerance, and they support organ homeostasis by differentiating into specialized tissue Treg cells. The underlying dataset characterises the epigenetic and transcriptomic modifications for specialized tissue Treg cells.

Depends R (>= 3.5)

License GPL (>= 2)

Encoding UTF-8

LazyData true

Imports

Suggests BiocStyle, knitr, rmarkdown, testthat, ExperimentHub, bsseq, SummarizedExperiment

VignetteBuilder knitr

biocViews ExperimentData, Tissue, Mus_musculus_Data, SequencingData, RNASeqData

URL `https://github.com/cimbusch/tissueTreg`

RoxygenNote 6.0.1

git_url https://git.bioconductor.org/packages/tissueTreg

git_branch RELEASE_3_10

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R topics documented:

`tissueTreg` *Epigenomes and transcriptomes of tissue resident regulatory T cells*

Description

The package provides ready to use epigenomes (obtained from TWGBS) and transcriptomes (RNA-seq) from various tissues. Regulatory T cells (Treg cells) perform two distinct functions: they maintain self-tolerance, and they support organ homeostasis by differentiating into specialized tissue Treg cells. The underlying dataset characterises the epigenetic and transcriptomic modifications for specialized tissue Treg cells.

Source

Delacher, M, Imbusch, CD, Weichenhan, D, Breiling, A, Hotz-Wagenblatt, A, Träger, U, Hofer, AC, Kägebein, D, Wang, Q, Frauhammer, F, Mallm, JP, Bauer, K, Herrmann, C, Lang, PA, Brors, B, Plass, C, Feuerer, M (2017). Genome-wide DNA-methylation landscape defines specialization of regulatory T cells in tissues. Nat. Immunol., 18, 10:1160-1172.

Examples

```
eh <- ExperimentHub::ExperimentHub()
se_rpkms <- eh[["EH1074"]]
```

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