Package ‘tissueTreg’

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

Version 1.28.0

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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

Suggests BiocStyle, knitr, rmarkdown, testthat, ExperimentHub, bsseq, SummarizedExperiment, ggplot2, reshape2

VignetteBuilder knitr

biocViews ExperimentData, Tissue, Mus_musculus_Data, SequencingData, RNASeqData

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

RoxygenNote 6.0.1

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

Description

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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()

# RNA-seq RPKM data:
se_rpkms <- eh[["EH1074"]]

# Whole genome bisulfite sequencing data as bsseq objects:
tregs_per_sample <- eh[["EH1072"]]
tregs_per_tissue <- eh[["EH1073"]]
```

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