Package ‘tissueTreg’

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Title   TWGBS and RNA-seq data from tissue T regulatory cells from mice
Version 1.22.0
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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, 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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**R topics documented:**

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<th>Epigenomes and transcriptomes of tissue resident regulatory T cells</th>
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**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**


**Examples**

```r
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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