Package ‘airway’

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Title RangedSummarizedExperiment for RNA-Seq in airway smooth muscle cells, by Himes et al PLoS One 2014

Version 1.27.0

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Description This package provides a RangedSummarizedExperiment object of read counts in genes for an RNA-Seq experiment on four human airway smooth muscle cell lines treated with dexamethasone. Details on the gene model and read counting procedure are provided in the package vignette. The citation for the experiment is: Himes BE, Jiang X, Wagner P, Hu R, Wang Q, Klanderman B, Whitaker RM, Duan Q, Lasky-Su J, Nikolos C, Jester W, Johnson M, Panettieri R Jr, Tantisira KG, Weiss ST, Lu Q. 'RNA-Seq Transcriptome Profiling Identifies CRISPLD2 as a Glucocorticoid Responsive Gene that Modulates Cytokine Function in Airway Smooth Muscle Cells.' PLoS One. 2014 Jun 13;9(6):e99625. PMID: 24926665. GEO: GSE52778.

biocViews ExperimentData, SequencingData, RNASeqData, GEO

License LGPL

Depends R (>= 3.5.0), SummarizedExperiment

Suggests knitr, GEOquery, markdown

VignetteBuilder knitr

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Contents

`airway` *Airway smooth muscle cells*

Description

Read counts per gene for airway smooth muscle cell lines RNA-Seq experiment

Usage

```
data("airway")
```

Format

RangedSummarizedExperiment

Details

For details on the gene model and read counting procedure, see the package vignette.

The dataset contains four cell lines in two conditions: control and treatment with dexamethasone.

Source

FASTQ files from SRA, phenotypic data from GEO

References

Himes BE, Jiang X, Wagner P, Hu R, Wang Q, Klanderman B, Whitaker RM, Duan Q, Lasky-Su J, Nikolos C, Jester W, Johnson M, Panettieri R Jr, Tantisira KG, Weiss ST, Lu Q. 'RNA-Seq Transcriptome Profiling Identifies CRISPLD2 as a Glucocorticoid Responsive Gene that Modulates Cytokine Function in Airway Smooth Muscle Cells.' PLoS One. 2014 Jun 13;9(6):e99625. PMID: 24926665. GEO: GSE52778.

`gse` *Airway smooth muscle cells - Salmon quantification*

Description

Estimated counts, abundance and effective length per gene for airway smooth muscle cell lines RNA-Seq experiment

Usage

```
data("gse")
```

Format

RangedSummarizedExperiment

Details

The dataset contains four cell lines in two conditions: control and treatment with dexamethasone.

In addition, in version 1.6, the package was updated to include two samples, SRR1039508 and SRR1039509, quantified using Salmon, in order to demonstrate the tximport/tximeta Bioconductor packages. For details on the quantification steps for these files, consult the airway2 package: `https://github.com/mikelove/airway2`.

This data object provides a SummarizedExperiment `gse` in which the Salmon quantification data for 8 samples have been loaded into R/Bioconductor using the tximeta package.

Source

FASTQ files from SRA, phenotypic data from GEO

References

Himes BE, Jiang X, Wagner P, Hu R, Wang Q, Klanderman B, Whitaker RM, Duan Q, Lasky-Su J, Nikolos C, Jester W, Johnson M, Panettieri R Jr, Tantisira KG, Weiss ST, Lu Q. 'RNA-Seq Transcriptome Profiling Identifies CRISPLD2 as a Glucocorticoid Responsive Gene that Modulates Cytokine Function in Airway Smooth Muscle Cells.' PLoS One. 2014 Jun 13;9(6):e99625. PMID: 24926665. GEO: GSE52778.

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