Package ‘airway’

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

Version 1.24.0

Author Michael Love

Maintainer Michael Love <michaelisaiahlove@gmail.com>


biocViews ExperimentData, SequencingData, RNASeqData, GEO

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Depends R (>= 3.5.0), SummarizedExperiment

Suggests knitr, GEOquery, markdown

VignetteBuilder knitr

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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

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

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