Package ‘airway’

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

Version 1.22.0

Author Michael Love

Maintainer Michael Love <michaelisaiaihlove@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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**R topics documented:**

- airway
- gse

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### Description

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

### Usage

```r
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

**gse**

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**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**

```r
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](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**

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