Package ‘curatedAdipoRNA’

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Type Package

Title A Curated RNA-Seq Dataset of MDI-induced Differentiated Adipocytes (3T3-L1)

Version 1.24.0

Year 2019

Description A curated dataset of RNA-Seq samples. The samples are MDI-induced pre-phagocytes (3T3-L1) at different time points/stage of differentiation. The package document the data collection, pre-processing and processing. In addition to the documentation, the package contains the scripts that was used to generated the data.

License GPL-3

URL https://github.com/MahShaaban/curatedAdipoRNA

BugReports https://github.com/MahShaaban/curatedAdipoRNA/issues

Encoding UTF-8

RoxygenNote 6.1.1

LazyData TRUE

Depends R (>= 3.6), SummarizedExperiment

Suggests knitr, rmarkdown, DESeq2, fastqcr, devtools, testthat, readr, dplyr, tidyr, ggplot2, S4Vectors

VignetteBuilder knitr

biocViews ExperimentData, GEO, RNASeqData, SequencingData

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Contents

`adipo_counts` *Gene counts in differentiating adipocytes*

Description

Gene counts in differentiating adipocytes

Usage

```
adipo_counts
```

Format

A `RangedSummarizedExperiment` object contains:

assay The gene counts `matrix`.

colData The phenotype data and quality control data of the samples.

rowRanges The feature data at gene level.

metadata The study level metadata which contains one object called `studies`. This is a `data.frame` of bibliography information of the studies from which the samples were collected.

Examples

```
# load the data object
data('adipo_counts')

# print the object
adipo_counts
```

`curatedAdipoRNA` `curatedAdipoRNA` *package*

Description

A Curated RNA-Seq Dataset of MDI-induced Differentiated Adipocytes (3T3-L1)

Details

A curated dataset of RNA-Seq samples. The samples are MDI-induced pre-phagocytes (3T3-L1) at different time points/stage of differentiation. The package document the data collection, pre-processing and processing. In addition to the documentation, the package contains the scripts that was used to generated the data. The datasets and the pipeline used to process it are documented in `adipo_counts` and the package vignette.

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