Package ‘curatedAdipoRNA’

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Type  Package
Title  A Curated RNA-Seq Dataset of MDI-induced Differentiated Adipocytes (3T3-L1)
Version 1.18.0
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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adipo_counts

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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
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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