Package ‘ObMiTi’

April 16, 2024

Type Package

Title Ob/ob Mice Data on Normal and High Fat Diet

Version 1.10.0

Year 2021

Description The package provide RNA-seq count for 2 strains of mus musclus; Wild type and Ob/Ob. Each strain was divided into two groups, and each group received either chow diet or high fat diet. RNA expression was measured after 20 weeks in 7 tissues.

License GPL-3

URL `https://github.com/OmarElAshkar/ObMiTi`

BugReports `https://github.com/OmarElAshkar/ObMiTi/issues`

Encoding UTF-8

RoxygenNote 7.1.1

Depends R (>= 4.1), SummarizedExperiment, ExperimentHub

Suggests knitr, rmarkdown, BiocManager, GenomicFeatures, S4Vectors, devtools, testthat

VignetteBuilder knitr

biocViews ExperimentHub, GEO, RNASeqData

git_url https://git.bioconductor.org/packages/ObMiTi

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Author Omar Elashkar [aut, cre] (<`https://orcid.org/0000-0002-5505-778X`>), Mahmoud Ahmed [aut] (<`https://orcid.org/0000-0002-4377-6541`>)

Maintainer Omar Elashkar <`omar.i.elashkar@gmail.com`>

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`ObMiTi` `ObMiTi` *package*

Description

Title: Ob/ob Mice Data on Normal and High Fat Diet The package provide RNA-seq count for 2 strains of mus musclus; Wild type and Ob/Ob. Each strain was divided into two groups, and each group received either chow diet or high fat diet. RNA expression was measured after 12 weeks in 7 tissues.

Details

The dataset can be accessed through the `ExperimentHub` as a `RangedSummarizedExperiment` object contains:

assay The read counts `matrix`.

colData The phenotype data of the samples

rowRanges The feature data and annotation of the peaks.

metadata extra details about the sample and associated phenotype `studies`. This is a `data.frame` of bibliography information of the studies from which the samples were collected for.

Examples

```
# load the data object
library(ExperimentHub)

# query package resources on ExperimentHub
eh <- ExperimentHub()
query(eh, "ObMiTi")

# load data from ExperimentHub
ob_counts <- query(eh, "ObMiTi")[[1]]

# print object
ob_counts
```

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