Package 'ObMiTi'

March 28, 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

git_branch RELEASE_3_18

git_last_commit 765fe6c

git_last_commit_date 2023-10-24

Repository Bioconductor 3.18

Date/Publication 2024-03-28

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>

1

R **topics documented:**

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
```

Index