Package ‘ObMiTi’

February 29, 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 musculus: 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 2024-02-29
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>
Description

Title: Ob/ob Mice Data on Normal and High Fat Diet The package provide RNA-seq count for 2 strains of mus musculus; 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

ObMiTi, 2