

Package ‘bodymapRat’

April 13, 2022

Title Experimental dataset from the rat BodyMap project

Version 1.10.0

Description This package contains a SummarizedExperiment from the Yu et al. (2013) paper that performed the rat BodyMap across 11 organs and 4 developmental stages. Raw FASTQ files were downloaded and mapped using STAR. Data is available on ExperimentHub as a data package.

Depends R (>= 3.6.0), SummarizedExperiment, ExperimentHub

Imports utils

Suggests rmarkdown, knitr, BiocStyle, testthat

biocViews SequencingData, RNASeqData, ExpressionData, ExperimentData, ExperimentHub

NeedsCompilation no

License CC BY 4.0

VignetteBuilder knitr

RoxygenNote 6.1.1

Encoding UTF-8

git_url <https://git.bioconductor.org/packages/bodymapRat>

git_branch RELEASE_3_14

git_last_commit 79dad34

git_last_commit_date 2021-10-26

Date/Publication 2022-04-13

Author Stephanie Hicks [aut, cre] (<<https://orcid.org/0000-0002-7858-0231>>), Kwame Okrah [aut]

Maintainer Stephanie Hicks <shicks19@jhu.edu>

R topics documented:

bodymapRat	2
Index	3

bodymapRat

Experimental dataset from the rat BodyMap project

Description

This package contains a SummarizedExperiment from the Yu et al. (2013) paper that performed the rat BodyMap across 11 organs and 4 developmental stages. Raw FASTQ files were downloaded and mapped using STAR. FlowSorted.DLPFC.450k data set from Bioconductor. The purpose is to create an example object for the man pages and vignette in this package.

The SummarizedExperiment object was created using the `/inst/scripts/make-data.Rmd` and is downloaded from ExperimentHub

Format

A SummarizedExperiment object with 652 RNA-seq samples (columns).

Examples

```
library(ExperimentHub)
bm_rat <- bodymapRat()
dim(bm_rat)
```

Index

bodymapRat, 2