Package 'pasilla'

October 16, 2021

Title Data package with per-exon and per-gene read counts of RNA-seq
samples of Pasilla knock-down by Brooks et al., Genome Research
2011.

Version 1.20.0

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Description This package provides per-exon and per-gene read counts
computed for selected genes from RNA-seq data that were presented in
the article ``Conservation of an RNA regulatory map between Drosophila
and mammals'' by Brooks AN, Yang L, Duff MO, Hansen KD, Park JW, Dudoit
S, Brenner SE, Graveley BR, Genome Res. 2011 Feb;21(2):193-202, Epub
2010 Oct 4, PMID: 20921232. The experiment studied the effect of RNAi
knockdown of Pasilla, the Drosophila melanogaster ortholog of
mammalian NOVA1 and NOVA2, on the transcriptome. The package vignette
describes how the data provided here were derived from the RNA-Seq
read sequence data that are provided by NCBI Gene Expression Omnibus
under accession numbers GSM461176 to GSM461181.

biocViews ExperimentData, Genome, Drosophila_melanogaster_Data,
RNASeqData

License LGPL

Suggests DEXSeq, rmarkdown, BiocStyle, knitr

Depends R (>= 3.3.0)

VignetteBuilder knitr

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

git_branch RELEASE_3_13

git_last_commit db2121e

git_last_commit_date 2021-05-19

Date/Publication 2021-10-16

R topics documented:

pasillaDEXSeqDataSet	*Read counts per exon, or per gene, from RNA-seq samples*

Description

pasillaDEXSeqDataSet is a DEXSeqDataSet object with exon counts.

Usage

```
data("pasillaDEXSeqDataSet")
```

Format

DEXSeqDataSet

Source

Processed data from NCBI Gene Expression Omnibus under accession numbers GSM461176 to GSM461181.

References

Brooks et al. Conservation of an RNA regulatory map between Drosophila and mammals. Genome Research, 2010

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