

Package ‘pasilla’

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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 1.25.0

Author Wolfgang Huber, Alejandro Reyes

Maintainer Alejandro Reyes <alejandro.reyes.ds@gmail.com>

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 rmarkdown, BiocStyle, knitr

Depends R (>= 3.5.0), DEXSeq

VignetteBuilder knitr

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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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