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 0.2.16

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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 is provided by NCBI Gene Expression Omnibus under accession numbers GSM461176 to GSM461181

biocViews ExperimentData, RNAseqData

License LGPL

Depends DEXSeq, DESeq

Suggests locfit, edgeR, xtable

R topics documented:

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

Description

`pasillaExons` is an `ExonCountSet` object containing exon counts for each of the samples from Brooks et al.'s RNA-seq data. `pasillaGenes` is an `CountDataSet` object with gene level counts.

Usage

```
data("pasillaExons")
data("pasillaGenes")
```

Format

ExonCountSet, CountDataSet

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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