

# 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** 1.6.0

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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

**NeedsCompilation** no

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pasillaExons

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

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### **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. dxd is a DEXSeqDataSet object with exon counts, the ExonCountSet has been deprecated and substituted by the object DEXSeqDataSet the object.

### **Usage**

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

### **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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