pasilla

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`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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