

# Package ‘pasillaBamSubset’

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**Title** Subset of BAM files from ‘‘Pasilla’’ experiment

**Description** Subset of BAM files untreated1.bam (single-end reads) and untreated3.bam (paired-end reads) from ‘‘Pasilla’’ experiment (Pasilla knock-down by Brooks et al., Genome Research 2011). See the vignette in the pasilla data package for how BAM files untreated1.bam and untreated3.bam were obtained from the RNA-Seq read sequence data that is provided by NCBI Gene Expression Omnibus under accession numbers GSM461176 to GSM461181. Also contains the DNA sequence for fly chromosome 4 to which the reads can be mapped.

**Version** 0.8.0

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**biocViews** ExperimentData, Genome, DNASEqData, RNASeqData

**Suggests** pasilla

**License** LGPL

**NeedsCompilation** no

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pasillaBamSubset-package

*Utilities returning the paths to BAM files untreated1\_chr4.bam and untreated3\_chr4.bam*

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**Description**

BAM file untreated1\_chr4.bam contains the subset of untreated1.bam (single-end reads, "Pasilla" experiment) where only alignments located on chr4 (Fly) were kept.

BAM file untreated3\_chr4.bam contains the subset of untreated3.bam (paired-end reads, "Pasilla" experiment) where only alignments located on chr4 (Fly) were kept.

FASTA file dm3\_chr4.fa contains the full sequence of the *D. melanogaster* chromosome 4.

untreated1\_chr4, untreated3\_chr4 and chr4 return the path to those files.

**Usage**

```
untreated1_chr4()  
untreated3_chr4()  
dm3_chr4()
```

**Details**

See the pasilla data package for details about the "Pasilla" experiment (RNA-seq, Fly).

BAM files untreated1.bam and untreated3.bam contain single-end and paired-end reads aligned to reference genome *BDGP Release 5* (aka the *dm3* genome on the UCSC Genome Browser).

Fasta file dm3\_chr4.fa from UCSC, the Apr. 2006 assembly of the *D. melanogaster* genome (dm3, BDGP Release 5): DNA sequence for fly chromosome 4.

**Examples**

```
untreated1_chr4()  
untreated3_chr4()  
dm3_chr4()
```

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