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.

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Suggests pasilla

License LGPL

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Contents

`pasillaBamSubset-package` *Utilities returning the paths to BAM files untreated1_chr4.bam and untreated3_chr4.bam*

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()
```

Index