pasillaBamSubset

March 23, 2012

`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.

`untreated1_chr4` and `untreated3_chr4` return the path to those files.

Usage

```
untreated1_chr4()
untreated3_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).

Examples

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

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