

Package ‘pasillaBamSubset’

November 28, 2023

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 0.40.0

Encoding UTF-8

Author Hervé Pagès

Maintainer Hervé Pagès <hpages.on.github@gmail.com>

biocViews ExperimentData, Genome, DNASEqData, RNASeqData

Suggests pasilla

License LGPL

git_url <https://git.bioconductor.org/packages/pasillaBamSubset>

git_branch RELEASE_3_18

git_last_commit 7254146

git_last_commit_date 2023-10-24

Repository Bioconductor 3.18

Date/Publication 2023-11-28

R topics documented:

pasillaBamSubset-package 2

Index 3

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

* **utilities**

pasillaBamSubset-package, [2](#)

dm3_chr4 (pasillaBamSubset-package), [2](#)

pasillaBamSubset
(pasillaBamSubset-package), [2](#)
pasillaBamSubset-package, [2](#)

untreated1_chr4
(pasillaBamSubset-package), [2](#)

untreated3_chr4
(pasillaBamSubset-package), [2](#)