

Package ‘breakpointRdata’

November 26, 2024

Type Package

Title Strand-seq data for demonstration purposes

Version 1.25.0

Date 2016-08

Author David Porubsky, Aaron Taudt, Ashley Sanders

Maintainer David Porubsky <david.porubsky@gmail.com>

Description Strand-seq data to demonstrate functionalities of breakpointR package.

Depends R (>= 3.5)

Suggests knitr, BiocStyle,

License file LICENSE

VignetteBuilder knitr

biocViews ExperimentData, Homo_sapiens_Data, SequencingData, DNaseqData, Genome, SingleCellData

NeedsCompilation no

URL <https://github.com/daewoooo/breakpointRdata>

RoxygenNote 6.1.0

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

git_branch devel

git_last_commit ff6412b

git_last_commit_date 2024-10-29

Repository Bioconductor 3.21

Date/Publication 2024-11-26

Contents

example_bams	2
example_results	2

Index	4
--------------	----------

example_bams

Example BAM-files

Description

A set of BAM-files for demonstration purposes of the functions in package **breakpointR**.

Format

A BAM files with aligned reads with one read per line.

Details

BAM files contain single-end reads aligned to GRCh38 reference genome.
Read sequences and quality values have been removed in order to reduce the file size.

Source

A lymphoblastoid cell line of Puerto Rican origin (HG00731). Raw reads were aligned to the GRCh38/hg38 reference assembly. The file has been downsampled to 20% of the coverage to reduce the file size.

References

<https://www.biorxiv.org/content/early/2017/09/23/193144>

example_results

Results for example BAM-files

Description

Localized breakpoints in example BAM-files, generated by the **breakpointR** package.

Format

Files containing BreakPoint object.

Details

A BreakPoint object is a list containing given elements: ID, fragments, deltas, breaks, confint, counts, lib.metrics and params.

- ID - unique identifier for a given library.
- fragments - A GRanges-class object that stores analyzed sequencing reads.
- deltas - A GRanges-class object that stores binned minus reads differences.

- `breaks` - A `GRanges`-class object that stores localized breaks.
- `confint` - A `GRanges`-class object that stores confidence intervals around localized breaks.
- `counts` - A `GRanges`-class object that stores directional read counts in between localized breaks.
- `lib.metrics` - A named vector with some useful library metrics.
- `params` - A named vector with user defined parameters used to run **breakpointR** package.

Source

A lymphoblastoid cell line of Puerto Rican origin (HG00731). Raw reads were aligned to the GRCh38/hg38 reference assembly.

References

<https://www.biorxiv.org/content/early/2017/09/23/193144>

Index

bams (example_bams), [2](#)

example_bams, [2](#)

example_results, [2](#)

results (example_results), [2](#)