Package ‘breakpointRdata’

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Type Package

Title Strand-seq data for demonstration purposes

Version 1.25.0

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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

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Repository Bioconductor 3.21

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Contents

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

References

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