

# Package ‘breakpointRdata’

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**Type** Package

**Title** Strand-seq data for demonstration purposes

**Version** 1.31.0

**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

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**Repository** Bioconductor 3.24

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example_bams	<i>Example BAM-files</i>
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**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>

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example_results	<i>Results for example BAM-files</i>
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**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>

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