

# 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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example\_bams

*Example BAM-files*

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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

*Results for example BAM-files*

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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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