

# Package ‘RnBeads.hg19’

August 8, 2024

**Title** RnBeads.hg19

**Description** Automatically generated RnBeads annotation package for the assembly hg19.

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**License** GPL-3

**Version** 1.37.0

**Depends** R (>= 3.0.0), GenomicRanges

**Suggests** RnBeads

**NeedsCompilation** no

**RoxygenNote** 6.0.1

**git\_url** <https://git.bioconductor.org/packages/RnBeads.hg19>

**git\_branch** devel

**git\_last\_commit** 5b0fba7

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hg19

*HG19 - Annotation tables***Description**

Scaffold of annotation tables for HG19. This structure is automatically loaded upon initialization of the annotation, that is, by the first valid call to any of the following functions: `rnb.get.assemblies`, `rnb.get.chromosomes`, `rnb.get.annotation`, `rnb.set.annotation`, `rnb.get.mapping`, `rnb.annotation.size`. Adding an annotation amounts to attaching its table(s) and mapping structures to this scaffold.

**Format**

list of four elements - "regions", "sites", "controls" and "mappings". These elements are described below.

"regions" list of NULLs; the names of the elements correspond to the built-in region annotation tables. Once the default annotations are loaded, the attribute "builtin" is a logical vector storing, for each region annotation, whether it is the default (built-in) or custom.

"sites" list of NULLs; the names of the elements correspond to the site and probe annotation tables.

"controls" list of NULLs; the names of the elements correspond to the control probe annotation tables. The attribute "sites" is a character vector pointing to the site annotation that encompasses the respective control probes.

"mappings" list of NULLs; the names of the elements correspond to the built-in region annotation tables.

**Author(s)**

Yassen Assenov

regions

*Names of the regions***Description**

This a a list of all regions available for the annotation.

**Usage**

regions

**Format**

list of NULLs; the names of the elements correspond to the built-in region annotation tables. Once the default annotations are loaded, the attribute "builtin" is a logical vector storing, for each region annotation, whether it is the default (built-in) or custom.

**Author(s)**

Michael Scherer

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rnb.set.example	<i>Example Data Set</i>
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**Description**

A small example dataset for testing RnBeads' basic functionality.

**Usage**

```
data(small.example.object)
```

**Format**

`RnBeadRawSet`-class object with 12 samples and 1,736 sites. It is an example object obtained from Illumina Infinium 450K BeadChip and contains coverage, intensity, and detection p-values. No preprocessing steps have been performed.

**Author(s)**

Michael Scherer

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sites	<i>Names of the sites</i>
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**Description**

This a a list of all sites available for the annotation.

**Usage**

```
sites
```

**Format**

list of NULLs; the names of the elements correspond to the site and probe annotation tables.

**Author(s)**

Michael Scherer

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