

# Package ‘RnBeads.hg19’

January 28, 2025

**Title** RnBeads.hg19

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

**Author** RnBeadsAnnotationCreator

**Maintainer** RnBeadsAnnotationCreator <rnbears@mpi-inf.mpg.de>

**Date** 2021-11-21

**License** GPL-3

**Version** 1.38.0

**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** RELEASE\_3\_20

**git\_last\_commit** dd160fa

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.20

**Date/Publication** 2025-01-28

## Contents

hg19 . . . . .	2
regions . . . . .	2
rnb.set.example . . . . .	3
sites . . . . .	3
<b>Index</b>	<b>4</b>

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 is 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

---

rnb.set.example	<i>Example Data Set</i>
-----------------	-------------------------

---

**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

---

sites	<i>Names of the sites</i>
-------	---------------------------

---

**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

# Index

## \* datasets

hg19, [2](#)

regions, [2](#)

rnb.set.example, [3](#)

sites, [3](#)

hg19, [2](#)

regions, [2](#)

rnb.annotation.size, [2](#)

rnb.get.annotation, [2](#)

rnb.get.assemblies, [2](#)

rnb.get.chromosomes, [2](#)

rnb.get.mapping, [2](#)

rnb.set.annotation, [2](#)

rnb.set.example, [3](#)

sites, [3](#)