

Package ‘RnBeads.hg19’

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Title RnBeads.hg19

Description Automatically generated RnBeads annotation package for the assembly hg19.

Author RnBeadsAnnotationCreator

Maintainer RnBeadsAnnotationCreator <rnbeads@mpi-inf.mpg.de>

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License GPL-3

Version 1.42.0

Depends R (>= 3.0.0), GenomicRanges

Suggests RnBeads

NeedsCompilation no

RoxygenNote 6.0.1

git_url <https://git.bioconductor.org/packages/RnBeads.hg19>

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hg19	<i>HG19 - Annotation tables</i>
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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	<i>Names of the regions</i>
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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

`rnb.set.example`*Example Data Set*

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`*Names of the sites*

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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