

# Package ‘seqCNA.annot’

October 16, 2021

**Type** Package

**Title** Annotation for the copy number analysis of deep sequencing cancer data with seqCNA

**Version** 1.28.0

**Date** 2013-03-27

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**Import**

**Depends** R (>= 2.10)

**Description**

Provides annotation on GC content, mappability and genomic features for various genomes

**License** GPL-3

**biocViews** Genome, CopyNumberVariationData

**git\_url** <https://git.bioconductor.org/packages/seqCNA.annot>

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seqCNA.annot-package *Annotation for the copy number analysis of deep sequencing cancer data with seqCNA*

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### Description

Provides annotation on GC content, mappability and genomic features for various genomes

### Details

Package: seqCNA.annot  
Type: Package  
Version: 0.99.0  
Date: 2013-03-27  
License: GPL-3

### Author(s)

David Mosen-Ansorena

Maintainer: David Mosen-Ansorena <dmosen.gn@cicbiogune.es>

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hg18 *A table with GC content, mappability and presence of common CNVs for the hg18 human genome build.*

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### Description

GC content can be used for read count correction, while mappability and CNV information can be used for window filtering.

### Usage

```
data(hg18)
```

### Format

A data frame with 2881044 observations on the following 3 variables.

GC A numeric vector with the proportion of G and C bases per 1000bp window over the total of non-N bases.

Mapp A numeric vector with the mean mappability of 35-mers within each 1000bp window.

CNV A numeric vector with the proportion of each window affected by the presence of a common CNV (frequency > 0.01).

**References**

Integrating common and rare genetic variation in diverse human populations. Altshuler DM, Gibbs RA, Brooks LD, McEwen JE. Nature. 2010 Sep 2; 467:52-8

**Examples**

```
data(hg18)
```

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hg18_len	<i>A table with information on chromosome lengths for the hg18 human genome build.</i>
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**Description**

The table is used to create genomic windows for the whole chromosome lengths.

**Usage**

```
data(hg18_len)
```

**Format**

A data frame with 24 observations on the following 2 variables.

chr A factor with levels 1 10 11 12 13 14 15 16 17 18 19 2 20 21 22 3 4 5 6 7 8 9 X Y.

length A numeric vector.

**Examples**

```
data(hg18_len)
```

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hg19	<i>A table with GC content, mappability and presence of common CNVs for the hg19 human genome build.</i>
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**Description**

GC content can be used for read count correction, while mappability and CNV information can be used for window filtering.

**Usage**

```
data(hg19)
```

**Format**

A data frame with 2881044 observations on the following 3 variables.

GC A numeric vector with the proportion of G and C bases per 1000bp window over the total of non-N bases.

Mapp A numeric vector with the mean mappability of 35-mers within each 1000bp window.

CNV A numeric vector with the proportion of each window affected by the presence of a common CNV (frequency > 0.01).

**References**

Integrating common and rare genetic variation in diverse human populations. Altshuler DM, Gibbs RA, Brooks LD, McEwen JE. Nature. 2010 Sep 2; 467:52-8

**Examples**

```
data(hg19)
```

---

hg19_len	<i>A table with information on chromosome lengths for the hg19 human genome build.</i>
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---

**Description**

The table is used to create genomic windows for the whole chromosome lengths.

**Usage**

```
data(hg19_len)
```

**Format**

A data frame with 24 observations on the following 2 variables.

chr A factor with levels 1 10 11 12 13 14 15 16 17 18 19 2 20 21 22 3 4 5 6 7 8 9 X Y.

length A numeric vector.

**Examples**

```
data(hg19_len)
```

---

supported.builds	<i>Names of the genome builds for which the package contains annotation.</i>
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**Description**

A vector with the names of the genome builds with annotation in the package.

**Usage**

```
supported.builds()
```

**Value**

A vector with the names of the genome builds with annotation in the package.

**Author(s)**

David Mosen-Ansorena

**Examples**

```
supported.builds()
```

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