

Package ‘seqCNA.annot’

October 18, 2017

Type Package

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

Version 1.12.0

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

NeedsCompilation no

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

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)

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hg18

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

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)
```

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)
```

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>
----------	--

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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