Package ‘seqCNA.annot’

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Type Package

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

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Import

Depends R (>= 2.10)

Description

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

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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
Author(s)

David Mosen-Ansorena

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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


Examples

data(hg18)
**hg18_len**

A table with information on chromosome lengths for the hg18 human genome build.

**Description**

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

**Usage**

```r
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**

```r
data(hg18_len)
```

---

**hg19**

A table with GC content, mappability and presence of common CNVs for the hg19 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**

```r
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**

supported.builds

Examples

data(hg19)

---

hg19.len

A table with information on chromosome lengths for the hg19 human genome build.

---

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

Names of the genome builds for which the package contains annotation.

---

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

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