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
License GPL-3
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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)

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**

**Examples**

```r
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**

```r
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**

```r
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**

```r
supported.builds()
```

**Value**

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

**Author(s)**

David Mosen-Ansorena

**Examples**

```r
supported.builds()
```
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