Package 'seqCNA.annot'

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Type Package

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

Version 1.32.0

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Author David Mosen-Ansorena

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

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

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

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` *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

```
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` *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

```
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)
```

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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

```
supported.builds()
```

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