Package ‘facopy.annot’

March 23, 2017

Type Package

Title Annotation for the copy number alteration association and enrichment analyses with facopy

Version 0.108.0

Date 2014-08-27

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Import

Depends R (&gt;= 2.10)

Description Provides facopy with genome annotation on chromosome arms, genomic features and copy number alterations.

License GPL-3

biocViews Genome

NeedsCompilation no

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Description

Provides facopy with genome annotation on chromosome arms, genomic features and copy number alterations.

Details

Package: facopy.annot
Type: Package
Version: 0.99.0
Date: 2014-08-27
License: GPL-3

Author(s)

David Mosen-Ansorena

Description

Modification of the biocarta object in graphite package, in order to list gene symbols instead of the native identifiers.

Source

graphite R package.

References

**facopy_kegg**

**Kegg Pathways with symbol identifiers**

**Description**
Modification of the Kegg object in graphite package, in order to list gene symbols instead of the native identifiers.

**Source**
graphite R package.

**References**

**facopy_msigdb**

**facopy MSigDB Data**

**Description**
Contains gene sets, classified into collections.

**Source**
MSigDB

**References**

**facopy_msigdbNames**

**facopy MSigDB Data Names**

**Description**
Contains the names of gene sets, classified into collections.

**Source**
MSigDB

**References**
Description

Modification of the reactome object in graphite package, in order to list gene symbols instead of the native identifiers.

Source

graphite R package.

References


Description

Chromosome arm upper limits (in base pairs) for the hg18 genome build.

Usage

data(hg18_armLimits)

Format

A data frame with 48 observations on the following 2 variables.

chr_q_arm  A factor with levels 1p 1q 2p 2q 3p 3q 4p 4q 5p 5q 6p 6q 7p 7q 8p 8q 9p 9q 10p 10q 11p 11q 12p 12q 13p 13q 14p 14q 15p 15q 16p 16q 17p 17q 18p 18q 19p 19q 20p 20q 21p 21q 22p 22q Xp Xq Yp Yq
limit  A numeric vector

Examples

data(hg18_armLimits)
Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg18_db_gsk_bladder)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr**: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st**: A numeric vector
- **pos_en**: A numeric vector
- **type**: A factor that comprises levels `amp` or `del` or just one of them
- **freq**: A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg18_db_gsk_bladder)

data(hg18_db_gsk_blood)
Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st  A numeric vector
pos_en  A numeric vector
type  A factor that comprises levels amp del or just one of them
freq  A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg18_db_gsk_blood)

Description

Copy number alteration frequencies for the corresponding genome build, database and dataset.
Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg18_db_gsk_bone)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st  A numeric vector
pos_en  A numeric vector
type  A factor that comprises levels amp del or just one of them
freq  A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.
**References**


**Examples**

```r
data(hg18_db_gsk_bone)
```

---

**Description**

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: `[genome][build]_db_[database]_[dataset]`.

**Usage**

```r
data(hg18_db_gsk_brain)
```

**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr**: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st**: A numeric vector
- **pos_en**: A numeric vector
- **type**: A factor that comprises levels `amp del` or just one of them
- **freq**: A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

**References**


**Examples**

```r
data(hg18_db_gsk_brain)
```
Description

Copy number alteration frequencies for the corresponding genome build, database and dataset.
Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg18_db_gsk_breast)

table(hg18_db_gsk_cervix)

data(hg18_db_gsk_breast)

data(hg18_db_gsk_cervix)

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another
 genome build.

References

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome Work-

Examples

data(hg18_db_gsk_breast)
Format
A data frame with amplification and/or deletion frequencies for different genomic regions.

chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st A numeric vector
pos_en A numeric vector
type A factor that comprises levels amp del or just one of them
freq A numeric vector

Source
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References

Examples
data(hg18_db_gsk_cervix)

Description
Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage
data(hg18_db_gsk_cns)

Format
A data frame with amplification and/or deletion frequencies for different genomic regions.

chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st A numeric vector
pos_en A numeric vector
type A factor that comprises levels amp del or just one of them
freq A numeric vector

Source
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.
**References**


**Examples**

```r
data(hg18_db_gsk_cns)
```

---

**Description**

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

**Usage**

```r
data(hg18_db_gsk_colon)
```

**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr**: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st**: A numeric vector
- **pos_en**: A numeric vector
- **type**: A factor that comprises levels amp del or just one of them
- **freq**: A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

**References**


**Examples**

```r
data(hg18_db_gsk_colon)
```
**Description**

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

**Usage**

```r
data(hg18_db_gsk_connective_tissue)
```

**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- `chr` A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- `pos_st` A numeric vector
- `pos_en` A numeric vector
- `type` A factor that comprises levels `amp` `del` or just one of them
- `freq` A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

**References**


**Examples**

```r
data(hg18_db_gsk_connective_tissue)
```

---

**Description**

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

**Usage**

```r
data(hg18_db_gsk_esophagus)
```
**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr** A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st** A numeric vector
- **pos_en** A numeric vector
- **type** A factor that comprises levels amp del or just one of them
- **freq** A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

**References**


**Examples**

data(hg18_db_gsk_esophagus)

---

**Description**

Copy number alteration frequencies for the corresponding genome build, database and dataset.

Naming format: [genome][build]_db_[database]_[dataset].

**Usage**

data(hg18_db_gsk_eye)

**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr** A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st** A numeric vector
- **pos_en** A numeric vector
- **type** A factor that comprises levels amp del or just one of them
- **freq** A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.
References


Examples

data(hg18_db_gsk_eye)

data(hg18_db_gsk_kidney)

Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg18_db_gsk_kidney)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st A numeric vector
pos_en A numeric vector
type  A factor that comprises levels amp de1 or just one of them
freq  A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg18_db_gsk_kidney)
Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg18_db_gsk_liver)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

chr A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st A numeric vector
pos_en A numeric vector
type A factor that comprises levels amp del or just one of them
freq A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg18_db_gsk_liver)
Format
A data frame with amplification and/or deletion frequencies for different genomic regions.

chr A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st A numeric vector
pos_en A numeric vector
type A factor that comprises levels amp del or just one of them
freq A numeric vector

Source
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References

Examples

data(hg18_db_gsk_lung)

Description
Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage
data(hg18_db_gsk_muscle)

Format
A data frame with amplification and/or deletion frequencies for different genomic regions.

chr A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st A numeric vector
pos_en A numeric vector
type A factor that comprises levels amp del or just one of them
freq A numeric vector

Source
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.
**References**


**Examples**

data(hg18_db_gsk_muscle)

data(hg18_db_gsk_ovary)

**Description**

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

**Usage**

data(hg18_db_gsk_ovary)

**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr**: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st**: A numeric vector
- **pos_en**: A numeric vector
- **type**: A factor that comprises levels amp del or just one of them
- **freq**: A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

**References**


**Examples**

data(hg18_db_gsk_ovary)
**Description**

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

**Usage**

data(hg18_db_gsk_pancreas)

**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr** A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st** A numeric vector
- **pos_en** A numeric vector
- **type** A factor that comprises levels amp del or just one of them
- **freq** A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

**References**


**Examples**

data(hg18_db_gsk_pancreas)

---

**Description**

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

**Usage**

data(hg18_db_gsk_pharynx)
**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr**: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st**: A numeric vector
- **pos_en**: A numeric vector
- **type**: A factor that comprises levels amp del or just one of them
- **freq**: A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

**References**


**Examples**

```r
data(hg18_db_gsk_pharynx)
```

---

**Description**

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_dataset.

**Usage**

```r
data(hg18_db_gsk_placenta)
```

**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr**: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st**: A numeric vector
- **pos_en**: A numeric vector
- **type**: A factor that comprises levels amp del or just one of them
- **freq**: A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.
References


Examples

data(hg18_db_gsk_placenta)

---

Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg18_db_gsk_prostate)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr**: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st**: A numeric vector
- **pos_en**: A numeric vector
- **type**: A factor that comprises levels amp de1 or just one of them
- **freq**: A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg18_db_gsk_prostate)
Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg18_db_gsk_rectum)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

- chr: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- pos_st: A numeric vector
- pos_en: A numeric vector
- type: A factor that comprises levels amp or del or just one of them
- freq: A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg18_db_gsk_rectum)
**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr**: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st**: A numeric vector
- **pos_en**: A numeric vector
- **type**: A factor that comprises levels amp del or just one of them
- **freq**: A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

**References**


**Examples**

```r
data(hg18_db_gsk_sarcoma)
```

```r
data(hg18_db_gsk_stomach)
```

**Description**

Copy number alteration frequencies for the corresponding genome build, database and dataset.

Naming format: [genome][build]_db_[database]_[dataset].

**Usage**

```r
data(hg18_db_gsk_stomach)
```

**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr**: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st**: A numeric vector
- **pos_en**: A numeric vector
- **type**: A factor that comprises levels amp del or just one of them
- **freq**: A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.
References


Examples

data(hg18_db_gsk_stomach)

data(hg18_db_gsk_synovium)

Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg18_db_gsk_synovium)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

- `chr` A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- `pos_st` A numeric vector
- `pos_en` A numeric vector
- `type` A factor that comprises levels amp del or just one of them
- `freq` A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg18_db_gsk_synovium)
Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg18_db_gsk_thyroid)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

<table>
<thead>
<tr>
<th>chr</th>
<th>A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X</th>
</tr>
</thead>
<tbody>
<tr>
<td>pos_st</td>
<td>A numeric vector</td>
</tr>
<tr>
<td>pos_en</td>
<td>A numeric vector</td>
</tr>
<tr>
<td>type</td>
<td>A factor that comprises levels amp del or just one of them</td>
</tr>
<tr>
<td>freq</td>
<td>A numeric vector</td>
</tr>
</tbody>
</table>

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg18_db_gsk_thyroid)
Format
A data frame with amplification and/or deletion frequencies for different genomic regions.

chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st  A numeric vector
pos_en  A numeric vector
type  A factor that comprises levels amp del or just one of them
freq  A numeric vector

Source
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References

Examples
data(hg18_db_gsk_uterus)

Description
Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage
data(hg18_db_nci60)

Format
A data frame with amplification and/or deletion frequencies for different genomic regions.

chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st  A numeric vector
pos_en  A numeric vector
type  A factor that comprises levels amp del or just one of them
freq  A numeric vector

Source
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.
hg18_db_tcga_blca

References


Examples

data(hg18_db_nci60)

Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg18_db_tcga_blca)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr**: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st**: A numeric vector
- **pos_en**: A numeric vector
- **type**: A factor that comprises levels amp del or just one of them
- **freq**: A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg18_db_tcga_blca)
Description
Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage
data(hg18_db_tcga_brca)

Format
A data frame with amplification and/or deletion frequencies for different genomic regions.

chr A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st A numeric vector
pos_en A numeric vector
type A factor that comprises levels amp del or just one of them
freq A numeric vector

Source
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References

Examples
data(hg18_db_tcga_brca)
Format
A data frame with amplification and/or deletion frequencies for different genomic regions.
chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st  A numeric vector
pos_en  A numeric vector
type  A factor that comprises levels amp del or just one of them
freq  A numeric vector

Source
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References

Examples
data(hg18_db_tcga_cesc)

Description
Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage
data(hg18_db_tcga_coad)

Format
A data frame with amplification and/or deletion frequencies for different genomic regions.
chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st  A numeric vector
pos_en  A numeric vector
type  A factor that comprises levels amp del or just one of them
freq  A numeric vector

Source
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.
References


Examples

data(hg18_db_tcga_coad)

---

Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg18_db_tcga_gbm)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

```r
chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st A numeric vector
pos_en A numeric vector
type  A factor that comprises levels amp del or just one of them
freq  A numeric vector
```

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg18_db_tcga_gbm)
### Description
Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

### Usage
```
data(hg18_db_tcga_hnsc)
```

### Format
A data frame with amplification and/or deletion frequencies for different genomic regions.

- `chr` A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- `pos_st` A numeric vector
- `pos_en` A numeric vector
- `type` A factor that comprises levels amp del or just one of them
- `freq` A numeric vector

### Source
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

### References

### Examples
```
data(hg18_db_tcga_hnsc)
```

---

### Description
Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

### Usage
```
data(hg18_db_tcga_kirc)
```
Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

chr A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st A numeric vector
pos_en A numeric vector
type A factor that comprises levels amp del or just one of them
freq A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg18_db_tcga_kirc)

data(hg18_db_tcga_kirc)

data(hg18_db_tcga_kirc)

Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg18_db_tcga_kirc)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

chr A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st A numeric vector
pos_en A numeric vector
type A factor that comprises levels amp del or just one of them
freq A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.
**References**


**Examples**

data(hg18_db_tcga_kirp)

data(hg18_db_tcga_lgg)

**Description**

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

**Usage**

data(hg18_db_tcga_lgg)

**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr**: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st**: A numeric vector
- **pos_en**: A numeric vector
- **type**: A factor that comprises levels amp del or just one of them
- **freq**: A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

**References**


**Examples**

data(hg18_db_tcga_lgg)
Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: \([\text{genome}]_[\text{build}]_\text{db}_\text{[database]}_\text{[dataset]}\).

Usage

data(hg18_db_tcga_lihc)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr**: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st**: A numeric vector
- **pos_en**: A numeric vector
- **type**: A factor that comprises levels amp del or just one of them
- **freq**: A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg18_db_tcga_lihc)
Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st  A numeric vector
pos_en  A numeric vector
type  A factor that comprises levels amp or del or just one of them
freq  A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg18_db_tcga_luad)

Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg18_db_tcga_lusc)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st  A numeric vector
pos_en  A numeric vector
type  A factor that comprises levels amp or del or just one of them
freq  A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.
References


Examples

data(hg18_db_tcga_lusc)

Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg18_db_tcga_ov)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

<table>
<thead>
<tr>
<th>chr</th>
<th>pos_st</th>
<th>pos_en</th>
<th>type</th>
<th>freq</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg18_db_tcga_ov)
Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg18_db_tcga_prad)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st  A numeric vector
pos_en  A numeric vector
type  A factor that comprises levels amp del or just one of them
freq  A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg18_db_tcga_prad)
**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- `chr`: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- `pos_st`: A numeric vector
- `pos_en`: A numeric vector
- `type`: A factor that comprises levels amp del or just one of them
- `freq`: A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

**References**


**Examples**

```r
data(hg18_db_tcga_read)
```

---

**Description**

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

**Usage**

```r
data(hg18_db_tcga_stad)
```

**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- `chr`: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- `pos_st`: A numeric vector
- `pos_en`: A numeric vector
- `type`: A factor that comprises levels amp del or just one of them
- `freq`: A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.
References


Examples

data(hg18_db_tcga_stad)

Description

Copy number alteration frequencies for the corresponding genome build, database and dataset.

Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg18_db_tcga_thca)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

<table>
<thead>
<tr>
<th>chr</th>
<th>A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X</th>
</tr>
</thead>
<tbody>
<tr>
<td>pos_st</td>
<td>A numeric vector</td>
</tr>
<tr>
<td>pos_en</td>
<td>A numeric vector</td>
</tr>
<tr>
<td>type</td>
<td>A factor that comprises levels amp del or just one of them</td>
</tr>
<tr>
<td>freq</td>
<td>A numeric vector</td>
</tr>
</tbody>
</table>

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg18_db_tcga_thca)
**Description**
Copy number alteration frequencies for the corresponding genome build, database and dataset.
Naming format: [genome][build] db_[database] [dataset].

**Usage**
data(hg18_db_tcga_ucec)

**Format**
A data frame with amplification and/or deletion frequencies for different genomic regions.

<table>
<thead>
<tr>
<th>chr</th>
<th>A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X</th>
</tr>
</thead>
<tbody>
<tr>
<td>pos_st</td>
<td>A numeric vector</td>
</tr>
<tr>
<td>pos_en</td>
<td>A numeric vector</td>
</tr>
<tr>
<td>type</td>
<td>A factor that comprises levels amp del or just one of them</td>
</tr>
<tr>
<td>freq</td>
<td>A numeric vector</td>
</tr>
</tbody>
</table>

**Source**
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

**References**

**Examples**
data(hg18_db_tcga_ucec)
**Format**

A data frame with positional information on a set of genomic features.

- **chr**  Chromosome harboring the genomic feature.
- **bp_st** Starting genomic position of the feature within the chromosome.
- **bp_en** Ending genomic position of the feature within the chromosome.
- **feature** Name of the genomic feature.
- **chr_q_arm** Chromosome arm in which the genomic feature lies.

**Source**

Collections **ensembl, mirna:**
- Extracted from Ensembl through BioMart. In the case of **mirna**, the collection was filter to keep only miRNAs.

Collections **oncogene, tumor suppressor, cancergene, lincRNA:**
- Gathered from CaSNP website’s BED files and reformatted.
- [http://cistrome.dfci.harvard.edu/CaSNP/gscore/](http://cistrome.dfci.harvard.edu/CaSNP/gscore/)

**References**


**Examples**

```r
data(hg18_feature_cancergene)
```

---

**Description**

Position of a collection of genomic features for the corresponding genome build.

Naming format: [genome][build]_feature_[collection].

**Usage**

```r
data(hg18_feature_ensembl)
```
Format

A data frame with positional information on a set of genomic features.

- **chr**: Chromosome harboring the genomic feature.
- **bp_st**: Starting genomic position of the feature within the chromosome.
- **bp_en**: Ending genomic position of the feature within the chromosome.
- **feature**: Name of the genomic feature.
- **chr_q_arm**: Chromosome arm in which the genomic feature lies.

Source

Collections **ensembl**, **mirna**:
- Extracted from Ensembl through BioMart. In the case of **mirna**, the collection was filter to keep only miRNAs.

Collections **oncogene**, **tumorsuppressor**, **cancergene**, **lincRNA**:
- Gathered from CaSNP website’s BED files and reformatted.
- [http://cistrome.dfci.harvard.edu/CaSNP/gscore/](http://cistrome.dfci.harvard.edu/CaSNP/gscore/)

References


Examples

```r
data(hg18_feature_ensembl)
```

```r
g18_feature_lincRNA
```

Description

Position of a collection of genomic features for the corresponding genome build. Naming format: **[genome][build]_feature_[collection]**.

Usage

```r
data(hg18_feature_lincRNA)
```
Format

A data frame with positional information on a set of genomic features.

- **chr**  Chromosome harboring the genomic feature.
- **bp_st** Starting genomic position of the feature within the chromosome.
- **bp_en** Ending genomic position of the feature within the chromosome.
- **feature** Name of the genomic feature.
- **chr_q_arm** Chromosome arm in which the genomic feature lies.

Source

Collections `ensembl`, `mirna`:
- Extracted from Ensembl through BioMart. In the case of `mirna`, the collection was filtered to keep only miRNAs.

Collections `oncogene`, `tumorsuppressor`, `cancergene`, `lincRNA`:
- Gathered from CaSNP website's BED files and re-formatted.
- [http://cistrome.dfci.harvard.edu/CaSNP/gscore/](http://cistrome.dfci.harvard.edu/CaSNP/gscore/)

References


Examples

```r
data(hg18_feature_lincRNA)
```

---

**hg18_feature_mirnas**  **hg18_feature_mirnas**

Description

Position of a collection of genomic features for the corresponding genome build.

Naming format: [genome][build]_feature_[collection].

Usage

```r
data(hg18_feature_mirnas)
```
Format

A data frame with positional information on a set of genomic features.

<table>
<thead>
<tr>
<th>chr</th>
<th>Chromosome harboring the genomic feature.</th>
</tr>
</thead>
<tbody>
<tr>
<td>bp_st</td>
<td>Starting genomic position of the feature within the chromosome.</td>
</tr>
<tr>
<td>bp_en</td>
<td>Ending genomic position of the feature within the chromosome.</td>
</tr>
<tr>
<td>feature</td>
<td>Name of the genomic feature.</td>
</tr>
<tr>
<td>chr_q_arm</td>
<td>Chromosome arm in which the genomic feature lies.</td>
</tr>
</tbody>
</table>

Source

Collections ensembl, mirna:
- Extracted from Ensembl through BioMart. In the case of mirna, the collection was filter to keep only miRNAs.
- http://www.ensembl.org/biomart/martview/

Collections oncogene, tumorsuppressor, cancergene, lincRNA:
- Gathered from CaSNP website’s BED files and reformatted.
- http://cistrome.dfci.harvard.edu/CaSNP/gscore/

References


Examples

data(hg18_feature_mirnas)

Description

Position of a collection of genomic features for the corresponding genome build.
Naming format: [genome][build]_feature_[collection].

Usage

data(hg18_feature_oncogene)
Format

A data frame with positional information on a set of genomic features.

- **chr**: Chromosome harboring the genomic feature.
- **bp_st**: Starting genomic position of the feature within the chromosome.
- **bp_en**: Ending genomic position of the feature within the chromosome.
- **feature**: Name of the genomic feature.
- **chr_q_arm**: Chromosome arm in which the genomic feature lies.

Source

Collections ensembl, mirna:
- Extracted from Ensembl through BioMart. In the case of mirna, the collection was filter to keep only miRNAs.

Collections oncogene, tumorsupressor, cancergene, lincRNA:
- Gathered from CaSNP website’s BED files and reformatted.
- [http://cistrome.dfci.harvard.edu/CaSNP/gscore/](http://cistrome.dfci.harvard.edu/CaSNP/gscore/)

References


Examples

```r
data(hg18_feature_oncogene)
```

Description

Position of a collection of genomic features for the corresponding genome build.

Naming format: [genome][build]_feature_[collection].

Usage

```r
data(hg18_feature_tumorsupressor)
```
Format
A data frame with positional information on a set of genomic features.

chr  Chromosome harboring the genomic feature.
bp_st Starting genomic position of the feature within the chromosome.
bp_en Ending genomic position of the feature within the chromosome.
feature Name of the genomic feature.
chr_q_arm Chromosome arm in which the genomic feature lies.

Source
Collections ensembl, mirna:
- Extracted from Ensembl through BioMart. In the case of mirna, the collection was filter to keep only miRNAs.
- http://www.ensembl.org/biomart/martview/

Collections oncogene, tumorsuppressor, cancergene, lincRNA:
- Gathered from CaSNP website’s BED files and reformatted.
- http://cistrome.dfci.harvard.edu/CaSNP/gscore/

References

Examples

data(hg18_feature_tumorsupressor)

<table>
<thead>
<tr>
<th>chr</th>
<th>bp_st</th>
<th>bp_en</th>
<th>feature</th>
</tr>
</thead>
<tbody>
<tr>
<td>chr1q</td>
<td>100000</td>
<td>100000</td>
<td>gene1</td>
</tr>
<tr>
<td>chr2q</td>
<td>200000</td>
<td>200000</td>
<td>gene2</td>
</tr>
</tbody>
</table>

Description
Chromosome arm upper limits (in base pairs) for the hg19 genome build.

Usage

data(hg19_armLimits)
Format

A data frame with 48 observations on the following 2 variables.

- **chr_q_arm**: A factor with levels 1p 1q 2p 2q 3p 3q 4p 4q 5p 5q 6p 6q 7p 7q 8p 8q 9p 9q 10p 10q 11p 11q 12p 12q 13p 13q 14p 14q 15p 15q 16p 16q 17p 17q 18p 18q 19p 19q 20p 20q 21p 21q 22p 22q Xp Xq Yp Yq
- **limit**: A numeric vector

Examples

```r
data(hg19_armLimits)
```

Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

```r
data(hg19_db_gsk_bladder)
```

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr**: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st**: A numeric vector
- **pos_en**: A numeric vector
- **type**: A factor that comprises levels amp del or just one of them
- **freq**: A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

```r
data(hg19_db_gsk_bladder)
```
Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg19_db_gsk_blood)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr**: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st**: A numeric vector
- **pos_en**: A numeric vector
- **type**: A factor that comprises levels amp del or just one of them
- **freq**: A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg19_db_gsk_blood)
\textbf{Format}

A data frame with amplification and/or deletion frequencies for different genomic regions.

\begin{itemize}
  \item \texttt{chr} A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
  \item \texttt{pos_st} A numeric vector
  \item \texttt{pos_en} A numeric vector
  \item \texttt{type} A factor that comprises levels \texttt{amp del} or just one of them
  \item \texttt{freq} A numeric vector
\end{itemize}

\textbf{Source}

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

\textbf{References}


\textbf{Examples}

\begin{verbatim}
data(hg19_db_gsk_bone)
\end{verbatim}

\begin{verbatim}
  \hline
  \texttt{hg19\_db\_gsk\_brain} & \texttt{hg19\_db\_gsk\_brain} \\
  \hline
\end{verbatim}

\textbf{Description}

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: \texttt{[genome][build]_db_[database]_[dataset]}.

\textbf{Usage}

\begin{verbatim}
data(hg19_db_gsk_brain)
\end{verbatim}

\textbf{Format}

A data frame with amplification and/or deletion frequencies for different genomic regions.

\begin{itemize}
  \item \texttt{chr} A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
  \item \texttt{pos_st} A numeric vector
  \item \texttt{pos_en} A numeric vector
  \item \texttt{type} A factor that comprises levels \texttt{amp del} or just one of them
  \item \texttt{freq} A numeric vector
\end{itemize}

\textbf{Source}

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.
References


Examples

data(hg19_db_gsk_brain)

Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg19_db_gsk_breast)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st A numeric vector
pos_en A numeric vector
type A factor that comprises levels amp del or just one of them
freq A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg19_db_gsk_breast)
Description
Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage
data(hg19_db_gsk_cervix)

Format
A data frame with amplification and/or deletion frequencies for different genomic regions.

- chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- pos_st  A numeric vector
- pos_en  A numeric vector
- type  A factor that comprises levels amp del or just one of them
- freq  A numeric vector

Source
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References

Examples
data(hg19_db_gsk_cervix)
Format
A data frame with amplification and/or deletion frequencies for different genomic regions.

chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st  A numeric vector
pos_en  A numeric vector
type  A factor that comprises levels amp del or just one of them
freq  A numeric vector

Source
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References

Examples
data(hg19_db_gsk_cns)

data(hg19_db_gsk_colon)

Description
Copy number alteration frequencies for the corresponding genome build, database and dataset.
Naming format: [genome][build]_db_[database]_[dataset].

Usage
data(hg19_db_gsk_colon)

Format
A data frame with amplification and/or deletion frequencies for different genomic regions.

chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st  A numeric vector
pos_en  A numeric vector
type  A factor that comprises levels amp del or just one of them
freq  A numeric vector

Source
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.
hg19_db_gsk_connective_tissue

References


Examples

data(hg19_db_gsk_colon)

hg19_db_gsk_connective_tissue

Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg19_db_gsk_connective_tissue)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st  A numeric vector
pos_en  A numeric vector
type  A factor that comprises levels amp del or just one of them
freq  A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg19_db_gsk_connective_tissue)
Description
Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage
\texttt{data(hg19\_db\_gsk\_esophagus)}

Format
A data frame with amplification and/or deletion frequencies for different genomic regions.
\begin{itemize}
  \item \texttt{chr} A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
  \item \texttt{pos\_st} A numeric vector
  \item \texttt{pos\_en} A numeric vector
  \item \texttt{type} A factor that comprises levels \texttt{amp} or \texttt{del} or just one of them
  \item \texttt{freq} A numeric vector
\end{itemize}

Source
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References

Examples
\texttt{data(hg19\_db\_gsk\_esophagus)}
**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr** A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st** A numeric vector
- **pos_en** A numeric vector
- **type** A factor that comprises levels amp del or just one of them
- **freq** A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

**References**


**Examples**

data(hg19_db_gsk_eye)

data(hg19_db_gsk_kidney)

---

**Description**

Copy number alteration frequencies for the corresponding genome build, database and dataset.

Naming format: [genome][build]_db_[database]_[dataset].

**Usage**

data(hg19_db_gsk_kidney)

**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr** A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st** A numeric vector
- **pos_en** A numeric vector
- **type** A factor that comprises levels amp del or just one of them
- **freq** A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.
References


Examples

data(hg19_db_gsk_kidney)

data(hg19_db_gsk_liver)

data(hg19_db_gsk_liver)

Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg19_db_gsk_liver)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr**: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st**: A numeric vector
- **pos_en**: A numeric vector
- **type**: A factor that comprises levels amp del or just one of them
- **freq**: A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg19_db_gsk_liver)
Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg19_db_gsk_lung)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

<table>
<thead>
<tr>
<th>chr</th>
<th>pos_st</th>
<th>pos_en</th>
<th>type</th>
<th>freq</th>
</tr>
</thead>
<tbody>
<tr>
<td>chr</td>
<td>pos_st</td>
<td>pos_en</td>
<td>type</td>
<td>freq</td>
</tr>
</tbody>
</table>

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg19_db_gsk_lung)
Format
A data frame with amplification and/or deletion frequencies for different genomic regions.

chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st  A numeric vector
pos_en  A numeric vector
type  A factor that comprises levels amp del or just one of them
freq  A numeric vector

Source
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References

Examples
data(hg19_db_gsk_muscle)

Description
Copy number alteration frequencies for the corresponding genome build, database and dataset.
Naming format: [genome][build]_db_[database]_[dataset].

Usage
data(hg19_db_gsk_ovary)

Format
A data frame with amplification and/or deletion frequencies for different genomic regions.

chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st  A numeric vector
pos_en  A numeric vector
type  A factor that comprises levels amp del or just one of them
freq  A numeric vector

Source
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.
References


Examples

data(hg19_db_gsk_ovary)

data(hg19_db_gsk_pancreas)

Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg19_db_gsk_pancreas)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st  A numeric vector
pos_en  A numeric vector
type  A factor that comprises levels amp de1 or just one of them
freq  A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg19_db_gsk_pancreas)
Description
Copy number alteration frequencies for the corresponding genome build, database and dataset.
Naming format: [genome][build]_db_[database]_[dataset].

Usage
data(hg19_db_gsk_pharynx)

Format
A data frame with amplification and/or deletion frequencies for different genomic regions.

chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st  A numeric vector
pos_en  A numeric vector
type  A factor that comprises levels amp del or just one of them
freq  A numeric vector

Source
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References

Examples
data(hg19_db_gsk_pharynx)

Description
Copy number alteration frequencies for the corresponding genome build, database and dataset.
Naming format: [genome][build]_db_[database]_[dataset].

Usage
data(hg19_db_gsk_placenta)
**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- chr: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- pos_st: A numeric vector
- pos_en: A numeric vector
- type: A factor that comprises levels amp del or just one of them
- freq: A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

**References**


**Examples**

```r
data(hg19_db_gsk_placenta)
```

---

**Description**

Copy number alteration frequencies for the corresponding genome build, database and dataset.

Naming format: [genome][build]_db_[database]_[dataset].

**Usage**

```r
data(hg19_db_gsk_prostate)
```

**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- chr: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- pos_st: A numeric vector
- pos_en: A numeric vector
- type: A factor that comprises levels amp del or just one of them
- freq: A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.
References


Examples

data(hg19_db_gsk_prostate)

data(hg19_db_gsk_rectum)

Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg19_db_gsk_rectum)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st  A numeric vector
pos_en  A numeric vector
type  A factor that comprises levels amp de1 or just one of them
freq  A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg19_db_gsk_rectum)
Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg19_db_gsk_sarcoma)

data(hg19_db_gsk_stomach)

Examples

data(hg19_db_gsk_sarcoma)

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st  A numeric vector
pos_en  A numeric vector
type  A factor that comprises levels amp del or just one of them
freq  A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg19_db_gsk_stomach)
**hg19_db_gsk_thyroid**

**References**


**Examples**

```r
data(hg19_db_gsk_synovium)
```

<table>
<thead>
<tr>
<th>chr</th>
<th>pos_st</th>
<th>pos_en</th>
<th>type</th>
<th>freq</th>
</tr>
</thead>
<tbody>
<tr>
<td>X</td>
<td>1</td>
<td>2</td>
<td>amp</td>
<td>0.1</td>
</tr>
<tr>
<td>X</td>
<td>3</td>
<td>4</td>
<td>del</td>
<td>0.2</td>
</tr>
</tbody>
</table>

**Description**

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

**Usage**

```r
data(hg19_db_gsk_thyroid)
```

**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr**: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st**: A numeric vector
- **pos_en**: A numeric vector
- **type**: A factor that comprises levels amp, del or just one of them
- **freq**: A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

**References**


**Examples**

```r
data(hg19_db_gsk_thyroid)
```
Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg19_db_gsk_uterus)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

chr  A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st  A numeric vector
pos_en  A numeric vector
type  A factor that comprises levels amp del or just one of them
freq  A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg19_db_gsk_uterus)
**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr** A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st** A numeric vector
- **pos_en** A numeric vector
- **type** A factor that comprises levels amp del or just one of them
- **freq** A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

**References**


**Examples**

data(hg19_db_nci60)

```r
hg19_db_tcga_blca
```

**Description**

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

**Usage**

data(hg19_db_tcga_blca)

**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr** A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st** A numeric vector
- **pos_en** A numeric vector
- **type** A factor that comprises levels amp del or just one of them
- **freq** A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.
References


Examples

data(hg19_db_tcga_blca)

Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg19_db_tcga_brca)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

<table>
<thead>
<tr>
<th>chr</th>
<th>pos_st</th>
<th>pos_en</th>
<th>type</th>
<th>freq</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td></td>
<td></td>
<td>amp</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td></td>
<td></td>
<td>del</td>
<td></td>
</tr>
</tbody>
</table>

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg19_db_tcga_brca)
Description
Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage
data(hg19_db_tcga_cesc)

Format
A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr**: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st**: A numeric vector
- **pos_en**: A numeric vector
- **type**: A factor that comprises levels amp del or just one of them
- **freq**: A numeric vector

Source
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References

Examples
data(hg19_db_tcga_cesc)
Format
A data frame with amplification and/or deletion frequencies for different genomic regions.

<table>
<thead>
<tr>
<th>chr</th>
<th>A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X</th>
</tr>
</thead>
<tbody>
<tr>
<td>pos_st</td>
<td>A numeric vector</td>
</tr>
<tr>
<td>pos_en</td>
<td>A numeric vector</td>
</tr>
<tr>
<td>type</td>
<td>A factor that comprises levels amp del or just one of them</td>
</tr>
<tr>
<td>freq</td>
<td>A numeric vector</td>
</tr>
</tbody>
</table>

Source
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References

Examples
```
data(hg19_db_tcga_coad)
```

Description
Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage
```
data(hg19_db_tcga_gbm)
```

Format
A data frame with amplification and/or deletion frequencies for different genomic regions.

<table>
<thead>
<tr>
<th>chr</th>
<th>A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X</th>
</tr>
</thead>
<tbody>
<tr>
<td>pos_st</td>
<td>A numeric vector</td>
</tr>
<tr>
<td>pos_en</td>
<td>A numeric vector</td>
</tr>
<tr>
<td>type</td>
<td>A factor that comprises levels amp del or just one of them</td>
</tr>
<tr>
<td>freq</td>
<td>A numeric vector</td>
</tr>
</tbody>
</table>

Source
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.
### Reference


### Examples

```r
data(hg19_db_tcga_gbm)
```

### Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

### Usage

```r
data(hg19_db_tcga_hnsc)
```

### Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr**: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st**: A numeric vector
- **pos_en**: A numeric vector
- **type**: A factor that comprises levels amp or del or just one of them
- **freq**: A numeric vector

### Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

### References


### Examples

```r
data(hg19_db_tcga_hnsc)
```
Description
Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage
data(hg19_db_tcga_kirc)

Format
A data frame with amplification and/or deletion frequencies for different genomic regions.

chr A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st A numeric vector
pos_en A numeric vector
type A factor that comprises levels amp del or just one of them
freq A numeric vector

Source
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References

Examples
data(hg19_db_tcga_kirc)
**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr**: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st**: A numeric vector
- **pos_en**: A numeric vector
- **type**: A factor that comprises levels amp del or just one of them
- **freq**: A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

**References**


**Examples**

```r
data(hg19_db_tcga_kirp)
```

---

**Description**

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

**Usage**

```r
data(hg19_db_tcga_lgg)
```

**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr**: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st**: A numeric vector
- **pos_en**: A numeric vector
- **type**: A factor that comprises levels amp del or just one of them
- **freq**: A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.
References


Examples

data(hg19_db_tcga_lgg)

Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg19_db_tcga_lihc)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr**: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st**: A numeric vector
- **pos_en**: A numeric vector
- **type**: A factor that comprises levels amp de1 or just one of them
- **freq**: A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg19_db_tcga_lihc)
**hg19_db_tcga_luad**

**Description**
Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

**Usage**
```
data(hg19_db_tcga_luad)
```

**Format**
A data frame with amplification and/or deletion frequencies for different genomic regions.

<table>
<thead>
<tr>
<th>chr</th>
<th>A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X</th>
</tr>
</thead>
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<tr>
<td>pos_st</td>
<td>A numeric vector</td>
</tr>
<tr>
<td>pos_en</td>
<td>A numeric vector</td>
</tr>
<tr>
<td>type</td>
<td>A factor that comprises levels amp del or just one of them</td>
</tr>
<tr>
<td>freq</td>
<td>A numeric vector</td>
</tr>
</tbody>
</table>

**Source**
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

**References**

**Examples**
```
data(hg19_db_tcga_luad)
```

**hg19_db_tcga_lusc**

**Description**
Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

**Usage**
```
data(hg19_db_tcga_lusc)
```
**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr**: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st**: A numeric vector
- **pos_en**: A numeric vector
- **type**: A factor that comprises levels amp del or just one of them
- **freq**: A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

**References**


**Examples**

data(hg19_db_tcga_lusc)

data(hg19_db_tcga_ov)

**Description**

Copy number alteration frequencies for the corresponding genome build, database and dataset.

Naming format: [genome][build]_db_[database]_[dataset].

**Usage**

data(hg19_db_tcga_ov)

**Format**

A data frame with amplification and/or deletion frequencies for different genomic regions.

- **chr**: A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
- **pos_st**: A numeric vector
- **pos_en**: A numeric vector
- **type**: A factor that comprises levels amp del or just one of them
- **freq**: A numeric vector

**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.
References


Examples

data(hg19_db_tcga_ov)

Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg19_db_tcga_prad)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

<table>
<thead>
<tr>
<th>chr</th>
<th>A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X</th>
</tr>
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<tbody>
<tr>
<td>pos_st</td>
<td>A numeric vector</td>
</tr>
<tr>
<td>pos_en</td>
<td>A numeric vector</td>
</tr>
<tr>
<td>type</td>
<td>A factor that comprises levels amp del or just one of them</td>
</tr>
<tr>
<td>freq</td>
<td>A numeric vector</td>
</tr>
</tbody>
</table>

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg19_db_tcga_prad)
hg19_db_tcga_read

Description
Copy number alteration frequencies for the corresponding genome build, database and dataset.
Naming format: \[genome\][build]_db_[database]_[dataset].

Usage
data(hg19_db_tcga_read)

Format
A data frame with amplification and/or deletion frequencies for different genomic regions.
chr A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st A numeric vector
pos_en A numeric vector
type A factor that comprises levels amp del or just one of them
freq A numeric vector

Source
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References

Examples
data(hg19_db_tcga_read)
**hg19_db_tcga_thca**

**Format**
A data frame with amplification and/or deletion frequencies for different genomic regions.

<table>
<thead>
<tr>
<th>chr</th>
<th>A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X</th>
</tr>
</thead>
<tbody>
<tr>
<td>pos_st</td>
<td>A numeric vector</td>
</tr>
<tr>
<td>pos_en</td>
<td>A numeric vector</td>
</tr>
<tr>
<td>type</td>
<td>A factor that comprises levels amp del or just one of them</td>
</tr>
<tr>
<td>freq</td>
<td>A numeric vector</td>
</tr>
</tbody>
</table>

**Source**
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

**References**

**Examples**
```r
data(hg19_db_tcga_stad)
```

**Description**
Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

**Usage**
```r
data(hg19_db_tcga_thca)
```

**Format**
A data frame with amplification and/or deletion frequencies for different genomic regions.

<table>
<thead>
<tr>
<th>chr</th>
<th>A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X</th>
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<tr>
<td>pos_st</td>
<td>A numeric vector</td>
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**Source**
Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.
References


Examples

data(hg19_db_tcga_thca)

table(hg19_db_tcga_ucec)

data(hg19_db_tcga_ucec)

Description

Copy number alteration frequencies for the corresponding genome build, database and dataset. Naming format: [genome][build]_db_[database]_[dataset].

Usage

data(hg19_db_tcga_ucec)

Format

A data frame with amplification and/or deletion frequencies for different genomic regions.

chr A factor with levels 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
pos_st A numeric vector
pos_en A numeric vector
type A factor that comprises levels amp de1 or just one of them
freq A numeric vector

Source

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.

References


Examples

data(hg19_db_tcga_ucec)
hg19_feature_cancergene

Description

Position of a collection of genomic features for the corresponding genome build.
Naming format: [genome][build]_feature_[collection].

Usage

data(hg19_feature_cancergene)

Format

A data frame with positional information on a set of genomic features.

chr  Chromosome harboring the genomic feature.
bp_st  Starting genomic position of the feature within the chromosome.
bp_en  Ending genomic position of the feature within the chromosome.
feature  Name of the genomic feature.
chr_q_arm  Chromosome arm in which the genomic feature lies.

Source

Collections ensembl, mirna:
- Extracted from Ensembl through BioMart. In the case of mirna, the collection was filter to keep only miRNAs.
- http://www.ensembl.org/biomart/martview/

Collections oncogene, tumorsuppressor, cancgene, lincRNA:
- Gathered from CaSNP website’s BED files and reformatted.
- http://cistrome.dfci.harvard.edu/CaSNP/gscore/

References


Examples

data(hg19_feature_cancergene)
Description

Position of a collection of genomic features for the corresponding genome build. Naming format: [genome][build]_feature_[collection].

Usage

data(hg19_feature_ensembl)

Format

A data frame with positional information on a set of genomic features.

- **chr**: Chromosome harboring the genomic feature.
- **bp_st**: Starting genomic position of the feature within the chromosome.
- **bp_en**: Ending genomic position of the feature within the chromosome.
- **feature**: Name of the genomic feature.
- **chr_q_arm**: Chromosome arm in which the genomic feature lies.

Source

Collections **ensembl**, **mirna**:
- Extracted from Ensembl through BioMart. In the case of **mirna**, the collection was filtered to keep only miRNAs.

Collections **oncogene**, **tumor_suppressor**, **cancer_gene**, **lincRNA**:
- Gathered from CaSNP website’s BED files and reformatted.
- [http://cistrome.dfci.harvard.edu/CaSNP/gscore/](http://cistrome.dfci.harvard.edu/CaSNP/gscore/)

References


Examples

data(hg19_feature_ensembl)
Description

Position of a collection of genomic features for the corresponding genome build. Naming format: [genome][build]_feature_[collection].

Usage

data(hg19_feature_lincRNA)

Format

A data frame with positional information on a set of genomic features.

- `chr` Chromosome harboring the genomic feature.
- `bp_st` Starting genomic position of the feature within the chromosome.
- `bp_en` Ending genomic position of the feature within the chromosome.
- `feature` Name of the genomic feature.
- `chr_q_arm` Chromosome arm in which the genomic feature lies.

Source

Collections ensembl, mirna:
- Extracted from Ensembl through BioMart. In the case of miRNA, the collection was filter to keep only miRNAs.
- http://www.ensembl.org/biomart/martview/

Collections oncogene, tumorsuppressor, cancergene, lincRNA:
- Gathered from CaSNP website’s BED files and reformatted.
- http://cistrome.dfci.harvard.edu/CaSNP/gscore/

References


Examples

data(hg19_feature_lincRNA)
Description

Position of a collection of genomic features for the corresponding genome build. Naming format: [genome][build]_feature_[collection].

Usage

data(hg19_feature_mirnas)

Format

A data frame with positional information on a set of genomic features.

- **chr**: Chromosome harboring the genomic feature.
- **bp_st**: Starting genomic position of the feature within the chromosome.
- **bp_en**: Ending genomic position of the feature within the chromosome.
- **feature**: Name of the genomic feature.
- **chr_q_arm**: Chromosome arm in which the genomic feature lies.

Source

Collections **ensembl, mirna**:
- Extracted from Ensembl through BioMart. In the case of **mirna**, the collection was filter to keep only miRNAs.

Collections **oncogene, tumorsuppressor, cancergene, lincRNA**:
- Gathered from CaSNP website’s BED files and reformatted.
- [http://cistrome.dfci.harvard.edu/CaSNP/gscore/](http://cistrome.dfci.harvard.edu/CaSNP/gscore/)

References


Examples

data(hg19_feature_mirnas)
Description

Position of a collection of genomic features for the corresponding genome build.
Naming format: [genome][build]_feature_[collection].

Usage

data(hg19_feature_oncogene)

Format

A data frame with positional information on a set of genomic features.

- **chr**: Chromosome harboring the genomic feature.
- **bp_st**: Starting genomic position of the feature within the chromosome.
- **bp_en**: Ending genomic position of the feature within the chromosome.
- **feature**: Name of the genomic feature.
- **chr_q_arm**: Chromosome arm in which the genomic feature lies.

Source

Collections ensembl, mirna:
- Extracted from Ensembl through BioMart. In the case of mirna, the collection was filter to keep only miRNAs.

Collections oncogene, tumorsuppressor, cancergene, lincRNA:
- Gathered from CaSNP website’s BED files and reformatted.
- [http://cistrome.dfci.harvard.edu/CaSNP/gscore/](http://cistrome.dfci.harvard.edu/CaSNP/gscore/)

References


Examples

data(hg19_feature_oncogene)
hg19_feature_tumorsupressor

Description
Position of a collection of genomic features for the corresponding genome build.
Naming format: [genome][build]_feature_[collection].

Usage
data(hg19_feature_tumorsupressor)

Format
A data frame with positional information on a set of genomic features.

chr  Chromosome harboring the genomic feature.
bp_st  Starting genomic position of the feature within the chromosome.
bp_en  Ending genomic position of the feature within the chromosome.
feature  Name of the genomic feature.
chr_q_arm  Chromosome arm in which the genomic feature lies.

Source
Collections ensembl, mirna:
- Extracted from Ensembl through BioMart. In the case of mirna, the collection was filter to keep only miRNAs.
- http://www.ensembl.org/biomart/martview/

Collections oncogene, tumorsuppressor, cancergene, lincRNA:
- Gathered from CaSNP website’s BED files and reformatted.
- http://cistrome.dfci.harvard.edu/CaSNP/gscore/

References

Examples
data(hg19_feature_tumorsupressor)
Description

Chromosome arm upper limits (in base pairs) for the mm8 genome build.

Usage

data(mm8_armLimits)

Format

A data frame with 21 observations on the following 2 variables.

- **chr_q_arm**: A factor with levels 1q 2q 3q 4q 5q 6q 7q 8q 9q 10q 11q 12q 13q 14q 15q 16q 17q 18q 19q Xq Yq
- **limit**: A numeric vector

Examples

data(mm8_armLimits)

Description

Position of a collection of genomic features for the corresponding genome build. Naming format: [genome][build]_feature_[collection].

Usage

data(mm8_feature_ensembl)

Format

A data frame with positional information on a set of genomic features.

- **chr**: Chromosome harboring the genomic feature.
- **bp_st**: Starting genomic position of the feature within the chromosome.
- **bp_en**: Ending genomic position of the feature within the chromosome.
- **feature**: Name of the genomic feature.
- **chr_q_arm**: Chromosome arm in which the genomic feature lies.
Source

Collections ensembl, mirna:
- Extracted from Ensembl through BioMart. In the case of mirna, the collection was filtered to keep only miRNAs.
- http://www.ensembl.org/biomart/martview/

Collections oncogene, tumorsuppressor, cancergene, lincRNA:
- Gathered from CaSNP website’s BED files and reformatted.
- http://cistrome.dfci.harvard.edu/CaSNP/gscore/

References


Examples

data(mm8_feature_ensembl)

---

mm8_feature_mirnas   mm8_feature_mirnas

Description

Position of a collection of genomic features for the corresponding genome build.
Naming format: [genome][build]_feature_[collection].

Usage

data(mm8_feature_mirnas)

Format

A data frame with positional information on a set of genomic features.

chr   Chromosome harboring the genomic feature.
bp_st  Starting genomic position of the feature within the chromosome.
bp_en  Ending genomic position of the feature within the chromosome.
feature Name of the genomic feature.
chr_q_arm  Chromosome arm in which the genomic feature lies.
Source

Collections ensembl, mirna:
- Extracted from Ensembl through BioMart. In the case of mirna, the collection was filtered to keep only miRNAs.
- http://www.ensembl.org/biomart/martview/

Collections oncogene, tumorsuppressor, cancergene, lincRNA:
- Gathered from CaSNP website’s BED files and reformatted.
- http://cistrome.dfci.harvard.edu/CaSNP/gscore/

References


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