Package ‘facopy.annot’

February 1, 2017

**Type** Package

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

**Version** 0.108.0

**Date** 2014-08-27

**Author** David Mosen-Ansorena

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

**Import**

**Depends** R (>= 2.10)

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

**License** GPL-3

**biocViews** Genome

**NeedsCompilation** no

R topics documented:

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facopy_annot-package  Companion annotation package for facopy

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

facopy_biocarta  Biocarta Pathways with symbol identifiers

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**


---

**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 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)`

---

**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_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**

```r
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**

```r
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

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

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

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)

data(hg18_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(hg18_db_gsk_breast)

data(hg18_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**

```r
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**

```r
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

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

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

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

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

data(hg18_db_gsk_connective_tissue)
**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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<tr>
<td>pos_st</td>
<td>A numeric vector</td>
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<td>pos_en</td>
<td>A numeric vector</td>
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<tr>
<td>type</td>
<td>A factor that comprises levels amp del or just one of them</td>
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<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(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**

```r
data(hg18_db_gsk_eye)
```

**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>
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<td>pos_en</td>
<td>A numeric vector</td>
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<tr>
<td>type</td>
<td>A factor that comprises levels amp del or just one of them</td>
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<tr>
<td>freq</td>
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**Source**

Source: Cancer Genome WorkBench. Reformatted, summarized and possibly lifted to another genome build.
hg18_db_gsk_kidney

References

Examples
data(hg18_db_gsk_eye)

<table>
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<tr>
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</table>

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)

data(hg18_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(hg18_db_gsk_liver)

data(hg18_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(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 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_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)

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` 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_pancreas)

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

data(hg18_db_gsk_pharynx)

---

hg18_db_gsk_placenta  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_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)

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_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(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)

data(hg18_db_gsk_sarcoma)

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)
```

---

**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)

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.

- 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_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(hg18_db_gsk_uterus)
```
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)

data(hg18_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(hg18_db_tcga_brca)
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_cesc)

data(hg18_db_tcga_coad)

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_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)

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_gbm)

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_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)
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)

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_tcgakirp)

Description

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

Usage

data(hg18_db_tcgakirp)

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_tcgakirp)
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_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)

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_luad)
**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_luad)
```

---

**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_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(hg18_db_tcga_lusc)

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

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.
- 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_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.

<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_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)
```

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.

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_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)

Description

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

Usage

data(hg18_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 filtered to keep only miRNAs.
- http://www.ensembl.org/biomart/martview/

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

References


Examples

data(hg18_feature_cancergene)

Description

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

Usage

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 reformedatted.
- [http://cistrome.dfci.harvard.edu/CaSNP/gscore/](http://cistrome.dfci.harvard.edu/CaSNP/gscore/)

References

Examples
```r
data(hg18_feature_ensembl)
```

```
  hg18_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*, *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

```r
data(hg18_feature_lincRNA)
```

```
chr1  chr2  chr3  chr4  chr5  chr6  chr7  chr8  chr9  chr10  chr11  chr12  chr13  chr14  chr15  chr16  chr17  chr18  chr19  chr20  chr21  chr22  chrX  chrY
598538 618474 686709 720377 720377 771383 795714 839106 878946 917386 952802 987648 1023675 1059432 1094422 1128504 1162704 1196938 1231175 1265410 1309651 1343816
```

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.

- **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 reformatted.
- [http://cistrome.dfci.harvard.edu/CaSNP/gscore/](http://cistrome.dfci.harvard.edu/CaSNP/gscore/)

**References**


**Examples**

```r
data(hg18_feature_mirnas)
```

```sh
hg18_feature_oncogene  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_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 filtered 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)
```
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>hg19_armLimits</th>
<th>hg19_armLimits</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></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

data(hg19_armLimits)

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

Examples

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)
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_bone)

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_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

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 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_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)

data(hg19_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

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)

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.
**References**


**Examples**

```r
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**

```r
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**

```r
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**

```r
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**

```r
data(hg19_db_gsk_esophagus)
```

```r
data(hg19_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(hg19_db_gsk_eye)

**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)

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.

- **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_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)

data(hg19_db_gsk_ovary)
References


Examples

data(hg19_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(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 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_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)

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

data(hg19_db_gsk_pharynx)

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**

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**

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)

---

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 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_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)

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_sarcoma)

data(hg19_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(hg19_db_gsk_stomach)

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_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(hg19_db_gsk_synovium)

data(hg19_db_gsk_thyroid)

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_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 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_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)

data(hg19_db_nci60)

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_gsk_uterus)

<table>
<thead>
<tr>
<th>hg19_db_gsk_uterus</th>
<th>hg19_db_gsk_uterus</th>
</tr>
</thead>
</table>

<table>
<thead>
<tr>
<th>hg19_db_nci60</th>
<th>hg19_db_nci60</th>
</tr>
</thead>
</table>

Description

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

Usage

data(hg19_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.

**References**

**Examples**
data(hg19_db_nci60)

---

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

**Usage**
data(hg19_db_tcgablca)

**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_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_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(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)

---

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_coad)
hg19_db_tcga_gbm

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_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.

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_gbm)

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_hnsc)

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 de1 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_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 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_lihc)
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)

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_luad)

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)
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.

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_prad)
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_stad)

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_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(hg19_db_tcga_stad)
References


Examples

data(hg19_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(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 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_ucec)
**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, cancergene, 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 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_ensembl)
**Description**

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

**Usage**

```r
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 filtered to keep only miRNAs.

Collections oncogene, tumorsuppressor, cancgene, 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(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.

<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(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.

<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, canergene, lincRNA:
- Gathered from CaSNP website’s BED files and reformatted.
- http://cistrome.dfci.harvard.edu/CaSNP/gscore/

References


Examples

data(hg19_feature_oncogene)
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 filtered 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_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 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(mm8_feature_ensembl)

data(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


Examples

data(mm8_feature_mirnas)
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