Package 'facopy.annot'

April 14, 2020

Type Package

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

Version 1.6.0

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

PackageStatus Deprecated

git_url https://git.bioconductor.org/packages/facopy.annot

git_branch RELEASE_3_10

git_last_commit c115349

git_last_commit_date 2019-10-29

Date/Publication 2020-04-14

R topics documented:

`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

Sales, G., Calura, E., Cavalieri, D. & Romualdi, C. graphite - a Bioconductor package to convert pathway topology to gene network. BMC Bioinformatics 13, 20 (2012).

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

Sales, G., Calura, E., Cavalieri, D. & Romualdi, C. graphite - a Bioconductor package to convert pathway topology to gene network. BMC Bioinformatics 13, 20 (2012).

facopy_msigdb *facopy MSigDB Data*

Description

Contains gene sets, classified into collections.

Source

MSigDB

References

Liberzon, A. et al. Molecular signatures database (MSigDB) 3.0. Bioinformatics 27, 1739-40 (2011).

facopy_msigdbNames *facopy MSigDB Data Names*

Description

Contains the names of gene sets, classified into collections.

Source

MSigDB

References

Liberzon, A. et al. Molecular signatures database (MSigDB) 3.0. Bioinformatics 27, 1739-40 (2011).

facopy_reactome *reactome Pathways with symbol identifiers*

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

Sales, G., Calura, E., Cavalieri, D. & Romualdi, C. graphite - a Bioconductor package to convert pathway topology to gene network. BMC Bioinformatics 13, 20 (2012).

hg18_armLimits *hg18_armLimits*

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)
```

hg18_db_gsk_bladder *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_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 WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_bladder)
```

hg18_db_gsk_blood *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_blood)
```

`hg18_db_gsk_bone` *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_bone)
```

`hg18_db_gsk_brain` *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_brain)
```

hg18_db_gsk_breast *hg18_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(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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_breast)
```

hg18_db_gsk_cervix *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_cervix)
```

`hg18_db_gsk_cns` *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_cns)
```

`hg18_db_gsk_colon` *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_colon)
```

hg18_db_gsk_connective_tissue *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

```
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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_connective_tissue)
```

hg18_db_gsk_esophagus *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_esophagus)
```

`hg18_db_gsk_eye` *hg18_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(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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_eye)
```

`hg18_db_gsk_kidney` *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` `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 WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_kidney)
```

hg18_db_gsk_liver *hg18_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(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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_liver)
```

hg18_db_gsk_lung *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_lung)
```

`hg18_db_gsk_muscle` *hg18_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(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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_muscle)
```

`hg18_db_gsk_ovary` *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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_ovary)
```

hg18_db_gsk_pancreas *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_pancreas)
```

hg18_db_gsk_pharynx *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

```
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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_placenta)
```

`hg18_db_gsk_prostate` *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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_prostate)
```

hg18_db_gsk_rectum *hg18_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(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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_rectum)
```

hg18_db_gsk_sarcoma *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

```
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 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 WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_sarcoma)
```

`hg18_db_gsk_stomach` *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_stomach)
```

`hg18_db_gsk_synovium` *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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_synovium)
```

hg18_db_gsk_thyroid *hg18_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(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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_thyroid)
```

hg18_db_gsk_uterus *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_gsk_uterus)
```

---

hg18_db_nci60 *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_nci60)
```

`hg18_db_tcga_blca` *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_tcga_blca)
```

hg18_db_tcga_brca *hg18_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(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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_tcga_brca)
```

hg18_db_tcga_cesc *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_tcga_cesc)
```

---

hg18_db_tcga_coad *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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_tcga_coad)
```

`hg18_db_tcga_gbm` *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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_tcga_gbm)
```

hg18_db_tcga_hnsc *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_tcga_hnsc)
```

hg18_db_tcga_kirc *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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_tcga_kirc)
```

`hg18_db_tcga_kirp` *hg18_db_tcga_kirp*

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_kirp)
```

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 WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_tcga_kirp)
```

`hg18_db_tcga_lgg` *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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_tcga_lgg)
```

hg18_db_tcga_lihc *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_tcga_lihc)
```

hg18_db_tcga_luad *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_tcga_luad)
```

---

hg18_db_tcga_lusc *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_tcga_lusc)
```

`hg18_db_tcga_ov` *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_tcga_ov)
```

hg18_db_tcga_prad *hg18_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(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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_tcga_prad)
```

hg18_db_tcga_read *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

```
data(hg18_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_tcga_read)
```

---

hg18_db_tcga_stad *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_tcga_stad)
```

`hg18_db_tcga_thca` *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_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` `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 WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_tcga_thca)
```

hg18_db_tcga_ucec *hg18_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(hg18_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg18_db_tcga_ucec)
```

hg18_feature_cancergene
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_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://may2009.archive.ensembl.org/biomart/martview/
- 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

Hubbard, T. The Ensembl genome database project. Nucleic Acids Res. 30, 38-41 (2002).

Durinck, S. et al. BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. Bioinformatics 21, 3439-40 (2005).

Cao, Q. et al. CaSNP: a database for interrogating copy number alterations of cancer genome from SNP array data. Nucleic Acids Res. 39, D968-74 (2011).

Examples

```
data(hg18_feature_cancergene)
```

`hg18_feature_ensembl` *hg18_feature_ensembl*

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.
- http://may2009.archive.ensembl.org/biomart/martview/
- 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

Hubbard, T. The Ensembl genome database project. Nucleic Acids Res. 30, 38-41 (2002).

Durinck, S. et al. BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. Bioinformatics 21, 3439-40 (2005).

Cao, Q. et al. CaSNP: a database for interrogating copy number alterations of cancer genome from SNP array data. Nucleic Acids Res. 39, D968-74 (2011).

Examples

```
data(hg18_feature_ensembl)
```

---

hg18_feature_lincRNA *hg18_feature_lincRNA*

Description

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

Usage

```
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 filter to keep only miRNAs.
- http://may2009.archive.ensembl.org/biomart/martview/
- 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

Hubbard, T. The Ensembl genome database project. Nucleic Acids Res. 30, 38-41 (2002).

Durinck, S. et al. BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. Bioinformatics 21, 3439-40 (2005).

Cao, Q. et al. CaSNP: a database for interrogating copy number alterations of cancer genome from SNP array data. Nucleic Acids Res. 39, D968-74 (2011).

Examples

```
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

```
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 filter to keep only miRNAs.
- http://may2009.archive.ensembl.org/biomart/martview/
- 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

Hubbard, T. The Ensembl genome database project. Nucleic Acids Res. 30, 38-41 (2002).

Durinck, S. et al. BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. Bioinformatics 21, 3439-40 (2005).

Cao, Q. et al. CaSNP: a database for interrogating copy number alterations of cancer genome from SNP array data. Nucleic Acids Res. 39, D968-74 (2011).

Examples

```
data(hg18_feature_mirnas)
```

`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

```
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.
- http://may2009.archive.ensembl.org/biomart/martview/
- 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

Hubbard, T. The Ensembl genome database project. Nucleic Acids Res. 30, 38-41 (2002).

Durinck, S. et al. BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. Bioinformatics 21, 3439-40 (2005).

Cao, Q. et al. CaSNP: a database for interrogating copy number alterations of cancer genome from SNP array data. Nucleic Acids Res. 39, D968-74 (2011).

Examples

```
data(hg18_feature_oncogene)
```

---

hg18_feature_tumorsupressor
hg18_feature_tumorsupressor

Description

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

Usage

```
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://may2009.archive.ensembl.org/biomart/martview/
- 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

Hubbard, T. The Ensembl genome database project. Nucleic Acids Res. 30, 38-41 (2002).

Durinck, S. et al. BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. Bioinformatics 21, 3439-40 (2005).

Cao, Q. et al. CaSNP: a database for interrogating copy number alterations of cancer genome from SNP array data. Nucleic Acids Res. 39, D968-74 (2011).

Examples

```
data(hg18_feature_tumorsupressor)
```

`hg19_armLimits` *hg19_armLimits*

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)
```

`hg19_db_gsk_bladder` *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_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 WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_bladder)
```

hg19_db_gsk_blood *hg19_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(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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_blood)
```

hg19_db_gsk_bone *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_bone)
```

`hg19_db_gsk_brain` *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_brain)
```

`hg19_db_gsk_breast` *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_breast)
```

hg19_db_gsk_cervix *hg19_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(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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_cervix)
```

hg19_db_gsk_cns *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_cns)
```

`hg19_db_gsk_colon` *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.

References

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_colon)
```

`hg19_db_gsk_connective_tissue`

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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_connective_tissue)
```

hg19_db_gsk_esophagus *hg19_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(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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_esophagus)
```

hg19_db_gsk_eye *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_eye)
```

---

hg19_db_gsk_kidney *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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_kidney)
```

`hg19_db_gsk_liver` *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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_liver)
```

hg19_db_gsk_lung *hg19_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(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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_lung)
```

hg19_db_gsk_muscle *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_muscle)
```

`hg19_db_gsk_ovary` *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_ovary)
```

---

hg19_db_gsk_pancreas *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` `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 WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_pancreas)
```

hg19_db_gsk_pharynx *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_pharynx)
```

hg19_db_gsk_placenta *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_placenta)
```

`hg19_db_gsk_prostate` *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_prostate)
```

`hg19_db_gsk_rectum` *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` `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 WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_rectum)
```

hg19_db_gsk_sarcoma *hg19_db_gsk_sarcoma*

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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_sarcoma)
```

hg19_db_gsk_stomach *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_stomach)
```

---

hg19_db_gsk_synovium *hg19_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(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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_synovium)
```

`hg19_db_gsk_thyroid` *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` `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 WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_thyroid)
```

hg19_db_gsk_uterus *hg19_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(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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_gsk_uterus)
```

hg19_db_nci60 *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_nci60)
```

`hg19_db_tcga_blca` *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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_tcga_blca)
```

`hg19_db_tcga_brca` *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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_tcga_brca)
```

hg19_db_tcga_cesc *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_tcga_cesc)
```

hg19_db_tcga_coad *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_tcga_coad)
```

---

hg19_db_tcga_gbm *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

```
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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_tcga_gbm)
```

`hg19_db_tcga_hnsc` *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.

`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 WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_tcga_hnsc)
```

hg19_db_tcga_kirc *hg19_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(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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_tcga_kirc)
```

hg19_db_tcga_kirp *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

```
data(hg19_db_tcga_kirp)
```

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 WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_tcga_kirp)
```

`hg19_db_tcga_lgg` *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_tcga_lgg)
```

`hg19_db_tcga_lihc` *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_tcga_lihc)
```

hg19_db_tcga_luad *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.

`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 WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_tcga_luad)
```

hg19_db_tcga_lusc *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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_tcga_lusc)
```

`hg19_db_tcga_ov` *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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_tcga_ov)
```

`hg19_db_tcga_prad` *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_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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_tcga_prad)
```

hg19_db_tcga_read *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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_tcga_read)
```

hg19_db_tcga_stad *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

```
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

Zhang, J. et al. Systematic analysis of genetic alterations in tumors using Cancer Genome WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_tcga_stad)
```

`hg19_db_tcga_thca` *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_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` `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 WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_tcga_thca)
```

`hg19_db_tcga_ucec` *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` `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 WorkBench (CGWB). Genome Res. 17, 1111-7 (2007).

Examples

```
data(hg19_db_tcga_ucec)
```

hg19_feature_cancergene
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://may2009.archive.ensembl.org/biomart/martview/
- 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

Hubbard, T. The Ensembl genome database project. Nucleic Acids Res. 30, 38-41 (2002).

Durinck, S. et al. BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. Bioinformatics 21, 3439-40 (2005).

Cao, Q. et al. CaSNP: a database for interrogating copy number alterations of cancer genome from SNP array data. Nucleic Acids Res. 39, D968-74 (2011).

Examples

```
data(hg19_feature_cancergene)
```

hg19_feature_ensembl *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_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://may2009.archive.ensembl.org/biomart/martview/
- 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

Hubbard, T. The Ensembl genome database project. Nucleic Acids Res. 30, 38-41 (2002).

Durinck, S. et al. BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. Bioinformatics 21, 3439-40 (2005).

Cao, Q. et al. CaSNP: a database for interrogating copy number alterations of cancer genome from SNP array data. Nucleic Acids Res. 39, D968-74 (2011).

Examples

```
data(hg19_feature_ensembl)
```

hg19_feature_lincRNA *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_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://may2009.archive.ensembl.org/biomart/martview/
- 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

Hubbard, T. The Ensembl genome database project. Nucleic Acids Res. 30, 38-41 (2002).

Durinck, S. et al. BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. Bioinformatics 21, 3439-40 (2005).

Cao, Q. et al. CaSNP: a database for interrogating copy number alterations of cancer genome from SNP array data. Nucleic Acids Res. 39, D968-74 (2011).

Examples

```
data(hg19_feature_lincRNA)
```

hg19_feature_mirnas *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_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.
- http://may2009.archive.ensembl.org/biomart/martview/
- 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

Hubbard, T. The Ensembl genome database project. Nucleic Acids Res. 30, 38-41 (2002).

Durinck, S. et al. BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. Bioinformatics 21, 3439-40 (2005).

Cao, Q. et al. CaSNP: a database for interrogating copy number alterations of cancer genome from SNP array data. Nucleic Acids Res. 39, D968-74 (2011).

Examples

```
data(hg19_feature_mirnas)
```

hg19_feature_oncogene *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_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.
- http://may2009.archive.ensembl.org/biomart/martview/
- 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

Hubbard, T. The Ensembl genome database project. Nucleic Acids Res. 30, 38-41 (2002).

Durinck, S. et al. BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. Bioinformatics 21, 3439-40 (2005).

Cao, Q. et al. CaSNP: a database for interrogating copy number alterations of cancer genome from SNP array data. Nucleic Acids Res. 39, D968-74 (2011).

Examples

```
data(hg19_feature_oncogene)
```

hg19_feature_tumorsupressor *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://may2009.archive.ensembl.org/biomart/martview/
- 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

Hubbard, T. The Ensembl genome database project. Nucleic Acids Res. 30, 38-41 (2002).

Durinck, S. et al. BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. Bioinformatics 21, 3439-40 (2005).

Cao, Q. et al. CaSNP: a database for interrogating copy number alterations of cancer genome from SNP array data. Nucleic Acids Res. 39, D968-74 (2011).

Examples

```
data(hg19_feature_tumorsupressor)
```

mm8_armLimits *mm8_armLimits*

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)
```

mm8_feature_ensembl *mm8_feature_ensembl*

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://may2009.archive.ensembl.org/biomart/martview/
- 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

Hubbard, T. The Ensembl genome database project. Nucleic Acids Res. 30, 38-41 (2002).

Durinck, S. et al. BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. Bioinformatics 21, 3439-40 (2005).

Cao, Q. et al. CaSNP: a database for interrogating copy number alterations of cancer genome from SNP array data. Nucleic Acids Res. 39, D968-74 (2011).

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 filter to keep only miRNAs.
- http://may2009.archive.ensembl.org/biomart/martview/
- 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

Hubbard, T. The Ensembl genome database project. Nucleic Acids Res. 30, 38-41 (2002).

Durinck, S. et al. BioMart and Bioconductor: a powerful link between biological databases and microarray data analysis. Bioinformatics 21, 3439-40 (2005).

Cao, Q. et al. CaSNP: a database for interrogating copy number alterations of cancer genome from SNP array data. Nucleic Acids Res. 39, D968-74 (2011).

Examples

```
data(mm8_feature_mirnas)
```

Index