

# Package ‘facopy.annot’

October 16, 2018

**Type** Package

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

**Version** 0.114.0

**Date** 2014-08-27

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**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

**git\_url** <https://git.bioconductor.org/packages/facopy.annot>

**git\_branch** RELEASE\_3\_7

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facopy.annot-package    *Companion annotation package for facopy*

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**Description**

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

**Details**

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

**Author(s)**

David Mosen-Ansorena

---

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	<i>kegg Pathways with symbol identifiers</i>
-------------	--

---

**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	<i>facopy MSigDB Data</i>
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---

**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	<i>facopy MSigDB Data Names</i>
--------------------	---------------------------------

---

**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	<i>reactome Pathways with symbol identifiers</i>
-----------------	--

---

### 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	<i>hg18_armLimits</i>
----------------	-----------------------

---

### 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	<i>hg18_db_gsk_bone</i>
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---

**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	<i>hg18_db_gsk_cns</i>
-----------------	------------------------

---

**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	<i>hg18_db_gsk_eye</i>
-----------------	------------------------

---

**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	<i>hg18_db_tcga_coad</i>
-------------------	--------------------------

---

**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_kirp)
```

---

hg18_db_tcga_kirp	<i>hg18_db_tcga_kirp</i>
-------------------	--------------------------

---

**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_lusc)
```

---

hg18_db_tcga_lusc	<i>hg18_db_tcga_lusc</i>
-------------------	--------------------------

---

**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_tcgav_lusc)
```

---

```
hg18_db_tcgav      hg18_db_tcgav
```

---

**Description**

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

**Usage**

```
data(hg18_db_tcgav)
```

**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_tcgav)
```

---

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)
```

---

<code>hg18_db_tcga_stad</code>	<i>hg18_db_tcga_stad</i>
--------------------------------	--------------------------

---

**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	<i>hg19_db_gsk_brain</i>
-------------------	--------------------------

---

**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	<i>hg19_db_gsk_colon</i>
-------------------	--------------------------

---

**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	<i>hg19_db_tcga_blca</i>
-------------------	--------------------------

---

**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)
```

---

<code>hg19_db_tcga_gbm</code>	<i>hg19_db_tcga_gbm</i>
-------------------------------	-------------------------

---

**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	<i>hg19_db_tcga_hnsc</i>
-------------------	--------------------------

---

**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)
```

---

<code>hg19_db_tcga_lgg</code>	<code>hg19_db_tcga_lgg</code>
-------------------------------	-------------------------------

---

**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_tcgav_lusc)
```

---

hg19_db_tcgav	<i>hg19_db_tcgav</i>
---------------	----------------------

---

**Description**

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

Naming format: [genome][build]\_db\_[database]\_[dataset].

**Usage**

```
data(hg19_db_tcgav)
```

**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	<i>hg19_db_tcga_prad</i>
-------------------	--------------------------

---

## 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	<i>hg19_db_tcga_thca</i>
-------------------	--------------------------

---

**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.dfc.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, tumorsupressor, cancergene, lincRNA:

- Gathered from CaSNP website's BED files and reformatted.

- <http://cistrome.dfc.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	<i>mm8_armLimits</i>
---------------	----------------------

---

**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	<i>mm8_feature_ensembl</i>
---------------------	----------------------------

---

**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)
```

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