

# Package ‘TCGAbiolinksGUI.data’

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**Title** Data for the TCGAbiolinksGUI package

**Version** 1.24.0

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**Description** Supporting data for the TCGAbiolinksGUI package.

**License** GPL-3

**LazyData** false

**Depends** R (>= 3.5.0)

**Suggests** BiocStyle, knitr, rmarkdown, readr, DT

**biocViews** AssayDomainData, TechnologyData, OrganismData

**URL** <https://github.com/BioinformaticsFMRP/TCGAbiolinksGUI.data>

**BugReports** <https://github.com/BioinformaticsFMRP/TCGAbiolinksGUI.data/issues>

**VignetteBuilder** knitr

**RoxygenNote** 7.1.2

**git\_url** <https://git.bioconductor.org/packages/TCGAbiolinksGUI.data>

**git\_branch** RELEASE\_3\_19

**git\_last\_commit** c98945d

**git\_last\_commit\_date** 2024-04-30

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## Contents

GDCdisease . . . . .	2
encode.v36.annotation.genes . . . . .	2
gene.location.hg19 . . . . .	3
gene.location.hg38 . . . . .	3
glioma.gcimp.model . . . . .	4
glioma.idh.model . . . . .	4

glioma.idhmut.model . . . . .	5
glioma.idhwt.model . . . . .	5
linkedOmics.data . . . . .	6
maf.tumor . . . . .	6
probes2rm . . . . .	7
TCGAbiolinksGUI.data . . . . .	7

## Index 8

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GDCdisease	<i>GDC projects</i>
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### Description

Contains all GDC projects with open data

### Usage

```
data("GDCdisease")
```

### Format

A named list with 39 projects

### Source

Retrieved from GDC API

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gencode.v36.annotation.genes	<i>GENCODE v36 gene information</i>
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### Description

GENCODE v36 gene information

### Usage

```
data("gencode.v36.annotation.genes")
```

### Format

A Granges object

### Source

Downloaded from GENCODE v36 [https://www.genencodegenes.org/human/release\\_36.html](https://www.genencodegenes.org/human/release_36.html) Comprehensive gene annotation and filtered to genes

---

`gene.location.hg19`     *Biomart hg19 gene information*

---

**Description**

Biomart hg19 gene information

**Usage**

```
data("gene.location.hg19")
```

**Format**

A table

**Source**

Downloaded with biomart

---

`gene.location.hg38`     *Biomart hg38 gene information*

---

**Description**

Biomart hg38 gene information

**Usage**

```
data("gene.location.hg38")
```

**Format**

A table

**Source**

Downloaded with biomart

---

glioma.gcimp.model     *gcimp RF model*

---

**Description**

A RF model able to classify DNA methylation samples in to GCIMP groups

**Usage**

```
data("glioma.gcimp.model")
```

**Format**

A random forest model with 276 samples and 145 predictors classifying into 3 classes

**Source**

RF model created from DNA methylation signatures retrieved from [www.cell.com/cell/abstract/S0092-8674\(15\)01692-X](http://www.cell.com/cell/abstract/S0092-8674(15)01692-X)

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glioma.idh.model     *IDH RF model*

---

**Description**

A RF model able to classify DNA methylation samples in to IDH groups

**Usage**

```
data("glioma.idh.model")
```

**Format**

A random forest model with 880 samples and 1205 predictors classifying into 6 classes

**Source**

RF model created from DNA methylation signatures retrieved from [www.cell.com/cell/abstract/S0092-8674\(15\)01692-X](http://www.cell.com/cell/abstract/S0092-8674(15)01692-X)

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`glioma.idhmut.model`     *IDHmut RF model*

---

**Description**

A RF model able to classify DNA methylation samples in to IDHmut groups

**Usage**

```
data("glioma.idhmut.model")
```

**Format**

A random forest model with 450 samples and 1216 predictors classifying into 3 classes

**Source**

RF model created from DNA methylation signatures retrieved from [www.cell.com/cell/abstract/S0092-8674\(15\)01692-X](http://www.cell.com/cell/abstract/S0092-8674(15)01692-X)

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`glioma.idhwt.model`     *IDHwt RF model*

---

**Description**

A RF model able to classify DNA methylation samples in to IDHwt groups

**Usage**

```
data("glioma.idhwt.model")
```

**Format**

A random forest model with 430 samples and 843 predictors classifying into 3 classes

**Source**

RF model created from DNA methylation signatures retrieved from [www.cell.com/cell/abstract/S0092-8674\(15\)01692-X](http://www.cell.com/cell/abstract/S0092-8674(15)01692-X)

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linkedOmics.data	<i>linkedOmics table</i>
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**Description**

linkedOmics table with links

**Usage**

```
data("linkedOmics.data")
```

**Format**

A table

**Source**

Parsed from <http://linkedomics.org/login.php#dataSource>

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maf.tumor	<i>GDC open MAF files</i>
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**Description**

Contains the list of GDC project with open MAF files available

**Usage**

```
data(maf.tumor)
```

**Format**

A named list with 33 tumors

**Source**

[https://gdc-docs.nci.nih.gov/Data/Release\\_Notes/Manifests/GDC\\_open\\_MAFs\\_manifest.txt](https://gdc-docs.nci.nih.gov/Data/Release_Notes/Manifests/GDC_open_MAFs_manifest.txt)

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 probes2rm

*EPIC probes removed from newer versions*


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**Description**

EPIC probes removed from newer versions that should not be used in the analysis

**Usage**

```
data("probes2rm")
```

**Format**

A list with 977 probes

**Source**

<https://support.illumina.com/downloads/infinium-methylationepic-v1-0-product-files.html>

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 TCGAbiolinksGUI.data

*Auxiliary data for TCGAbiolinksGUI package.*


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**Description**

**Package:** TCGAbiolinksGUI.data provide the necessary data for TCGAbiolinksGUI glioma classifier menu. It includes the following objects:

**glioma.gcimp.model** A train model for GCIMP DNA methylation signatures.

**glioma.idhwt.model** A train model for IDHwt DNA methylation signatures

**glioma.idhmut.model** A train model for IDHmut DNA methylation signatures

**glioma.idh.model** A train model for IDH DNA methylation signatures

**probes2rm** List of probes that should be removed from EPIC array due to different versions of the platform.

Source: <https://support.illumina.com/downloads/infinium-methylationepic-v1-0-product-files.html>

**maf.tumor** TCGA projects with open MAF files retrieved from the NCI's Genomic Data Commons (GDC).

Source: [https://gdc-docs.nci.nih.gov/Data/Release\\_Notes/Manifests/GDC\\_open\\_MAFs\\_manifest.txt](https://gdc-docs.nci.nih.gov/Data/Release_Notes/Manifests/GDC_open_MAFs_manifest.txt)

**GDCdisease** The NCI's Genomic Data Commons (GDC) projects list

# Index

## \* datasets

- GDCdisease, [2](#)
- gencode.v36.annotation.genes, [2](#)
- gene.location.hg19, [3](#)
- gene.location.hg38, [3](#)
- glioma.gcimp.model, [4](#)
- glioma.idh.model, [4](#)
- glioma.idhmut.model, [5](#)
- glioma.idhwt.model, [5](#)
- linkedOmics.data, [6](#)
- maf.tumor, [6](#)
- probes2rm, [7](#)

## \* utilities

- TCGAbiolinksGUI.data, [7](#)

- GDCdisease, [2](#), [7](#)
- gencode.v36.annotation.genes, [2](#)
- gene.location.hg19, [3](#)
- gene.location.hg38, [3](#)
- glioma.gcimp.model, [4](#), [7](#)
- glioma.idh.model, [4](#), [7](#)
- glioma.idhmut.model, [5](#), [7](#)
- glioma.idhwt.model, [5](#), [7](#)

- linkedOmics.data, [6](#)

- maf.tumor, [6](#), [7](#)

- probes2rm, [7](#), [7](#)

- TCGAbiolinksGUI.data, [7](#)