

Package ‘RTCGA.CNV’

September 22, 2026

Type Package

Title CNV (Copy-number variation) datasets from The Cancer Genome Atlas Project

Version 1.40.0

Date 2015-12-14

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Description Package provides CNV (based on Merge snp) datasets from The Cancer Genome Atlas Project for all cohorts types from <http://gdac.broadinstitute.org/>. Data format is explained here <https://wiki.nci.nih.gov/display/TCGA/Retrieving+Data+Using+the+Data+Matrix>. Data from 2015-11-01 snapshot.

License GPL-2

LazyData TRUE

BugReports <https://github.com/RTCGA/RTCGA/issues>

Depends R (>= 3.3.0), RTCGA

Suggests knitr, rmarkdown

biocViews AnnotationData

VignetteBuilder knitr

NeedsCompilation no

RoxygenNote 5.0.1

git_url <https://git.bioconductor.org/packages/RTCGA.CNV>

git_branch RELEASE_3_23

git_last_commit 1f968ff

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

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CNV	<i>CNV datasets from TCGA project</i>
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Description

Package provides CNV datasets from The Cancer Genome Atlas Project for all cohorts types from <http://gdac.broadinstitute.org/>. Data were downloaded using [RTCGA-package](#) and contain snapshots for the date: 2015-11-01. The process is described here: <http://rtcga.github.io/RTCGA/>. Use cases, examples and information about datasets in **RTCGA.data** family can be found here: `browseVignettes("RTCGA")` Data format is explained here <https://wiki.nci.nih.gov/display/TCGA/Retrieving+Data+U> Converting **RTCGA.CNV** datasets from `data.frames` to Bioconductor classes is explained here [convertTCGA](#).

Usage

- ACC.CNV
- BLCA.CNV
- BRCA.CNV
- CESC.CNV
- CHOL.CNV
- COAD.CNV
- COADREAD.CNV
- DLBC.CNV
- ESCA.CNV
- GBM.CNV
- GBMLGG.CNV
- HNSC.CNV
- KICH.CNV
- KIPAN.CNV
- KIRC.CNV
- KIRP.CNV

LAML.CNV

LGG.CNV

LIHC.CNV

LUAD.CNV

LUSC.CNV

MESO.CNV

OV.CNV

PAAD.CNV

PCPG.CNV

PRAD.CNV

READ.CNV

SARC.CNV

SKCM.CNV

STAD.CNV

STES.CNV

TGCT.CNV

THCA.CNV

THYM.CNV

UCEC.CNV

UCS.CNV

UVM.CNV

Details

```
browseVignettes("RTCGA")
```

Value

Data frames with CNV data.

Source

<http://gdac.broadinstitute.org/>

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* **datasets**

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