

# Package ‘RTCGA.CNV’

October 24, 2025

**Type** Package

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

**Version** 1.37.0

**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** devel

**git\_last\_commit** ef17564

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.23

**Date/Publication** 2025-10-24

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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
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- GBM.CNV
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LAML.CNV

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LIHC.CNV

LUAD.CNV

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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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