

# COSMIC 67

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## 1 Introduction

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The *COSMIC.67* package provides the curated mutations published with the COSMIC release version 67 (2013-10-24). Both variants found in coding and non-coding regions are included and offered as a single object of class 'CollapsedVCF' and a bgzipped and tabix-index 'VCF' file.

Additionally, the package contains the Cancer Gene Census, a list of genes causally linked to cancer.

## 2 Accessing and Using the Data

---

```
library(VariantAnnotation)

Loading required package: BiocGenerics
Loading required package: generics

Attaching package: 'generics'

The following objects are masked from 'package:base':
```

```
as.difftime, as.factor, as.ordered, intersect,
is.element, setdiff, setequal, union
```

Attaching package: 'BiocGenerics'

The following objects are masked from 'package:stats':

```
IQR, mad, sd, var, xtabs
```

The following objects are masked from 'package:base':

```
Filter, Find, Map, Position, Reduce, anyDuplicated,
aperm, append, as.data.frame, basename, cbind,
colnames, dirname, do.call, duplicated, eval, evalq,
get, grep, grepl, is.unsorted, lapply, mapply, match,
mget, order, paste, pmax, pmax.int, pmin, pmin.int,
rank, rbind, rownames, sapply, saveRDS, table,
tapply, unique, unsplit, which.max, which.min
```

Loading required package: MatrixGenerics

Loading required package: matrixStats

Attaching package: 'MatrixGenerics'

The following objects are masked from 'package:matrixStats':

```
colAlls, colAnyNAs, colAnys, colAvesPerRowSet,
colCollapse, colCounts, colCummaxs, colCummins,
colCumprods, colCumsums, colDiffs, colIQRDiffs,
colIQRs, colLogSumExps, colMadDiffs, colMads,
colMaxs, colMeans2, colMedians, colMins,
colOrderStats, colProds, colQuantiles, colRanges,
colRanks, colSdDiffs, colSds, colSums2, colTabulates,
colVarDiffs, colVars, colWeightedMads,
colWeightedMeans, colWeightedMedians, colWeightedSds,
colWeightedVars, rowAlls, rowAnyNAs, rowAnys,
rowAvesPerColSet, rowCollapse, rowCounts, rowCummaxs,
rowCummins, rowCumprods, rowCumsums, rowDiffs,
rowIQRDiffs, rowIQRs, rowLogSumExps, rowMadDiffs,
rowMads, rowMaxs, rowMeans2, rowMedians, rowMins,
rowOrderStats, rowProds, rowQuantiles, rowRanges,
rowRanks, rowSdDiffs, rowSds, rowSums2, rowTabulates,
rowVarDiffs, rowVars, rowWeightedMads,
rowWeightedMeans, rowWeightedMedians, rowWeightedSds,
rowWeightedVars
```

Loading required package: Seqinfo

Loading required package: GenomicRanges

Loading required package: stats4

Loading required package: S4Vectors

Attaching package: 'S4Vectors'

The following object is masked from 'package:utils':

`findMatches`

The following objects are masked from 'package:base':

`I`, `expand.grid`, `unname`

Loading required package: IRanges

Loading required package: SummarizedExperiment

Loading required package: Biobase

Welcome to Bioconductor

Vignettes contain introductory material; view with  
'browseVignettes()'. To cite Bioconductor, see  
'citation("Biobase")', and for packages  
'citation("pkgname")'.

Attaching package: 'Biobase'

The following object is masked from 'package:MatrixGenerics':

`rowMedians`

The following objects are masked from 'package:matrixStats':

`anyMissing`, `rowMedians`

Loading required package: Rsamtools

Loading required package: Biostrings

Loading required package: XVector

Attaching package: 'Biostrings'

The following object is masked from 'package:base':

`strsplit`

Attaching package: 'VariantAnnotation'

The following object is masked from 'package:base':

`tabulate`

```
library(GenomicRanges)
```

```
data(package = "COSMIC.67")
```

```
data(cosmic_67, package = "COSMIC.67")
```

```
tp53_range = GRanges("17", IRanges(7565097, 7590856))
```

```
vcf_path = system.file("vcf", "cosmic_67.vcf.gz", package = "COSMIC.67")
```

```
cosmic_tp53 = readVcf(vcf_path, genome = "GRCh37", ScanVcfParam(which = tp53_range))
```

```

cosmic_tp53
class: CollapsedVCF
dim: 5892 0
rowRanges(vcf):
  GRanges with 5 metadata columns: paramRangeID, REF, ALT, QUAL, FILTER
info(vcf):
  DataFrame with 5 columns: GENE, STRAND, CDS, AA, CNT
info(header(vcf)):
  Number Type      Description
  GENE    1      String  Gene name
  STRAND  1      String  Gene strand
  CDS     1      String  CDS annotation
  AA      1      String  Peptide annotation
  CNT     1      Integer How many samples have this mutation
geno(vcf):
  List of length 0:

data(cgc_67, package = "COSMIC.67")
head(cgc_67)

```

	SYMBOL	ENTREZID	ENSEMBL
1	ABI1	10006	ENSG000000136754
2	ABL1	25	ENSG000000097007
3	ABL2	27	ENSG000000143322
4	ACSL3	2181	ENSG000000123983
5	CASC5	57082	ENSG000000137812
6	MLLT11	10962	ENSG000000213190

For details on the collection and curation of the original data, please see the webpage of the COSMIC project: <http://cancer.sanger.ac.uk/cancergenome/projects/cosmic/>.

## 3 Data Provenance

### 3.1 COSMIC Mutations

The following steps are performed for importing and processing of the VCF data:

1. Downloading of the VCF files 'CosmicCodingMuts\_v67\_20131024.vcf.gz' and 'Cosmic-NonCodingVariants\_v67\_20131024.vcf.gz' from 'ftp://ngs.sanger.ac.uk/production/cosmic/' to 'inst/raw/'.
2. Importing of both files to R using 'readVcf'.
3. Sorting of the seqlevels and adding 'seqinfo' data for the toplevel chromosomes of 'GRCh37'.
4. Merging of both objects, sorting according to genomic position.
5. Converting the object to class `VariantAnnotation::VRanges`.
6. Converting the 'character' columns to 'factors'.
7. Saving the merged object to 'data/cosmic\_v67\_vcf.rda'.

8. Exporting the merged object as a bgzipped and tabix-indexed 'VCF' to 'inst/vcf/cosmic\_v67.vcf.gz'.

## 3.2 Cancer Gene Census

The following steps are performed for importing and processing of the Cancer Gene Census data:

1. Downloading of the 'cancer\_gene\_census.tsv' file from [ftp://ftp.sanger.ac.uk/pub/CGP/cosmic/data\\_export](ftp://ftp.sanger.ac.uk/pub/CGP/cosmic/data_export) to 'inst/raw'.
2. Import of the files as a data frame.
3. Annotation of the 'HGNC' and 'ENSEMBLID' identifiers, using the 'ENTREZ gene ID' as query with the 'org.Hs.eg.db' object.
4. Saving the object to 'data/cgc\_67.rda'.

## 4 Data Source

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The mutation data was obtained from the Sanger Institute Catalogue Of Somatic Mutations In Cancer web site, <http://www.sanger.ac.uk/cosmic>

Bamford et al (2004):

The COSMIC (Catalogue of Somatic Mutations in Cancer) database and website.  
Br J Cancer, 91,355-358.

For details on the usage and redistribution of the data, please see [ftp://ftp.sanger.ac.uk/pub/CGP/cosmic/GUIDELINES\\_ON\\_THE\\_USE\\_OF\\_THIS\\_DATA.txt](ftp://ftp.sanger.ac.uk/pub/CGP/cosmic/GUIDELINES_ON_THE_USE_OF_THIS_DATA.txt).

## 5 References

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- <http://cancer.sanger.ac.uk/cancergenome/projects/cosmic/>
- [http://nar.oxfordjournals.org/content/39/suppl\\_1/D945.long](http://nar.oxfordjournals.org/content/39/suppl_1/D945.long)
- [ftp://ftp.sanger.ac.uk/pub/CGP/cosmic/GUIDELINES\\_ON\\_THE\\_USE\\_OF\\_THIS\\_DATA.txt](ftp://ftp.sanger.ac.uk/pub/CGP/cosmic/GUIDELINES_ON_THE_USE_OF_THIS_DATA.txt)

## 6 Session Info

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R version 4.5.1 Patched (2025-08-23 r88802)

Platform: x86\_64-pc-linux-gnu

Running under: Ubuntu 24.04.3 LTS

Matrix products: default

BLAS: /home/biocbuild/bbs-3.22-bioc/R/lib/libRblas.so

LAPACK: /usr/lib/x86\_64-linux-gnu/lapack/liblapack.so.3.12.0 LAPACK version 3.12.0

locale:

[1] LC_CTYPE=en_US.UTF-8	LC_NUMERIC=C
[3] LC_TIME=en_GB	LC_COLLATE=C
[5] LC_MONETARY=en_US.UTF-8	LC_MESSAGES=en_US.UTF-8

```
[7] LC_PAPER=en_US.UTF-8      LC_NAME=C
[9] LC_ADDRESS=C               LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

```
time zone: America/New_York
tzcode source: system (glibc)
```

```
attached base packages:
```

```
[1] stats4      stats      graphics  grDevices  utils      datasets
[7] methods     base
```

```
other attached packages:
```

```
[1] VariantAnnotation_1.56.0   Rsamtools_2.26.0
[3] Biostrings_2.78.0         XVector_0.50.0
[5] SummarizedExperiment_1.40.0 Biobase_2.70.0
[7] GenomicRanges_1.62.0      IRanges_2.44.0
[9] S4Vectors_0.48.0          Seqinfo_1.0.0
[11] MatrixGenerics_1.22.0     matrixStats_1.5.0
[13] BiocGenerics_0.56.0       generics_0.1.4
[15] knitr_1.50
```

```
loaded via a namespace (and not attached):
```

```
[1] SparseArray_1.10.1        bitops_1.0-9
[3] RSQLite_2.4.3             lattice_0.22-7
[5] digest_0.6.37            evaluate_1.0.5
[7] grid_4.5.1               fastmap_1.2.0
[9] blob_1.2.4               Matrix_1.7-4
[11] cigarillo_1.0.0          AnnotationDbi_1.72.0
[13] restfulr_0.0.16          DBI_1.2.3
[15] BiocManager_1.30.26      httr_1.4.7
[17] BSgenome_1.78.0          XML_3.99-0.19
[19] codetools_0.2-20        abind_1.4-8
[21] cli_3.6.5               rlang_1.1.6
[23] crayon_1.5.3             BiocStyle_2.38.0
[25] bit64_4.6.0-1           cachem_1.1.0
[27] DelayedArray_0.36.0      yaml_2.3.10
[29] GenomicFeatures_1.62.0   S4Arrays_1.10.0
[31] tools_4.5.1             parallel_4.5.1
[33] BiocParallel_1.44.0      memoise_2.0.1
[35] curl_7.0.0              vctrs_0.6.5
[37] R6_2.6.1                png_0.1-8
[39] BiocIO_1.20.0           rtracklayer_1.70.0
[41] KEGGREST_1.50.0         bit_4.6.0
[43] highr_0.11              GenomicAlignments_1.46.0
[45] xfun_0.54               rjson_0.2.23
[47] htmltools_0.5.8.1       rmarkdown_2.30
[49] compiler_4.5.1          RCurl_1.98-1.17
```