

# Package ‘CaMutQC’

January 19, 2026

**Type** Package

**Title** An R Package for Comprehensive Filtration and Selection of  
Cancer Somatic Mutations

**Version** 1.6.0

**Description** CaMutQC is able to filter false positive mutations generated due to technical issues, as well as to select candidate cancer mutations through a series of well-structured functions by labeling mutations with various flags. And a detailed and vivid filter report will be offered after completing a whole filtration or selection section. Also, CaMutQC integrates several methods and gene panels for Tumor Mutational Burden (TMB) estimation.

**biocViews** Software, QualityControl, GeneTarget

**Encoding** UTF-8

**LazyData** false

**Suggests** knitr, rmarkdown, BiocStyle, shiny

**VignetteBuilder** knitr

**RoxygenNote** 7.3.3

**NeedsCompilation** no

**BugReports** <https://github.com/likelet/CaMutQC/issues>

**URL** <https://github.com/likelet/CaMutQC>

**Depends** R (>= 4.5.0)

**Imports** ggplot2, dplyr, org.Hs.eg.db, vcfR, clusterProfiler, stringr,  
DT, MesKit, maftools, data.table, utils, stats, methods, tidyr

**License** GPL-3

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

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|        |               |
|--------|---------------|
| calTMB | <i>calTMB</i> |
|--------|---------------|

---

## Description

Calculate Tumor Mutational Burden (TMB) in specific regions.

## Usage

```
calTMB(
  maf,
  bedFile = NULL,
  bedHeader = FALSE,
  assay = "MSK-v3",
  genelist = NULL,
  mutType = "nonsynonymous",
  bedFilter = TRUE
)
```

## Arguments

|           |                                                                                                                                                                        |
|-----------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| maf       | An MAF data frame, generated by <a href="#">vcfToMAF</a> function.                                                                                                     |
| bedFile   | A file in bed format that contains region information. Default: NULL.                                                                                                  |
| bedHeader | Whether the input bed file has a header or not. Default: FALSE.                                                                                                        |
| assay     | Methodology and assay will be applied as a reference, including 'MSK-v3', 'MSK-v2', 'MSK-v1', 'FoundationOne', 'Pan-Cancer Panel' and 'Customized'. Default: 'MSK-v3'. |
| genelist  | A vector of panel gene list, only useful when assay is set to 'Customized'.                                                                                            |

|           |                                                                                                                                                                                                     |
|-----------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| mutType   | A group of variant classifications that will be kept, only useful when assay is set to 'Pan-Cancer Panel' or 'Customized', including 'exonic', 'nonsynonymous', and 'all' Default: 'nonsynonymous'. |
| bedFilter | Whether to filter the information in bed file or not, which only leaves segments in Chr1-Ch22, ChrX and ChrY. Default: TRUE.                                                                        |

### Value

A TMB value.

### Examples

```
maf <- vcfToMAF(system.file("extdata", "WES_EA_T_1_mutect2.vcf",
package="CaMutQC"))
TMB_value <- calTMB(maf, bedFile=system.file("extdata/bed/panel_hg38",
"Pan-cancer-hg38.rds", package="CaMutQC"), assay = "Customized")
```

---

|              |                     |
|--------------|---------------------|
| mutFilterAdj | <i>mutFilterAdj</i> |
|--------------|---------------------|

---

### Description

Filter SNVs with adjacent indels

### Usage

```
mutFilterAdj(maf, maxIndelLen = 50, minInterval = 10)
```

### Arguments

|             |                                                                                             |
|-------------|---------------------------------------------------------------------------------------------|
| maf         | An MAF data frame, generated by <a href="#">vcfToMAF</a> function.                          |
| maxIndelLen | Maximum length of indel accepted to be included. Default: 50                                |
| minInterval | Minimum length of interval between an SNV and an indel accepted to be included. Default: 10 |

### Value

An MAF data frame after filtration for adjacent variants.

### Examples

```
maf <- vcfToMAF(system.file("extdata",
"WES_EA_T_1_mutect2.vcf", package="CaMutQC"))
mafF <- mutFilterAdj(maf)
```

---

mutFilterCan

*mutFilterCan*


---

## Description

Apply common filtering strategies on a MAF data frame for different cancer types.

## Usage

```
mutFilterCan(
  maf,
  cancerType,
  PONfile = NULL,
  PONformat = "vcf",
  panel = "Customized",
  tumorDP = 0,
  normalDP = 0,
  tumorAD = 0,
  normalAD = Inf,
  VAF = 0,
  VAFratio = 0,
  dbsnpCutoff = 0,
  nonCutoff = 0,
  SBmethod = "SOR",
  SBscore = Inf,
  maxIndelLen = Inf,
  minInterval = 0,
  tagFILTER = NULL,
  dbVAF = 0.01,
  ExAC = FALSE,
  Genomesprojects1000 = FALSE,
  ESP6500 = FALSE,
  gnomAD = FALSE,
  dbSNP = FALSE,
  keepCOSMIC = FALSE,
  keepType = "all",
  bedFile = NULL,
  bedFilter = FALSE,
  bedHeader = FALSE,
  mutFilter = FALSE,
  selectCols = FALSE,
  report = TRUE,
  reportFile = "FilterReport.html",
  reportDir = "./",
  TMB = FALSE,
  progressBar = TRUE,
  codelog = FALSE,
  codelogFile = "mutFilterCan.log",
  verbose = TRUE
)
```

**Arguments**

|                     |                                                                                                                                                                                                                                                                                                                                                              |
|---------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| maf                 | An MAF data frame.                                                                                                                                                                                                                                                                                                                                           |
| cancerType          | Type of cancer whose filtering parameters need to be referred to. Options are: "COADREAD", "BRCA", "LIHC", "LAML", "LCML", "UCEC", "UCS", "BLCA", "KIRC", "KIRP" and "STAD".                                                                                                                                                                                 |
| PONfile             | Panel-of-Normals files, which can be either obtained through GATK ( <a href="https://gatk.broadinstitute.org/hc/en-us/articles/360035890631-Panel-of-Normals-PON-">https://gatk.broadinstitute.org/hc/en-us/articles/360035890631-Panel-of-Normals-PON-</a> ) or generated by users. Should have at least four columns: CHROM, POS, REF, ALT. Default: NULL. |
| PONformat           | The format of PON file, either "vcf" or "txt". Default: "vcf"                                                                                                                                                                                                                                                                                                |
| panel               | The sequencing panel applied on the dataset. Parameters for <code>mutFilterQual</code> function are set differently for different panels. Default: "Customized". Options: "MSKCC", "WES".                                                                                                                                                                    |
| tumorDP             | Threshold of tumor total depth. Default: 0.                                                                                                                                                                                                                                                                                                                  |
| normalDP            | Threshold of normal total depth. Default: 0.                                                                                                                                                                                                                                                                                                                 |
| tumorAD             | Threshold of tumor alternative allele depth. Default: 0.                                                                                                                                                                                                                                                                                                     |
| normalAD            | Threshold of normal alternative allele depth. Default: Inf.                                                                                                                                                                                                                                                                                                  |
| VAF                 | Threshold of VAF value. Default: 0.                                                                                                                                                                                                                                                                                                                          |
| VAFratio            | Threshold of VAF ratio (tVAF/nVAF). Default: 0.                                                                                                                                                                                                                                                                                                              |
| dbsnpcutoff         | Cutoff of normal depth for dbSNP variants. Default: 0.                                                                                                                                                                                                                                                                                                       |
| nonCutoff           | Cutoff of normal depth for non-dbSNP variants. Default: 0.                                                                                                                                                                                                                                                                                                   |
| SBmethod            | Method will be used to detect strand bias, including 'SOR' and 'Fisher'. Default: 'SOR'. SOR: StrandOddsRatio ( <a href="https://gatk.broadinstitute.org/hc/en-us/articles/360041849111-StrandOddsRatio">https://gatk.broadinstitute.org/hc/en-us/articles/360041849111-StrandOddsRatio</a> ).                                                               |
| SBscore             | Cutoff strand bias score used to filter variants. Default: 0.                                                                                                                                                                                                                                                                                                |
| maxIndelLen         | Maximum length of indel accepted to be included. Default: Inf.                                                                                                                                                                                                                                                                                               |
| minInterval         | Maximum length of interval between an SNV and an indel accepted to be included. Default: 0.                                                                                                                                                                                                                                                                  |
| tagFILTER           | Variants with specific tag in the FILTER column will be kept, Default: NULL.                                                                                                                                                                                                                                                                                 |
| dbVAF               | Threshold of VAF of certain population for variants in database. Default: 0.                                                                                                                                                                                                                                                                                 |
| ExAC                | Whether to filter variants listed in ExAC with VAF higher than cutoff(set in VAF parameter). Default: FALSE                                                                                                                                                                                                                                                  |
| Genomesprojects1000 | Whether to filter variants listed in Genomesprojects1000 with VAF higher than cutoff(set in VAF parameter). Default: FALSE.                                                                                                                                                                                                                                  |
| ESP6500             | Whether to filter variants listed in ESP6500 with VAF higher than cutoff(set in VAF parameter). Default: FALSE.                                                                                                                                                                                                                                              |
| gnomAD              | Whether to filter variants listed in gnomAD with VAF higher than cutoff(set in VAF parameter). Default: FALSE.                                                                                                                                                                                                                                               |
| dbSNP               | Whether to filter variants listed in dbSNP. Default: FALSE.                                                                                                                                                                                                                                                                                                  |
| keepCOSMIC          | Whether to keep variants in COSMIC even they have are present in germline database. Default: FALSE.                                                                                                                                                                                                                                                          |
| keepType            | A group of variant classifications will be kept, including 'exonic', 'nonsynonymous' and 'all'. Default: 'all'.                                                                                                                                                                                                                                              |
| bedFile             | A file in bed format that contains region information. Default: NULL                                                                                                                                                                                                                                                                                         |

|             |                                                                                                                                                                                                                                                                                                        |
|-------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| bedFilter   | Whether to filter the information in bed file or not, which only leaves segments in Chr1-Ch22, ChrX and ChrY. Default: FALSE                                                                                                                                                                           |
| bedHeader   | Whether the input bed file has a header or not. Default: FALSE.                                                                                                                                                                                                                                        |
| mutFilter   | Whether to directly return a filtered MAF data frame. If FALSE, a simulation filtration process will be run, and the original MAF data frame with tags in CaTag column, and a filter report will be returned. If TRUE, a filtered MAF data frame and a filter report will be generated. Default: FALSE |
| selectCols  | Columns will be contained in the filtered data frame. By default (FALSE), the first 13 columns and 'Tumor_Sample_Barcode' column. Or a vector contains column names will be kept.                                                                                                                      |
| report      | Whether to generate report automatically. Default: TRUE.                                                                                                                                                                                                                                               |
| reportFile  | File name of the report. Default: 'FilterReport.html'                                                                                                                                                                                                                                                  |
| reportDir   | Path to the output report file. Default: './'                                                                                                                                                                                                                                                          |
| TMB         | Whether to calculate TMB. Default: FALSE.                                                                                                                                                                                                                                                              |
| progressbar | Whether to show progress bar when running this function Default: TRUE                                                                                                                                                                                                                                  |
| codelog     | If TRUE, your code, along with the parameters you set, will be export in a log file. It will be convenient for users to repeat experiments. Default: FALSE                                                                                                                                             |
| codelogFile | Where to store the codelog, only useful when codelog is set to TRUE. Default: "mutFilterCan.log"                                                                                                                                                                                                       |
| verbose     | Whether to generate message/notification during the filtration process. Default: TRUE.                                                                                                                                                                                                                 |

### Value

An MAF data frame after common strategy filtration for a cancer type.

A filter report in HTML format

### Examples

```
maf <- vcfToMAF(system.file("extdata",
"WES_EA_T_1_mutect2.vcf", package="CaMutQC"))
maff <- mutFilterCan(maf, cancerType='BRCA',
PONfile=system.file("extdata", "PON_test.txt", package="CaMutQC"),
PONformat="txt", TMB=FALSE, report=FALSE)
```

---

mutFilterCom

*mutFilterCom*


---

### Description

Apply common filtering strategies on a MAF data frame.

**Usage**

```
mutFilterCom(
  maf,
  PONfile = NULL,
  PONformat = "vcf",
  panel = "Customized",
  tumorDP = 20,
  normalDP = 10,
  tumorAD = 5,
  normalAD = Inf,
  VAF = 0.05,
  VAFratio = 0,
  dbsnpCutoff = 19,
  nonCutoff = 8,
  SBmethod = "SOR",
  SBscore = 3,
  maxIndelLen = 50,
  minInterval = 10,
  tagFILTER = "PASS",
  dbVAF = 0.01,
  ExAC = TRUE,
  Genomesprojects1000 = TRUE,
  gnomAD = TRUE,
  dbSNP = FALSE,
  keepCOSMIC = TRUE,
  keepType = "exonic",
  bedFile = NULL,
  bedHeader = FALSE,
  bedFilter = FALSE,
  mutFilter = FALSE,
  ESP6500 = TRUE,
  selectCols = TRUE,
  report = TRUE,
  assay = "MSK-v3",
  genelist = NULL,
  mutType = "nonsynonymous",
  reportFile = "FilterReport.html",
  reportDir = "./",
  TMB = TRUE,
  cancerType = NULL,
  reference = NULL,
  progressbar = TRUE,
  codelog = FALSE,
  codelogFile = "mutFilterCom.log",
  verbose = TRUE
)
```

**Arguments**

|         |                                                                                                                                                                                                                                                                                             |
|---------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| maf     | An MAF data frame.                                                                                                                                                                                                                                                                          |
| PONfile | Panel-of-Normals files, which can be either obtained through GATK ( <a href="https://gatk.broadinstitute.org/hc/en-us/articles/360035890631-Panel-of-Normals-PON-">https://gatk.broadinstitute.org/hc/en-us/articles/360035890631-Panel-of-Normals-PON-</a> ) or generated by users. Should |

|                     |                                                                                                                                                                                                                                                                                                         |
|---------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|                     | have at least four columns: CHROM, POS, REF, ALT Default: NULL.                                                                                                                                                                                                                                         |
| PONformat           | The format of PON file, either "vcf" or "txt". Default: "vcf"                                                                                                                                                                                                                                           |
| panel               | The sequencing panel applied on the dataset. Parameters for <code>mutFilterQual</code> function are set differently for different panels. Default: "Customized". Options: "MSKCC", "WES".                                                                                                               |
| tumorDP             | Threshold of tumor total depth. Default: 20                                                                                                                                                                                                                                                             |
| normalDP            | Threshold of normal total depth. Default: 10                                                                                                                                                                                                                                                            |
| tumorAD             | Threshold of tumor alternative allele depth. Default: 5                                                                                                                                                                                                                                                 |
| normalAD            | Threshold of normal alternative allele depth. Default: Inf                                                                                                                                                                                                                                              |
| VAF                 | Threshold of VAF value. Default: 0.05                                                                                                                                                                                                                                                                   |
| VAFratio            | Threshold of VAF ratio (tVAF/nVAF). Default: 0.                                                                                                                                                                                                                                                         |
| dbsnpcutoff         | Cutoff of normal depth for dbSNP variants. Default: 19.                                                                                                                                                                                                                                                 |
| nonCutoff           | Cutoff of normal depth for non-dbSNP variants. Default: 8.                                                                                                                                                                                                                                              |
| SBmethod            | Method will be used to detect strand bias, including 'SOR' and 'Fisher'. Default: 'SOR'. SOR: StrandOddsRatio ( <a href="https://gatk.broadinstitute.org/hc/en-us/articles/360041849111">https://gatk.broadinstitute.org/hc/en-us/articles/360041849111</a> StrandOddsRatio)                            |
| SBscore             | Cutoff strand bias score used to filter variants. Default: 3.                                                                                                                                                                                                                                           |
| maxIndelLen         | Maximum length of indel accepted to be included. Default: 50.                                                                                                                                                                                                                                           |
| minInterval         | Maximum length of interval between an SNV and an indel accepted to be included. Default: 10.                                                                                                                                                                                                            |
| tagFILTER           | Variants with specific tag in the FILTER column will be kept, Default: 'PASS'.                                                                                                                                                                                                                          |
| dbVAF               | Threshold of VAF value for databases. Default: 0.01.                                                                                                                                                                                                                                                    |
| ExAC                | Whether to filter variants listed in ExAC with VAF higher than cutoff(set in VAF parameter). Default: TRUE.                                                                                                                                                                                             |
| Genomesprojects1000 | Whether to filter variants listed in Genomesprojects1000 with VAF higher than cutoff(set in VAF parameter). Default: TRUE.                                                                                                                                                                              |
| gnomAD              | Whether to filter variants listed in gnomAD with VAF higher than cutoff(set in VAF parameter). Default: TRUE.                                                                                                                                                                                           |
| dbSNP               | Whether to filter variants listed in dbSNP. Default: FALSE.                                                                                                                                                                                                                                             |
| keepCOSMIC          | Whether to keep variants in COSMIC even they have are present in germline database. Default: TRUE.                                                                                                                                                                                                      |
| keepType            | A group of variant classifications will be kept, including 'exonic', 'nonsynonymous' and 'all'. Default: 'exonic'.                                                                                                                                                                                      |
| bedFile             | A file in bed format that contains region information. Default: NULL.                                                                                                                                                                                                                                   |
| bedHeader           | Whether the input bed file has a header or not. Default: FALSE.                                                                                                                                                                                                                                         |
| bedFilter           | Whether to filter the information in bed file or not, which only leaves segments in Chr1-Ch22, ChrX and ChrY. Default: FALSE.                                                                                                                                                                           |
| mutFilter           | Whether to directly return a filtered MAF data frame. If FALSE, a simulation filtration process will be run, and the original MAF data frame with tags in CaTag column, and a filter report will be returned. If TRUE, a filtered MAF data frame and a filter report will be generated. Default: FALSE. |
| ESP6500             | Whether to filter variants listed in ESP6500 with VAF higher than cutoff(set in VAF parameter). Default: TRUE.                                                                                                                                                                                          |

|             |                                                                                                                                                                                                                                                                                                                                                              |
|-------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| selectCols  | Columns will be contained in the filtered data frame. By default (TRUE), the first 13 columns and 'Tumor_Sample_Barcode' column. Or a vector contains column names will be kept.                                                                                                                                                                             |
| report      | Whether to generate report automatically. Default: TRUE                                                                                                                                                                                                                                                                                                      |
| assay       | Methodology and assay will be applied as a reference, including 'MSK-v3', 'MSK-v2', 'MSK-v1', 'FoundationOne', 'Pan-Cancer Panel' and 'Customized'. Default: 'MSK-v3'.                                                                                                                                                                                       |
| genelist    | A vector of panel gene list, only useful when assay is set to 'Customized'.                                                                                                                                                                                                                                                                                  |
| mutType     | A group of variant classifications that will be kept in TMB calculation, only useful when assay is set to 'Pan-Cancer Panel' or 'Customized', including 'exonic' and 'nonsynonymous'. Default: 'nonsynonymous'.                                                                                                                                              |
| reportFile  | File name of the report. Default: 'FilterReport.html'                                                                                                                                                                                                                                                                                                        |
| reportDir   | Path to the output report file. Default: './'.                                                                                                                                                                                                                                                                                                               |
| TMB         | Whether to calculate TMB. Default: TRUE. Note: CaMutQC uses unfiltered maf to calculate TMB value.                                                                                                                                                                                                                                                           |
| cancerType  | Type of cancer whose filtering parameters need to be referred to. Options are: "COADREAD", "BRCA", "LIHC", "LAML", "LCML", "UCEC", "UCS", "BLCA", "KIRC" and "KIRP"                                                                                                                                                                                          |
| reference   | A specific study whose filtering strategies need to be referred to. Format: "Last_name_of_the_first_author-Journal-Year-Cancer_type" Options are: "Haralddottir_et_al-Gastroenterology-2014-UCEC", "Cherniack_et_al-Cancer_Cell-2017-UCS", "Mason_et_al-Leukemia-2015-LCML", "Gerlinger_et_al-Engl_J_Med-2012-KIRC" "Zhu_et_al-Nat_Communications-2020-KIRP" |
| progressbar | Whether to show progress bar when running this function Default: TRUE                                                                                                                                                                                                                                                                                        |
| codelog     | If TRUE, your code, along with the parameters you set, will be export in a log file. It will be convenient for users to repeat experiments. Default: FALSE                                                                                                                                                                                                   |
| codelogFile | Where to store the codelog, only useful when codelog is set to TRUE. Default: "mutFilterCom.log"                                                                                                                                                                                                                                                             |
| verbose     | Whether to generate message/notification during the filtration process. Default: TRUE.                                                                                                                                                                                                                                                                       |

## Value

An MAF data frame after common strategy filtration

A filter report in HTML format

## Examples

```
maf <- vcfToMAF(system.file("extdata",
"WES_EA_T_1_mutect2.vcf", package="CaMutQC"))
mafF <- mutFilterCom(maf,
PONfile=system.file("extdata", "PON_test.txt", package="CaMutQC"),
TMB=FALSE, report=FALSE, PONformat="txt", verbose=FALSE)
```

mutFilterDB

*mutFilterDB***Description**

Filter variants in germline database.

**Usage**

```
mutFilterDB(
  maf,
  dbVAF = 0.01,
  ExAC = TRUE,
  Genomesprojects1000 = TRUE,
  ESP6500 = TRUE,
  gnomAD = TRUE,
  dbSNP = FALSE,
  keepCOSMIC = TRUE,
  verbose = TRUE
)
```

**Arguments**

|                     |                                                                                                                               |
|---------------------|-------------------------------------------------------------------------------------------------------------------------------|
| maf                 | An MAF data frame, generated by <a href="#">vcfToMAF</a> function.                                                            |
| dbVAF               | Threshold of VAF value for database annotations. Default: 0.01.                                                               |
| ExAC                | Whether to filter variants listed in ExAC with VAF higher than cutoff (set in dbVAF parameter). Default: TRUE.                |
| Genomesprojects1000 | Whether to filter variants listed in Genomesprojects1000 with VAF higher than cutoff (set in dbVAF parameter). Default: TRUE. |
| ESP6500             | Whether to filter variants listed in ESP6500 with VAF higher than cutoff (set in dbVAF parameter). Default: TRUE.             |
| gnomAD              | Whether to filter variants listed in gnomAD with VAF higher than cutoff (set in dbVAF parameter). Default: TRUE.              |
| dbSNP               | Whether to filter variants listed in dbSNP. Default: FALSE.                                                                   |
| keepCOSMIC          | Whether to keep variants in COSMIC even they are present in germline database. Default: TRUE.                                 |
| verbose             | Whether to generate message/notification during the filtration process. Default: TRUE.                                        |

**Value**

An MAF data frame after filtration for database and clinical significance

**Examples**

```
maf <- vcfToMAF(system.file("extdata",
  "WES_EA_T_1_mutect2.vcf", package="CaMutQC"))
maff <- mutFilterDB(maf)
```

---

|                   |                          |
|-------------------|--------------------------|
| mutFilterNormalDP | <i>mutFilterNormalDP</i> |
|-------------------|--------------------------|

---

### Description

Filter dbsnp/non-dbsnp variants based on their normal depth. Variants in dbSNP database should have normal depth  $\geq 19$ , while non-dbSNP variants should have normal depth  $\geq 8$  to avoid being filtered.

### Usage

```
mutFilterNormalDP(maf, dbsnpCutoff = 19, nonCutoff = 8, verbose = TRUE)
```

### Arguments

|             |                                                                                        |
|-------------|----------------------------------------------------------------------------------------|
| maf         | An MAF data frame, generated by <a href="#">vcfToMAF</a> function.                     |
| dbsnpCutoff | Cutoff of normal depth for dbSNP variants. Default: 19.                                |
| nonCutoff   | Cutoff of normal depth for non-dbSNP variants. Default: 8.                             |
| verbose     | Whether to generate message/notification during the filtration process. Default: TRUE. |

### Value

An MAF data frame where some variants has N tag in CaTag column for Normal depth filtration.

### Examples

```
maf <- vcfToMAF(system.file("extdata",
  "WES_EA_T_1_mutect2.vcf", package="CaMutQC"))
mafF <- mutFilterNormalDP(maf)
```

---

|              |                     |
|--------------|---------------------|
| mutFilterPON | <i>mutFilterPON</i> |
|--------------|---------------------|

---

### Description

Filter variants based on Panel of Normals

### Usage

```
mutFilterPON(maf, PONfile = NULL, PONformat = "vcf", verbose = TRUE)
```

### Arguments

|           |                                                                                                                                                                                                                                                                                                                                                              |
|-----------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| maf       | An MAF data frame, generated by <a href="#">vcfToMAF</a> function.                                                                                                                                                                                                                                                                                           |
| PONfile   | Panel-of-Normals files, which can be either obtained through GATK ( <a href="https://gatk.broadinstitute.org/hc/en-us/articles/360035890631-Panel-of-Normals-PON-">https://gatk.broadinstitute.org/hc/en-us/articles/360035890631-Panel-of-Normals-PON-</a> ) or generated by users. Should have at least four columns: CHROM, POS, REF, ALT. Defalut: NULL. |
| PONformat | The format of PON file, either "vcf" or "txt". Default: "vcf"                                                                                                                                                                                                                                                                                                |
| verbose   | Whether to generate message/notification during the filtration process. Default: TRUE.                                                                                                                                                                                                                                                                       |

**Value**

An MAF data frame where some variants have P tag in CaTag column for PON filtration.

**Examples**

```
maf <- vcfToMAF(system.file("extdata",
"WES_EA_T_1_mutect2.vcf", package="CaMutQC"))
maff <- mutFilterPON(maf, PONfile=system.file("extdata",
"PON_test.txt", package="CaMutQC"), PONformat="txt")
```

---

|               |                      |
|---------------|----------------------|
| mutFilterQual | <i>mutFilterQual</i> |
|---------------|----------------------|

---

**Description**

Filter variants in low sequencing quality or low confidence.

**Usage**

```
mutFilterQual(
  maf,
  panel = "Customized",
  tumorDP = 20,
  normalDP = 10,
  tumorAD = 5,
  normalAD = Inf,
  VAF = 0.05,
  VAFratio = 0
)
```

**Arguments**

|          |                                                                                                                                                                                              |
|----------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| maf      | An MAF data frame, generated by <a href="#">vcfToMAF</a> function.                                                                                                                           |
| panel    | The sequencing panel applied on the dataset. Parameters for <a href="#">mutFilterQual</a> function are set differently for different panels. Default: "Customized". Options: "MSKCC", "WES". |
| tumorDP  | Threshold of tumor total depth. Default: 20                                                                                                                                                  |
| normalDP | Threshold of normal total depth. Default: 10                                                                                                                                                 |
| tumorAD  | Threshold of tumor alternative allele depth. Default: 5                                                                                                                                      |
| normalAD | Threshold of normal alternative allele depth. Default: Inf                                                                                                                                   |
| VAF      | Threshold of VAF value. Default: 0.05                                                                                                                                                        |
| VAFratio | Threshold of VAF ratio (tVAF/nVAF). Default: 0                                                                                                                                               |

**Value**

An MAF data frame where some variants have Q tag in CaTag column for sequencing quality filtration

## Examples

```
maf <- vcfToMAF(system.file("extdata",
  "WES_EA_T_1_mutect2.vcf", package="CaMutQC"))
mafF <- mutFilterQual(maf)
```

---

mutFilterRef

*mutFilterRef*


---

## Description

Use the same filtering strategies that a specific study used, or top-rated strategies shared by users.

## Usage

```
mutFilterRef(
  maf,
  reference,
  PONfile,
  PONformat = "vcf",
  tumorDP = 0,
  normalDP = 0,
  tumorAD = 0,
  normalAD = Inf,
  VAF = 0,
  VAFratio = 0,
  SBmethod = "SOR",
  SBscore = Inf,
  maxIndelLen = Inf,
  minInterval = 0,
  tagFILTER = NULL,
  dbVAF = 0.01,
  ExAC = FALSE,
  Genomesprojects1000 = FALSE,
  ESP6500 = FALSE,
  gnomAD = FALSE,
  dbSNP = FALSE,
  keepCOSMIC = FALSE,
  keepType = "all",
  bedFile = NULL,
  bedFilter = TRUE,
  mutFilter = FALSE,
  selectCols = FALSE,
  report = TRUE,
  reportFile = "FilterReport.html",
  reportDir = "./",
  TMB = FALSE,
  progressBar = TRUE,
  codelog = FALSE,
  codelogFile = "mutFilterCom.log",
  verbose = TRUE
)
```

**Arguments**

|                     |                                                                                                                                                                                                                                                                                                                                                                |
|---------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| maf                 | An MAF data frame.                                                                                                                                                                                                                                                                                                                                             |
| reference           | A specific study whose filtering strategies need to be referred to. Format: "Last_name_of_the_first_author-Journal-Year-Cancer_type" Options are: "Haraldsdottir_et_al-Gastroenterology-2014-UCEC", "Cherniack_et_al-Cancer_Cell-2017-UCS", "Mason_et_al-Leukemia-2015-LCML", "Gerlinger_et_al-Engl_J_Med-2012-KIRC", "Zhu_et_al-Nat_Communications-2020-KIRC" |
| PONfile             | Panel-of-Normals files, which can be either obtained through GATK ( <a href="https://gatk.broadinstitute.org/hc/en-us/articles/360035890631-Panel-of-Normals-PON-">https://gatk.broadinstitute.org/hc/en-us/articles/360035890631-Panel-of-Normals-PON-</a> ) or generated by users. Should have at least four columns: CHROM, POS, REF, ALT                   |
| PONformat           | The format of PON file, either "vcf" or "txt". Default: "vcf"                                                                                                                                                                                                                                                                                                  |
| tumorDP             | Threshold of tumor total depth. Default: 0                                                                                                                                                                                                                                                                                                                     |
| normalDP            | Threshold of normal total depth. Default: 0                                                                                                                                                                                                                                                                                                                    |
| tumorAD             | Threshold of tumor alternative allele depth. Default: 0                                                                                                                                                                                                                                                                                                        |
| normalAD            | Threshold of normal alternative allele depth. Default: Inf                                                                                                                                                                                                                                                                                                     |
| VAF                 | Threshold of VAF value. Default: 0                                                                                                                                                                                                                                                                                                                             |
| VAFratio            | Threshold of VAF ratio (tVAF/nVAF). Default: 0                                                                                                                                                                                                                                                                                                                 |
| SBmethod            | Method will be used to detect strand bias, including 'SOR' and 'Fisher'. Default: 'SOR'. SOR: StrandOddsRatio ( <a href="https://gatk.broadinstitute.org/hc/en-us/articles/360041849111-StrandOddsRatio">https://gatk.broadinstitute.org/hc/en-us/articles/360041849111-StrandOddsRatio</a> )                                                                  |
| SBscore             | Cutoff strand bias score used to filter variants. Default: 3                                                                                                                                                                                                                                                                                                   |
| maxIndelLen         | Maximum length of indel accepted to be included. Default: Inf                                                                                                                                                                                                                                                                                                  |
| minInterval         | Maximum length of interval between an SNV and an indel accepted to be included. Default: 0                                                                                                                                                                                                                                                                     |
| tagFILTER           | Variants with specific tag in the FILTER column will be kept, Default: NULL                                                                                                                                                                                                                                                                                    |
| dbVAF               | Threshold of VAF of certain population for variants in database. Default: 0.01                                                                                                                                                                                                                                                                                 |
| ExAC                | Whether to filter variants listed in ExAC with VAF higher than cutoff(set in VAF parameter). Default: TRUE.                                                                                                                                                                                                                                                    |
| Genomesprojects1000 | Whether to filter variants listed in Genomesprojects1000 with VAF higher than cutoff(set in VAF parameter). Default: TRUE.                                                                                                                                                                                                                                     |
| ESP6500             | Whether to filter variants listed in ESP6500 with VAF higher than cutoff(set in VAF parameter). Default: TRUE.                                                                                                                                                                                                                                                 |
| gnomAD              | Whether to filter variants listed in gnomAD with VAF higher than cutoff(set in VAF parameter). Default: TRUE.                                                                                                                                                                                                                                                  |
| dbSNP               | Whether to filter variants listed in dbSNP. Default: FALSE.                                                                                                                                                                                                                                                                                                    |
| keepCOSMIC          | Whether to keep variants in COSMIC even they have are present in germline database. Default: FALSE.                                                                                                                                                                                                                                                            |
| keepType            | A group of variant classifications will be kept, including 'exonic', 'nonsynonymous' and 'all'. Default: 'all'.                                                                                                                                                                                                                                                |
| bedFile             | A file in bed format that contains region information. Default: NULL.                                                                                                                                                                                                                                                                                          |
| bedFilter           | Whether to filter the information in bed file or not, which only leaves segments in Chr1-Ch22, ChrX and ChrY. Default: TRUE                                                                                                                                                                                                                                    |

|             |                                                                                                                                                                                                                                                                                                        |
|-------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| mutFilter   | Whether to directly return a filtered MAF data frame. If FALSE, a simulation filtration process will be run, and the original MAF data frame with tags in CaTag column, and a filter report will be returned. If TRUE, a filtered MAF data frame and a filter report will be generated. Default: FALSE |
| selectCols  | Columns will be contained in the filtered data frame. By default (TRUE), the first 13 columns and 'Tumor_Sample_Barcode' column. Or a vector contains column names will be kept.                                                                                                                       |
| report      | Whether to generate report automatically. Default: TRUE                                                                                                                                                                                                                                                |
| reportFile  | File name of the report. Default: 'FilterReport.html'                                                                                                                                                                                                                                                  |
| reportDir   | Path to the output report file. Default: './'                                                                                                                                                                                                                                                          |
| TMB         | Whether to calculate TMB. Default: TRUE                                                                                                                                                                                                                                                                |
| progressbar | Whether to show progress bar when running this function Default: TRUE                                                                                                                                                                                                                                  |
| codelog     | If TRUE, your code, along with the parameters you set, will be export in a log file. It will be convenient for users to repeat experiments. Default: FALSE                                                                                                                                             |
| codelogFile | Where to store the codelog, only useful when codelog is set to TRUE. Default: "mutFilterCom.log"                                                                                                                                                                                                       |
| verbose     | Whether to generate message/notification during the filtration process. Default: TRUE.                                                                                                                                                                                                                 |

### Value

An MAF data frame after applied filtering strategies in another study

A filter report in HTML format

### Examples

```
maf <- vcfToMAF(system.file("extdata",
"WES_EA_T_1_mutect2.vcf", package="CaMutQC"))
mafR <- mutFilterReg(maf, reference="Zhu_et_al-Nat_Comm-2020-KIRP",
PONfile=system.file("extdata", "PON_test.txt", package="CaMutQC"),
PONformat="txt", TMB=FALSE, verbose=FALSE, report=FALSE)
```

---

mutFilterReg

*mutFilterReg*


---

### Description

Filter variants not in specific regions.

### Usage

```
mutFilterReg(
  maf,
  bedFile = NULL,
  bedHeader = FALSE,
  bedFilter = FALSE,
  verbose = TRUE
)
```

**Arguments**

|           |                                                                                                                              |
|-----------|------------------------------------------------------------------------------------------------------------------------------|
| maf       | An MAF data frame, generated by <a href="#">vcfToMAF</a> function.                                                           |
| bedFile   | A bed file that contains region information. Default: NULL                                                                   |
| bedHeader | Whether the input bed file has a header or not. Default: FALSE.                                                              |
| bedFilter | Whether to filter the information in bed file or not, which only leaves segments in Chr1-Ch22, ChrX and ChrY. Default: FALSE |
| verbose   | Whether to generate message/notification during the filtration process. Default: TRUE.                                       |

**Value**

An MAF data frame where some variants have R tag in CaTag column for region filtration.

**Examples**

```
maf <- vcfToMAF(system.file("extdata", "WES_EA_T_1_mutect2.vcf",
package="CaMutQC"))
mafF <- mutFilterReg(maf, bedFile=system.file("extdata/bed/panel_hg38",
"Pan-cancer-hg38.rds", package="CaMutQC"), bedFilter = FALSE)
```

---

|             |                    |
|-------------|--------------------|
| mutFilterSB | <i>mutFilterSB</i> |
|-------------|--------------------|

---

**Description**

Filter variants based on strand bias.

**Usage**

```
mutFilterSB(maf, method = "SOR", SBscore = 3)
```

**Arguments**

|         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
|---------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| maf     | An MAF object, generated by <a href="#">vcfToMAF</a> function.                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| method  | Method will be used to detect strand bias, including 'SOR' and 'Fisher'. Default: 'SOR'. SOR: StrandOddsRatio ( <a href="https://gatk.broadinstitute.org/hc/en-us/articles/360041849111-StrandOddsRatio">https://gatk.broadinstitute.org/hc/en-us/articles/360041849111-StrandOddsRatio</a> ) Fisher's Exat Test: Switch to Phred socre ( <a href="https://gatk.broadinstitute.org/hc/en-us/articles/360035532152-Fisher-s-Exact-Test">https://gatk.broadinstitute.org/hc/en-us/articles/360035532152-Fisher-s-Exact-Test</a> ) |
| SBscore | Cutoff strand bias score used to filter variants. Default: 3                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |

**Value**

An MAF data frame where some variants have S tag in CaTag column for strand bias filtration

**Examples**

```
maf <- vcfToMAF(system.file("extdata",
"WES_EA_T_1_mutect2.vcf", package="CaMutQC"))
mafF <- mutFilterSB(maf)
```

---

|               |                      |
|---------------|----------------------|
| mutFilterTech | <i>mutFilterTech</i> |
|---------------|----------------------|

---

## Description

Filter potential artifacts produced through technical issue, including filtration for sequencing quality, strand bias, adjacent indel tag, normal depth, panel of normal (PON) and FILTER field.

## Usage

```
mutFilterTech(
  maf,
  PONfile = NULL,
  PONformat = "vcf",
  panel = "Customized",
  tumorDP = 20,
  normalDP = 10,
  tumorAD = 5,
  normalAD = Inf,
  VAF = 0.05,
  VAFratio = 0,
  dbsnpCutoff = 19,
  nonCutoff = 8,
  SBmethod = "SOR",
  SBscore = 3,
  maxIndelLen = 50,
  minInterval = 10,
  tagFILTER = "PASS",
  progressbar = TRUE,
  verbose = TRUE
)
```

## Arguments

|           |                                                                                                                                                                                                                                                                                                                                                             |
|-----------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| maf       | An MAF data frame, generated by <a href="#">vcfToMAF</a> function.                                                                                                                                                                                                                                                                                          |
| PONfile   | Panel-of-Normals files, which can be either obtained through GATK ( <a href="https://gatk.broadinstitute.org/hc/en-us/articles/360035890631-Panel-of-Normals-PON-">https://gatk.broadinstitute.org/hc/en-us/articles/360035890631-Panel-of-Normals-PON-</a> ) or generated by users. Should have at least four columns: CHROM, POS, REF, ALT Defalut: NULL. |
| PONformat | The format of PON file, either "vcf" or "txt". Default: "vcf"                                                                                                                                                                                                                                                                                               |
| panel     | The sequencing panel applied on the dataset. Parameters for <a href="#">mutFilterQual</a> function are set differently for different panels. Default: "Customized". Options: "MSKCC", "WES".                                                                                                                                                                |
| tumorDP   | Threshold of tumor total depth. Default: 20                                                                                                                                                                                                                                                                                                                 |
| normalDP  | Threshold of normal total depth. Default: 10                                                                                                                                                                                                                                                                                                                |
| tumorAD   | Threshold of tumor alternative allele depth. Default: 5                                                                                                                                                                                                                                                                                                     |
| normalAD  | Threshold of normal alternative allele depth. Default: Inf                                                                                                                                                                                                                                                                                                  |
| VAF       | Threshold of VAF value. Default: 0.05                                                                                                                                                                                                                                                                                                                       |
| VAFratio  | Threshold of VAF ratio (tVAF/nVAF). Default: 0                                                                                                                                                                                                                                                                                                              |

|             |                                                                                                                                                                                                                                                                              |
|-------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| dbSNPCutoff | Cutoff of normal depth for dbSNP variants. Default: 19.                                                                                                                                                                                                                      |
| nonCutoff   | Cutoff of normal depth for non-dbSNP variants. Default: 8.                                                                                                                                                                                                                   |
| SBmethod    | Method will be used to detect strand bias, including 'SOR' and 'Fisher'. Default: 'SOR'. SOR: StrandOddsRatio ( <a href="https://gatk.broadinstitute.org/hc/en-us/articles/360041849111">https://gatk.broadinstitute.org/hc/en-us/articles/360041849111</a> StrandOddsRatio) |
| SBscore     | Cutoff strand bias score used to filter variants. Default: 3                                                                                                                                                                                                                 |
| maxIndelLen | Maximum length of indel accepted to be included. Default: 50                                                                                                                                                                                                                 |
| minInterval | Minimum length of interval between an SNV and an indel accepted to be included. Default: 10                                                                                                                                                                                  |
| tagFILTER   | Variants with specific tag in FILTER column will be kept, set to NULL if you want to skip this filter. Default: 'PASS'                                                                                                                                                       |
| progressbar | Whether to show progress bar when running this function Default: TRUE                                                                                                                                                                                                        |
| verbose     | Whether to generate message/notification during the filtration process. Default: TRUE.                                                                                                                                                                                       |

### Value

An MAF data frame after filtration for technical issue

### Examples

```
maf <- vcfToMAF(system.file("extdata",
"WES_EA_T_1_mutect2.vcf", package="CaMutQC"))
maff <- mutFilterTech(maf, PONfile=system.file("extdata",
"PON_test.txt", package="CaMutQC"), PONformat="txt")
```

---

|               |                      |
|---------------|----------------------|
| mutFilterType | <i>mutFilterType</i> |
|---------------|----------------------|

---

### Description

Filter variants based on variant types

### Usage

```
mutFilterType(maf, keepType = "exonic")
```

### Arguments

|          |                                                                                                                    |
|----------|--------------------------------------------------------------------------------------------------------------------|
| maf      | An MAF data frame, generated by <a href="#">vcfToMAF</a> function.                                                 |
| keepType | A group of variant classifications will be kept, including 'exonic', 'nonsynonymous' and 'all'. Default: 'exonic'. |

### Value

An MAF data frame where some variants has T tag in CaTag column for variant type filtration

### Examples

```
maf <- vcfToMAF(system.file("extdata",
"WES_EA_T_1_mutect2.vcf", package="CaMutQC"))
maff <- mutFilterType(maf)
```

mutSelection

*mutSelection***Description**

Select candidate variants for cancer research.

**Usage**

```
mutSelection(
  maf,
  dbVAF = 0.01,
  ExAC = TRUE,
  Genomesprojects1000 = TRUE,
  ESP6500 = TRUE,
  gnomAD = TRUE,
  dbSNP = FALSE,
  keepCOSMIC = TRUE,
  keepType = "exonic",
  bedFile = NULL,
  bedHeader = FALSE,
  bedFilter = FALSE,
  progressbar = TRUE,
  verbose = TRUE
)
```

**Arguments**

|                     |                                                                                                                              |
|---------------------|------------------------------------------------------------------------------------------------------------------------------|
| maf                 | An MAF data frame, generated by <a href="#">vcfToMAF</a> function.                                                           |
| dbVAF               | Threshold of VAF of certain population for variants in database. Default: 0.01                                               |
| ExAC                | Whether to filter variants listed in ExAC with VAF higher than cutoff(set in VAF parameter). Default: TRUE.                  |
| Genomesprojects1000 | Whether to filter variants listed in Genomesprojects1000 with VAF higher than cutoff(set in VAF parameter). Default: TRUE.   |
| ESP6500             | Whether to filter variants listed in ESP6500 with VAF higher than cutoff(set in VAF parameter). Default: TRUE.               |
| gnomAD              | Whether to filter variants listed in gnomAD with VAF higher than cutoff(set in VAF parameter). Default: TRUE.                |
| dbSNP               | Whether to filter variants listed in dbSNP. Default: FALSE.                                                                  |
| keepCOSMIC          | Whether to keep variants in COSMIC even they have are present in germline database. Default: TRUE.                           |
| keepType            | A group of variant classifications will be kept, including 'exonic', 'nonsynonymous' and 'all'. Default: 'exonic'.           |
| bedFile             | A file in bed format that contains region information. Default: NULL                                                         |
| bedHeader           | Whether the input bed file has a header or not. Default: FALSE.                                                              |
| bedFilter           | Whether to filter the information in bed file or not, which only leaves segments in Chr1-Ch22, ChrX and ChrY. Default: FALSE |

|             |                                                                                        |
|-------------|----------------------------------------------------------------------------------------|
| progressbar | Whether to show progress bar when running this function Default: TRUE                  |
| verbose     | Whether to generate message/notification during the filtration process. Default: TRUE. |

### Value

An MAF data frame with variants after selection.

### Examples

```
maf <- vcfToMAF(system.file("extdata",
"WES_EA_T_1_mutect2.vcf", package="CaMutQC"))
mafF <- mutSelection(maf)
```

---

|            |                   |
|------------|-------------------|
| processMut | <i>processMut</i> |
|------------|-------------------|

---

### Description

Takes union or intersection on multiple MAF data frame, and return 7 important columns.

### Usage

```
processMut(mafList, processMethod = "union")
```

### Arguments

|               |                                                                                                                          |
|---------------|--------------------------------------------------------------------------------------------------------------------------|
| mafList       | A list of MAF data frames after going through at least one CaMutQC filtration function, and the length of the list <= 3. |
| processMethod | Methods for processing mutations, including "union" and "intersection". Default: "union".                                |

### Value

A data frame includes mutations after taking union or intersection.

### Examples

```
maf_MuSE <- vcfToMAF(system.file("extdata/Multi-caller",
"WES_EA_T_1.MuSE.vcf", package="CaMutQC"))
maf_MuSE_f <- mutFilterCom(maf_MuSE, report=FALSE, TMB=FALSE,
PONfile=system.file("extdata", "PON_test.txt", package="CaMutQC"),
PONformat="txt")
maf_VarScan2 <- vcfToMAF(system.file("extdata/Multi-caller",
"WES_EA_T_1_varscan_filter_snp.vcf", package="CaMutQC"))
maf_VarScan2_f <- mutFilterCom(maf_VarScan2, report=FALSE, TMB=FALSE,
PONfile=system.file("extdata", "PON_test.txt", package="CaMutQC"),
PONformat="txt")
mafs <- list(maf_MuSE_f, maf_VarScan2_f)
maf_union <- processMut(mafs, processMethod="union")
```

tomaftools

*tomaftools***Description**

Transform a CaMutQC maf object to a maftools maf object.

**Usage**

```
tomaftools(
  maf,
  clinicalData = NULL,
  rmFlags = FALSE,
  removeDuplicatedVariants = TRUE,
  useAll = TRUE,
  gisticAllLesionsFile = NULL,
  gisticAmpGenesFile = NULL,
  gisticDelGenesFile = NULL,
  gisticScoresFile = NULL,
  cnLevel = "all",
  cnTable = NULL,
  isTCGA = FALSE,
  vc_nonSyn = NULL,
  verbose = TRUE
)
```

**Arguments**

|                          |                                                                                                                                                                     |
|--------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| maf                      | An MAF data frame, generated by <a href="#">vcfToMAF</a> function.                                                                                                  |
| clinicalData             | Clinical data associated with each # sample/Tumor_Sample_Barcode in MAF. Could be a text file or a data.frame. Default NULL. Inherited from maftools.               |
| rmFlags                  | Default FALSE. Can be TRUE or an integer. If TRUE, removes all the top 20 FLAG genes. If integer, remove top n FLAG genes. Inherited from maftools.                 |
| removeDuplicatedVariants | removes repeated variants in a particular sample, mapped to multiple transcripts of same Gene. See Description. Default TRUE. Inherited from maftools.              |
| useAll                   | logical. Whether to use all variants irrespective of values in Mutation_Status. Defaults to TRUE. If FALSE, only uses with values Somatic. Inherited from maftools. |
| gisticAllLesionsFile     | All Lesions file generated by gistic. e.g; all_lesions.conf_XX.txt, where XX is the confidence level. Default NULL. Inherited from maftools.                        |
| gisticAmpGenesFile       | Amplification Genes file generated by gistic. e.g; amp_genes.conf_XX.txt, where XX is the confidence level. Default NULL. Inherited from maftools.                  |
| gisticDelGenesFile       | Deletion Genes file generated by gistic. e.g; del_genes.conf_XX.txt, where XX is the confidence level. Default NULL. Inherited from maftools.                       |
| gisticScoresFile         | scores.gistic file generated by gistic. Default NULL Inherited from maftools.                                                                                       |

|           |                                                                                                                                                                                                                                                                |
|-----------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| cnLevel   | level of CN changes to use. Can be 'all', 'deep' or 'shallow'. Default uses all i.e, genes with both 'shallow' or 'deep' CN changes. Inherited from maftools.                                                                                                  |
| cnTable   | Custom copynumber data if gistic results are not available. Input file or a data.frame should contain three columns in aforementioned order with gene name, Sample name and copy number status (either 'Amp' or 'Del'). Default NULL. Inherited from maftools. |
| isTCGA    | Is input MAF file from TCGA source. If TRUE uses only first 12 characters from Tumor_Sample_Barcode. Inherited from maftools.                                                                                                                                  |
| vc_nonSyn | NULL. Provide manual list of variant classifications to be considered as non-synonymous. Rest will be considered as silent variants. Default uses Variant Classifications with High/Moderate variant consequences. Inherited from maftools.                    |
| verbose   | TRUE logical. Default to be talkative and prints summary. Inherited from maftools.                                                                                                                                                                             |

### Value

An maf object that can be recognized by maftools.

### Examples

```
maf_CaMutQC <- vcfToMAF(system.file("extdata/Multi-caller/",
package="CaMutQC"), multiVCF=TRUE)
maf_maftools <- tomaftools(maf_CaMutQC)
```

---

toMesKit

toMeskit

---

### Description

Transform a CaMutQC maf object to a MesKit maf object.

### Usage

```
toMesKit(
  maf,
  clinicalFile,
  ccFile = NULL,
  nonSyn.vc = NULL,
  use.indel.ccf = FALSE,
  ccf.conf.level = 0.95
)
```

### Arguments

|              |                                                                                                           |
|--------------|-----------------------------------------------------------------------------------------------------------|
| maf          | An MAF data frame, generated by <a href="#">vcfToMAF</a> function.                                        |
| clinicalFile | A clinical data file includes Tumor_Sample_Barcode, Tumor_ID, Patient_ID. Tumor_Sample_Label is optional. |
| ccFile       | A CCF file of somatic mutations. Default NULL.                                                            |
| nonSyn.vc    | List of Variant classifications which are considered as non-silent. Default NULL.                         |

`use.indel.ccf` Whether include indels in `ccfFile`. Default FALSE.

`ccf.conf.level` The confidence level of CCF to identify clonal or subclonal. Only works when "CCF\_std" or "CCF\_CI\_high" is provided in `ccfFile`. Default 0.95.

### Value

An maf object that can be recognized by MesKit.

### Examples

```
maf_CaMutQC <- vcfToMAF(system.file("extdata/Multi-caller/",
package="CaMutQC"), multiVCF=TRUE)
clin_file <- system.file("extdata", "clin.txt", package="CaMutQC")
maf_MesKit <- toMesKit(maf_CaMutQC, clinicalFile=clin_file)
```

vcfToMAF

*vcfToMAF*

### Description

Format transformation from VCF to MAF.

### Usage

```
vcfToMAF(
  vcfFile,
  multiVCF = FALSE,
  inputStrelka = FALSE,
  writeFile = FALSE,
  MAFfile = "MAF.maf",
  MAFdir = "./",
  tumorSampleName = "Extracted",
  normalSampleName = "Extracted",
  ncbiBuild = "Extracted",
  MAFcenter = ".",
  MAFstrand = "+",
  filterGene = FALSE,
  simplified = FALSE
)
```

### Arguments

|                           |                                                                                                                                                 |
|---------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>vcfFile</code>      | Directory of a VCF file, or the path to several VCF files that is going to be transformed. Files should be in .vcf or .vcf.gz format.           |
| <code>multiVCF</code>     | Logical, whether the input is a path that leads to several VCFs that come from multi-region/sample/caller sequencing. Default: FALSE            |
| <code>inputStrelka</code> | The type of variants ('INDEL' or 'SNV') in VCF file if it is from Strelka. Default: FALSE                                                       |
| <code>writeFile</code>    | Whether to directly write MAF file to the disk. If FALSE, a MAF data frame will be returned. If TRUE, a MAF file will be saved. Default: FALSE. |

|                  |                                                                                                                                                                        |
|------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| MAFfile          | File name of the exported MAF file, if writeFile is set as TRUE.                                                                                                       |
| MAFdir           | Directory of the exported MAF file, if writeFile is set as TRUE.                                                                                                       |
| tumorSampleName  | Name of the tumor sample(s) in the VCF file(s). If it is set as 'Extracted', tumorSampleName would be extracted automatically from the VCF file. Default: 'Extracted'. |
| normalSampleName | Name the normal sample in the VCF file. If it is set as 'Extracted', normalSampleName would be extracted automatically from the VCF file. Default: 'Extracted'.        |
| ncbiBuild        | The reference genome used for the alignment, which will be presented as value in 'NCBIbuild' column in MAF file. Default: 'GRCh38'.                                    |
| MAFcenter        | One or more genome sequencing center reporting the variant, which will be presented as value in 'Center' column in MAF. Default: '.'.                                  |
| MAFstrand        | Genomic strand of the reported allele, which will be presented as value in 'Strand' column in MAF file. Default: '+'.                                                  |
| filterGene       | Logical. Whether to filter variants without Hugo Symbol. Default: FALSE                                                                                                |
| simplified       | Logical. Whether to extract the first thirteen columns after converting to MAF file. Default: FALSE                                                                    |

### Value

A detailed MAF data frame

### Examples

```
maf <- vcfToMAF(system.file("extdata", "WES_EA_T_1_mutect2.vcf",
package="CaMutQC"))
```

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