

# Package ‘MTseeker’

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**Type** Package

**Title** Bioconductor Tools for Human Mitochondrial Variant Analysis

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**Description** Variant analysis tools for mitochondrial genetics.

**biocViews** Genetics, Metabolomics, VariantAnnotation

**Depends** viridis, S4Vectors, GenomeInfoDb, GenomicAlignments,  
VariantAnnotation

**Imports** xml2, utils, gmapR, methods, IRanges, Biobase, circlize,  
jsonlite, graphics, Rsamtools, grDevices, Biostrings,  
rtracklayer, VariantTools, Homo.sapiens, BiocGenerics,  
GenomicRanges, GenomicFeatures, SummarizedExperiment

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---

anno\_rCRS

*annotation for the regions (genic and not) of the rCRS mitogenome*


---

## Description

annotation for the regions (genic and not) of the rCRS mitogenome

## Usage

```
anno_rCRS
```

## Format

a GRanges object

## Examples

```
data(anno_rCRS)
subset(anno_rCRS, region == "D-loop")
```

---

byStrand	<i>simple helper function to split a *RangesList by the strand of its mt target</i>
----------	---

---

### Description

If presented with a GAlignments/MAlignments, this method will split the element by strand, i.e. + alignments and - alignments. Otherwise the method retrieves ranges/variant calls that overlap genic elements on the heavy and light strands of the mitochondrial genome.

### Usage

```
byStrand(x, anno = NULL)
```

### Arguments

x	a *Ranges[List] or *Alignments[List]
anno	optional feature annotation, will use mtAnno.rCRS if NULL

### Value

elements of x over features on each strand OR x split by strand

### Examples

```
data(RONKSvariants, package="MTseekerData")
byStrand(RONKSvariants)
```

---

callMT	<i>call mitochondrial variants against rCRS from an MAlignments[List] object</i>
--------	--

---

### Description

‘callMTVars’ is a helper function for callMT

### Usage

```
callMT(mal, ..., parallel = FALSE, verbose = FALSE)

callMTVars(BAM, SIZE = 75, GENOME = "rCRS", CHR = "chrM",
           COV = NULL, verbose = FALSE)
```

**Arguments**

mal	an MAlignments (or, potentially, an MAlignmentsList)
...	other arguments to pass to VariantTools::callVariants
parallel	try to run in parallel? (FALSE; this is super unstable)
verbose	be verbose? (FALSE; turn on for debugging purposes)
BAM	the BAM filename (for callMTVars)
SIZE	the read length (for callMTVars; default is 75)
GENOME	the reference genome (for callMTVars; default is rCRS)
CHR	the mt contig name (for callMTVars; default is chrM)
COV	average read coverage (so we don't have to countBam)

**Details**

FIXME: transition gmapR from import to suggestion  
 FIXME: use Rsamtools::pileup by default  
 FIXME: optional haplogroup masking?

**Value**

an MVRanges (or, potentially, an MVRangesList)

**Examples**

```
library(MTseekerData)
BAMdir <- system.file("extdata", "BAMs", package="MTseekerData")
BAMs <- paste0(BAMdir, "/", list.files(BAMdir, pattern=".bam$"))
(mal <- getMT(BAMs[1]))
if (requireNamespace("GmapGenome.Hsapiens.rCRS", quietly=TRUE)) {
  (mvr <- callMT(mal))
  filt(snpCall(mvr))
} else {
  message("You have not yet installed an rCRS reference genome.")
  message("Consider running the indexMTgenome() function to do so.")
  message("The RONKSvariants object in MTseekerData is a result of callMT.")
}
```

---

chrominfo.rCRS

*Sequence information (seqinfo) for the rCRS mitogenome*

---

**Description**

Sequence information (seqinfo) for the rCRS mitogenome

**Usage**

```
chrominfo.rCRS
```

**Format**

a Seqinfo object

**Examples**

```
data(chrominfo.rCRS)
library(GenomeInfoDb) # wat
seqlengths(chrominfo.rCRS)
```

---

filterMT	<i>Filter SummarizedExperiment or DataFrame values based on its \$mtCovg column</i>
----------	---

---

**Description**

Griffin et al. (Genetics in Medicine 2014) recommends 20x coverage for mtDNA sequencing to have comparable error rates to Sanger sequencing. By default, that is the cutoff applied here to ensure halfway decent variant annotation.

**Usage**

```
filterMT(DFSE, minCovg = 20, fpFilter = FALSE, NuMT = FALSE)
```

**Arguments**

DFSE	a DataFrame/SummarizedExperiment with colData()\$'mtCovg'
minCovg	minimum covg (20, cf. Griffin, Genetics in Medicine 2014)
fpFilter	apply Triska's homopolymer false positive filter? (FALSE)
NuMT	apply the 0.03 VAF NuMT filter from Ju (GR 2015)? (FALSE)

**Details**

Triska (Cancer Res, in revision) suggests a small number of masked regions where homopolymers can be a problem; these are avoided if fpFilter

The NuMT filtration step (Ju, in eLife 2014, suggests a variant allele cutoff of 0.03 to avoid false positive calls from nuclear-mitochondrial translocated or 'NuMT' fragments) is also a useful tool to cut down on nonsensical calls, although it may be important to use caution as low heteroplasmy can also resolve into apparent near-homoplasmy at the single-cell level, at least in our (TJT & co) experience.

As a consequence of the Wild West nature for published methods of high-throughput mitochondrial sequence variant analysis at the time of writing (2018), the default for this function is to filter on coverage only, as the user is expected to determine what additional filters to apply. We could envision changing these defaults down the road as standards congeal.

If DFSE is an MVRanges[List], the function will call filterMTvars instead.

**Value**

a filtered SE or data.frame

**Examples**

```
filterMT(data.frame(sample="foo", mtCovg=1000))
```

---

filterMTvars	<i>sanitize PASSing mitochondrial variant calls to a moderate degree</i>
--------------	--

---

**Description**

sanitize PASSing mitochondrial variant calls to a moderate degree

**Usage**

```
filterMTvars(vars, fp = TRUE, NuMT = 0.03, covg = 20)
```

**Arguments**

vars	an MVRanges or MVRangesList (will be unlisted and relisted)
fp	use false positive filter[s]? (TRUE: use Triska fpFilter)
NuMT	variants with VAF < [this number] will be presumed NuMTs (0.03)
covg	minimum median read coverage across chrM to be considered (20)

**Value**

a filtered set of variants

**Examples**

```
library(MTseekerData)
filterMTvars(RONKSvariants$RO_1)
```

---

fixMetadata	<i>fix metadata for an MAlignmentsList or MVRangesList, if needed and possible.</i>
-------------	---

---

**Description**

This function is punishingly simple – it just calls validMetadata() and assigns attr('fixedMeta') from the result. If no fixing is required, the object's existing metadata is used. The object (with fixed metadata) is then returned. If automatic fixes are impossible, a message is generated.

**Usage**

```
fixMetadata(x)
```

**Arguments**

x	an MAlignmentsList or MVRangesList
---	------------------------------------

**Value**

the object, with fixed metadata (if needed and possible)

**Examples**

```
library(MTseekerData)
data(RONKSreads)
fixed <- fixMetadata(RONKSreads)
```

---

fpFilter_RSRS	<i>false positive filter (fpFilter) for RSRS haplogroup-determining variants</i>
---------------	--

---

**Description**

false positive filter (fpFilter) for RSRS haplogroup-determining variants

**Usage**

```
fpFilter_RSRS
```

**Format**

a GRanges object

**Examples**

```
data(fpFilter_RSRS)
subset(fpFilter_RSRS, !is.na(L0))
subset(fpFilter_RSRS, !is.na(rCRS))
```

---

fpFilter_Triska	<i>a false positive (fp) filter from Petr Triska's manuscript on mtDNA variants</i>
-----------------	---

---

**Description**

a false positive (fp) filter from Petr Triska's manuscript on mtDNA variants

**Usage**

```
fpFilter_Triska
```

**Format**

a GRanges object

**Examples**

```
data(fpFilter_Triska)
show(fpFilter_Triska)
```

---

getMT	<i>grab the mitochondrial reads from a BAM &amp; estimate their fraction (of total)</i>
-------	---

---

### Description

This purely a convenience function, and an incredibly convenient one at that.

### Usage

```
getMT(bam, filter = FALSE, parallel = FALSE, plotMAPQ = FALSE, ...)
```

### Arguments

bam	a BAM filename, or DataFrame/SummarizedExperiment with \$BAM
filter	filter on bam\$mtCovg? (default is FALSE, don't filter)
parallel	load multiple BAMs in parallel, if possible? (FALSE)
plotMAPQ	plot distribution of mitochondrial mapping quality? (FALSE)
...	additional args to pass scanBamParam(), such as mapqFilter

### Value

an MAlignments or MAlignmentsList object

### Examples

```
library(MTseekerData)
BAMdir <- system.file("extdata", "BAMs", package="MTseekerData")
BAMs <- paste0(BAMdir, "/", list.files(BAMdir, pattern=".bam$"))
(mal <- getMT(BAMs[1]))
class(mal)

targets <- data.frame(BAM=BAMs, stringsAsFactors=FALSE)
rownames(targets) <- sapply(strsplit(basename(BAMs), "\\."), `[`, 1)
(mall <- getMT(targets))
class(mall)
```

---

hg19TorCRS	<i>a liftOver chain for hg19 to rCRS attempts. We do not recommend this.</i>
------------	--

---

### Description

a liftOver chain for hg19 to rCRS attempts. We do not recommend this.

### Usage

```
hg19TorCRS
```

**Format**

a Chain object

**Examples**

```
data(hg19TorCRS)
sapply(hg19TorCRS, offset)
```

---

indexMTGenome	<i>build and install GmapGenome.[organism].[mtGenome], currently Hsapiens.rCRS</i>
---------------	--

---

**Description**

gmapR needs a reference genome index in order for it to call any variants. We support rCRS (and only rCRS) as that reference, at least for the moment. This function creates & installs a reference (rCRS, the default) Gmap index. In principle, hg19 and mm10 could be supported; in practice, support is poor. (Also, the Yoruban chrM in hg19 is a terrible reference for variant calling.) We would be grateful for a patch to add mm10/GRCm38 support; eventually, we plan to add it in ourselves (as one might have guessed from Mouse Mitocarta).

**Usage**

```
indexMTGenome(mtGenome = "rCRS", fa = NULL, organism = "Hsapiens",
  destDir = NULL, install = TRUE, unlink = FALSE)
```

**Arguments**

mtGenome	mitochondrial reference genome to index (default is rCRS)
fa	FASTA file (default is to find included 'mtGenome'.fa)
organism	organism whose mitochondrial genome is indexed (Hsapiens)
destDir	optional destination for the package (\$HOME is default)
install	install the package after creation? (default is TRUE)
unlink	if an index package already exists, remove it? (FALSE)

**Details**

Note: this function creates a "skeleton key" rCRS index for contigs named 'chrM', 'MT', 'rCRS', 'NC\_012920.1', and/or 'gil251831106|ref|NC\_012920.1|'. The point of this kludge is to allow gmapR to call variants against various styles of contig names, whether NCBI, UCSC, Genbank, or colloquial rCRS.

**Value**

the path to the created package as a character string

**Examples**

```

if (.Platform$OS.type != "windows") {
  mtGenome <- "rCRS"
  fa <- system.file(paste0("extdata/", mtGenome, ".fa"), package="MTseeker")
  indexMTGenome(mtGenome=mtGenome, fa=fa, destDir=tempdir())
}

```

---

injectMTVariants	<i>Inject (one or more) variants against rCRS.</i>
------------------	--

---

**Description**

FIXME: this function could most likely be orders of magnitude faster. FIXME: this ONLY considers variants injected against rCRS, not RSRS or hg19.

**Usage**

```

injectMTVariants(mvr, gr = NULL, aa = TRUE, canon = 0.99, refX = 1,
  altX = 1)

```

**Arguments**

mvr	An MVRanges, usually from callMT, often subsetted
gr	A GRanges, usually of protein-coding regions (the default)
aa	Attempt to translate codon(s) affected by variant(s)? (TRUE)
canon	Minimum VAF to treat variants as canonical by subject (0.99)
refX	Reference depth below which variant is deemed canonical (1)
altX	Alternative depth above which variants deemed canonical (1)

**Value**

The GRanges, with ref/var DNA and AA and

**Examples**

```

library(MTseekerData)
RO_2 <- RONKSvariants[["RO_2"]]
injectMTVariants(RO_2)

```

---

MAlignments	<i>wrap a GAlignments for easier stats</i>
-------------	--

---

### Description

Normally the MAlignments constructor will be called by getMT(bam).

Depending on how a generic was originally designated, the arguments to these methods can have various argument names, but all of them tend to take an MAlignments as their argument.

### Usage

```
MAlignments(gal, bam)

genomeCoverage(x)

## S4 method for signature 'MAlignments'
Summary(x)

## S4 method for signature 'MAlignments'
show(object)

## S4 method for signature 'MAlignments'
fileName(object)

## S4 method for signature 'MAlignments'
scanBamHeader(files)

readLength(x)

## S4 method for signature 'MAlignments'
readLength(x)

genomeLength(x)

## S4 method for signature 'MAlignments'
genomeLength(x)
```

### Arguments

gal	a GAlignments
bam	a bam filename
x	an MAlignments
object	an MAlignments
files	an MAlignments

### Value

an MAlignments  
various things, as appropriate to the methods

**Examples**

```

library(MTseekerData)
BAMdir <- system.file("extdata", "BAMs", package="MTseekerData")
BAMs <- paste0(BAMdir, "/", list.files(BAMdir, pattern=".bam$"))
mal <- getMT(BAMs[1])
class(mal)
show(mal)

```

---

MAlignments-class	<i>wraps a GAlignments with information about coverage and its target BAM file</i>
-------------------	--

---

**Description**

The runLength slot stores readLength and named for historic reasons.

---

MAlignmentsList	<i>wrap a GAlignmentsList for viewing</i>
-----------------	---

---

**Description**

Normally the MAlignmentsList constructor will be called by getMT.

Depending on how a generic was originally designated, the arguments to these methods can have various argument names, but all of them tend to take an MAlignmentsList as their argument.

**Usage**

```

MAlignmentsList(...)

## S4 method for signature 'MAlignmentsList'
genomeCoverage(x)

## S4 method for signature 'MAlignmentsList'
readLength(x)

## S4 method for signature 'MAlignmentsList'
fileName(object)

## S4 method for signature 'MAlignmentsList'
Summary(x)

## S4 method for signature 'MAlignmentsList'
show(object)

```

**Arguments**

... MAlignments  
 x an MAlignmentsList  
 object an MAlignmentsList

**Value**

an MAlignments  
 various objects, as appropriate to the method

**Examples**

```
library(MTseekerData)
BAMdir <- system.file("extdata", "BAMs", package="MTseekerData")
print(BAMdir)
BAMs <- paste0(BAMdir, "/", list.files(BAMdir, pattern=".bam$"))
print(BAMs)
targets <- data.frame(BAM=BAMs, stringsAsFactors=FALSE)
rownames(targets) <- sapply(strsplit(basename(BAMs), "\\."), `[`, 1)
mall <- getMT(targets)
class(mall)
show(mall)
```

---

MAlignmentsList-class *wraps a GAlignmentsList (made up of MAlignments) for nicer viewing*

---

**Description**

wraps a GAlignmentsList (made up of MAlignments) for nicer viewing

---

mtAnno *annotation for the rCRS genome*

---

**Description**

annotation for the rCRS genome

**Usage**

mtAnno

**Format**

a GRanges object

---

 MTcircos

*plot a canonical human (or, in principle, any) mitochondrial genome*


---

## Description

The default font sizes, orientations, etc. are optimized for a "cold" start; if you want to fiddle with the details, crack open the code and modify it... or alternatively, add sectors/dendrograms inside of this "framed" version.

## Usage

```
MTcircos(variants = NULL, outside = NULL, inside = NULL,
          outcol = NULL, incol = NULL, anno = NULL, how = c("matrix",
          "VAF"), ...)
```

## Arguments

variants	optional MVRanges or MVRangesList to split by strand & plot
outside	optional MVRanges or MVRangesList to plot outside the circle
inside	optional MVRanges or MVRangesList to plot inside the circle
outcol	optional color assignment function or matrix for outside
incol	optional color assignment function or matrix for inside
anno	a GRanges (optional, defaults to mtAnno.rCRS if none given)
how	optional specification for how to plot multiple samples
...	other arguments to pass on to called functions

## Details

FIXME: add variant type coloration (del=blue, SNV=black, ins=red)

## Value

invisibly, a list: 'anno' (data.frame) + 'pfun' (panel.fun)

## Examples

```
library(MTseekerData)
data(ROKNSvariants)
MTcircos(ROKNSvariants)
# same as plot(ROKNSvariants)
title("Renal oncocyomas and normal kidney samples")
```

---

MTcomplex	<i>plot the (putative) functional impact of mutations to ETP genes as SVG</i>
-----------	---

---

**Description**

Tim Vickers created a beautiful illustration of the mitochondrial electron transport chain, and that's where coding mitochondrial DNA mutations will usually hit (we aren't plotting the mitoribosome or tRNAs just yet). So why reinvent the wheel (and possibly make it square)?

**Usage**

```
MTcomplex(variants, defColor = "#c9eded", verbose = FALSE)
```

**Arguments**

variants	an MVRanges or MVRangesList
defColor	default color (#c9eded is standard)
verbose	be verbose, for debugging? (FALSE)

**Value**

invisibly, the temporary file to which the SVG was written

**Examples**

```
library(MTseekerData)
data(RONKSvariants)
MTcomplex(RONKSvariants$RO_1)
```

---

MTcoverage	<i>Mitochondrial genome coverage and plots for MAlignments or MVRanges objects</i>
------------	--

---

**Description**

We co-opted the 'coverage' method to retrieve approximate coverage depth across the mitochondrial genome in MAlignments[List] and MVRanges[list], so this function gives back what it was supposed to do (provide an Rle) and can allow for some subsetting (e.g. variant-supporting-read coverage) that may be of interest when interpreting results.

**Usage**

```
MTcoverage(x, ...)

plotMTCoverage(x, ...)

plotStrandedMTCoverage(x, ...)
```

**Arguments**

x                    an MAlignments or MVRanges  
 ...                  other arguments to pass to GenomicAlignments::coverage()

**Details**

The plotting functions can handle MAlignments or MVRanges objects directly. plotMTCoverage does what one might expect, and plots (read or call) coverage. plotStrandedMTCoverage does the same thing, but keeps track of which strand.

**Value**

an RleList (or, invisibly for plot functions, a result list)

**Examples**

```
library(MTseekerData)

data(RONKSreads)
MTCoverage(RONKSreads$RO_1)
plotMTCoverage(RONKSreads$RO_1)

data(RONKSvariants)
MTCoverage(RONKSvariants$RO_1)
plotMTCoverage(RONKSvariants$RO_1)

par(mfrow=c(1,2))
plotMTCoverage(RONKSreads$NKS_1)
title("Read coverage for normal kidney sample 1")
plotMTCoverage(RONKSreads$RO_1)
title("Read coverage for renal oncocyoma sample 1")

par(mfrow=c(1,2))
plotStrandedMTCoverage(RONKSreads$NKS_1)
title("Stranded read coverage for normal kidney sample 1")
plotStrandedMTCoverage(RONKSreads$RO_1)
title("Stranded read coverage for renal oncocyoma sample 1")
```

---

mtGenes

*Base sequences of mitochondrial coding genes.*


---

**Description**

Base sequences of mitochondrial coding genes.

**Usage**

```
mtGenes
```

**Format**

a GRanges with a DNASTringSet of the base sequences as its mcols.

**Examples**

```
data(mtGenes)
width(mtGenes)
names(mtGenes$DNA)
```

---

mtGenes.rCRS

*All annotated gene regions (not just coding genes) from rCRS.*


---

**Description**

All annotated gene regions (not just coding genes) from rCRS.

**Usage**

```
mtGenes.rCRS
```

**Format**

a GRanges

**Examples**

```
data(mtGenes.rCRS)
subset(mtGenes.rCRS, region == "coding")
subset(mtGenes.rCRS, region == "tRNA")
```

---

MTHGVS

*convert mitochondrial variant calls to HGVS format for naming*


---

**Description**

convert mitochondrial variant calls to HGVS format for naming

**Usage**

```
MTHGVS(x, asMVR = FALSE, verbose = FALSE)
```

**Arguments**

x	an MVRanges (or, in a pinch, a GRanges)
asMVR	return a renamed MVRanges? (default is FALSE)
verbose	be yappy? (default is FALSE)

**Value**

proper HGVS names for the \*Ranges (or a renamed \*Ranges)

**Examples**

```
library(MTseekerData)
data(RONKSvariants)
MTHGVS(RONKSvariants$RO_1)
```

---

MVRanges

*wrap a VRanges for mitochondrial use*


---

**Description**

Usually the MVRanges constructor will be called by callMT().

Many of these methods can be dispatched from an MVRangesList OR an MVRanges. In such cases, the method will usually, but not always, be apply()ed.

**Usage**

```
MVRanges(vr, coverage = NA_real_)

## S4 method for signature 'MVRanges'
genomeCoverage(x)

## S4 method for signature 'MVRanges'
coverage(x)

## S4 method for signature 'MVRanges'
type(x)

## S4 method for signature 'MVRanges'
genes(x)

## S4 method for signature 'MVRanges'
snpCall(object)

## S4 method for signature 'MVRanges'
pos(x)

## S4 method for signature 'MVRanges'
show(object)

## S4 method for signature 'MVRanges'
annotation(object)

## S4 method for signature 'MVRanges'
getAnnotations(annotations)

## S4 method for signature 'MVRanges'
encoding(x)

## S4 method for signature 'MVRanges'
```

```

filt(x)

## S4 method for signature 'MVRanges'
genome(x)

## S4 method for signature 'MVRanges,missing,missing'
locateVariants(query,
  filterLowQual = FALSE, ...)

## S4 method for signature 'MVRanges'
tallyVariants(x, filterLowQual = TRUE, ...)

## S4 method for signature 'MVRanges,missing,missing,missing'
predictCoding(query, subject,
  seqSource, varAllele, ...)

## S4 method for signature 'MVRanges,missing,missing'
summarizeVariants(query, subject,
  mode, ...)

## S4 method for signature 'MVRanges,ANY'
plot(x, y, ...)

## S4 method for signature 'MVRanges'
consensusString(x, ...)

```

### Arguments

vr	the VRanges
coverage	estimated coverage
x	an MVRanges
object	an MVRanges
annotations	an MVRanges
query	an MVRanges
filterLowQual	boolean; drop non-PASSing variants from locateVariants?
...	miscellaneous args, passed through
subject	a GRanges, usually
seqSource	a BSgenome, usually
varAllele	variant alleles
mode	miscellaneous arguments
y	another MVRanges

### Value

an MVRanges  
 depends on the method invoked.

**Utility methods**

‘pos’ returns a character vector describing variant positions. ‘filt’ returns a subset of variant calls where PASS == TRUE (i.e. filtered) ‘coverage’ returns an Rle of coverage across the mitochondrial genome ‘genomeCoverage’ returns the estimated mitochondrial read coverage depth

**Annotation methods**

‘type’ returns a character vector describing variant type (SNV or indel) ‘genes’ retrieves a GRanges of mitochondrial gene locations for an MVRanges ‘snpCall’ retrieves single nucleotide variant polymorphisms PASSing filters ‘annotation’ gets (perhaps oddly) an MVRanges object annotated against rCRS ‘getAnnotations’ returns the GRanges of gene/region annotations for an MVR ‘encoding’ returns variants residing in coding regions (consequence unknown) ‘locateVariants’ annotates variants w/region, gene, and localStart/localEnd ‘predictCoding’ returns variants consequence predictions as one might expect ‘tallyVariants’ returns a named vector of variant types by annotated region. ‘summarizeVariants’ uses MitImpact to attempt annotation of coding variants. ‘consensusString’ edits rCRS to create a consensus genotype for eg Haplogrep

**Visualization methods**

‘plot’ creates a circular plot of mitochondrial variant calls with annotation

**Examples**

```
library(MTseekerData)
BAMdir <- system.file("extdata", "BAMs", package="MTseekerData")
BAMs <- paste0(BAMdir, "/", list.files(BAMdir, pattern=".bam$"))
(mal <- getMT(BAMs[1]))
if (requireNamespace("GmapGenome.Hsapiens.rCRS", quietly=TRUE)) {
  (mvr <- callMT(mal))
  locateVariants(mvr)
  predictCoding(mvr)
} else {
  message("You have not yet installed an rCRS reference genome.")
  message("Consider running the indexMTgenome() function to do so.")
  message("An example MVRanges is RONKSvariants$RO_1 from MTseekerData.")
}

# summarizeVariants can take too long to run, and requires internet access
```

---

MVRanges-class

*like a VRanges, but for mitochondria*


---

**Description**

like a VRanges, but for mitochondria

---

MVRangesList

*Wrap a VRangesList for mitochondrial use.*

---

## Description

Usually an MVRangesList will be created by callMT.

## Usage

```
MVRangesList(...)
```

```
## S4 method for signature 'MVRangesList'  
genomeCoverage(x)
```

```
## S4 method for signature 'MVRangesList'  
genes(x)
```

```
## S4 method for signature 'MVRangesList'  
snpCall(object)
```

```
## S4 method for signature 'MVRangesList'  
getAnnotations(annotations)
```

```
## S4 method for signature 'MVRangesList'  
encoding(x)
```

```
## S4 method for signature 'MVRangesList'  
coverage(x)
```

```
## S4 method for signature 'MVRangesList,missing,missing,missing'  
predictCoding(query,  
  subject, seqSource, varAllele, ...)
```

```
## S4 method for signature 'MVRangesList'  
show(object)
```

```
## S4 method for signature 'MVRangesList'  
filt(x)
```

```
## S4 method for signature 'MVRangesList'  
granges(x, filterLowQual = TRUE)
```

```
## S4 method for signature 'MVRangesList,missing,missing'  
summarizeVariants(query,  
  filterLowQual = TRUE, ...)
```

```
## S4 method for signature 'MVRangesList'  
genome(x)
```

```
## S4 method for signature 'MVRangesList,missing,missing'  
locateVariants(query,
```

```

    filterLowQual = TRUE, ...)

## S4 method for signature 'MVRangesList,ANY'
plot(x, y, ...)

## S4 method for signature 'MVRangesList'
consensusString(x, ...)

```

### Arguments

...	miscellaneous args, passed through
x	an MVRangesList (for some methods)
object	an MVRangesList (for other methods)
annotations	an MVRangesList (for getAnnotations)
query	an MVRangesList (for predictCoding)
subject	a GRanges, usually
seqSource	a BSgenome, usually
varAllele	variant alleles
filterLowQual	opt. for 'granges'/'summarizeVariants'
y	another MVRangesList

### Value

the MVRangesList  
depends on the method invoked.

### Utility methods

'genomeCoverage' returns estimated mitochondrial read coverage depth 'coverage' returns an RleList of coverage for each sample's chrM 'filt' removes variants where PASS != TRUE for each element

### Annotation methods

'genes' returns an annotated GRanges of mitochondrial genes 'getAnnotations' returns a GRanges of annotated mitochondrial features 'genome' returns the genome (or, perhaps, genomes) in an MVRL 'encoding' returns mutations in coding regions for each element 'granges' returns mildly annotated aggregates of variant sites 'snpCall' retrieves single nucleotide variant polymorphisms 'locateVariants' locates variants within genes, tRNA, rRNA, or D-loop 'summarizeVariants' attempts mass functional annotation of variant sites 'consensusString' creates consensus genotypes from rCRS for eg Haplogrep

### Visualization methods

'plot' creates circular plot of mitochondrial variant calls

**Examples**

```

library(MTseekerData)
BAMdir <- system.file("extdata", "BAMs", package="MTseekerData")
BAMs <- paste0(BAMdir, "/", list.files(BAMdir, pattern=".bam$"))
targets <- data.frame(BAM=BAMs, stringsAsFactors=FALSE)
rownames(targets) <- sapply(strsplit(basename(BAMs), "\\."), `\[`, 1)
(mall <- getMT(targets))

if (requireNamespace("GmapGenome.Hsapiens.rCRS", quietly=TRUE)) {
  (mvr1 <- callMT(mall))
  filt(mvr1$pt1_cell11)
} else {
  message("You have not yet installed an rCRS reference genome.")
  message("Consider running the indexMTgenome() function to do so.")
  message("An example MVRangesList is RONKSvariants from MTseekerData.")
}

```

---

MVRangesList-class     *like a VRangesList, but for mitochondria*

---

**Description**

like a VRangesList, but for mitochondria

---

rCRSeq	<i>The complete sequence of the human rCRS mitogenome. Yes, it's that small.</i>
--------	--

---

**Description**

The complete sequence of the human rCRS mitogenome. Yes, it's that small.

**Usage**

rCRSeq

**Format**

a DNASTringSet of length 1

**Examples**

```

data(rCRSeq)
width(rCRSeq)
data(mtGenes.rCRS)
getSeq(rCRSeq, mtGenes.rCRS)

```

---

s4Methods	<i>List all defined methods for an S4 class (or classes, if you must)</i>
-----------	---

---

**Description**

Mostly for debugging and making architectural choices, e.g. about coverage()

**Usage**

```
s4Methods(...)
```

**Arguments**

... name[s] of class[es] (please note, results will be union'ed)

**Details**

Note: this is borrowed from Hadley, who borrowed it from a BioC workshop!

**Value**

methods for the class[es], union'ed into a character vector

**Examples**

```
s4Methods("MVRangesList")
s4Methods("MAlignmentsList")
```

---

validMetadata	<i>Ensure that the metadata caches in MAlignmentsLists and MVRangesLists are OK</i>
---------------	---

---

**Description**

In order to avoid a lot of lengthy calculations, both MAlignmentsList and MVRangesList objects keep a cache of some relevant statistics and filenames in their metadata slot. If these caches get stale, it can cause problems.

**Usage**

```
validMetadata(x)
```

**Arguments**

x an MAlignmentsList or an MVRangesList

**Details**

This function performs some sanity checks on the caches so that the above problems are unlikely to occur, provided that checkMetadataCache() is called at sensible times. This function is NOT a replacement for validObject().

**Value**

TRUE or FALSE (if FALSE, attr(res)\$mismatches shows why)

**Examples**

```
library(MTseekerData)
data(RONKSreads)
if(validMetadata(RONKSreads)) message("RONKSreads has valid metadata")
```

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