

Package ‘MTseekerData’

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Type Package

Title Supporting Data for the MTseeker Package

Description Provides examples for the MTseeker package vignette.

Version 1.3.0

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Depends R (>= 3.5)

Imports utils, IRanges, GenomeInfoDb, GenomicRanges, GenomicFeatures,
VariantAnnotation, Homo.sapiens, MTseeker

Suggests gmapR, xml2, rtracklayer

biocViews ExperimentData, Genome

NeedsCompilation no

RoxygenNote 6.1.0

Encoding UTF-8

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R topics documented:

.onAttach	2
mitocarta2.hg19	2
mitocarta2.mm10	3
RONKSreads	4
RONKSvariants	4
Index	6

```
.onAttach
```

Data for the MTseeker package examples.

Description

Data for the MTseeker package examples.

Usage

```
.onAttach(lib, pkgname = "MTseekerData")
```

Arguments

lib	the library
pkgname	the package name

Value

nothing, it's a package

```
mitocarta2.hg19
```

MitoCarta 2.0: an atlas of mitochondrial genes and proteins

Description

This is the hg19 (human) version of MitoCarta 2.0, downloaded from <https://www.broadinstitute.org/scientific-community/science/programs/metabolic-disease-program/publications/mitocarta/mitocarta-in-0>

Usage

```
mitocarta2.hg19
```

Format

A GRanges object.

Details

The associated publication is Calvo, S.E., Klauser, C.R., Mootha, V.K. MitoCarta2.0: an updated inventory of mammalian mitochondrial proteins (2015). Nucleic Acids Research.

The publication is available from <http://nar.oxfordjournals.org/content/early/2015/10/07/nar.gkv1003.full>

Please cite the publication if you use the MitoCarta database.

Source

<http://www.broadinstitute.org/ftp/distribution/metabolic/papers/Pagliarini/MitoCarta2.0/Human.MitoCarta2.0.bed>

Examples

```
data(mitocarta2.hg19)
show(mitocarta2.hg19)
```

mitocarta2.mm10

MitoCarta 2.0: an atlas of mitochondrial genes and proteins

Description

This is the mm10 (mouse) version of MitoCarta 2.0, downloaded from <https://www.broadinstitute.org/scientific-community/science/programs/metabolic-disease-program/publications/mitocarta/mitocarta-in-0>

Usage

```
mitocarta2.mm10
```

Format

A GRanges object.

Details

The associated publication is Calvo, S.E., Klauser, C.R., Mootha, V.K. MitoCarta2.0: an updated inventory of mammalian mitochondrial proteins (2015). Nucleic Acids Research.

The publication is available from <http://nar.oxfordjournals.org/content/early/2015/10/07/nar.gkv1003.full>

Please cite the publication if you use the MitoCarta database.

Source

<http://www.broadinstitute.org/ftp/distribution/metabolic/papers/Pagliarini/MitoCarta2.0/Mouse.MitoCarta2.0.bed>

Examples

```
data(mitocarta2.mm10)
show(mitocarta2.mm10)
```

RONKSreads	<i>RONKSreads: chrM reads from Renal Oncocytomas and Normal Kidney Samples</i>
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Description

RONKS == "Renal Oncocytoma, Normal Kidney Sample" matched by patient This object was produced by applying MTseeker::getMT(BAMs) to the full exome BAMs, aligned against hg19_rCRSchrM (i.e. GRCh37 with UCSC contigs).

Usage

```
RONKSreads
```

Format

An MAlignmentsList object, which subclasses GAlignmentsList

Source

<https://www.ncbi.nlm.nih.gov/bioproject/PRJNA271036/>

Examples

```
library(MTseeker)
data(RONKSreads)
show(RONKSreads)
```

RONKSvariants	<i>RONKSvariants: mitochondrial variant calls from RONKSreads</i>
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Description

RONKS == "Renal Oncocytoma, Normal Kidney Sample" matched by patient This object was produced by applying MTseeker::callMT(RONKSreads).

Usage

```
RONKSvariants
```

Format

An MVRangesList object, which subclasses VRangesList

Source

<https://www.ncbi.nlm.nih.gov/bioproject/PRJNA271036/>

Examples

```
library(MTseeker)
data(RONKSvariants)
show(RONKSvariants)
endoapply(RONKSvariants, subset, PASS == TRUE)
```

Index

*Topic **datasets**

mitocarta2.hg19, [2](#)

mitocarta2.mm10, [3](#)

RONKSreads, [4](#)

RONKSvariants, [4](#)

.onAttach, [2](#)

mitocarta2.hg19, [2](#)

mitocarta2.mm10, [3](#)

RONKSreads, [4](#)

RONKSvariants, [4](#)