

# Package ‘MTseekerData’

May 14, 2019

**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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**License** Artistic-2.0

**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

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

**git\_branch** master

**git\_last\_commit** 64da329

**git\_last\_commit\_date** 2019-05-02

**Date/Publication** 2019-05-14

## R topics documented:

|                           |          |
|---------------------------|----------|
| .onAttach . . . . .       | 2        |
| mitocarta2.hg19 . . . . . | 2        |
| mitocarta2.mm10 . . . . . | 3        |
| RONKSreads . . . . .      | 4        |
| RONKSvariants . . . . .   | 4        |
| <b>Index</b>              | <b>6</b> |

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```
.onAttach
```

*Data for the MTseeker package examples.*

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**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

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```
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)
```

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mitocarta2.mm10

*MitoCarta 2.0: an atlas of mitochondrial genes and proteins*

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**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)
```

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|            |  |
|------------|--|
| 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](#)