

# Package ‘MTseekerData’

October 12, 2020

**Type** Package

**Title** Supporting Data for the MTseeker Package

**Description** Provides examples for the MTseeker package vignette.

**Version** 1.6.0

**Author** Tim Triche, Jr; Noor Sohail; Ben Johnson

**Maintainer** Tim Triche, Jr. <tim.triche@gmail.com>

**License** Artistic-2.0

**Depends** R (>= 3.5)

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

**Suggests** xml2, rtracklayer

**biocViews** ExperimentData, Genome

**NeedsCompilation** no

**RoxygenNote** 7.0.0

**Encoding** UTF-8

**PackageStatus** Deprecated

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

**git\_branch** RELEASE\_3\_11

**git\_last\_commit** cf1e02c

**git\_last\_commit\_date** 2020-04-27

**Date/Publication** 2020-10-12

## R topics documented:

.onAttach . . . . .	2
mitocarta2.hg19 . . . . .	2
mitocarta2.mm10 . . . . .	3
RONKSvariants . . . . .	4

<b>Index</b>	<b>5</b>
--------------	----------

---

```
.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)
```

---

RONKSvariants

*RONKSvariants: mitochondrial variant calls from RONKSreads*

---

### **Description**

RONKS == "Renal Oncocytoma, Normal Kidney Sample" matched by patient This object was produced by applying `MTseeker::callMT()` to PRJNA271036. An updated version called with `pile-upMT()` will be added presently.

### **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

## \* datasets

mitocarta2.hg19, [2](#)

mitocarta2.mm10, [3](#)

RONKSvariants, [4](#)

.onAttach, [2](#)

mitocarta2.hg19, [2](#)

mitocarta2.mm10, [3](#)

RONKSvariants, [4](#)