

# Package ‘MTseekerData’

April 11, 2019

**Type** Package

**Title** Supporting Data for the MTseeker Package

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

**Version** 1.0.0

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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** RELEASE\_3\_8

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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

<code>lib</code>	the library
<code>pkgname</code>	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*

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### 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)
```

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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(ROMKSreads).

**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)
```

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