

BSgenome.Mmulatta.UCSC.rheMac2

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Mmulatta

Macaca mulatta (Rhesus) full genome (UCSC version rheMac2)

Description

Macaca mulatta (Rhesus) full genome as provided by UCSC (rheMac2, Jan. 2006) and stored in Biostrings objects. NOTE: In most assemblies available at UCSC, Tandem Repeats Finder repeats were filtered to retain only the repeats with period ≤ 12 . However, the filtering was omitted for this assembly, so the TRF masks contain all Tandem Repeats Finder results.

Note

This BSgenome data package was made from the following source data files:

sequences: chromFa.tar.gz, upstream1000.fa.gz, upstream2000.fa.gz, upstream5000.fa.gz
from <http://hgdownload.cse.ucsc.edu/goldenPath/rheMac2/bigZips/>
AGAPS masks: gap.txt.gz from <http://hgdownload.cse.ucsc.edu/goldenPath/rheMac2/database/>
RM and TRF masks: chromOut.tar.gz and chromTrf.tar.gz
from <http://hgdownload.cse.ucsc.edu/goldenPath/rheMac2/bigZips/>

See [?BSgenomeForge](#) and the BSgenomeForge vignette (vignette("BSgenomeForge")) in the BSgenome software package for how to make a BSgenome data package.

Author(s)

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See Also

[BSgenome-class](#), [DNAString-class](#), [available.genomes](#), [BSgenomeForge](#)

Examples

```

Mmulatta
seqlengths(Mmulatta)
Mmulatta$chr1 # same as Mmulatta[["chr1"]]
## NOTE: In most assemblies available at UCSC, Tandem Repeats
## Finder repeats were filtered to retain only the repeats
## with period <= 12. However, the filtering was omitted for
## this assembly, so, despite the description being displayed
## for this mask, it contains all the Tandem Repeats Finder
## results.
masks(Mmulatta$chr1)$TRF
## To get rid of the masks altogether:
unmasked(Mmulatta$chr1)

if ("AGAPS" %in% masknames(Mmulatta)) {

  ## Check that the assembly gaps contain only Ns:
  checkOnlyNsInGaps <- function(seq)
  {
    ## Replace all masks by the inverted AGAPS mask
    masks(seq) <- gaps(masks(seq)["AGAPS"])
    unique_letters <- uniqueLetters(seq)
    if (any(unique_letters != "N"))
      stop("assembly gaps contain more than just Ns")
  }

  ## A message will be printed each time a sequence is removed
  ## from the cache:
  options(verbose=TRUE)

  for (seqname in seqnames(Mmulatta)) {
    cat("Checking sequence", seqname, "... ")
    seq <- Mmulatta[[seqname]]
    checkOnlyNsInGaps(seq)
    cat("OK\n")
  }
}

## See the GenomeSearching vignette in the BSgenome software
## package for some examples of genome-wide motif searching using
## Biostrings and the BSgenome data packages:
if (interactive())
  vignette("GenomeSearching", package="BSgenome")

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