

# BSgenome.Mmusculus.UCSC.mm10

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Mmusculus

*Mus musculus (Mouse) full genome (UCSC version mm10)*

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## Description

Mus musculus (Mouse) full genome as provided by UCSC (mm10, Dec. 2011) and stored in Biostrings objects.

## Note

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

sequences: chr1.fa.gz chr2.fa.gz chr3.fa.gz chr4.fa.gz chr5.fa.gz chr6.fa.gz chr7.fa.gz chr8.fa.gz  
from <http://hgdownload.cse.ucsc.edu/goldenPath/mm10/chromosomes/>  
AGAPS masks: <http://hgdownload.cse.ucsc.edu/goldenPath/mm10/database/gap.txt.gz>

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

```
Mmusculus
seqlengths(Mmusculus)
Mmusculus$chr1 # same as Mmusculus[["chr1"]]

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

  ## 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(Mmusculus)) {
    cat("Checking sequence", seqname, "... ")
    seq <- Mmusculus[[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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