

# BSgenome.Cfamiliaris.UCSC.canFam2

June 9, 2011

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Cfamiliaris

*Canis lupus familiaris* full genome (UCSC version canFam2)

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## Description

Canis lupus familiaris full genome as provided by UCSC (canFam2, May 2005) and stored in Biostrings objects.

## Note

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

```
sequences: chromFa.tar.gz
from http://hgdownload.cse.ucsc.edu/goldenPath/canFam2/bigZips/
AGAPS masks: all the chr*_gap.txt.gz files from ftp://hgdownload.cse.ucsc.edu/go
RM masks: http://hgdownload.cse.ucsc.edu/goldenPath/canFam2/bigZips/chromOut.tar
TRF masks: http://hgdownload.cse.ucsc.edu/goldenPath/canFam2/bigZips/chromTrf.ta
```

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

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

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

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

# Index

## \*Topic **data**

Cfamiliaris, [1](#)

## \*Topic **package**

Cfamiliaris, [1](#)

available.genomes, [1](#)

BSgenome-class, [1](#)

BSgenome.Cfamiliaris.UCSC.canFam2  
(*Cfamiliaris*), [1](#)

BSgenome.Cfamiliaris.UCSC.canFam2-package  
(*Cfamiliaris*), [1](#)

BSgenomeForge, [1](#)

Cfamiliaris, [1](#)

DNAStrng-class, [1](#)