

# BSgenome.Cfamiliaris.UCSC.canFam2

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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/goldenPath/canFam2/data/>

RM masks: <http://hgdownload.cse.ucsc.edu/goldenPath/canFam2/bigZips/chromOut.tar.gz>

TRF masks: <http://hgdownload.cse.ucsc.edu/goldenPath/canFam2/bigZips/chromTrf.tar.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**

```
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")
```

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