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

**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/](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/database/](ftp://hgdownload.cse.ucsc.edu/goldenPath/canFam2/database/)
- RM masks: [http://hgdownload.cse.ucsc.edu/goldenPath/canFam2/bigZips/chromOut.tar.gz](http://hgdownload.cse.ucsc.edu/goldenPath/canFam2/bigZips/chromOut.tar.gz)
- TRF masks: [http://hgdownload.cse.ucsc.edu/goldenPath/canFam2/bigZips/chromTrf.tar.gz](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**

```r
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

```r
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)
```

```r
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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