# BSgenome.Cfamiliaris.UCSC.canFam3

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*Canis lupus familiaris (Dog) full genome (UCSC version canFam3)*

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### Description

Canis lupus familiaris (Dog) full genome as provided by UCSC (canFam3, Sep. 2011) and stored in Biostrings objects.

### Note

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

```
sequences: canFam3.fa.gz and the upstream*.fa.gz files
from http://hgdownload.cse.ucsc.edu/goldenPath/canFam3/bigZips/
AGAPS masks: http://hgdownload.cse.ucsc.edu/goldenPath/canFam3/database/gap.txt.gz
RM masks: http://hgdownload.cse.ucsc.edu/goldenPath/canFam3/bigZips/canFam3.fa.out.gz
TRF masks: http://hgdownload.cse.ucsc.edu/goldenPath/canFam3/bigZips/canFam3.trf.bed.gz
```

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

### Author(s)

The Bioconductor Dev Team

### See Also

BSgenome-class, DNAString-class, available.genomes, BSgenomeForge

### Examples

```
BSgenome.Cfamiliaris.UCSC.canFam3
genome <- BSgenome.Cfamiliaris.UCSC.canFam3
seqlengths(genome)
genome$chr1  # same as genome[["chr1"]]

if ("AGAPS" %in% masknames(genome)) {
```

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