

# BSgenome.Cfamiliaris.UCSC.canFam2

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BSgenome.Cfamiliaris.UCSC.canFam2

*Full genome sequences for Canis lupus familiaris (UCSC version can-Fam2)*

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## Description

Full genome sequences for Canis lupus familiaris (Dog) 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:

chromFa.tar.gz from <http://hgdownload.cse.ucsc.edu/goldenPath/canFam2/bigZips/>

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](#) objects and the [available.genomes](#) function in the **BSgenome** software package.
- [DNAString](#) objects in the **Biostrings** package.
- The BSgenomeForge vignette (`vignette("BSgenomeForge")`) in the **BSgenome** software package for how to make a BSgenome data package.

**Examples**

```

BSgenome.Cfamilaris.UCSC.canFam2
genome <- BSgenome.Cfamilaris.UCSC.canFam2
seqlengths(genome)
genome$chr1 # same as genome[["chr1"]]

## -----
## Upstream sequences
## -----
## The upstream sequences for canFam2 (i.e. the sequences 1000 bases
## upstream of annotated transcription starts) can easily be extracted
## from the full genome sequences with something like:

library(GenomicFeatures)
txdb <- makeTranscriptDbFromUCSC("canFam2", "refGene")
gn <- sort(genes(txdb))
up1000 <- flank(gn, width=1000)
up1000seqs <- getSeq(genome, up1000)

## IMPORTANT: Make sure you use a TxDb package (or TranscriptDb object),
## that contains a gene model based on the exact same reference genome
## as the BSgenome object you pass to getSeq(). Note that you can make
## your own custom TranscriptDb object from various annotation resources.
## See the makeTranscriptDbFromUCSC(), makeTranscriptDbFromBiomart(),
## and makeTranscriptDbFromGFF() functions in the GenomicFeatures
## package.

## -----
## Genome-wide motif searching
## -----
## 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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