BSgenome.Cfamiliaris.UCSC.canFam2

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*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)**

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**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.Cfamiliaris.UCSC.canFam2
genome <- BSgenome.Cfamiliaris.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")
*Topic data
  BSgenome.Cfamiliaris.UCSC.canFam2, 1

*Topic package
  BSgenome.Cfamiliaris.UCSC.canFam2, 1

available.genomes, /

BSgenome, /
BSgenome.Cfamiliaris.UCSC.canFam2, 1
BSgenome.Cfamiliaris.UCSC.canFam2-package
  (BSgenome.Cfamiliaris.UCSC.canFam2), 1
BSgenomeForge, /
Cfamiliaris
  (BSgenome.Cfamiliaris.UCSC.canFam2), 1

DNAString, /