BSgenome.Cfamiliaris.UCSC.canFam2

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`BSgenome.Cfamiliaris.UCSC.canFam2`
Full genome sequences for Canis lupus familiaris (UCSC version canFam2)

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")
```

Index

∗ **data**
BSgenome.Cfamiliaris.UCSC.canFam2, 1
∗ **package**
BSgenome.Cfamiliaris.UCSC.canFam2, 1

available.genomes, *1*

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

Cfamiliaris (BSgenome.Cfamiliaris.UCSC.canFam2), 1

DNAString, *1*