BSgenome.Cfamiliaris.UCSC.canFam3

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Full genome sequences for Canis lupus familiaris (UCSC version canFam3)

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Description

Full genome sequences for Canis lupus familiaris (Dog) 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:

canFam3.fa.gz from http://hgdownload.cse.ucsc.edu/goldenPath/canFam3/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

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

## Upstream sequences

library(GenomicFeatures)
txdb <- makeTranscriptDbFromUCSC("canFam3", "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

if (interactive())
  vignette("GenomeSearching", package="BSgenome")
```
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