BSgenome.Cfamiliaris.UCSC.canFam2

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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"]]

## 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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