

BSgenome.Cfamiliaris.UCSC.canFam3

October 7, 2014

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

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 and the upstream*.fa.gz files
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)

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.canFam3
genome <- BSgenome.Cfamilaris.UCSC.canFam3
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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