BSgenome.Btaurus.UCSC.bosTau3

October 16, 2009

**Btaurus**

*Bos taurus (Cow) full genome (UCSC version bosTau3)*

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**Description**

*Bos taurus* (Cow) full genome as provided by UCSC (bosTau3, Aug. 2006) and stored in Biostrings objects.

**Note**

This BSgenome data package was made from the following source data files:

- **sequences**: all the *.fa.gz* files from [http://hgdownload.cse.ucsc.edu/goldenPath/bosTau3/chromosomes/](http://hgdownload.cse.ucsc.edu/goldenPath/bosTau3/chromosomes/)

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-class, DNAString-class, available.genomes, BSgenomeForge

**Examples**

```r
Btaurus
seqlengths(Btaurus)
Btaurus$chr1 # same as Btaurus["chr1"]

if ("AGAPS" %in% masknames(Btaurus)) {
  ## Check that the assembly gaps contain only Ns:
  checkOnlyNsInGaps <- function(seq)
  |
  ## Replace all masks by the inverted AGAPS mask
```
```r
masks(seq) <- gaps(masks(seq)["AGAPS"])
unique_letters <- uniqueLetters(seq)
if (any(unique_letters != "N"))
  stop("assembly gaps contain more than just Ns")
}

## A message will be printed each time a sequence is removed
## from the cache:
options(verbose=TRUE)

for (seqname in seqnames(Btaurus)) {
  cat("Checking sequence", seqname, "...")
  seq <- Btaurus[[seqname]]
  checkOnlyNsInGaps(seq)
  cat("OK\n")
}

## 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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