BSgenome.Dmelanogaster.UCSC.dm2

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Dmelanogaster  
Drosophila melanogaster full genome (UCSC version dm2)

Description
Drosophila melanogaster full genome as provided by UCSC (dm2, Apr. 2004) and stored in Biostrings objects.

Note
This BSgenome data package was made from the following source data files:
AGAPS masks: all the chr*_gap.txt.gz files from ftp://hgdownload.cse.ucsc.edu/goldenPath/dm2/database/
RM masks: http://hgdownload.cse.ucsc.edu/goldenPath/dm2/bigZips/chromOut.zip
TRF masks: http://hgdownload.cse.ucsc.edu/goldenPath/dm2/bigZips/chromTrf.zip

See ?BSgenomeForge and the BSgenomeForge vignette(vignette("BSgenomeForge")) in the BSgenome software package for how to make a BSgenome data package.

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See Also
BSgenome-class, DNAString-class, available.genomes, BSgenomeForge

Examples
Dmelanogaster
seqlengths(Dmelanogaster)
Dmelanogaster$chr2L  # same as Dmelanogaster["chr2L"]

if (!"AGAPS" %in% masknames(Dmelanogaster)) {
  ## 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:
```r
options(verbose=TRUE)
```

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

## See the GenomeSearching vignette in the BSgenome software
## package for some examples of genome-wide motif searching using
## Biostings and the BSgenome data packages:
```r
if (interactive())  
    vignette("GenomeSearching", package="BSgenome")
```
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