

BSgenome.Scerevisiae.UCSC.sacCer2

September 28, 2010

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| Scerevisiae | <i>Saccharomyces cerevisiae</i> (Yeast) full genome (UCSC version sac-Cer2) |
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Description

Saccharomyces cerevisiae (Yeast) full genome as provided by UCSC (sacCer2, June 2008) and stored in Biostrings objects.

Note

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

<http://hgdownload.cse.ucsc.edu/goldenPath/sacCer2/bigZips/chromFa.tar.gz>

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

```
Scerevisiae
seqlengths(Scerevisiae)
Scerevisiae$chrI # same as Scerevisiae[["chrI"]]

if ("AGAPS" %in% masknames(Scerevisiae)) {

  ## Check that the assembly gaps contain only Ns:
  checkOnlyNsInGaps <- function(seq)
  {
    ## Replace all masks by the inverted AGAPS mask
```

```
    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(Scerevisiae)) {
    cat("Checking sequence", seqname, "... ")
    seq <- Scerevisiae[[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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