**BSgenome.Hsapiens.UCSC.hg19**

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**Hsapiens**  
*Homo sapiens full genome (UCSC version hg19)*

**Description**

Homo sapiens full genome as provided by UCSC (hg19, Feb. 2009) and stored in Biostrings objects.

**Note**

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

- **AGAPS masks**: [http://hgdownload.cse.ucsc.edu/goldenPath/hg19/database/gap.txt.gz](http://hgdownload.cse.ucsc.edu/goldenPath/hg19/database/gap.txt.gz)
- **RM masks**: [http://hgdownload.cse.ucsc.edu/goldenPath/hg19/bigZips/chromOut.tar.gz](http://hgdownload.cse.ucsc.edu/goldenPath/hg19/bigZips/chromOut.tar.gz)
- **TRF masks**: [http://hgdownload.cse.ucsc.edu/goldenPath/hg19/bigZips/chromTrf.tar.gz](http://hgdownload.cse.ucsc.edu/goldenPath/hg19/bigZips/chromTrf.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**

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

if ("AGAPS" %in% masknames(Hsapiens)) {
  ## 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(Hsapiens)) {
  cat("Checking sequence", seqname, "...
  seq <- Hsapiens[[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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