**BSgenome.Hsapiens.UCSC.hg18**

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| Hsapiens | Homo sapiens (Human) full genome (UCSC version hg18) |

**Description**

Homo sapiens (Human) full genome as provided by UCSC (hg18, Mar. 2006) 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/hg18/database/
- RM masks: http://hgdownload.cse.ucsc.edu/goldenPath/hg18/bigZips/chromOut.zip
- TRF masks: http://hgdownload.cse.ucsc.edu/goldenPath/hg18/bigZips/chromTrf.zip

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

```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)

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:

```r
if (interactive())
    vignette("GenomeSearching", package="BSgenome")
```
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