

# BSgenome.Hsapiens.UCSC.hg17

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Hsapiens

*Homo sapiens full genome (UCSC version hg17)*

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## Description

Homo sapiens full genome as provided by UCSC (hg17, May 2004) and stored in Biostrings objects.

## Note

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

```
sequences: chromFa.zip, upstream1000.zip, upstream2000.zip, upstream5000.zip
from http://hgdownload.cse.ucsc.edu/goldenPath/hg17/bigZips/
AGAPS masks: all the chr*_gap.txt.gz files from ftp://hgdownload.cse.ucsc.edu/g
RM masks: http://hgdownload.cse.ucsc.edu/goldenPath/hg17/bigZips/chromOut.zip
TRF masks: http://hgdownload.cse.ucsc.edu/goldenPath/hg17/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)

H. Pages

## See Also

[BSgenome-class](#), [DNASTring-class](#), [available.genomes](#), [BSgenomeForge](#)

## Examples

```
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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