

# BSgenome.Hsapiens.UCSC.hg18

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Hsapiens

*Homo sapiens (Human) full genome (UCSC version hg18)*

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## 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:

sequences: chromFa.zip, upstream1000.zip, upstream2000.zip, upstream5000.zip  
from <http://hgdownload.cse.ucsc.edu/goldenPath/hg18/bigZips/>  
AGAPS masks: all the chr\*\_gap.txt.gz files from <ftp://hgdownload.cse.ucsc.edu/goldenPath/hg18/bigZips/>  
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

```
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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