# BSgenome.Hsapiens.UCSC.hg38

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`BSgenome.Hsapiens.UCSC.hg38`
*Full genomic sequences for Homo sapiens (UCSC genome hg38)*

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## Description

Full genomic sequences for Homo sapiens as provided by UCSC (genome hg38, based on assembly GRCh38.p14 since 2023/01/31). The sequences are stored in DNAString objects.

## Note

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

`hg38.p14.2bit, downloaded from https://hgdownload.soe.ucsc.edu/goldenPath/hg38/bigZips/p14/ on Feb`

See `?BSgenomeForge` and the BSgenomeForge vignette (`vignette("BSgenomeForge")`) in the **BSgenome** software package for how to create a BSgenome data package.

## Author(s)

The Bioconductor Dev Team

## See Also

- BSgenome objects in the **BSgenome** software package.
- The `seqinfo` getter and Seqinfo objects in the **GenomeInfoDb** package.
- The `seqlevelsStyle` getter and setter in the **GenomeInfoDb** package.
- DNAString objects in the **Biostrings** package.
- The `available.genomes` function in the **BSgenome** software package.
- The BSgenomeForge vignette (`vignette("BSgenomeForge")`) in the **BSgenome** software package for how to create a BSgenome data package.

## Examples

```
BSgenome.Hsapiens.UCSC.hg38
bsg <- BSgenome.Hsapiens.UCSC.hg38
head(seqlengths(bsg))
seqinfo(bsg)

## Access individual sequences:

bsg$chr1  # same as bsg[["chr1"]]
alphabetFrequency(bsg[["chr1"]])

bsg[["chrM"]]  # same as bsg$chrM
reverseComplement(bsg$chrM)

## ---------------------------------------------------------------------
## Switch the sequence names back and forth between UCSC and NCBI
## ---------------------------------------------------------------------

## IMPORTANT NOTE: Even though hg38 is officially based on the
## GRCh38.p14 assembly (this is as of Jan 31, 2023, hg38 was based on
## GRCh38.p13 before that), it contains 2 sequences that do not belong
## to GRCh38.p14: chr11_KQ759759v1_fix and chr22_KQ759762v1_fix
## These 2 foreign sequences belong to GRCh38.p13 (they are named
## HG107_PATCH and HG1311_PATCH there), but they've been replaced with
## sequences HG107_HG2565_PATCH and HG1311_HG2539_PATCH in GRCh38.p14.

seqinfo(bsg)
seqlevelsStyle(bsg)  # UCSC

## --- switch to NCBI names ---

bsg0 <- bsg
seqlevelsStyle(bsg) <- "NCBI"
bsg
seqinfo(bsg)
bsg[["1"]]

## Surprise!
table(genome(bsg))   # 2 sequences belong to GRCh38.p13!
foreign_idx <- which(genome(bsg) == "GRCh38.p13")
seqinfo(bsg)[seqnames(bsg)[foreign_idx]]
seqlevelsStyle(bsg)  # NCBI

## --- switch back ---

seqlevelsStyle(bsg) <- "UCSC"
bsg
stopifnot(identical(bsg0, bsg))
seqinfo(bsg)[seqnames(bsg)[foreign_idx]]

## ---------------------------------------------------------------------
## Genome-wide motif searching
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## 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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