BSgenome.Hsapiens.UCSC.hg38.dbSNP151.major

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`BSgenome.Hsapiens.UCSC.hg38.dbSNP151.major`
Full genome sequences for Homo sapiens (UCSC version hg38, based on GRCh38.p12) with injected major alleles (dbSNP151)

Description

Full genome sequences for Homo sapiens (Human) as provided by UCSC (hg38, based on GRCh38.p12) with major allele injected from dbSNP151, and stored in Biostrings objects. Only single nucleotide variants (SNVs) were considered. At each SNV, the most frequent allele was chosen at the major allele to be injected into the reference genome.

Author(s)

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See Also

- BSgenome objects and the `available.genomes` function in the **BSgenome** software package.
- DNAString objects in the **Biostrings** package.
- The BSgenomeForge vignette (`vignette("BSgenomeForge")`) in the **BSgenome** software package for how to make a BSgenome data package.

Examples

```
BSgenome.Hsapiens.UCSC.hg38.dbSNP151.major
genome_maj <- BSgenome.Hsapiens.UCSC.hg38.dbSNP151.major
head(seqlengths(genome_maj))

# Getting nucleotide at SNP rs12813551 (C/T, MAF>0.5)
# Major allele genome has a T:
chr <- "chr12"
pos <- 25241845L
getSeq(genome_maj, chr, start=pos, end=pos)

# Reference genome has the minor allele, C:
if (require(BSgenome.Hsapiens.UCSC.hg38)){
    genome_ref <- BSgenome.Hsapiens.UCSC.hg38
```

```
    getSeq(genome_ref, chr, start=pos, end=pos)
}

# Minor allele genome agrees with reference genome (C):
if (require(BSgenome.Hsapiens.UCSC.hg38.dbSNP151.minor)){
    genome_min <- BSgenome.Hsapiens.UCSC.hg38.dbSNP151.minor
    getSeq(genome_min, chr, start=pos, end=pos)
}
```

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