

SNPlocs.Hsapiens.dbSNP.20090506

February 3, 2010

```
SNPlocs.Hsapiens.dbSNP.20090506
      SNP locations for Homo sapiens (dbSNP BUILD 130)
```

Description

SNP locations and alleles for Homo sapiens extracted from dbSNP BUILD 130.

Usage

```
## Convenience wrappers for loading the SNP data:
getSNPcount()
getSNPlocs(seqname)

## Datasets:
data(SNPcount)
data(chr1_snplocs)
data(chr2_snplocs)
data(chr3_snplocs)
data(chr4_snplocs)
data(chr5_snplocs)
data(chr6_snplocs)
data(chr7_snplocs)
data(chr8_snplocs)
data(chr9_snplocs)
data(chr10_snplocs)
data(chr11_snplocs)
data(chr12_snplocs)
data(chr13_snplocs)
data(chr14_snplocs)
data(chr15_snplocs)
data(chr16_snplocs)
data(chr17_snplocs)
data(chr18_snplocs)
data(chr19_snplocs)
data(chr20_snplocs)
data(chr21_snplocs)
data(chr22_snplocs)
```

```
data(chrX_snplocs)  
data(chrY_snplocs)
```

Arguments

seqname The name of the sequence for which to get the SNP locations.

Details

`getSNPcount` and `getSNPlocs` are convenience wrappers for loading the SNP data. `getSNPcount` returns a named integer vector containing the number of SNPs mapped to each sequence in the genome. `getSNPlocs` returns a data frame containing the RefSNP id, alleles and location for each SNP mapped to the specified sequence. The alleles is represented by an IUPAC nucleotide ambiguity code. See [?IUPAC_CODE_MAP](#) in the Biostrings package for more information.

Note

The source data files used for this package were created by NCBI on 5-6 May 2009. The SNPs in this package map the hg18 genome (NCBI Build 36.1) and therefore can be "injected" in BSgenome.Hsapiens.UCSC.hg18. See [?injectSNPs](#) in the BSgenome software package for more information.

Author(s)

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See Also

[IUPAC_CODE_MAP](#), [injectSNPs](#)

Examples

```
getSNPcount()  
chr22snps <- getSNPlocs("chr22")  
dim(chr22snps)  
colnames(chr22snps)  
head(chr22snps)
```

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