

# SNPlocs.Hsapiens.dbSNP.20090506

February 3, 2010

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

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## 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)

H. Pages

### See Also

[IUPAC\\_CODE\\_MAP](#), [injectSNPs](#)

### Examples

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

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