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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