

# SNPlocs.Hsapiens.dbSNP.20101109

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getSNPlocs

*Accessing the data stored in SNPlocs.Hsapiens.dbSNP.20101109*

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## Description

The data sets stored in SNPlocs.Hsapiens.dbSNP.20101109 and how to access them.

## Usage

```
## Datasets:
data(SNPcount)
data(all_rsids)
data(ch1_snplocs)
data(ch2_snplocs)
data(ch3_snplocs)
data(ch4_snplocs)
data(ch5_snplocs)
data(ch6_snplocs)
data(ch7_snplocs)
data(ch8_snplocs)
data(ch9_snplocs)
data(ch10_snplocs)
data(ch11_snplocs)
data(ch12_snplocs)
data(ch13_snplocs)
data(ch14_snplocs)
data(ch15_snplocs)
data(ch16_snplocs)
data(ch17_snplocs)
data(ch18_snplocs)
data(ch19_snplocs)
data(ch20_snplocs)
data(ch21_snplocs)
data(ch22_snplocs)
data(chX_snplocs)
data(chY_snplocs)
data(chMT_snplocs)
```

```
## Convenience wrappers for loading the SNP data:
getSNPcount()
getSNPlocs(seqname, as.GRanges=FALSE, caching=TRUE)

## Extract SNP information for a set of rs ids:
rsid2loc(rsids, caching=TRUE)
rsid2alleles(rsids, caching=TRUE)
rsidsToGRanges(rsids, caching=TRUE)
```

### Arguments

seqname	The name of the sequence for which to get the SNP locations and alleles. If <code>as.GRanges</code> is <code>FALSE</code> , only one sequence can be specified (i.e. <code>seqname</code> must be a single string). If <code>as.GRanges</code> is <code>TRUE</code> , an arbitrary number of sequences can be specified (i.e. <code>seqname</code> can be a character vector of arbitrary length).
as.GRanges	<code>TRUE</code> or <code>FALSE</code> . If <code>TRUE</code> , then the SNP locations and alleles are returned in a <a href="#">GRanges</a> object. Otherwise (the default), they are returned in a data frame (see below).
caching	Should the loaded SNPs be cached in memory for faster further retrieval but at the cost of increased memory usage?
rsids	A vector of rs ids. Can be integer or character vector, with or without the "rs" prefix. NAs are not allowed.

### Details

See [SNPlocs.Hsapiens.dbSNP.20101109](#) for general information about this package.

The SNP data are split by chromosome i.e. the package contains one data set per chromosome, each of them being a serialized data frame with 1 row per SNP and the 2 following columns:

- `loc`: The 1-based location of the SNP relative to the first base at the 5' end of the plus strand of the reference sequence.
- `alleles`: A raw vector with no NAs which can be converted into a character vector containing the alleles for each SNP represented by an IUPAC nucleotide ambiguity code (see [?IUPAC\\_CODE\\_MAP](#) in the Biostrings package for more information).

Note that those data sets are not intended to be used directly but the user should instead use the `getSNPcount` and `getSNPlocs` convenience wrappers for loading the SNP data. When used with `as.GRanges=FALSE` (the default), `getSNPlocs` returns a data frame with 1 row per SNP and the 3 following columns:

- `RefSNP_id`: RefSNP ID (aka "rs id") with "rs" prefix removed. Character vector with no NAs and no duplicates.
- `alleles_as_ambig`: A character vector with no NAs containing the alleles for each SNP represented by an IUPAC nucleotide ambiguity code.
- `loc`: Same as for the 2-col serialized data frame described previously.

### Value

`getSNPcount` returns a named integer vector containing the number of SNPs for each sequence in the reference genome.

By default (`as.GRanges=FALSE`), `getSNPlocs` returns the 3-col data frame described above containing the SNP data for the specified chromosome. Otherwise (`as.GRanges=TRUE`), it returns a

**GRanges** object with extra columns "RefSNP\_id" and "alleles\_as\_ambig". Note that all the elements (genomic ranges) in this **GRanges** object have their strand set to \* and that all the sequence lengths are set to NA.

rsid2loc and rsid2alleles both return a named vector (integer vector for the former, character vector for the latter) where each (name, value) pair corresponds to a supplied rs id. For both functions the name in (name, value) is the chromosome of the rs id. The value in (name, value) is the position of the rs id on the chromosome for rsid2loc, and a single IUPAC code representing the associated alleles for rsid2alleles.

rsidsToGRanges returns a **GRanges** object similar to the one returned by getSNPlocs (when used with as.GRanges=TRUE) and where each element corresponds to a supplied rs id.

### Author(s)

H. Pages

### See Also

[SNPlocs.Hsapiens.dbSNP.20101109](#), [IUPAC\\_CODE\\_MAP](#), [GRanges-class](#), [BSgenome-class](#), [injectSNPs](#), [findOverlaps](#)

### Examples

```
## -----
## A. BASIC USAGE
## -----

getSNPcount()

## Get the locations and alleles of all SNPs on chromosome 22:
ch22snps <- getSNPlocs("ch22")
dim(ch22snps)
colnames(ch22snps)
head(ch22snps)

## Get the locations and alleles of all SNPs on chromosomes 22 and MT
## as a GRanges object:
getSNPlocs(c("ch22", "chMT"), as.GRanges=TRUE)

## -----
## B. EXTRACT SNP INFORMATION FOR A SET OF RS IDS...
## -----

## ... and return it in a GRanges object:
myrsids <- c("rs2639606", "rs75264089", "rs73396229", "rs55871206",
            "rs10932221", "rs56219727", "rs73709730", "rs55838886",
            "rs3734153", "rs79381275", "rs75350930", "rs1516535")
rsidsToGRanges(myrsids)

## -----
## C. INJECTION IN THE REFERENCE GENOME
## -----

library(BSgenome.Hsapiens.UCSC.hg19)
Hsapiens
## Note that the chromosome names in BSgenome.Hsapiens.UCSC.hg19
```

```

## are those used by UCSC and they differ from those used by dbSNP.

## Inject the SNPs in hg19 (injectSNPs() "knows" how to map dbSNP
## chromosome names to UCSC names):
Hs2 <- injectSNPs(Hsapiens, "SNPlocs.Hsapiens.dbSNP.20101109")
Hs2
alphabetFrequency(unmasked(Hs2$chr22))
alphabetFrequency(unmasked(Hsapiens$chr22))

## Get the number of nucleotides that were modified by this injection:
neditAt(unmasked(Hs2$chr22), unmasked(Hsapiens$chr22))

## -----
## D. SOME BASIC QUALITY CONTROL (WITH SURPRISING RESULTS!)
## -----

## Note that dbSNP can assign distinct ids to SNPs located at the same
## position:
any(duplicated(ch22snps$RefSNP_id)) # rs ids are all distinct...
any(duplicated(ch22snps$loc)) # but some locations are repeated!
ch22snps <- ch22snps[order(ch22snps$loc), ] # sort by location
which(duplicated(ch22snps$loc))[1] # 777
ch22snps[775:778, ] # rs75258394 and rs78180314 have same locations
# and alleles

## Also note that not all SNP alleles are consistent with the hg19 genome
## i.e. the alleles reported for a given SNP are not always compatible
## with the nucleotide found at the SNP location in hg19.
## For example, to get the number of inconsistent SNPs in chr1:
ch1snps <- getSNPlocs("chr1")
all_alleles <- paste(ch1snps$alleles_as_ambig, collapse="")
nchar(all_alleles) # 1849438 SNPs on chr1
neditAt(all_alleles, unmasked(Hsapiens$chr1)[ch1snps$loc], fixed=FALSE)
## ==> 3181 SNPs (0.17%) are inconsistent with hg19 chr1!

## Finally, let's check that no SNP falls in an assembly gap:
agaps <- masks(Hsapiens$chr1)$AGAPS
agaps # the assembly gaps
## Looping over the assembly gaps:
sapply(1:length(agaps),
       function(i)
         any(ch1snps$loc >= start(agaps)[i] &
            ch1snps$loc <= end(agaps)[i]))
## Or, in a more efficient way:
length(findOverlaps(ch1snps$loc, agaps)) # 0

```

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SNPlocs.Hsapiens.dbSNP.20101109

*The SNPlocs.Hsapiens.dbSNP.20101109 package*

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## Description

This package contains SNP locations and alleles for Homo sapiens extracted from dbSNP Build 132.

**Details**

SNPs from dbSNP were filtered to keep only those satisfying the 3 following criteria:

- The SNP is a single-base substitution i.e. its type is "snp". Other types used by dbSNP are: "indel", "mixed", "microsatellite", "named-locus", "multinucleotide-polymorphism", etc... All those SNPs were dropped.
- The SNP is marked as notwithdrawn.
- A single location on the reference genome (GRCh37) is reported for the SNP.

**Note**

The source data files used for this package were created by the dbSNP Development Team at NCBI on 9 November 2010.

WARNING: The SNPs in this package are mapped to reference genome GRCh37. Note that the GRCh37 genome is the same as the hg19 genome from UCSC except for the mitochondrion chromosome. Therefore, the SNPs in this package can be "injected" in BSgenome.Hsapiens.UCSC.hg19 but this injection will exclude chrM (i.e. nothing will be injected in that sequence).

See <http://www.ncbi.nlm.nih.gov/snp>, the SNP Home at NCBI, for more information about dbSNP.

See [injectSNPs](#) in the BSgenome software package for more information about the SNP injection mechanism.

See <http://genome.ucsc.edu/cgi-bin/hgGateway?clade=mammal&org=Human&db=hg19> for more information about the Human Feb. 2009 (GRCh37/hg19) assembly used by the UCSC Genome Browser.

**Author(s)**

H. Pages

**References**

SNP Home at NCBI: <http://www.ncbi.nlm.nih.gov/snp>

dbSNP Build 132 announcement: <http://www.ncbi.nlm.nih.gov/mailman/pipermail/dbsnp-announce/2010q4/000097.html>

About the Human Feb. 2009 (GRCh37/hg19) assembly used by the UCSC Genome Browser: <http://genome.ucsc.edu/cgi-bin/hgGateway?clade=mammal&org=Human&db=hg19>

**See Also**

[getSNPlocs](#) for how to access the data stored in this package.

[injectSNPs](#) in the BSgenome package for more information about SNP injection.

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