

# Package ‘hmyriB36’

April 12, 2018

**Title** YRI hapmap + expression (GENEVAR), Build 36, r23a genotypes

**Description** YRI hapmap + expression (GENEVAR), Build 36, r23a genotypes

**Version** 1.14.0

**Author** Vincent Carey <stvjc@channing.harvard.edu>

**Maintainer** Vincent Carey <stvjc@channing.harvard.edu>

**Depends** R (>= 2.13.0), methods, Biobase (>= 2.5.5), GGBase

**Suggests** GGtools, illuminaHumanv1.db

**License** Artistic-2.0

**biocViews** ExperimentData, Genome, SNPData, HapMap

**NeedsCompilation** no

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hmyriB36	<i>representations of HapMap phaseII snp data + expression data</i>
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## Description

representations of HapMap snp data + expression data

## Usage

```
# getSS("hmyriB36", "20") # for example, to get full expression, + genotypes  
# on chr20
```

## Format

ExpressionSet and SnpMatrix instances to be combined using getSS

## Details

Instances of class `smlSet` are created from two basic sources.

First, the expression data for 90 YRI families were obtained from SANGER GENEVAR project.

Second, data on forward non-redundant SNPs in these individuals the HapMap build 36 ftp site (r23a) in march 2008. Full provenance information still to be supplied.

## Value

instances of class `smlSet`

## Note

As of March 2011 the `smlSet` is no longer serialized. Instead, use `getSS("hmyriB36", [chrs])` to create an `smlSet` with all probes and selected chromosomes. There is an instance of `ExpressionSet-class` named `ex` in the data folder of this package that will be united with genotype data using `getSS`.

## Author(s)

Vince Carey <stvjc@channing.harvard.edu>

## References

Cheung VG., Spielman RS., Ewens KG., Weber TM., Morley M & Burdick JT.: *Mapping determinants of human gene expression by regional and whole genome association*. Nature, 437: 1365-1369, 2005

## Examples

```
library(GGtools)
hmyriB36 = getSS("hmyriB36", c("20")) # just 1 chromosome
exprs(hmyriB36)[1:4,1:4]
as(smlList(hmyriB36)[[1]][1:4,1:4], "character")
library(GGtools)
library(illuminaHumanv1.db)
cptag = get("CPNE1", revmap(illuminaHumanv1SYMBOL))
tt = eqtlTests(hmyriB36[probeId(cptag),], ~male)
topFeats(probeId(cptag), mgr=tt, ffind=1)
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