Package ‘hmyriB36’

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

R topics documented:

hmyriB36

Description
representations of HapMap phaseII 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)

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References


Examples

```r
library(GGtools)
hmyriB36 = getSS("hmyriB36", c("20")) # just 1 chromosome
exprs(hmyriB36)[1:4,1:4]
as(smList(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)
```
Index

«Topic packages
  hmyriB36, 1
ex (hmyriB36), 1
getSS, 2
hmyriB36, 1
hmyriB36-package (hmyriB36), 1
smlSet, 2