Package ‘hmyriB36’

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Title YRI hapmap + expression (GENEVAR), Build 36, r23a genotypes
Description YRI hapmap + expression (GENEVAR), Build 36, r23a genotypes
Version 1.10.0
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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:

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hmyriB36  representations of HapMap phaseII snp data + expression data

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 GENEV AR 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
```
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)
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