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

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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 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

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(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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