hmyriB36

March 23, 2012

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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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