

# GGdata

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hmceuB36

*representations of HapMap snp data + expression data*

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## Description

representations of HapMap snp data + expression data

## Usage

```
# getSS("GGdata", "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 CEU families in CEPH were obtained from SANGER GENEVAR project.

Second, data on forward non-redundant SNPs in these individuals the HapMap build 36 ftp site 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("GGdata", [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)
hmceuB36 = getSS("GGdata", c("20", "21")) # just 2 chromosomes
exprs(hmceuB36)[1:4,1:4]
as(smList(hmceuB36)[[1]][1:4,1:4], "character")
library(GGtools)
library(illuminaHumanv1.db)
cptag = get("CPNE1", revmap(illuminaHumanv1SYMBOL))
tt = eqtlTests(hmceuB36[probeId(cptag),], ~male)
topFeats(probeId(cptag), mgr=tt, ffind=1)
```

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## \*Topic **packages**

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