

# Package ‘GGdata’

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**Title** all 90 hapmap CEU samples, 47K expression, 4mm SNP

**Description** data exemplars dealing with hapmap SNP reports, GWAS, etc.

**Version** 1.28.0

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**biocViews** ExperimentData, HapMap, Genome, SequencingData,  
MicroarrayData, SNPData

**Depends** R (>= 2.12.0), methods, Biobase (>= 2.5.5), GGBase, snpStats,  
illuminaHumanv1.db, AnnotationDbi

**Enhances** GGtools

**LazyLoad** yes

**License** LGPL

**PackageStatus** Deprecated

**git\_url** <https://git.bioconductor.org/packages/GGdata>

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hmceuB36	<i>representations of HapMap snp data + expression data</i>
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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")) # just 1 chromosome
exprs(hmceuB36)[1:4,1:4]
as(smlList(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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