

# GGdata

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fheadFits	<i>forkhead box F2 gene set eQTL search result using CEU</i>
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## Description

forkhead box F2 gene set eQTL search result using CEU

## Usage

```
data(fheadFits)
```

## Format

The format is: Formal class 'filteredMultiGwSnpScreenResult' [package "GGBase"] with 4 slots, the list of filtered results (.Data), geneset (the set of genes tested), call, and sessionInfo.

## Examples

```
data(fheadFits)
fheadFits
fheadFits[["CPNE1"]]
library(GGtools)
topSnps(fheadFits[["CPNE1"]])[[20]]
```

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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**

```
data(hmceuB36)
```

**Details**

These 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`

**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**

```
data(hmceuB36)
# be patient
exprs(hmceuB36)[1:4,1:4]
as(smlList(hmceuB36)[[1]][1:4,1:4], "character")
library(GGtools)
tt = gwSnpTests(genesym("CPNE1")~male, hmceuB36, snpdepth(500))
tt
plot(tt)
```

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