

# Package ‘gap.datasets’

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**Title** Datasets for 'gap'

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**Description** Datasets associated with the 'gap' package. Currently, it includes an example data for regional association plot (CDKN), an example data for a genomewide association meta-analysis (OPG), Manhattan plots with (hr1420, mhdata) and without (w4) gene annotations.

**LazyData** Yes

**LazyLoad** Yes

**License** GPL (>= 2)

**URL** <https://jinghuazhao.github.io/R/>

**NeedsCompilation** no

**Depends** R (>= 2.10)

**Repository** CRAN

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CDKN

*An example data for regional association plot*

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### Description

These data are adapted from the DGI study on CDKN2A/CDKN2B region.

### Usage

```
data(CDKN)
```

### Format

There are three data objects in the dataset: CDKNgenes, the gene list from the Chromosome 9 according to UCSC browser (<http://genome.ucsc.edu/>); CDKNmap, the genetic map as from the HapMap website ([http://www.hapmap.org/downloads/recombination/2006-10\\_re121\\_phaseII/rates/](http://www.hapmap.org/downloads/recombination/2006-10_re121_phaseII/rates/)); CDKNlocus, the results from the association analysis of the locus based on DGI data.

### Source

The data were obtained from the Harvard-MIT Broad Institute (see <http://www.broad.mit.edu/diabetes/>)

### References

Diabetes Genetics Initiative of Broad Institute of Harvard and MIT, Lund University and Novartis Institute for Biomedical Research. *Whole-genome association analysis identifies novel loci for type 2 diabetes and triglyceride levels* Science 2007;316(5829):1331-6

### Examples

```
data(CDKN)
head(CDKNlocus)
```

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hr1420

*An example data for Manhattan plot with annotation*

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### Description

This example contains p values for a list of SNPs with information on chromosome, position and gene symbol.

In the reference below, seven established SNPs are in light blue, 14 new SNPs in dark blue and those failed to replicate in red. The paper size is set to 189 width x 189/2 height (mm) and 1200 dpi resolution. The font is Verdana.

**Usage**

```
data(hr1420)
```

**Format**

A data frame

**Source**

Dr Marcel den Hoed

**References**

de Hoed M et al. (2013) Heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. *Nature Genetics* 45(6):621-31, doi: 10.1038/ng.2610.

**Examples**

```
head(hr1420)
```

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mhtdata

*An example data for Manhattan plot with annotation (mhtplot)*

---

**Description**

This example contains p values for a list of SNPs whose information regarding chromosome, position and reference sequence as with gene annotation is obtained separately.

**Usage**

```
data(mhtdata)
```

**Format**

A data frame

**Source**

Dr Tuomas Kilpelainen at the MRC Epidemiology Unit

**References**

Kilpelainen TO, et al. (2011) Genetic variation near *IRS1* associates with reduced adiposity and an impaired metabolic profile. *Nature Genetics* 43(8):753-60, doi: 10.1038/ng.866.

**Examples**

```
head(mhtdata)
```

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OPG

*An example data for forest plot using METAL output*

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### **Description**

This example contains METAL outputs (OPGtbl) as with association statistics from contributing studies (OPGall). It is appropriate to use chr:pos\_A1\_A2 (A1<=A2) (SNPID) rather than reference id (rsid) due to its variability – therefore a SNPID-rsid mapping file (OPGrsid) is also provided.

### **Usage**

```
data(OPG)
```

### **Format**

Three data frames

### **Source**

SCALLOP consortium

### **References**

pending to give.

### **Examples**

```
data(OPG)
head(OPGtbl)
head(OPGall)
head(OPGrsid)
```

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w4

*Results from a GWAS on Chickens*

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### **Description**

This example contains p values for a list of SNPs with information on chromosome and positions.

### **Usage**

```
data(w4)
```

### **Format**

A data frame

w4

5

**Source**

Guo Jun <guojun.yz@gmail.com>

**Examples**

head(w4)

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