

# Package ‘hapmapsnp6’

December 5, 2023

**Title** Sample data - Hapmap SNP 6.0 Affymetrix

**Version** 1.45.0

**Author** Hapmap Consortium

**Depends** R (>= 2.15)

**Suggests** oligo, oligoClasses

**Maintainer** Benilton Carvalho <Benilton.Carvalho@cancer.org.uk>

**Description** Sample dataset obtained from <http://www.hapmap.org>

**biocViews** ExperimentData, HapMap, SNPData

**License** GPL

**git\_url** <https://git.bioconductor.org/packages/hapmapsnp6>

**git\_branch** devel

**git\_last\_commit** 0aaa30c

**git\_last\_commit\_date** 2023-10-24

**Repository** Bioconductor 3.19

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hapmapsnp6-package      *Sample HapMap SNP 6.0*

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## Description

Sample dataset on the SNP 6.0 Affymetrix platform. Data obtained from <http://www.hapmap.org> .  
The package is meant to be used only for demonstration of BioConductor tools.

## Details

Package: hapmapsnp6  
Type: Package  
Version: 1.0  
Date: March/2007  
License: GPL

Details on the data are available at <http://www.hapmap.org> .

The maintainer does not warrant the accuracy of the data.

## Author(s)

Data generated by the HapMap Consortium.

Package maintained by Benilton Carvalho <[Benilton.Carvalho@cancer.org.uk](mailto:Benilton.Carvalho@cancer.org.uk)>.

## References

The International HapMap Consortium. The International HapMap Project. Nature 426, 789-796 (2003).

## Examples

```
## library(oligo)
## library(hapmapsnp6)
## the.path <- system.file("celFiles", package="hapmapsnp6")
## cels <- list.celfiles(path=the.path, full.names=TRUE)
## temporaryDir <- tempdir()
## rawData <- read.celfiles(fullfilenames, tmpdir=temporaryDir)
```

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`crlmmResult`*Results for crlmm on 90 CEU HapMap samples*

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**Description**

Results for crlmm on 90 CEU HapMap samples. These results were produced straight from the CEL files available on hapmap.org and are meant to be used for demonstration.

**Usage**

```
data(crlmmResult)
```

**Format**

SnpSet object.

**Source**

<http://www.hapmap.org>

**Examples**

```
data(crlmmResult)
```

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