

# Package ‘hapmapsnp6’

April 11, 2019

**Title** Sample data - Hapmap SNP 6.0 Affymetrix  
**Version** 1.24.0  
**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** RELEASE\_3\_8  
**git\_last\_commit** c7e3bc2  
**git\_last\_commit\_date** 2018-10-30  
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hapmapsnp6-package	<i>Sample HapMap SNP 6.0</i>
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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>.

**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>

*crlmmResult*

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**Examples**

```
data(crlmmResult)
```

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