

# Package ‘hapmapsnp5’

September 18, 2025

**Title** Sample data - Hapmap SNP 5.0 Affymetrix

**Version** 1.51.0

**Author** Hapmap Consortium

**Suggests** oligo

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

**biocViews** ExperimentData, HapMap, CancerData, SNPData

**License** GPL

**git\_url** <https://git.bioconductor.org/packages/hapmapsnp5>

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## Contents

|                              |          |
|------------------------------|----------|
| hapmapsnp5-package . . . . . | 1        |
| <b>Index</b>                 | <b>3</b> |

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|                    |                              |
|--------------------|------------------------------|
| hapmapsnp5-package | <i>Sample HapMap SNP 5.0</i> |
|--------------------|------------------------------|

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## Description

Sample dataset on the SNP 5.0 Affymetrix platform. Data obtained from <http://www.hapmap.org> .  
The package is meant to be used only for demonstration of BioConductor tools.

**Details**

Package: hapmapsnp5  
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(hapmapsnp5)
## the.path <- system.file("celFiles", package="hapmapsnp5")
## cels <- list.celfiles(path=the.path, full.names=TRUE)
## temporaryDir <- tempdir()
## rawData <- read.celfiles(fullFileNames, tmpdir=temporaryDir)
```

# Index

## \* **package**

hapmapsnp5-package, [1](#)

hapmapsnp5 (hapmapsnp5-package), [1](#)

hapmapsnp5-package, [1](#)