

# Package ‘hapmap100khind’

March 29, 2021

**Title** Sample data - Hapmap 100K HIND Affymetrix

**Version** 1.32.0

**Author** Hapmap Consortium

**Suggests** oligo

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

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

**biocViews** ExperimentData, HapMap, CancerData

**License** GPL

**git\_url** <https://git.bioconductor.org/packages/hapmap100khind>

**git\_branch** RELEASE\_3\_12

**git\_last\_commit** dc1968d

**git\_last\_commit\_date** 2020-10-27

**Date/Publication** 2021-03-29

## R topics documented:

hapmap100khind-package . . . . . 1

**Index** . . . . . 3

---

hapmap100khind-package  
*Sample HapMap 100K Hind*

---

## Description

Sample dataset on the 100K Hind Affymetrix platform. Data obtained from <http://www.hapmap.org>. The package is meant to be used only for demonstration of BioConductor tools.

## Details

Package: hapmap100khind  
Type: Package  
Version: 1.0  
Date: March/2007  
License: GPL  
1

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(hapmap100khind)
## the.path <- system.file("celFiles", package="hapmap100khind")
## cels <- list.celfiles(path=the.path, full.names=TRUE)
## temporaryDir <- tempdir()
## rawData <- read.celfiles(fullfilenames, tmpdir=temporaryDir)
```

# Index

\* **package**

hapmap100khind-package, [1](#)

hapmap100khind

(hapmap100khind-package), [1](#)

hapmap100khind-package, [1](#)