

# Package ‘hapmap100kxba’

October 22, 2019

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

**Version** 1.27.0

**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/hapmap100kxba>

**git\_branch** master

**git\_last\_commit** 1335e5a

**git\_last\_commit\_date** 2019-05-02

**Date/Publication** 2019-10-22

## R topics documented:

hapmap100kxba-package . . . . . 1

**Index** . . . . . 3

---

hapmap100kxba-package *Sample HapMap 100K Xba*

---

## Description

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

## Details

Package: hapmap100kxba  
Type: Package  
Version: 1.0  
Date: 2007-03-03  
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(hapmap100kxba)
## the.path <- system.file("celFiles", package="hapmap100kxba")
## cels <- list.celfiles(path=the.path, full.names=TRUE)
## temporaryDir <- tempdir()
## rawData <- read.celfiles(fullfilenames, tmpdir=temporaryDir)
```

# Index

\*Topic **package**

hapmap100kxba-package, [1](#)

hapmap100kxba (hapmap100kxba-package), [1](#)

hapmap100kxba-package, [1](#)