

# hapmap100kxba

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hapmap100kxba-package

*Sample HapMap 100K Xba*

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## 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 <[bcarvalh@jhsph.edu](mailto:bcarvalh@jhsph.edu)>.

## 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)
```

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