Package ‘hapmapsnp6’

March 23, 2017

Title Sample data - Hapmap SNP 6.0 Affymetrix
Version 1.16.0
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
NeedsCompilation no

R topics documented:

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hapmapsnp6-package  Sample HapMap SNP 6.0

Description


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


Examples

```r
## 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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### 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

```r
data(crlmmResult)
```

### Format

SnpSet object.

### Source

http://www.hapmap.org

### Examples

```r
data(crlmmResult)
```
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