

Package ‘hapmapsnp6’

March 9, 2022

Title Sample data - Hapmap SNP 6.0 Affymetrix

Version 1.36.0

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

git_url <https://git.bioconductor.org/packages/hapmapsnp6>

git_branch RELEASE_3_14

git_last_commit 2d4d790

git_last_commit_date 2021-10-26

Date/Publication 2022-03-09

R topics documented:

hapmapsnp6-package	1
crlmmResult	2

Index	4
--------------	---

hapmapsnp6-package	<i>Sample HapMap SNP 6.0</i>
--------------------	------------------------------

Description

Sample dataset on the SNP 6.0 Affymetrix platform. Data obtained from <http://www.hapmap.org> .
The package is meant to be used only for demonstration of BioConductor tools.

Details

Package: 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

The International HapMap Consortium. The International HapMap Project. Nature 426, 789-796 (2003).

Examples

```
## 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)
```

crlmmResult

Results for crlmm on 90 CEU HapMap samples

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

```
data(crlmmResult)
```

Format

SnpSet object.

Source

<http://www.hapmap.org>

crlmmResult

3

Examples

```
data(crlmmResult)
```

Index

- * **datasets**

- [cr1mmResult](#), [2](#)

- * **package**

- [hapmapsnp6-package](#), [1](#)

[cr1mmResult](#), [2](#)

[hapmapsnp6 \(hapmapsnp6-package\)](#), [1](#)

[hapmapsnp6-package](#), [1](#)