

Package ‘hapmapsnp6’

December 16, 2025

Title Sample data - Hapmap SNP 6.0 Affymetrix

Version 1.53.0

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 devel

git_last_commit 3be1258

git_last_commit_date 2025-10-29

Repository Bioconductor 3.23

Date/Publication 2025-12-16

Contents

hapmapsnp6-package	2
crLmmResult	3
Index	4

hapmapsnp6-package *Sample HapMap SNP 6.0*

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>

Examples

```
data(crlmmResult)
```

Index

- * **datasets**

- [crlmmResult](#), [3](#)

- * **package**

- [hapmapsnp6-package](#), [2](#)

[crlmmResult](#), [3](#)

[hapmapsnp6 \(hapmapsnp6-package\)](#), [2](#)

[hapmapsnp6-package](#), [2](#)