

Package ‘ceuhm3’

October 7, 2015

Title ceuhm3: genotype (HapMap phase III) and expression data for CEPH CEU cohort

Version 0.6.0

Author VJ Carey

Description ceuhm3: genotype (HapMap phase III) and expression data for CEPH CEU cohort

Depends R (>= 2.12.0), GGBase, Biobase

Imports GGtools

Maintainer VJ Carey <stvjc@channing.harvard.edu>

License Artistic-2.0

LazyLoad yes

biocViews SNPData, HapMap

NeedsCompilation no

R topics documented:

ceuhm3-package	1
Index	3

ceuhm3-package	<i>ceuhm3 HapMap phase III genotype calls for CEU subpopulation</i>
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Description

ceuhm3 HapMap phase III genotype calls for CEU subpopulation

Details

Package: ceuhm3
Version: 0.0.0
Depends: GGBase
License: Artistic-2.0
LazyLoad: yes
Built: R 2.12.0; ; 2010-07-16 13:28:01 UTC; unix

There are multiple representations of HapMap Phase III genotypes in this package. First, the full data derived from HapMap are provided in `ceuhm3.sms`. Second, the samples for which March 2007 expression data was provided by Wellcome Trust GENEVAR project are coupled in the `hm3ceuSMS` data set. Finally genomic coordinates for all referenced SNP are in `hm3ceuLocs`.

Author(s)

VJ Carey

Maintainer: VJ Carey <stvjc@channing.harvard.edu>

Examples

```
library(GGtools)
h3_20 = getSS("ceuhm3", "chr20")
t1 = gwSnpTests(genesym("CPNE1")~male, h3_20, chrnum("chr20"))
topSnps(t1)
```

Index

*Topic **package**

ceuhm3-package, [1](#)

ceuhm3 (ceuhm3-package), [1](#)

ceuhm3-package, [1](#)

ceuhm3.sm1 (ceuhm3-package), [1](#)

ex (ceuhm3-package), [1](#)

hm3ceuLocs (ceuhm3-package), [1](#)

hm3ceuSMS (ceuhm3-package), [1](#)