Package ‘ceuhm3’

March 23, 2017

Title ceuhm3: genotype (HapMap phase III) and expression data for CEPH CEU cohort
Version 0.12.0
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

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ceuhm3-package ceuhm3 HapMap phase III genotype calls for CEU subpopulation

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

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Examples

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