

# Package ‘ceuhm3’

March 29, 2021

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

**Version** 0.28.0

**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

**git\_url** <https://git.bioconductor.org/packages/ceuhm3>

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

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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

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**Examples**

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