

# Package ‘ceuhm3’

April 11, 2019

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

**Version** 0.20.0

**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>

**git\_branch** RELEASE\_3\_8

**git\_last\_commit** 953195b

**git\_last\_commit\_date** 2018-10-30

**Date/Publication** 2019-04-11

## R topics documented:

ceuhm3-package . . . . . 1

**Index** 3

---

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

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](#)