

# ceulkg

October 25, 2011

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ceulkg-package      *CEU (N=60) genotypes from 1000 genomes pilot phase I*

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## Description

CEU genotypes from 1000 genomes pilot phase I (approx 8 million SNP); includes wellcome trust GENEVAR expression for 41 individuals

## Details

Package:      ceulkg  
Version:      0.0.10  
Depends:      R (>= 2.11.1), GGBase (>= 3.9.0)  
License:      Artistic-2.0  
LazyLoad:     yes  
Built:        R 2.12.0; ; 2010-07-01 01:14:27 UTC; unix

## Index:

ceulkg-package      60 hapmap CEU samples, 47K expression, 8mm 1000 genomes SNP

There are three two data resources provided here.

First, the 1000 genomes SNP calls for 60 CEU individuals were extracted from the pilot data VCF file [ftp://ftp-trace.ncbi.nih.gov/1000genomes/ftp/pilot\\_data/release/2010\\_07/low\\_coverage/snps/CEU.low\\_coverage.2010\\_07.genotypes.vcf.gz](ftp://ftp-trace.ncbi.nih.gov/1000genomes/ftp/pilot_data/release/2010_07/low_coverage/snps/CEU.low_coverage.2010_07.genotypes.vcf.gz).

Second, a `smlSet-class` is provided for 43 individuals in the 1000 genomes CEU SNP call set for whom expression data are available via the Sanger GENEVAR distribution ([ftp://ftp.sanger.ac.uk/pub/genevar/CEU\\_parents\\_norm\\_march2007.zip](ftp://ftp.sanger.ac.uk/pub/genevar/CEU_parents_norm_march2007.zip)).

## Author(s)

The R package was created by VJ Carey <stvjc@channing.harvard.edu>

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**Examples**

```
library(ceulkg)
```

# Index

## \*Topic **package**

[ceulkg-package](#), 1

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

[ceulkg-package](#), 1

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

[smlSet-class](#), 1