

# 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

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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)
```

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