Computations related to the Bioinformatics Applications Note, 2009

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The main illustrations in the Applications note involve a gene set. All chunks have eval=FALSE; to run this code, please manually reset.

```
> library(GGtools)
> data(hla2set)
> hla2set
```

We need to filter the full HapMap CEU cohort to founders:

```
> library(GGdata)
> data(hmceuB36)
> hmFou = hmceuB36[, which(hmceuB36$isFounder == TRUE)]
```

Now we run the tests:

```
> hla2run = gwSnpTests(hla2set ~ male, hmFou, snpdepth(250))
```