Supplementary File S2. Benchmarking of the r^2 calculations

The benchmarking of the r^2 calculations was performed in a Dell Precision T7610 workstation with 16 GB RAM and 12 x 64-bit Intel Xeon 2.10 GHz CPUs, running PLINK v1.9 under Ubuntu 14.04 LTS.

Performance was evaluated in a single run, in each breed for each chromosome, using ten cores. Considering 886 samples and 564,865 autosomal SNPs and 811 samples and 485,455 autosomal SNPs in HOL and NEL, respectively, the processing time was a function of the number of r^2 calculations, which in turn is given by:

$$NC = 0.5 \cdot x \cdot (x-1)$$

where,

NC is the number of calculations performed;

x is the number of markers.

A total of 1.60×10^{11} and 1.18×10^{11} calculations were performed for HOL and NEL, resulting in 18h26m and 11h58m of processing time, respectively. Figure 1 shows the benchmark, for each chromosome in each breed. Such calculations may be affected by sample size.

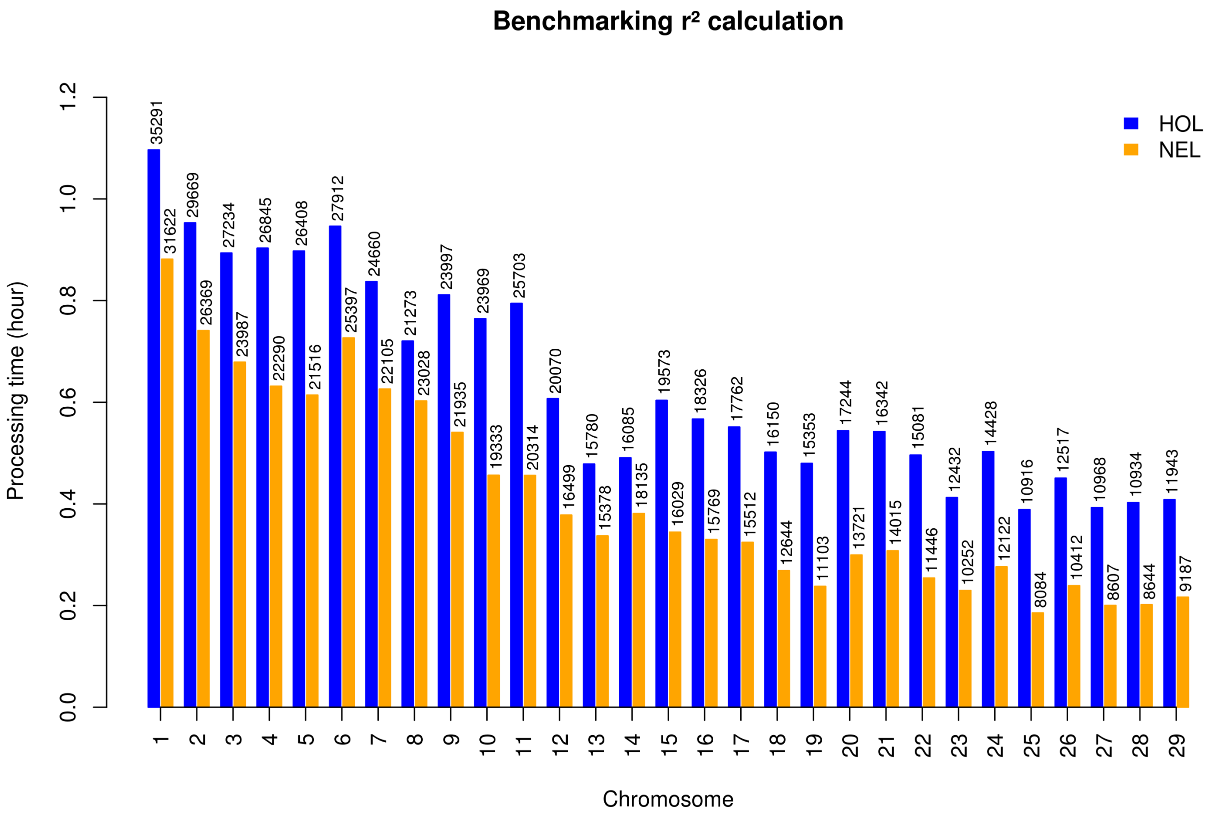

Figure 1. Histogram of the processing time to perform r^2 calculations. The numbers over the bars represent the amount of SNPs in the chromosome.