Supplemental Table

Genes that lie within eQTL 95% confidence intervals containing five or fewer genes. The table gives the name of the gene associated with the transcript detected by the illumine probe, followed by the location of the eQTL (chromosome, start and end positions of the 95% confidence interval), the genes within the interval, the tissue in which the trans-eQTL was detected and the type of eQTL (cis or trans).

Supplemental Figure Legend

The relationship between the number of eQTLs (vertical axis) and the distance between eQTL peak position and the eQTL transcript (horizontal axis). eQTLs are categorized as either cis or trans eQTL based on the linkage disequilibrium within the HS. Increasing beyond 2 Mb does not increase the number of eQTLs categorized as cis, which approaches an asymptote at this distance, as expected from the genetic correlation between markers.