Figure S2. Power to detect eQTL as a function of gene expression level. Genes were grouped into 24 bins of 1,000 genes sorted by expression level. We performed eQTL mapping and permutations within each abundance bin, and plotted the resulting FDR as a function of the mean expression level within the given bin. For clarity, the four bins with the lowest abundance are not shown. The dashed horizontal line indicates the threshold of an FDR of 5%. We used the result shown in this figure to limit eQTL mapping to genes whose expression level was high enough so that eQTL can be reliably detected.