



Figure S5. Relationship of MAF and dN/dS with eQTLs.

A. Histogram illustrating the distribution of minor allele frequencies (MAF) of eQTL variants. The data plotted is the MAF of the top variant (lowest P-value) for each gene tested. We observe that the MAF of X Chromosome eQTLs was significantly smaller than the mean MAF of autosomal eQTLs (0.189 versus 0.229; t-test P-value = 3.8×10^{-7}). **B.** Histogram illustrating the distribution of mean expression levels of genes tested for eQTLs. We observe that the mean expression levels of X Chromosome eQTLs are slightly smaller than the mean expression levels of autosomal eQTLs (t-test P-value = 2.0×10^{-3}). **C.** Comparison of FST estimates for the top cis-eQTLs (FDR 5%) and gene-matched controls on the autosomes and the X Chromosome. Control variants were chosen as variants tested as cis-eQTLs for the same gene as the top cis-eQTL. In addition, each control variant was required to be within 5kb of the top cis-eQTL. We found that the mean difference in FST statistics between cis-eQTLs and their matched controls on the X Chromosome was 0.0847 compared to 0.0287 for the autosomes (t-test P-value = 0.0433). **D.** Relationship of eQTL effect size and strength of purifying selection. Boxplots for the effect size of eQTLs on the autosomes (n = 11967) and the X Chromosome (n = 303) at genes five dN/dS bins. eQTLs on the X Chromosome have lower effect sizes compared to eQTLs on the autosomes across different dN/dS bins (one-sided Wilcoxon-rank-sum test; **P value < 5×10^{-4} ; * P value < 5×10^{-2}).