Figure S1. Difference between average π_N/π_S (δ_{LH}) estimated for genes belonging to two extreme categories of gene expression level, tissue specificity, gene essentiality and protein interactions. For this analysis, we used only the genes belonging to one functional attribute (see main text) **(A)** Results based on the ratio of nonsynonymous-to-synonymous diversity (π_N/π_S) **(B)** Based on the ratio of nonsynonymous-to-intron diversity (π_N/π_I). The error bars show the standard error of the mean. The differences between δ_{LH} estimated for the two

extreme classes of genes were tested for significance using a permutation test (see methods). ** $P < 0.01$; * $P < 0.05$.