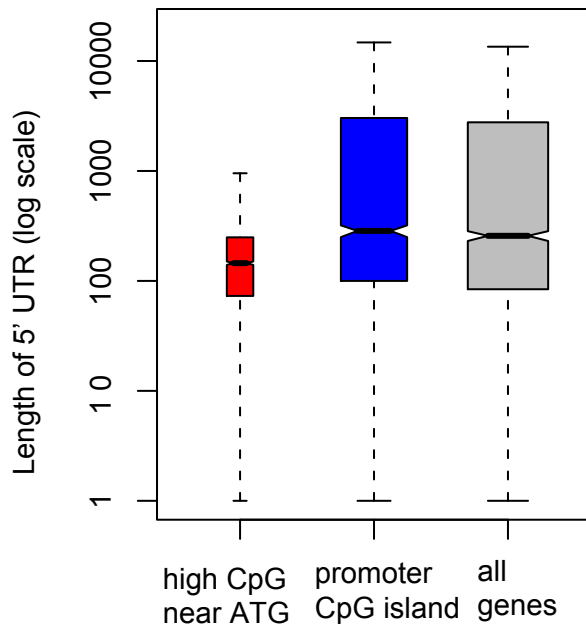
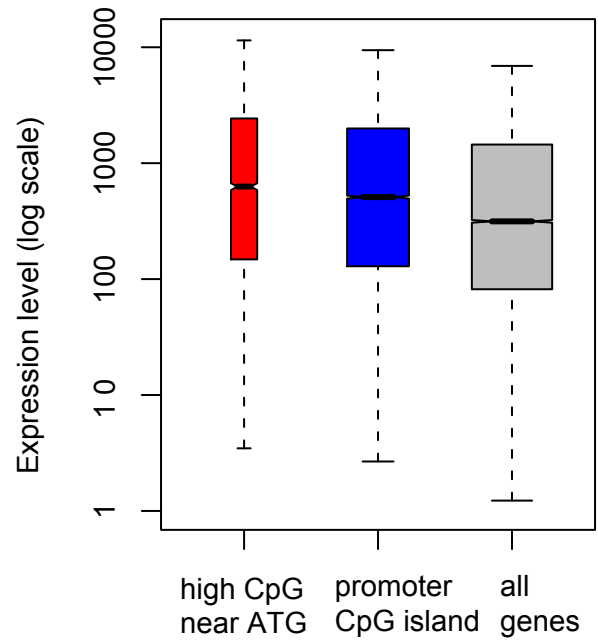


Figure S8

A



B



The size of the 5' UTR (A) and gene expression level in human T cells (B) were surveyed for genes with high CpG density near their start codon (2,777 genes) and those with a CpG island in their promoter (17,308 genes), in comparison to all genes in the genome. The y axis is shown on a log scale. The boxes are shown with widths proportional to the square roots of the number of genes in the groups. The whiskers are extended to the most extreme data point which is no more than four times the interquartile range from the box. The outliers are not drawn.