



Supplementary Figure S2: Plots of proportions as in fig. 1. (A) Data for our full set of 5,547 genes plotted along with those for a stringent 'no gene' set of 2,390 genes. For this set we used more stringent criteria in eliminating upstream sequence which might have a gene in it. (B) We divided our 10kb sequence in half. Here we plot data for the 5' and 3' regions separately. (C) Data for our full set of genes plotted along with a subset of 627 which were manually annotated in Vega.