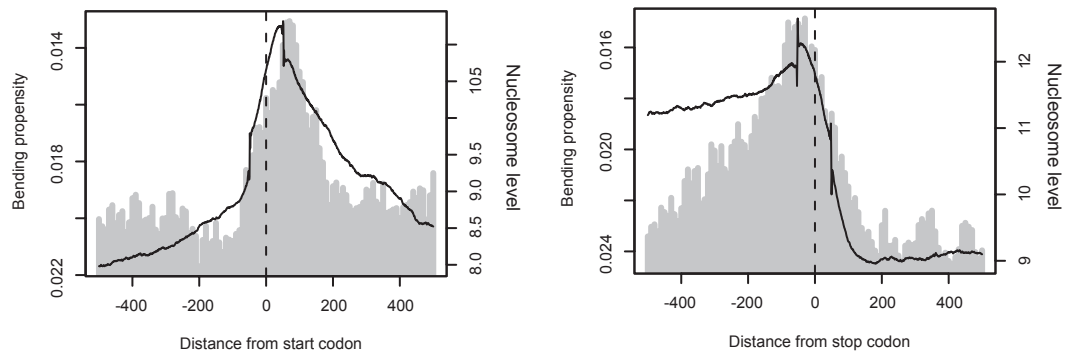
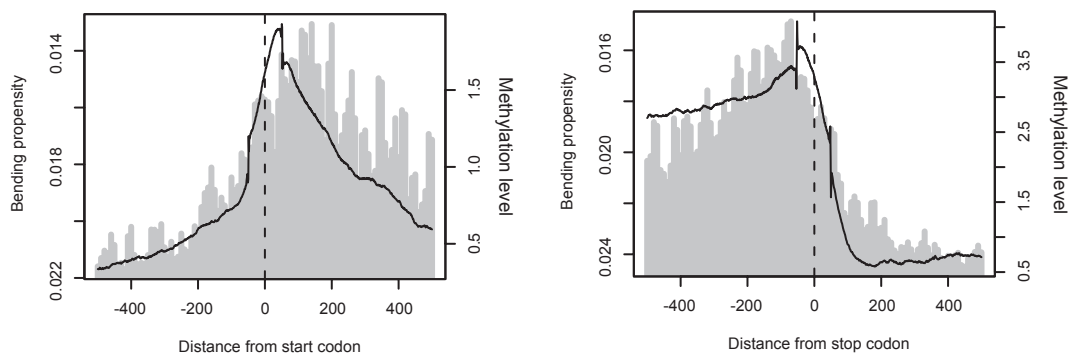


Figure S7

A



B



DNA-bending propensity, nucleosome occupancy, and methylation density surrounding the start codon and stop codon. A bending parameter was obtained for each trinucleotide across the surrounding region (see Materials and Methods). For each gene, bending propensity was averaged in a sliding window of 100 nucleotides. Genomewide average of bending propensity (black trace scaled on the left-side axis), nucleosome level (gray shade in A scaled on the right-side axis), and methylation level (gray shade in B scaled on the right-side axis) were obtained for genes aligned at the start codon or stop codon. While correlated with bending propensity, nucleosome level and methylation level appear to be independent.