

Figure S3: The x-axis represents the maximum absolute variation observed in a mono-nucleotide pattern derived by averaging 438,000 individual DNA sequences of length 151 bp each. The null-model distribution was obtained empirically from 800,000 random sets of DNA fragments. (a) shows the null model distributions based on random sampling for each of the 4 nucleotides as well as the observed Δ 's based on the nucleosome pattern derived from the Zhang positions, and (b) shows the null distributions at higher resolution.