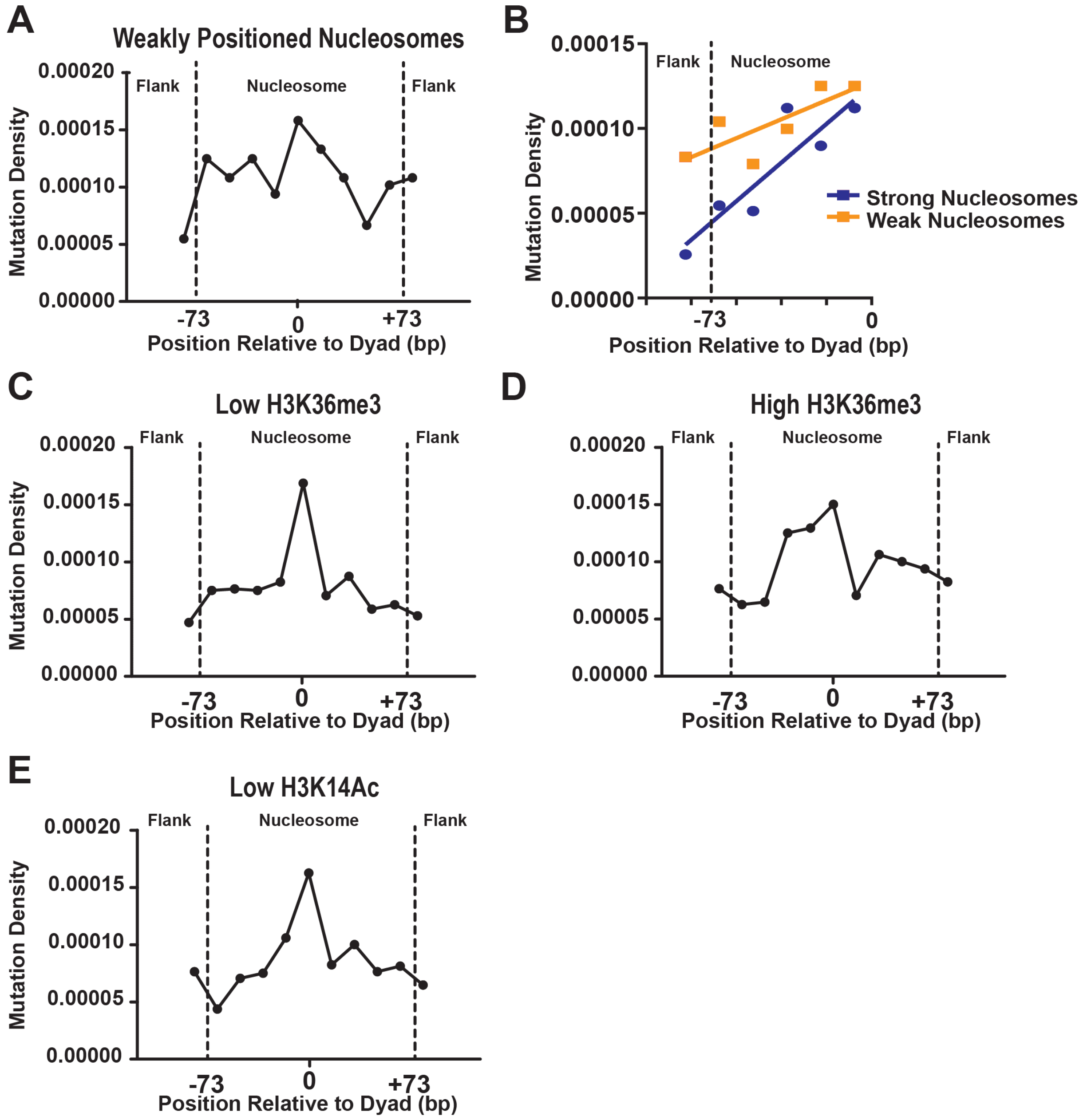
Supplemental Fig. S9



Supplemental Figure S9. (*A*) Mutations were mapped relative to weakly positioned nucleosomes and normalized by sequence context. An area of 180 bp was examined, which consisted of the main nucleosome (147bp) and an additional flank on either side (~30 bp total). The 180 bp was then divided into 11 bins, each of ~16bp. Weak nucleosomes were identified as having a positioning strength score less than 1. Comparisons of the number of mutations observed between nucleosome-bound and flanking DNA was performed using Chi-square analysis. (*B*) Mutations observed in strongly positioned (blue) and weakly positioned (orange) nucleosomes were counted in successive 15 nucleotide bins extending from the dyad axis. Corresponding bins on either side of the axis of symmetry were combined and the resulting mutation densities were compared to the nucleotide position relative to the dyad by Pearson correlation test. Mutations were mapped relative to nucleosomes with (*C*) low H3K36me3, (*D*) high H3K36me3, or (*E*) low H3K14ac, and analyzed as in part *A*.