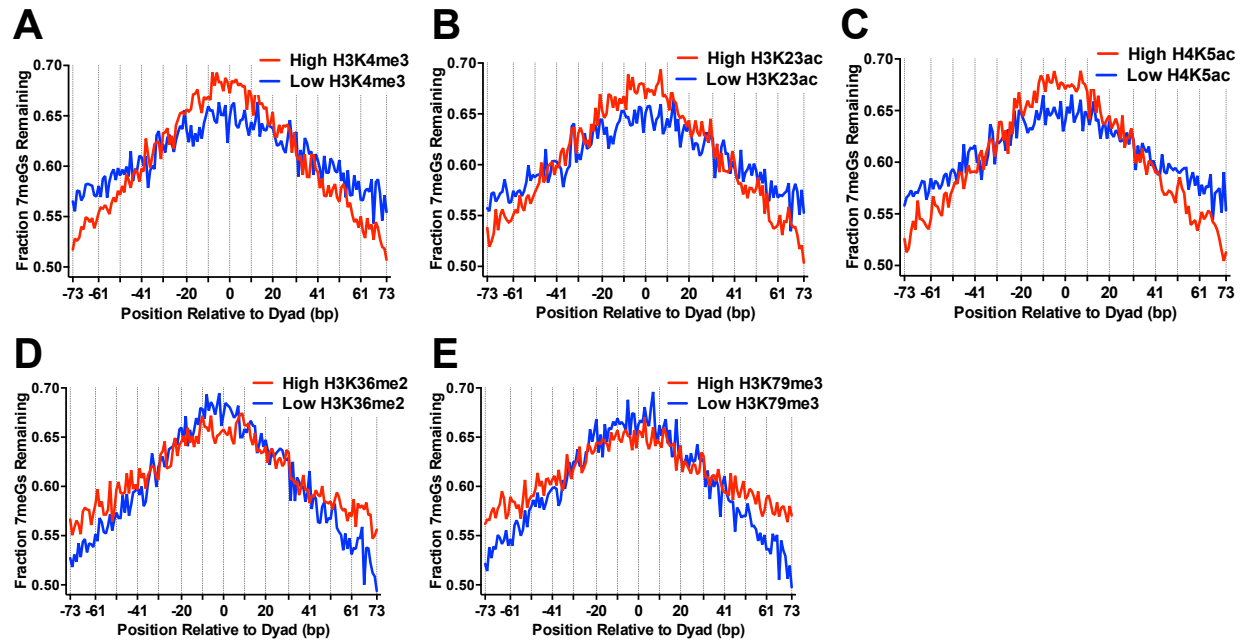


Supplemental Fig. S6



Supplemental Figure S6. Histone post-translational modifications (PTMs) affect repair of 7meG lesions within nucleosomes. (A-E) Comparison of fraction of lesions remaining following 2hr repair in WT cells following MMS treatment relative to 0hr *mag1Δ* control. In each case, the fraction of lesions remaining was analyzed among the top 10,000 nucleosomes with the highest levels of the indicated histone PTM (colored red) were compared with the bottom 10,000 nucleosomes with the lowest levels of the indicated histone PTM (colored blue). Nucleosomes overlapping with the *MAG1* gene, which is deleted in the *mag1Δ* control strain, were excluded from this analysis. (A) Histone H3K4me3, (B) H3K23ac, and (C) H4K5ac are group 1 histone PTMs (Weiner et al. 2015) and share a similar repair pattern, while (D) H3K36me2 and (E) H3K79me3 are group 2 histone PTMs.