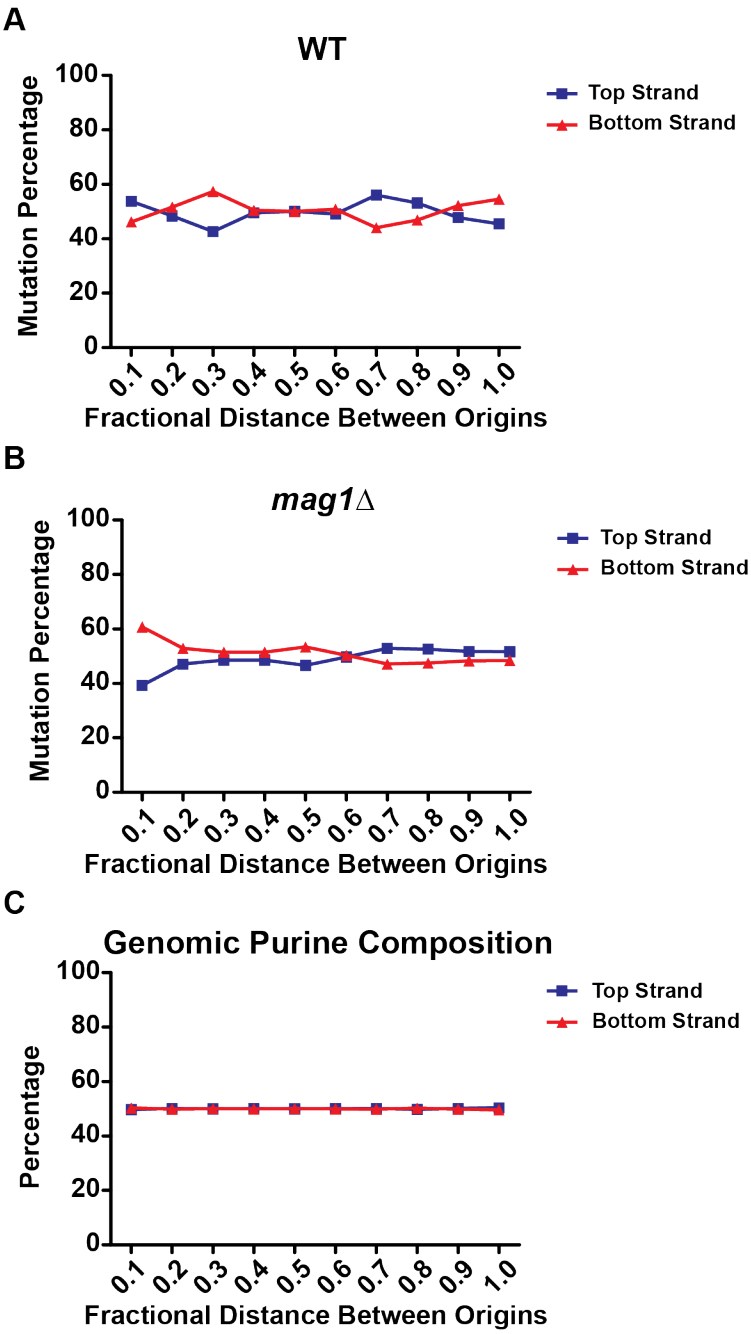
Supplemental Fig. S13



Supplemental Fig. S13. The percent distance between replication origins were split into 10 bins and number of A and G mutations (Top Strand) and the number of T and C mutations (Bottom Strand) were counted in each bin. The number of mutations were converted to percentages occurring in each bin and graphed to show the overall trend in (*A*) WT and (*B*) *mag1*Δ strains. (*C*) Additionally, the number of A and G nucleotides (Top Strand) and T and C nucleotides (Bottom Strand) occurring in each bin were counted to represent the expected frequency of mutations if MMS mutagenesis were random. Statistical significance was determined by comparing the number of mutations associated with lesions in the on the top and bottom strands

to the corresponding strand's purine nucleotide content in each genotype by Chi-square. The frequency of mutations between the top and bottom strands of MMS-treated WT yeast was not significantly different from their respective purine content ($p=0.9247$ for the Top Strand, $p=0.9309$ for the Bottom Strand). Mutations associated with the top and bottom strands in MMS-treated *mag1*Δ yeast were significantly different ($p=0.0007$, $p=0.0025$, respectively).