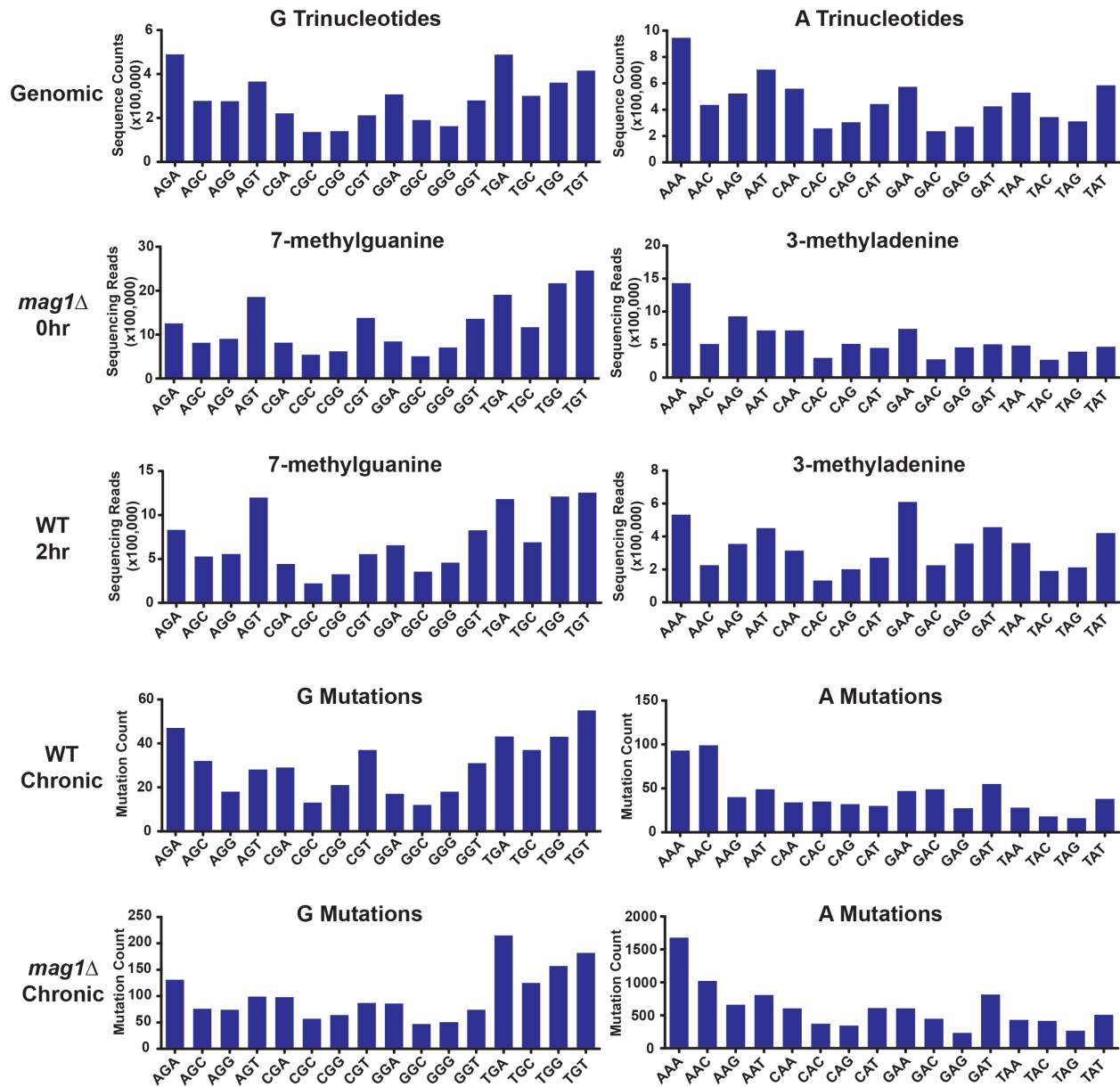


## Supplemental Fig. S7



**Supplemental Figure S7.** Trinucleotide sequences in the yeast genome (Genomic) with either A or G as the center nucleotide were counted to determine the relative abundance of potential sequences to be damaged or mutated. MMS-induced lesions (3-methyladenine and 7-methylguanine) and mutations (A-mutations and G-mutations) were counted with respect to their trinucleotide context in WT and *mag1Δ* yeast, and were then compared to the genomic distribution using a Pearson correlation test. Complementary sequences counted together.