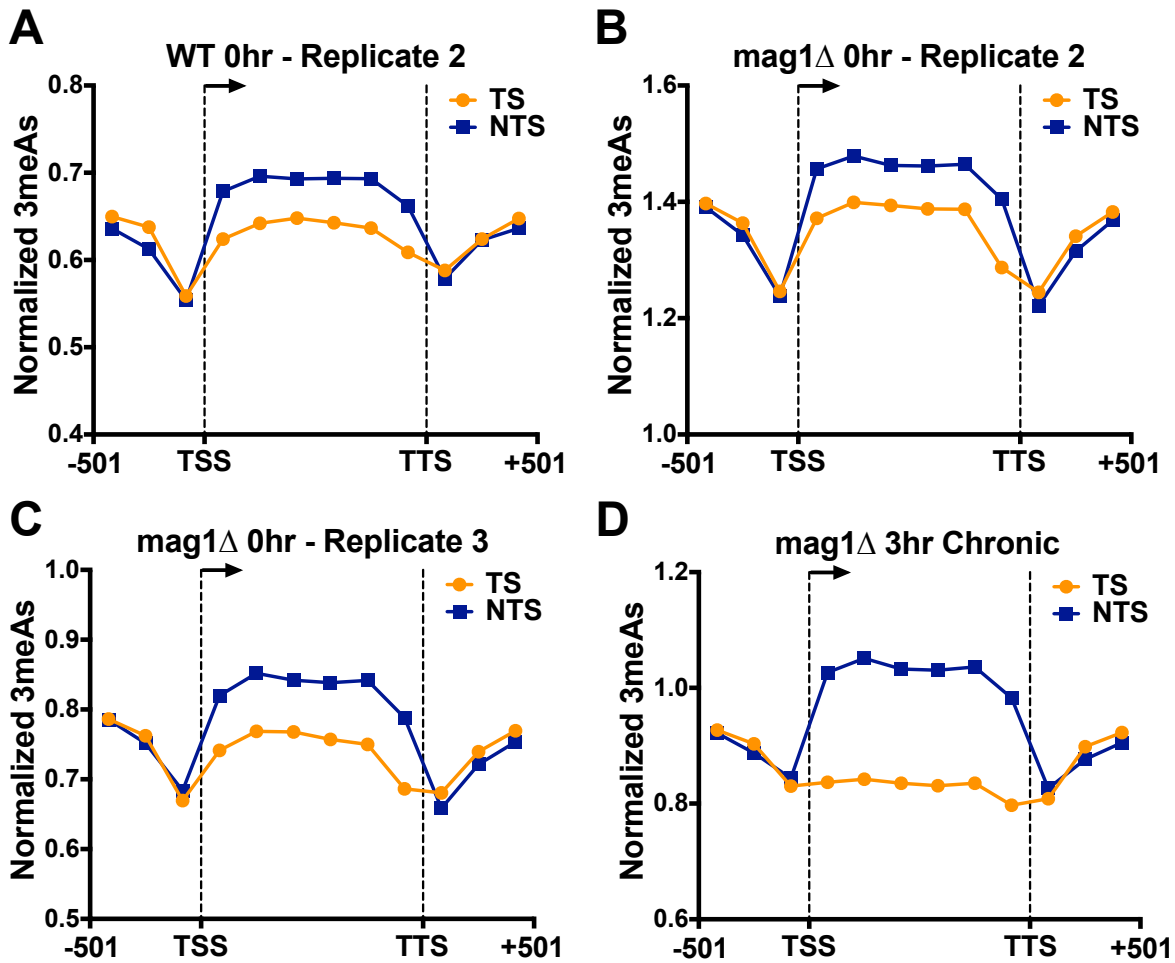


Supplemental Fig. S10



Supplemental Figure S10. MMS-induced 3-methyladenine (3meA) lesions are enriched on the non-transcribed strand (NTS) relative to the transcribed strand (TS) of 5762 yeast genes following acute (10 minutes) or chronic (3hr) treatment with MMS. (A) Replicate WT experiment analyzing 3meA lesions on the TS versus NTS following MMS treatment (0hr). WT strain was treated with 0.2% MMS for 10 minutes, and 3meA lesions mapped using NMP-seq were plotted for bins spanning 501 bp upstream of the transcription start site (TSS), the transcribed region of the gene, and 501 bp downstream of transcription termination site (TTS) for 5762 yeast genes. 3meA lesion data was normalized by the number of A nucleotides in each bin. (B-C) Replicate *mag1*Δ experiments analyzing 3meA formation on the TS versus NTS following MMS treatment (0hr). Same as in part A, except the *mag1*Δ strain was treated with 0.4% MMS for 10 minutes prior to DNA isolation and NMP-seq analysis. (D) Average number of 3meA lesions in *mag1*Δ strain chronically treated with 0.02% MMS for 3hr was analyzed for 5762 yeast genes. 3meA lesion data was normalized by the number of A nucleotides in each bin, as described above.