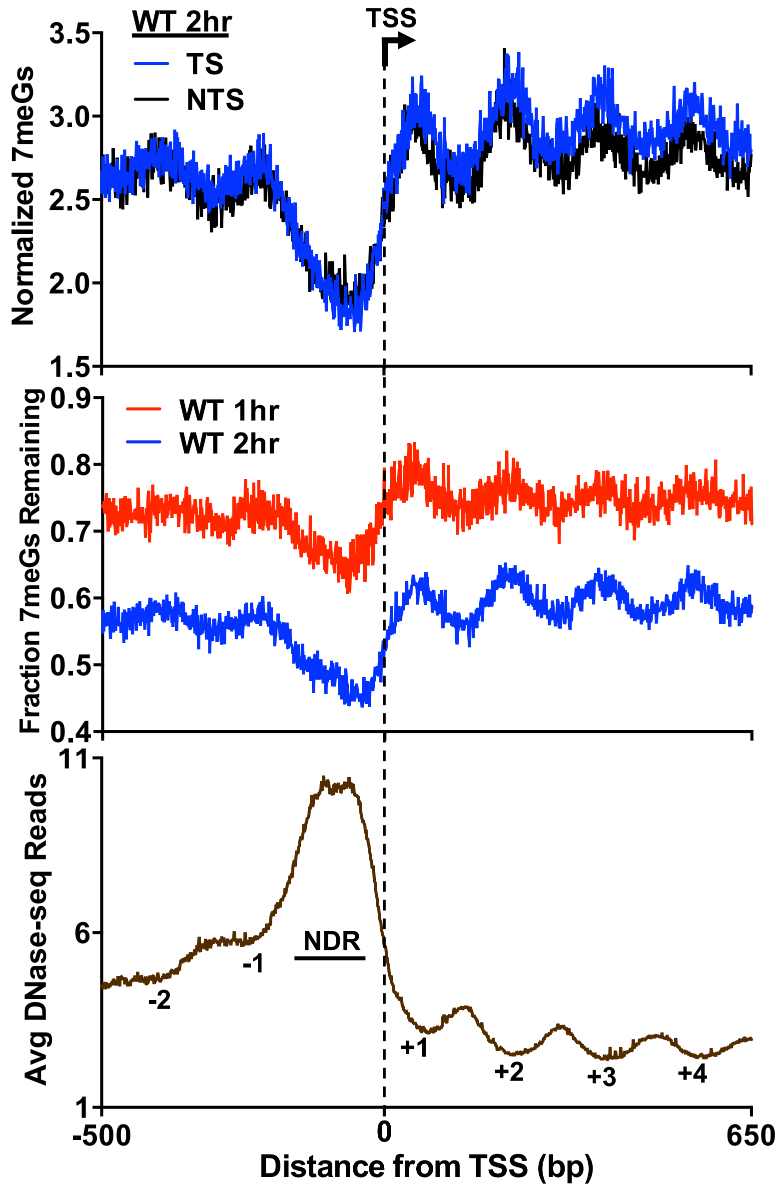
Supplemental Fig. S3



Supplemental Figure S3. Pattern of chromatin accessibility surrounding the transcription start sites (TSS) of 5762 yeast genes modulates repair of 7meG lesions. Top panel depicts the average number of 7meG lesions per G nucleotide following 2hr repair in WT yeast strain. Middle panel depicts the fraction of 7meG lesions remaining following 1hr or 2hr repair in WT relative to a matched 0hr *mag1*Δ control (data same as in Fig. 1C). Lower panel depicts the average number of DNA-seq reads (Zhong et al. 2016), which is a measure of chromatin accessibility.