



**Figure S8** Transcription-matched version of Fig. 3. (A) The distribution of MNase-Seq read counts relative to the transcription start site (TSS) for wild type (WT) and cells over-expressing Yta7 (*YTA7oe*) for transcriptionally-matched regions bound and unbound by overexpressed Yta7 in YPGal. To control for possible confounding effects of transcription level, genes classified as bound were compared to unbound genes matched for similar expression. FPKM of bound genes was calculated and unbound genes with optimally similar expression were selected to create the expression-matched gene set. (B) As A, but at regions bound and unbound by normally expressed Yta7 in YPGal. (C) The distribution of MNase-Seq read counts relative to the transcription start site for wild type and cells not expressing Yta7 (*yta7*<sup>-</sup>) for transcriptionally-matched regions bound and unbound by Yta7 in YPD.