



B

Sample	-1	+1	+2	+3	+4	+5	+6
yta7 ⁻	-209 (9x10 ⁻⁹)	59 (8x10 ⁻⁶)	228 (10 ⁻²⁰)	394 (3x10 ⁻³¹)	558 (7x10 ⁻⁴³)	722 (6x10 ⁻⁴⁰)	887 (4x10 ⁻³³)
WT	-213	61	233	401	569	736	903
YTA7oe	-214 (0.1)	63 (0.01)	240 (7x10 ⁻⁴¹)	415 (10 ⁻¹⁰⁴)	590 (9x10 ⁻¹⁵⁴)	763 (2x10 ⁻¹⁵⁸)	936 (5x10 ⁻¹³¹)

Figure S5 As Fig. 1B, but using independent biological replicates. (A) The distribution of nucleosome centers relative to the transcription start site (TSS) for called nucleosomes in wild type (WT), cells not expressing Yta7 (*yta7*⁻), and cells over-expressing Yta7 (*YTA7oe*). MNase-seq data were used to identify nucleosome centers, and the distance of each nucleosome center from the transcription start site (TSS) was plotted. Distances were smoothed with a Hanning window. The relative nucleosome count was normalized per position. (B) Average distance of the indicated nucleosome's centers to the transcription start site and the associated p-value (two-tailed *t*-test) compared to wild type.