Figure S1 Heatmap analysis of MNase-Seq read counts. (A) For the indicated genotypes, the distribution of log$_2$-transformed MNase-Seq read counts relative to the center of the +1 nucleosome. Data for each gene was plotted as a separate row. The rows are ordered top-to-bottom by increasing distance between the +1 nucleosome and the TSS in wild type. Similar to metagene analysis, comparison between strains grown in YPD, wild-type (WT YPD) and cells not expressing Yta7 (yta7), indicated contraction of nucleosome spacing. In contrast, comparison between cells grown in YPGal, wild-type (WT YPGal) and cells over-expressing Yta7 (YTA7oe), demonstrated increased nucleosome spacing upon Yta7 over-expression. (B) As above, for wild-type (WT YPD), cells lacking Rtt106 (rtt106Δ), cells not expressing Yta7 (yta7) and cells not expressing Rtt106 or Yta7 (rtt106Δ yta7). Again, as displayed by metagene analysis, rtt106Δ and yta7 exhibited opposite effects on nucleosome spacing.