Expanded View Figures

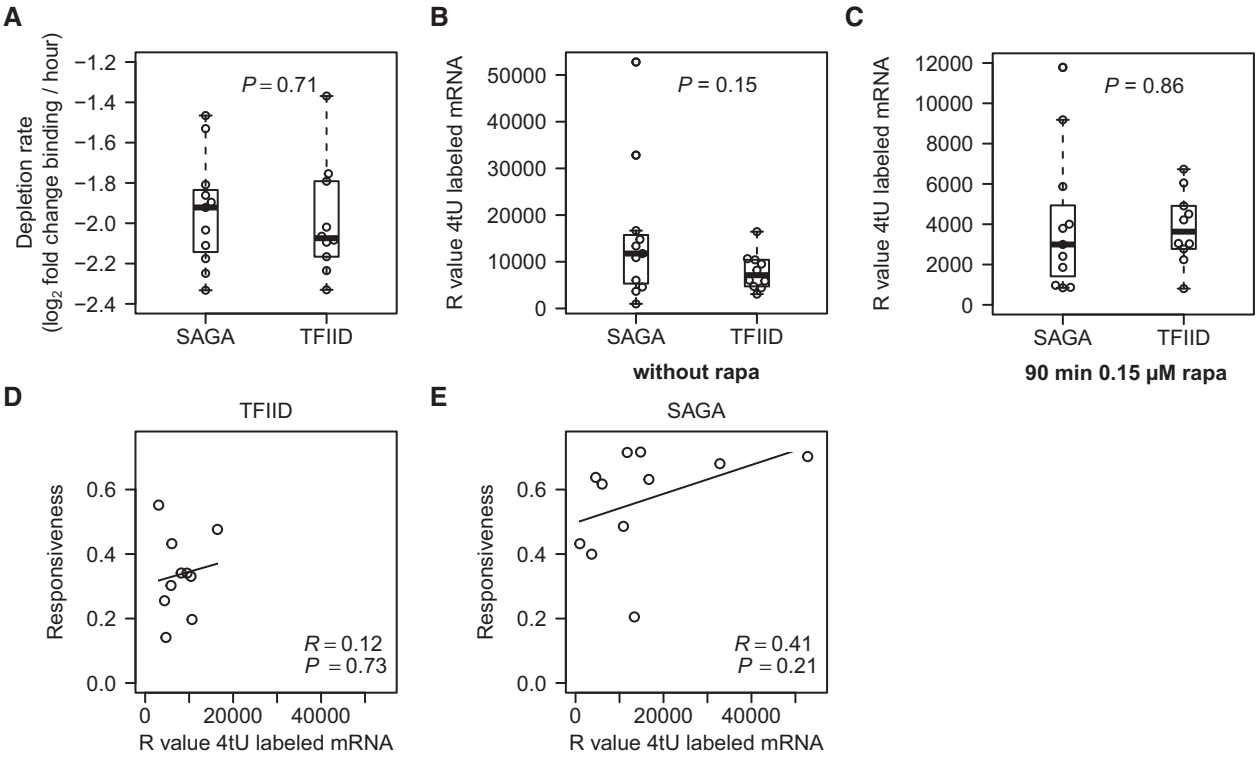

Figure EV1. Depletion rate and mRNA synthesis levels do not explain differences in responsiveness.

A Boxplot showing the comparison of the depletion rate of Hsf1 from the promoter of the SAGA- and TFIID-dominated genes. Depletion rate was calculated by plotting Hsf1 binding versus time and taking the slope of the line fitted through these points.

B Boxplot of initial mRNA synthesis before addition of rapamycin, as measured by the raw microarray intensity values (R values), compared between the SAGA- and TFIID-dominated genes.

C Boxplot with the mRNA synthesis rates (R values) after 90 min of slow depletion.

D, E Correlation of the mRNA synthesis before depletion (R values) with the responsiveness of (D) the TFIID-dominated and (E) the SAGA-dominated targets.

Data information: *P*-values in (A–C) were calculated using a two-tailed *t*-test; solid horizontal lines show the median, the box represents the interquartile range and the whiskers are at the most extreme data point no further away from the closest quartile than 1.5 times the interquartile range. *P*-values in (D, E) were obtained using the function "cor.test" in the statistical language R.

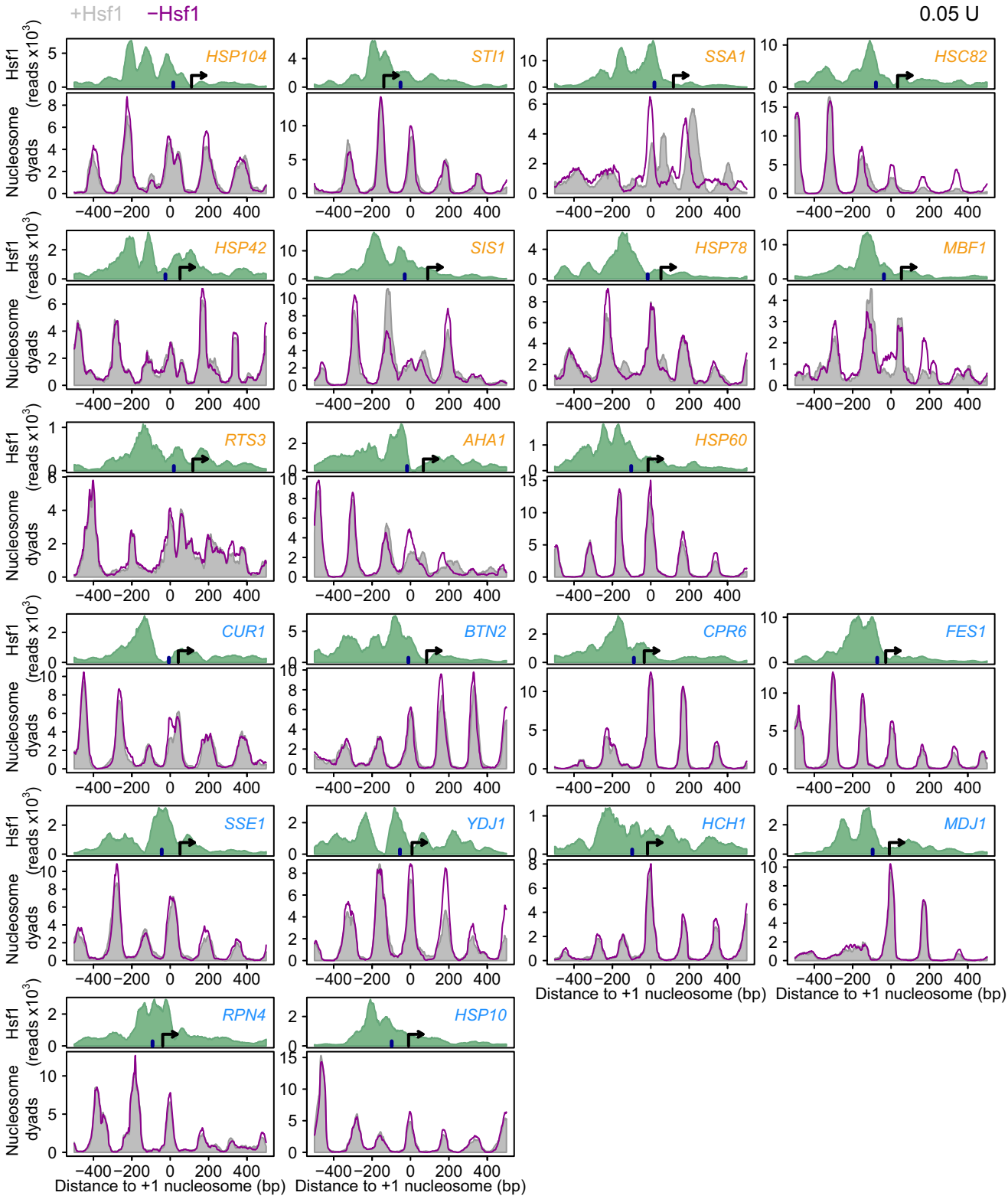

Figure EV2. Hsf1 removal results in nucleosomal repositioning on SAGA-dominated promoters.
MNase-seq nucleosomal DNA midpoint mapping with and without Hsf1 for all 11 SAGA-dominated targets (orange) and all 10 TFIID-dominated targets (blue). The arrow denotes the transcriptional start site (Nagalakshmi *et al*, 2008). The dark blue bar indicates the location of the TATA(-like) element (Rhee & Pugh, 2012). For STI1 either the TATA-box or the start site is likely incorrectly called. All the tracks are aligned to the +1 nucleosome. These tracks were used to create the average plot shown in Fig 6.