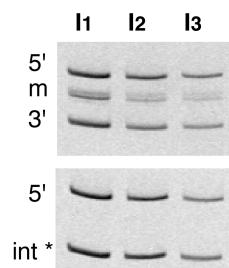


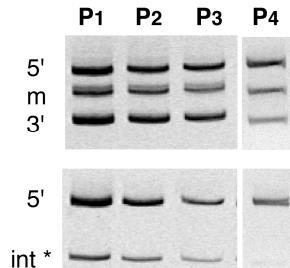
Figure S1 (Jimeno et al.)

A

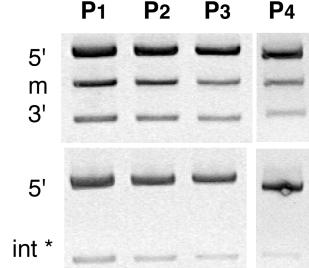
I(Inputs)



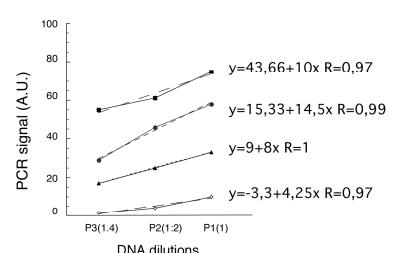
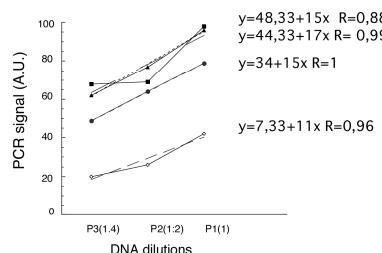
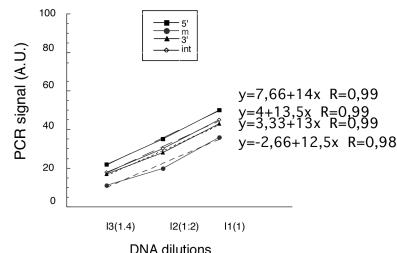
WT



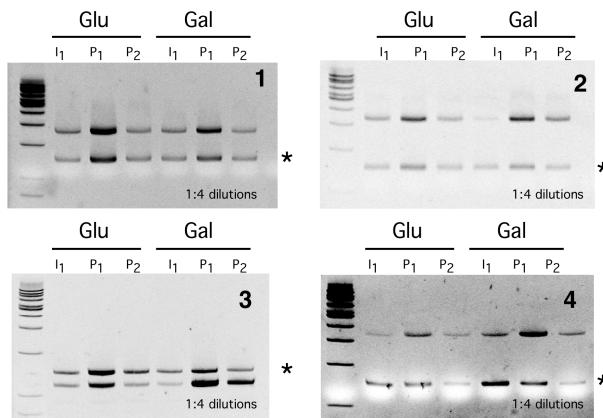
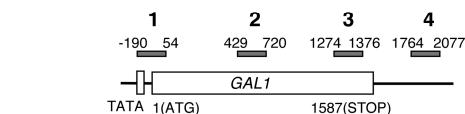
hpr1Δ



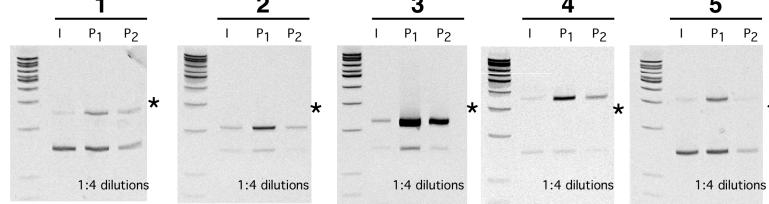
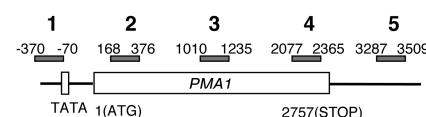
B



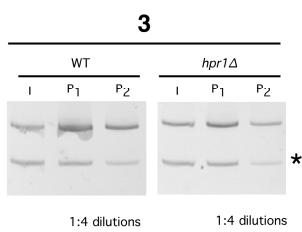
C



D



E



F

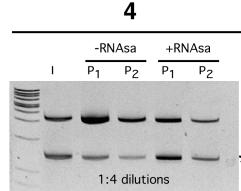


Figure S1. Titration of different DNA amounts in order to work within linear range in the PCRs corresponding to ChIP experiments involving the YLR454 coding region (A, B) and the *GAL1* and *PMA1* genes (C,D, E, F). **A)** Amplification were performed with serial dilutions of the total (input) (I) and immunoprecipitated (P) DNA. One representative acrylamide electrophoresis for each PCR reaction is shown (int*= intergenic fragment used as control). **B)** Regression analysis of quantified PCR signals (R=regression coefficient). **C, D, E, F)** Example of different DNA dilutions used in the PCRs corresponding to ChIP experiments shown in Figure 4 (A, B, C and D respectively). (*) Intergenic region of chromosome V (9716-9863) used as control.