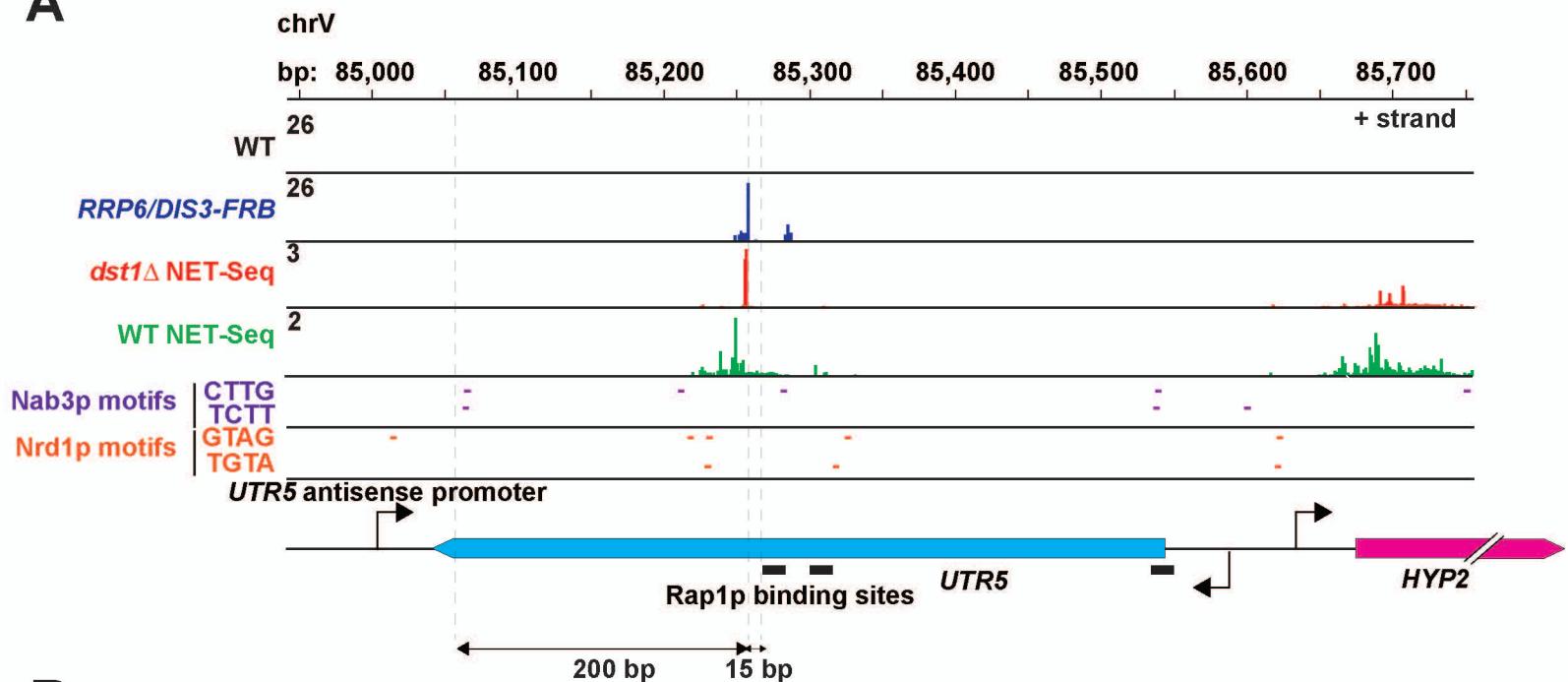
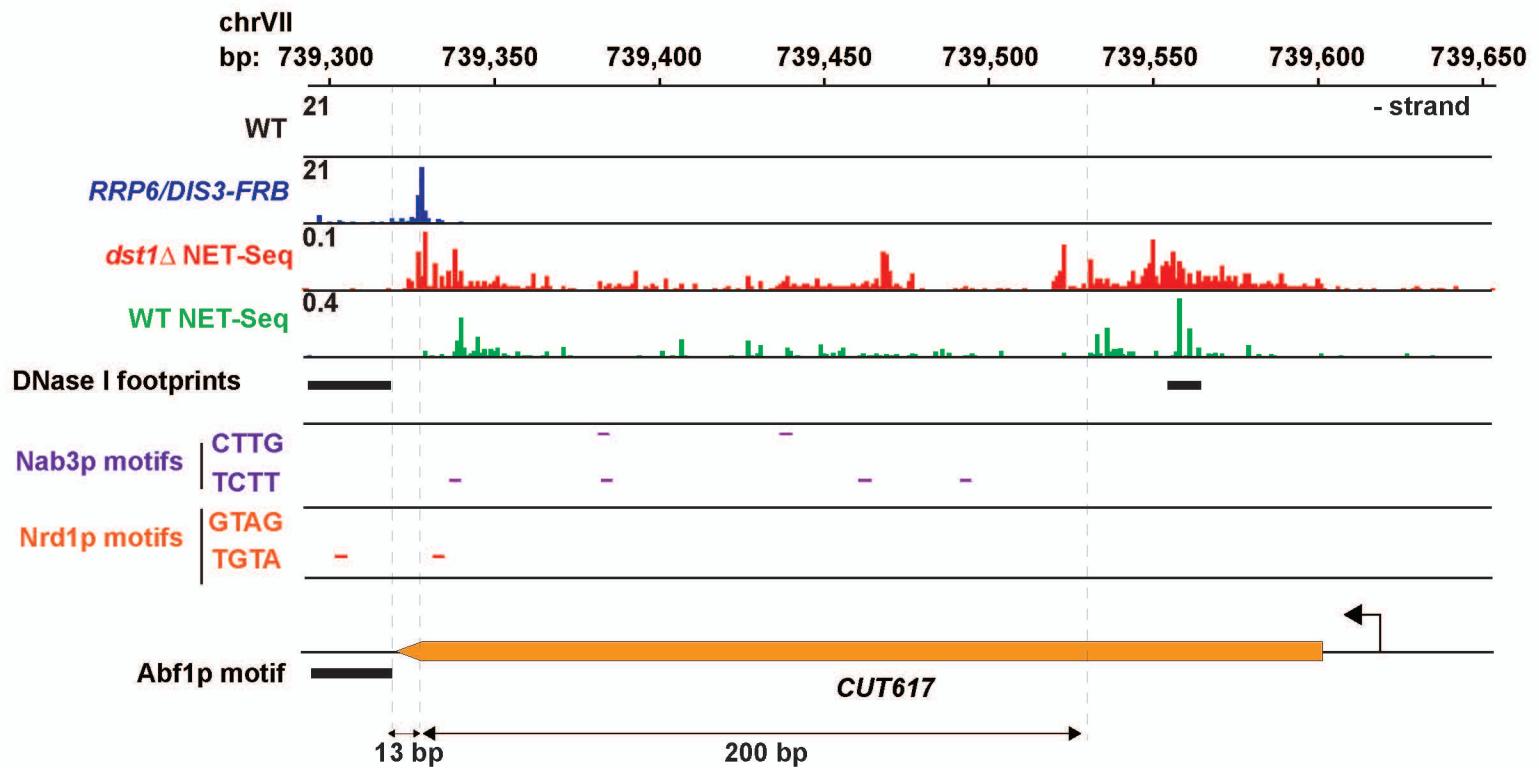


Roy_et_al_Supplemental_Fig.S6

A



B



Supplemental Figure S6. Termination of cryptic transcripts by the general regulatory factors (GRFs) Rap1p and Abf1p, Related to Figure 6

(A) Genome browser view of the region surrounding the *UTR5* gene, which gives rise to cryptic antisense transcription. The position of the three Rap1p binding sites were obtained from motif predictions (de Boer and Hughes 2012), and ChIP-exo (Rhee and Pugh 2011), and are indicated by black boxes. The positions of consensus motifs are shown for Nab3p (purple) and Nrd1p (orange).

(B) Genome browser view of the region surrounding the *CUT617* transcription unit. The position of the Abf1p binding site (black box) was obtained from motif predictions (de Boer and Hughes 2012), and confirmed by DRS mapping (Hesselberth et al. 2009).