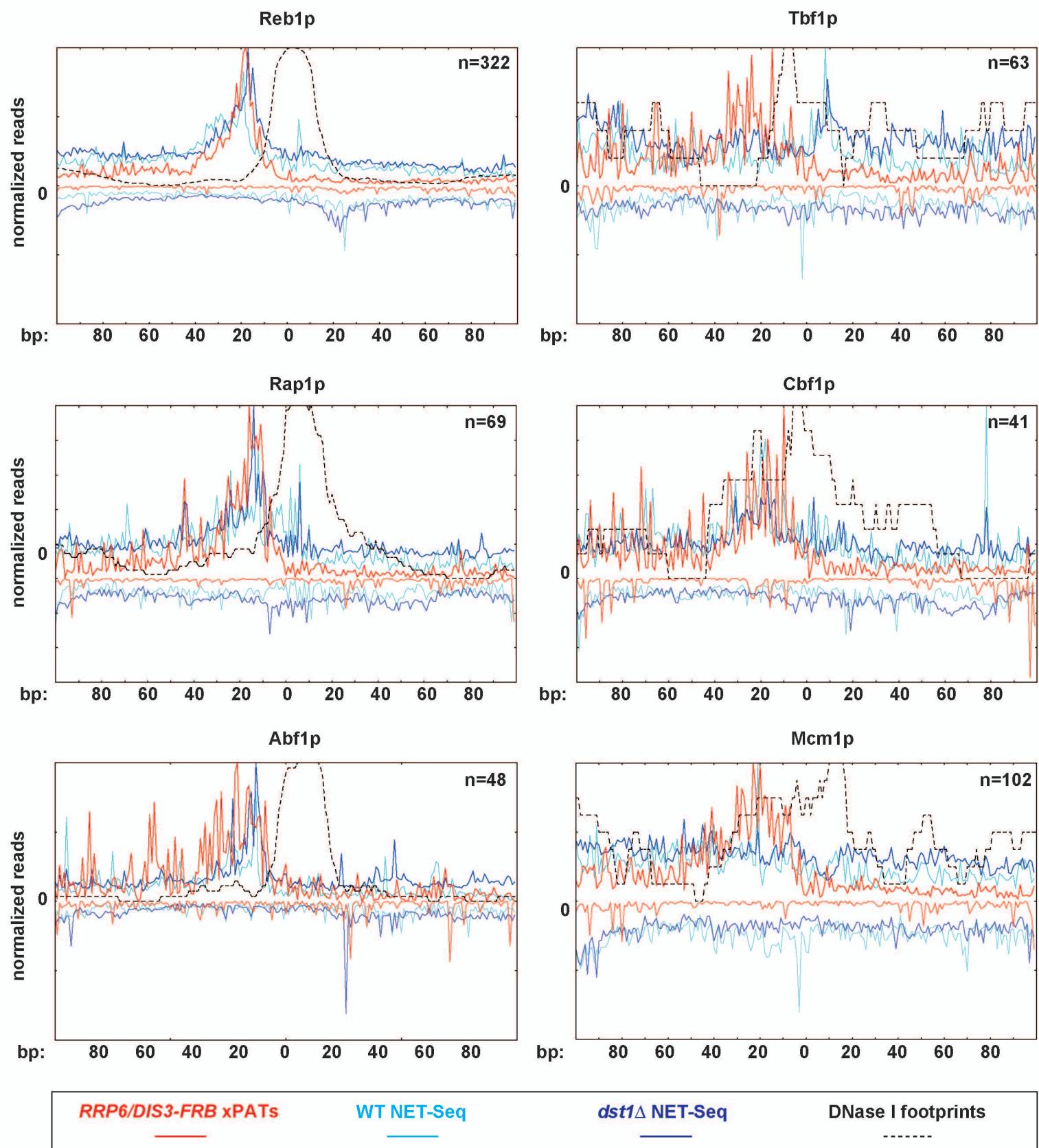


# Roy\_et\_al\_Supplemental\_Fig.S7



**Supplemental Figure S7. Meta-site analysis for general regulatory factors (GRFs) and non-GRF DNA-binding proteins, Related to Figure 4**

Meta-site analysis for GRFs (left side) and non-GRF DNA-binding proteins (right side). Binding sites for the indicated proteins were screened for the presence of nuclear exosome targeted PATs (xPATs) in a window from 5-20 bp upstream of the edge of the binding site (minimum of 1 read per million and 2 fold upregulated over WT). Each binding site is oriented so that the xPATs (cyan) are upstream and have a positive value. Pol II associated 3'-ends are shown for WT (green), and *dst1Δ* (red). Reb1p, Rap1p, and Abf1p binding sites were obtained from experimentally mapped binding sites (see Methods). Mcm1p, Tbf1p, and Cbf1p binding sites were obtained from motif predictions (see Methods). The x-axis indicates distance in bp from the upstream edge of the binding motif.