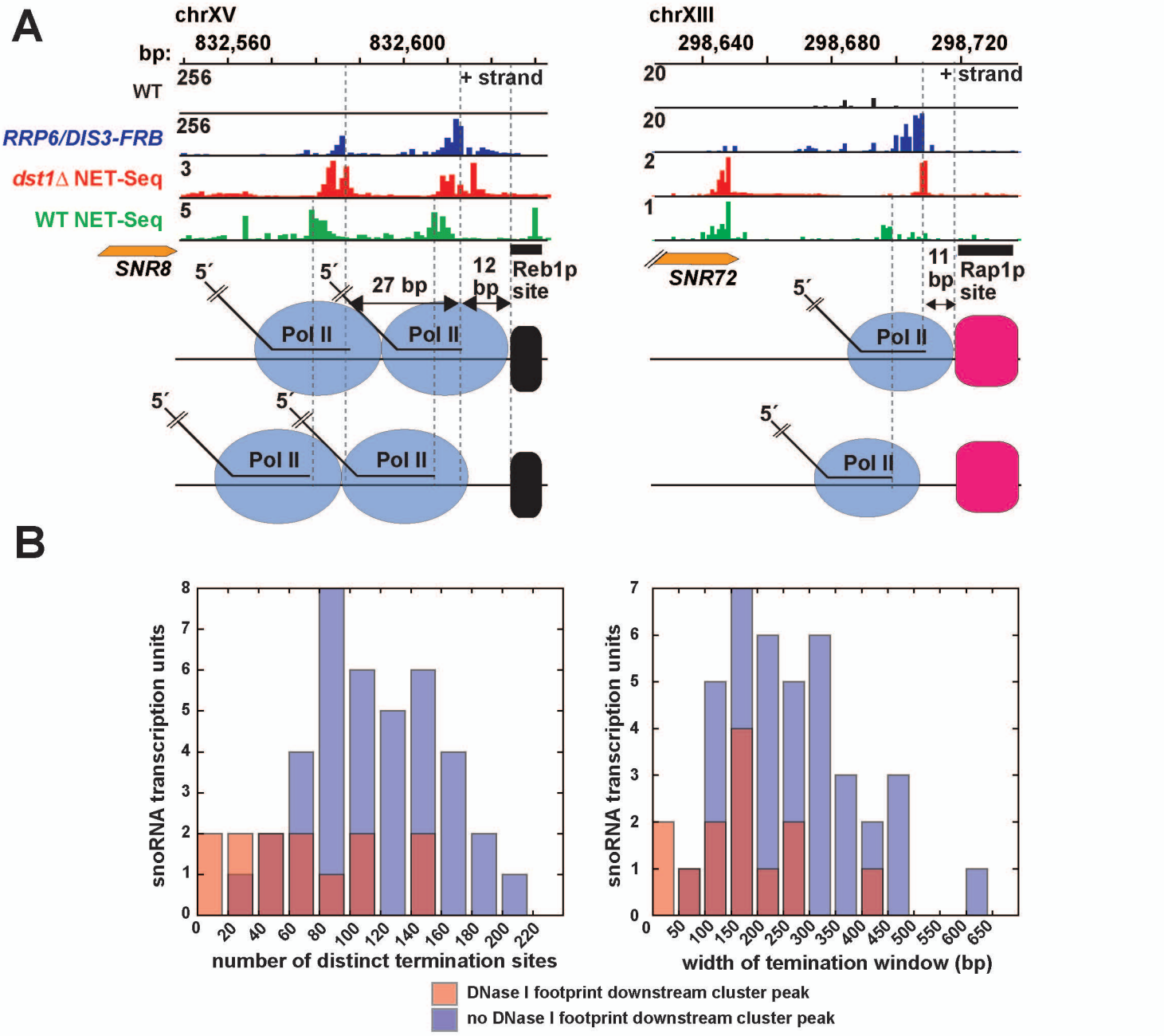
Roy_et_al_Supplemental_Fig.S4



Supplemental Figure S4. NNS termination window distribution for roadblocked and non-roadblocked snoRNAs, Related to Figure 2

(A) Genome browser views for regions encompassing the NNS termination regions of the roadblocked snoRNAs *SNR8* (left panel) and *SNR72* (right panel). The top two tracks show PATs in WT and the *RRP6/DIS3-FRB* strain. Nascent Pol II-associated 3´ ends in WT and *dst1Δ* are shown in red and green, respectively (Churchman and Weissman 2011; Kaplan et al. 2009). The y-scale represents reads per million. The binding sites for the general regulatory factors (GRFs) Reb1p and Rap1p are shown for each panel, and the distance between the leading edge of the GRF binding site and the Pol II active site is indicated.

(B) Histogram depicting the distinct number of termination sites (left panel) or the width of the termination window (right panel) required to account for 80% of the total termination signal within the genomic window 25 bp to 775 bp downstream of the snoRNA 3´ ends. The snoRNAs undergoing NNS-dependent termination are grouped according to the presence (red) or absence (blue) of a DNase I resistant site (DRS) within a 20 bp window downstream of the PAT cluster peaks.