



**Supplemental Figure S1. Pol I NET-seq is reproducible across triplicate samples.** After alignment, reads mapping to the rDNA were isolated, normalized (as described in the methods and the results (3.1) sections), and plotted for the (A) WT and (B) *hmo1Δ* strains. Histograms were generated for each of the three separate replicates (left panels) and with all replicates overlaid (middle panels), where “counts” represents the number of polymerases at that single-nucleotide position on the rDNA at the time of harvest. Spearman correlation coefficient values (where 1 represents total similarity between two replicates) are included in the right panels for the comparison between one replicate vs. each of the other two within either the WT or the *hmo1Δ* strain.