Supplemental Figure 5. Start-RNAs document pausing at enhancers and super-enhancers. A, (Top) List of enriched GO categories for TSS clusters containing 50 or more uTSSs in mES cells. (Bottom) Overlap between genes associated with clusters of uTSSs (≥50, N=583, green) and genes associated with super-enhancers (N=231, red) identified by enrichment of Med1 (Whyte et al. 2013). P-value (p=9.63e-90) from hypergeometric test. B, Distributions of Start-RNAs around mRNA TSSs and uTSSs in mES cells. Sites are rank ordered by decreasing Start-RNAs reads (±50bp; mRNA TSSs N=15,066 genes and uTSSs N=21,763). Related to Fig. 5.