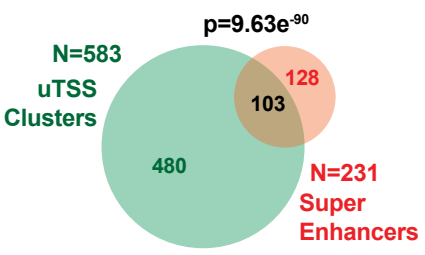


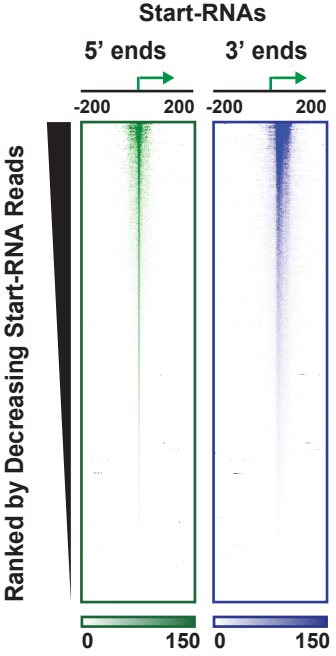
A

**Top 5 GO categories
(mESC cells; N=583 genes)**

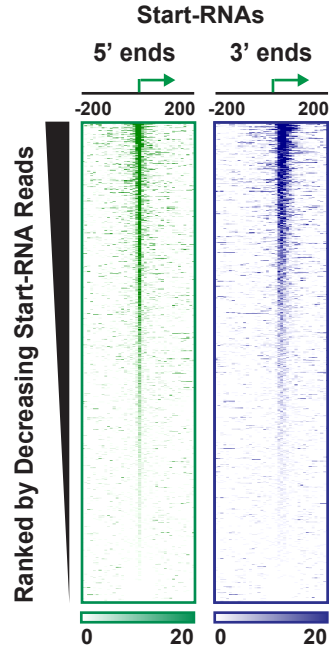
- Protein binding
- DNA binding
- Sequence-specific DNA binding
- Chromatin binding
- Transcription factor activity



B mRNA TSSs



uTSSs



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 (± 50 bp; mRNA TSSs N=15,066 genes and uTSSs N=21,763). Related to Fig. 5.