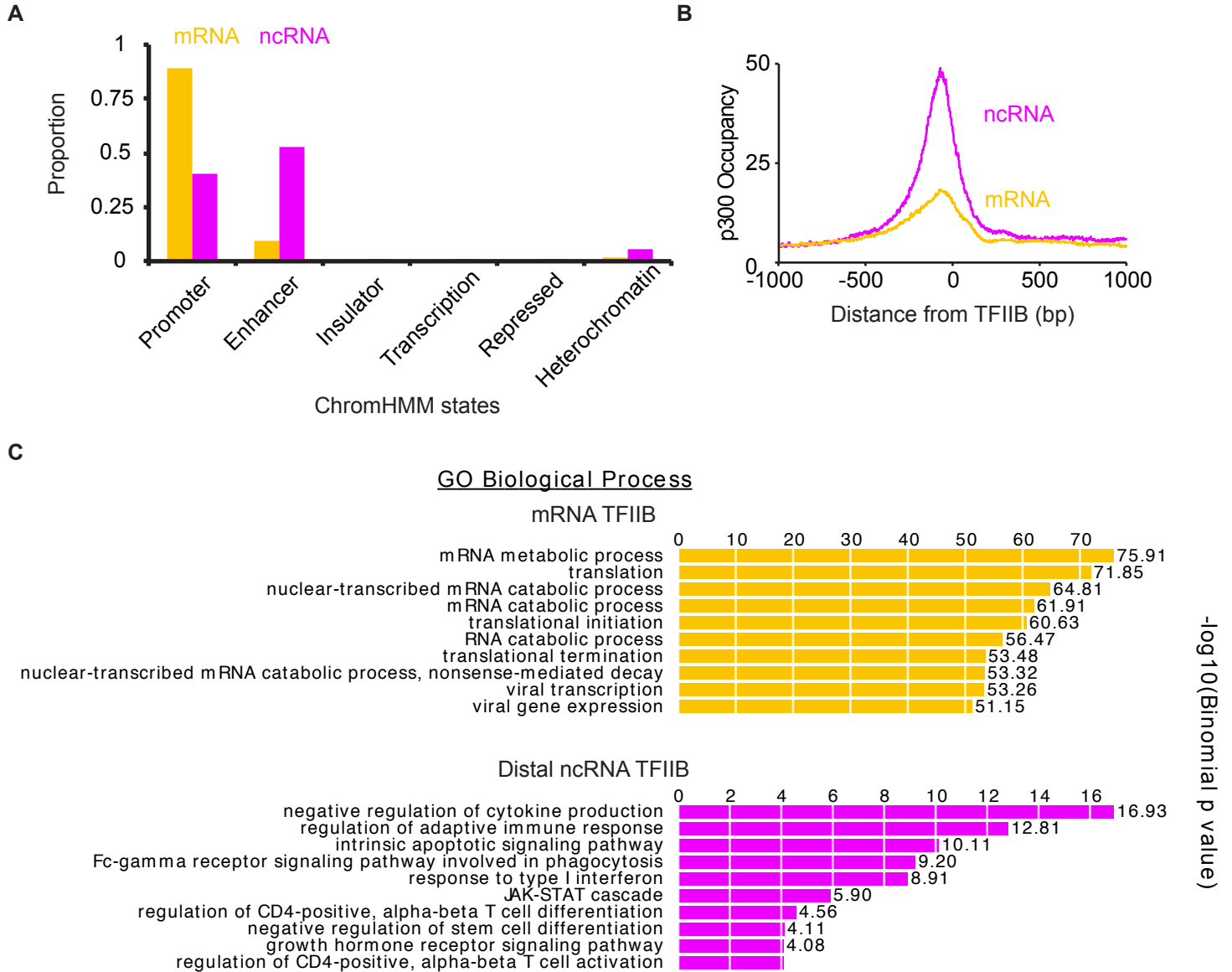


Supplemental Fig S10



Supplemental Figure S10. ncRNA and mRNA TFIIB meta-analysis. (A) Proportion of predicted regulatory functions based on chromatin state maps (ENCODE K562 ChromHMM) for mRNA and ncRNA TFIIB locations. (B) Composite plot of ENCODE K562 p300 ChIP-seq occupancy plotted relative to mRNA and ncRNA TFIIB PIP-seq peaks. (C) GO enrichment of closest annotated genes for mRNA and distal ncRNA TFIIB locations using GREAT enrichment.