

SUPPLEMENTAL FIGURE LEGENDS

Supplemental Figure 1: PAR-CLIP identifies and maps the cell-type specific and condition specific binding sites of ELAVL1

(S1A) Gene expression analysis using qPCR measuring the mRNA levels of *IFNB1*. THP-1 cells were stimulated with the STING agonist cGAMP (EC50) and RNA was collected at indicated timepoints.

(S1B) Bar graph showing the number of clusters that mapped either to exons and introns across the two cellular conditions. Inset shows the average number of unique reads for each exonic- or intronic- cluster across the conditions.

(S1C) Venn diagram showing the overlap of target mRNAs from HEK293 (Mukherjee et al. 2011) and THP-1 naïve.

(S1D) Reactome pathway analysis for the mRNAs that were unique bound by THP-1s compared to HEK293.

(S1E) Metagene analysis showing the normalized distribution of binding sites across introns or **(S1F)** the 3'UTR across both conditions.

(S1G) Metagene analysis showing the distribution of binding sites in the 3'UTR that are 200 nucleotides downstream of the poly-A tail.

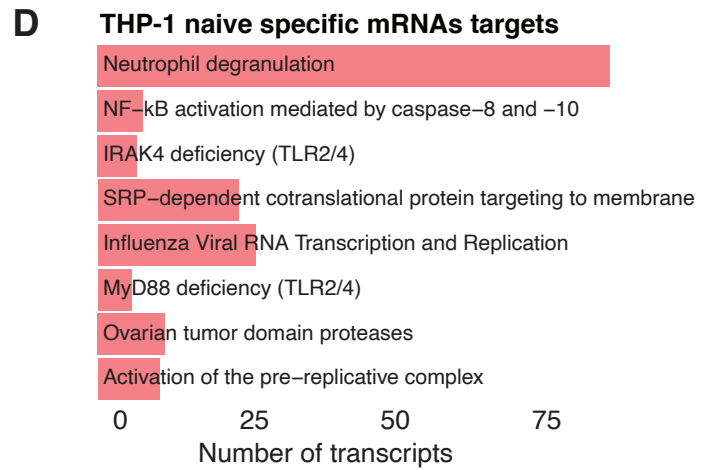
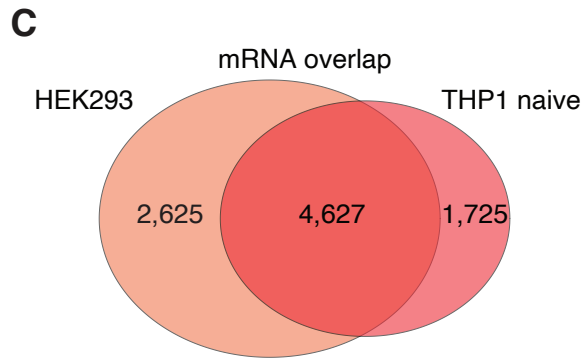
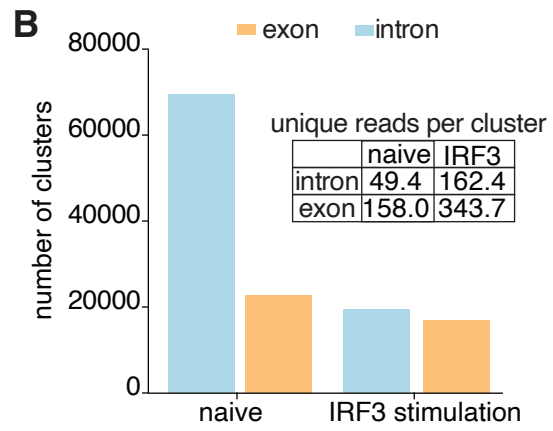
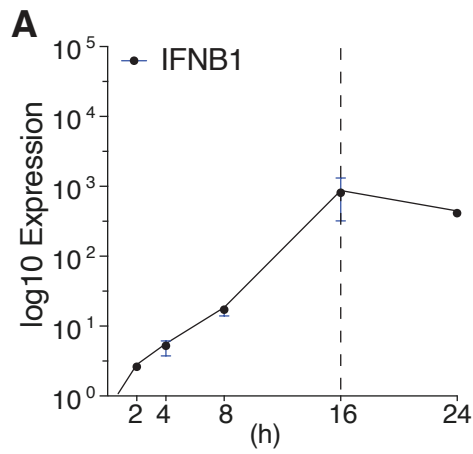
Supplemental Figure 2: PAR-CLIP and RIP-Seq identify enriched transcripts that are condition independent or dependent

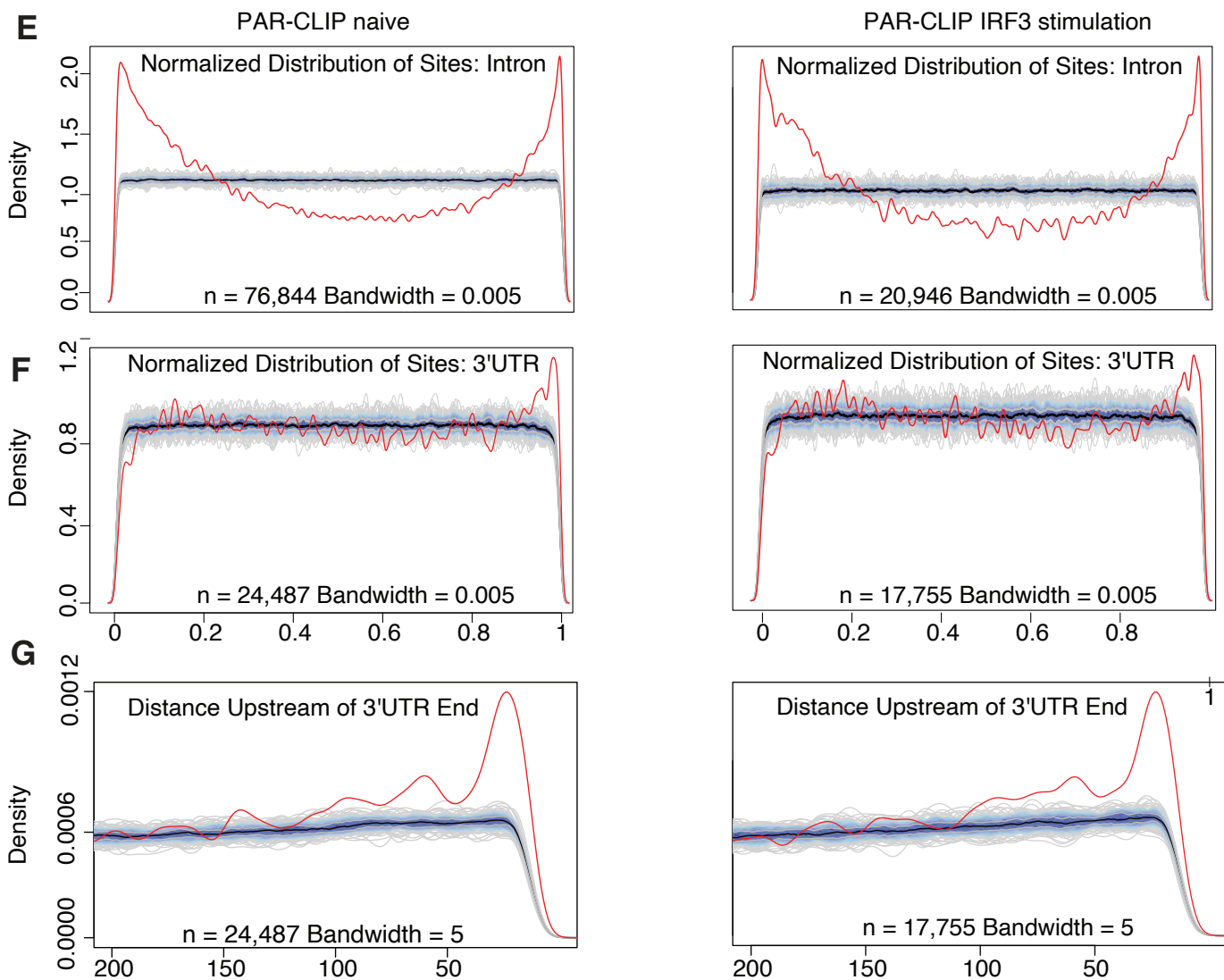
(S2A) Venn diagram showing the overlap between the bound (PAR-CLIP) and enriched (RIP-Seq) mRNA transcripts across conditions.

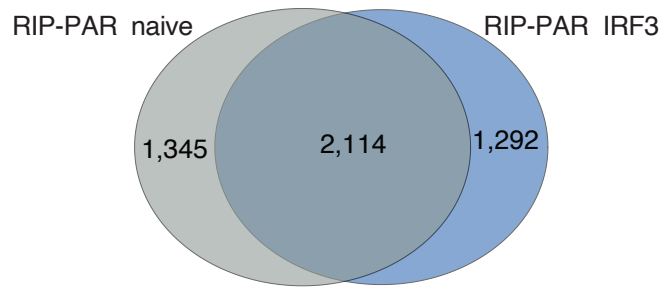
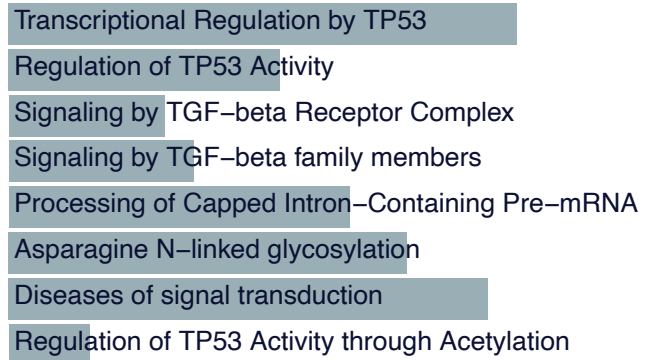
(S2B) Bar graph of a Reactome pathway analysis for each group of transcripts that were either shared (from S2A) between the two conditions or unique bound and enriched in the naïve **(S2C)** or **(S2D)** the stimulated states.

Supplemental Figure 3: KO determines transcripts whose half-lives are dependent on the presence of ELAVL1

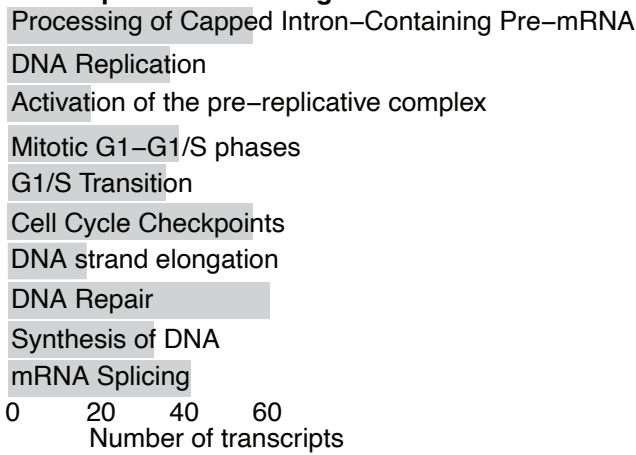
(S3A) Cumulative distribution plot of the log₂ foldchange (KO/wt) in half-life showing the group of transcripts whose half-lives are most affected by the loss of ELAVL1.



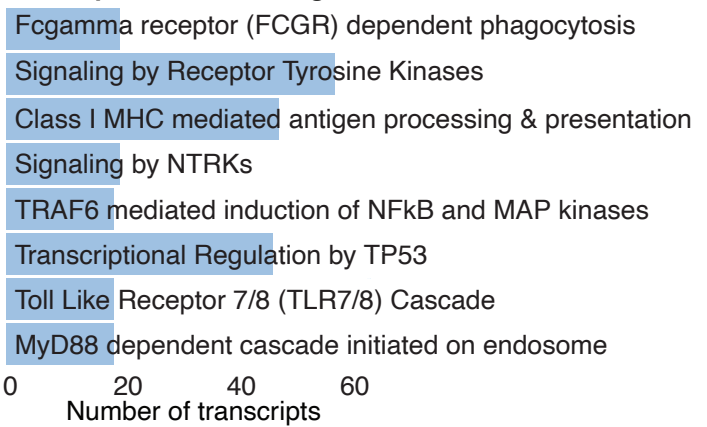


A**B****condition independent THP-1 mRNA targets**

0 25 50 75
Number of transcripts

C**naive specific mRNA targets**

0 20 40 60
Number of transcripts

D**IRF3 specific mRNA targets**

0 20 40 60
Number of transcripts

Supplemental Figure 3

