#### 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.

(SIB) 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.

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

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

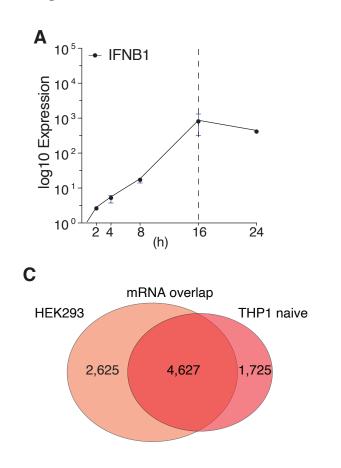
## Supplemental Figure 2: PAR-CLIP and RIP-Seq identify enriched transcripts that are condition independent or dependent

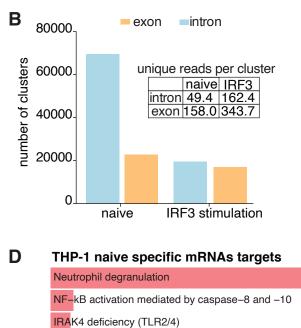
(**S2A**) Venn diagram showing the overlap between the bound (PAR-CLIP) and enriched (RIP-Seq) mRNA transcripts across conditions.

(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 log<sub>2</sub> foldchange (KO/wt) in half-life showing the group of transcripts whose half-lives are most affected by the loss of ELAVL1.





SRP-dependent cotranslational protein targeting to membrane

50

75

Influenza Viral RNA Transcription and Replication

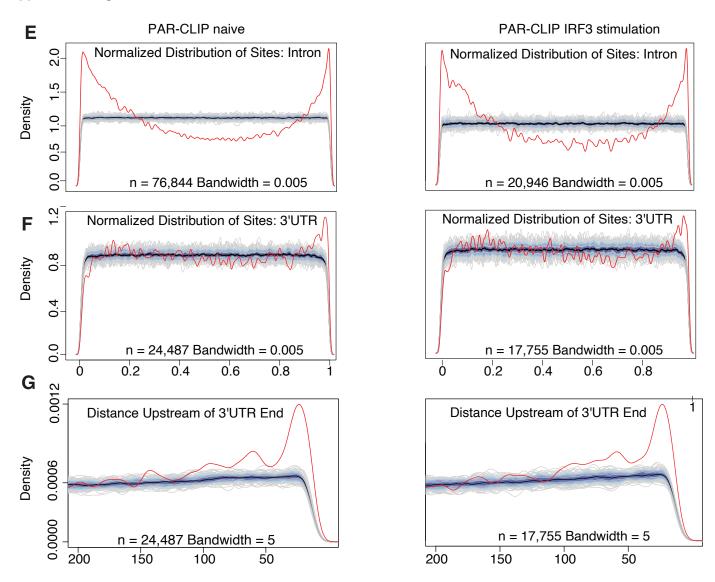
Activation of the pre-replicative complex

Number of transcripts

25

MyD88 deficiency (TLR2/4) Ovarian tumor domain proteases

0



**Supplemental Figure 2** 

# A RIP-PAR naive 1,345 2,114 1,292

#### С

#### naive specific mRNA targets

Processing of Capped Intron-Containing Pre-mRNA

**DNA Replication** 

Activation of the pre-replicative complex

Mitotic G1–G1/S phases

G1/S Transition

Cell Cycle Checkpoints

DNA strand elongation

**DNA** Repair

Synthesis of DNA

mRNA Splicing

0 20 40 60 Number of transcripts

	condition independent THP-1 mRNA targets
	Transcriptional Regulation by TP53
	Regulation of TP53 Activity
	Signaling by TGF-beta Receptor Complex
	Signaling by TGF-beta family members
	Processing of Capped Intron-Containing Pre-mRNA
	Asparagine N-linked glycosylation
	Diseases of signal transduction
	Regulation of TP53 Activity through Acetylation
	0 25 50 75 Number of transcripts
D	
	IRF3 specific mRNA targets
	Fcgamma receptor (FCGR) dependent phagocytosis
	Signaling by Receptor Tyrosine Kinases
	Class I MHC mediated antigen processing & presentation
	Signaling by NTRKs
	TRAF6 mediated induction of NFkB and MAP kinases
	Transcriptional Regulation by TP53
	Toll Like Receptor 7/8 (TLR7/8) Cascade
	MyD88 dependent cascade initiated on endosome

0 20 40 60 Number of transcripts

