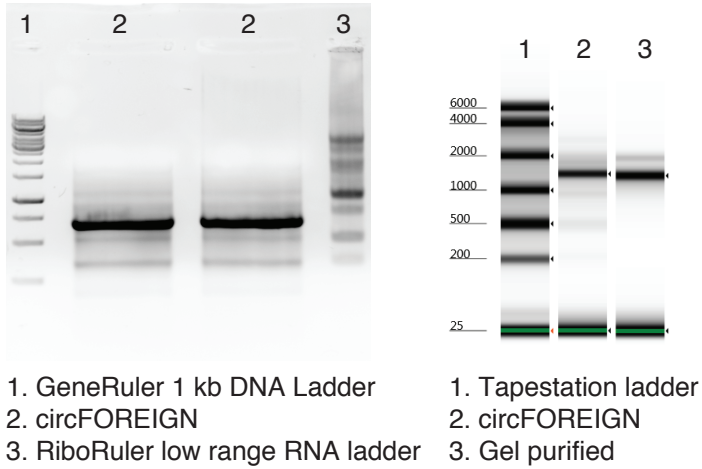
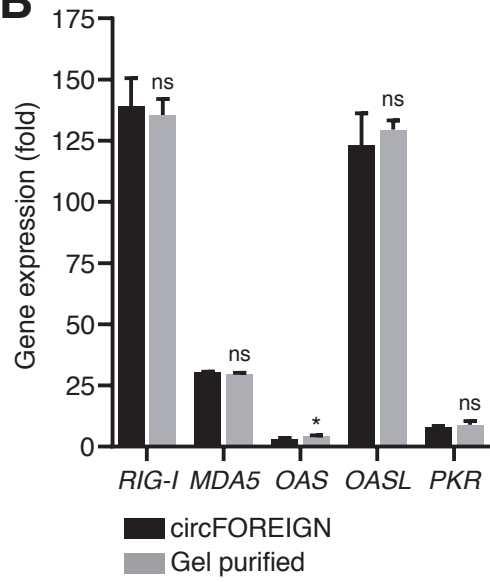


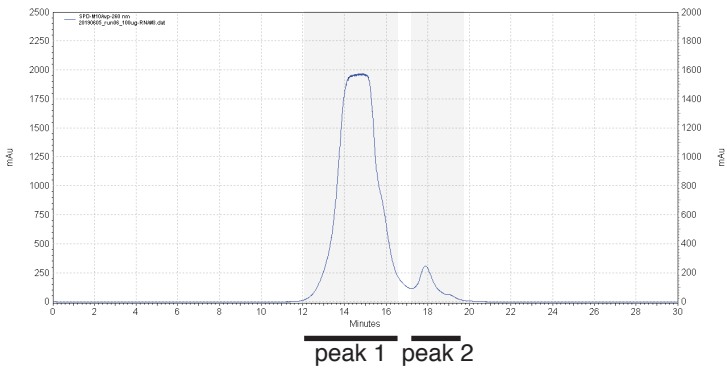
A



B



C



D

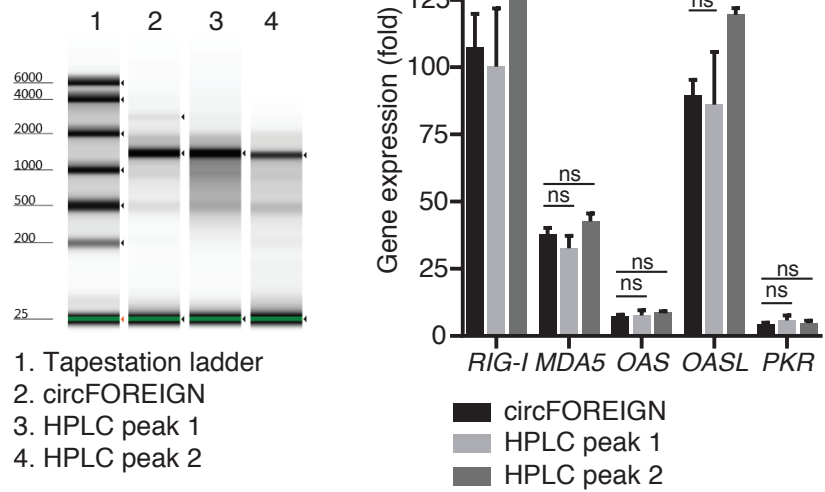


Figure S1. Gel and HPLC purification of circFOREIGN, related to STAR Methods.

- A. Agarose gel electrophoresis of circFOREIGN prior to gel purification (left) and Tapestation analysis of resulting purified RNA (right).
- B. Graph showing gene expression of innate immune genes 24 hours following RNA transfection into HeLa cells. Relative expression of the indicated mRNA and transfected RNA are measured by qRT-PCR, results normalized mock transfection. Means \pm SEM are shown (n = 3).). *p<0.05, Student's t-test, comparing circFOREIGN to gel purified RNA transfection.
- C. HPLC chromatogram of circFOREIGN purification. Collected fractions indicated on trace (left) and Tapestation analysis of purified RNA (right).
- D. Graph showing gene expression of innate immune genes 24 hours following RNA transfection into HeLa cells. Relative expression of the indicated mRNA and transfected RNA are measured by qRT-PCR, results normalized to expression following mock transfection. Means \pm SEM are shown (n = 3).). *p<0.05, Student's t-test, comparing circFOREIGN to indicated RNA transfection.

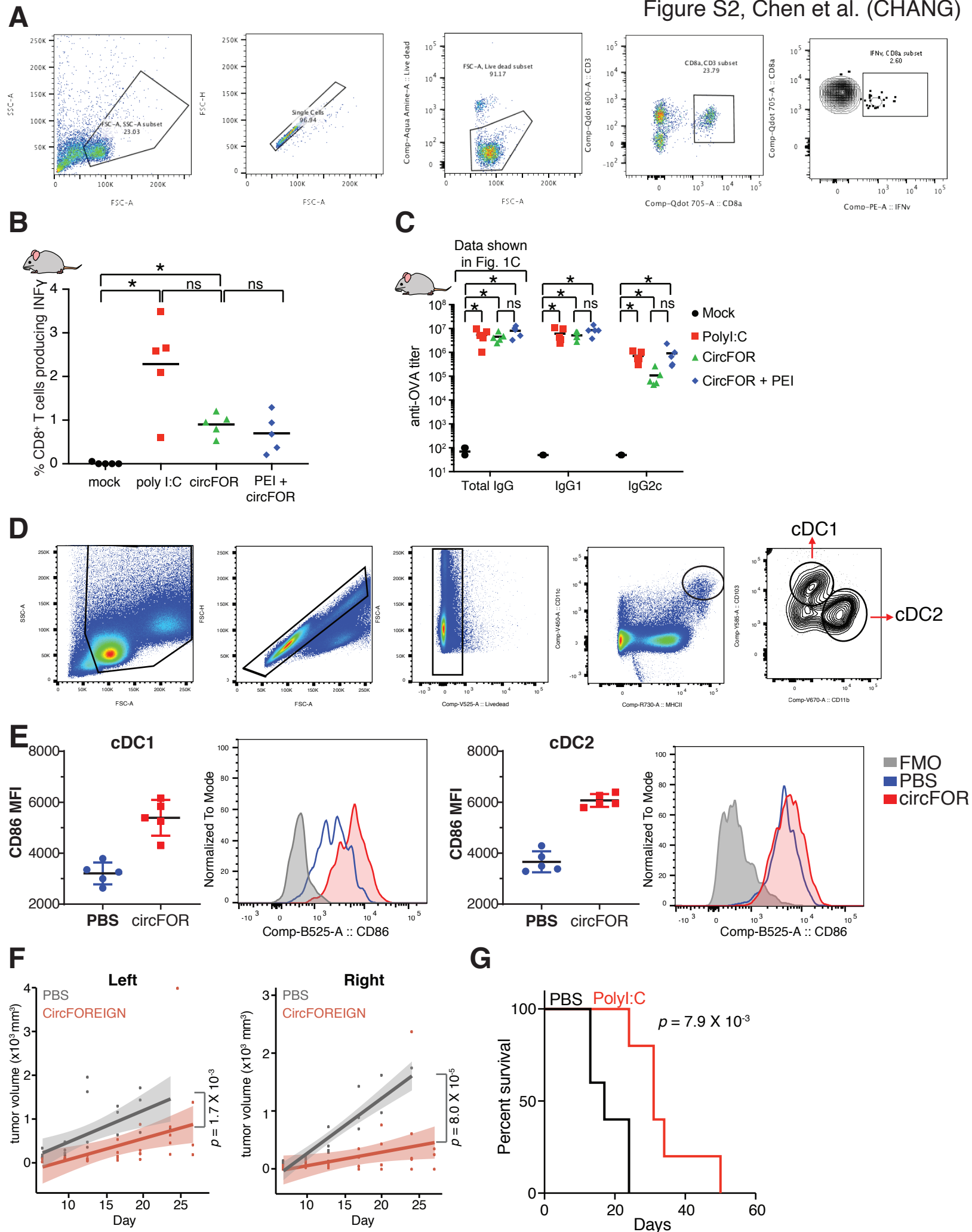
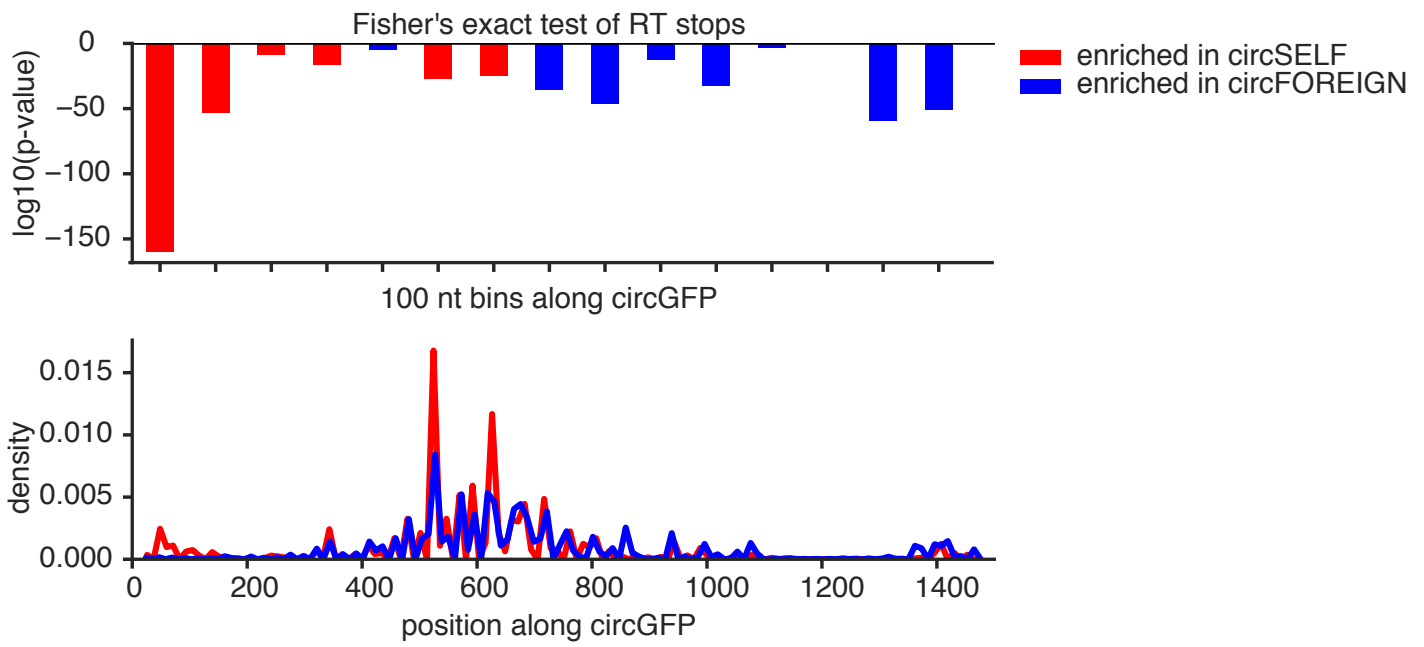
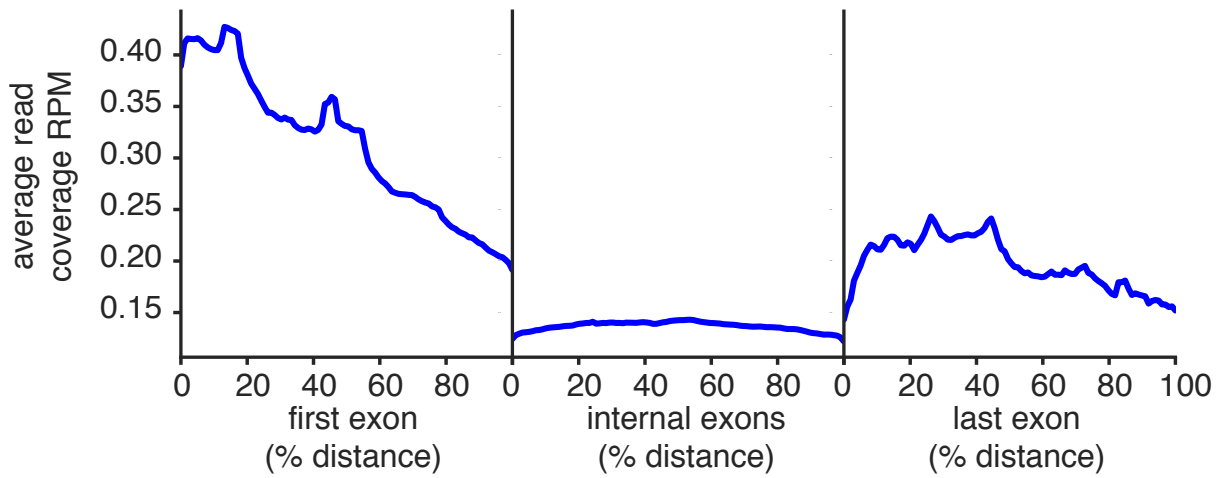


Figure S2. CircFOREIGN kinetics and vaccination effects in vivo, related to Figure 1.

- A. Gating strategy for FACS analysis of IFN γ + CD8 + T cells.
- B. CircFOREIGN stimulates anti-OVA specific T cell response independent of PEI after secondary immunization. Means are shown (n =5), *p<0.05, Anova-Tukey's test.
- C. CircFOREIGN stimulates anti-OVA antibody titers independent of PEI after secondary immunization. Means are shown (n = 5), *p<0.05, Anova-Tukey's test.
- D. Gating strategy for FACS analysis of cDC1 and cDC2 cells.
- E. CircFOREIGN immunization activates DCs in mice.
- F. Measurements of left and right tumor volumes in mice vaccinated with PBS or circFOREIGN. p value calculated by Wilcoxon signed-rank test.
- G. Survival curve of mice vaccinated with PBS or positive control polyI:C. p value calculated by log-rank test.

A**B****C**

circRNA: 0% m⁶A 1% m⁶A 10% m⁶A
Rnase R: - + - + - +

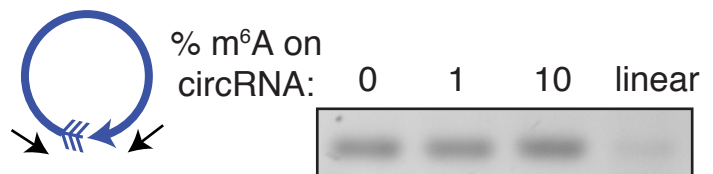
**D**

Figure S3. m⁶A modification on endogenous RNAs and circFOREIGN, related to Figure 2.

- A. m⁶A-irCLIP identifies high confidence m⁶A positions of circSELF or circFOREIGN. Fisher's exact test of RT stops enriched in circSELF (red) or circFOREIGN (blue). Density of m⁶A-irCLIP reads normalized to reads per million.
- B. Analysis determines m⁶A frequency on endogenous linear RNA.
- C. TapeStation analysis of in vitro transcribed circFOREIGN with the indicated levels of m⁶A modification incorporated and with or without RNase R treatment.
- D. qRT-PCR over splice junction confirms unmodified and m⁶A-modified circRNA formation during in vitro transcription. Agarose gel of unmodified and m⁶A-modified circRNA after qRT-PCR using "inverted" primers as indicated.

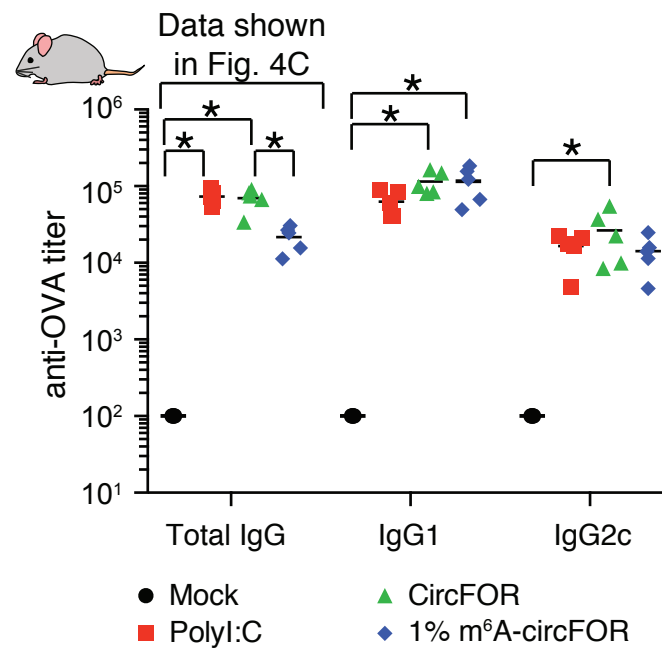
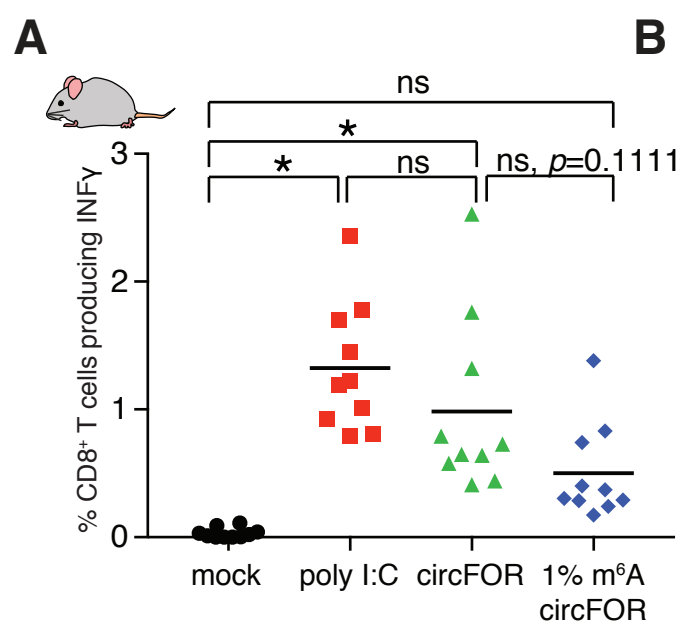


Figure S4. Effects of circFOREIGN immunization, related to Figure 3.

- A. CircFOREIGN stimulates anti-OVA specific T cell response and 1% m⁶A-modified circFOREIGN attenuates immunity after secondary immunization. Means are shown (n = 10), * $p < 0.05$, Anova-Tukey's test.
- B. CircFOREIGN stimulates anti-OVA antibody titers and 1% m⁶A-modified circRNA attenuates immunity after secondary immunization. Means are shown (n = 5), * $p < 0.05$, Anova-Tukey's test.

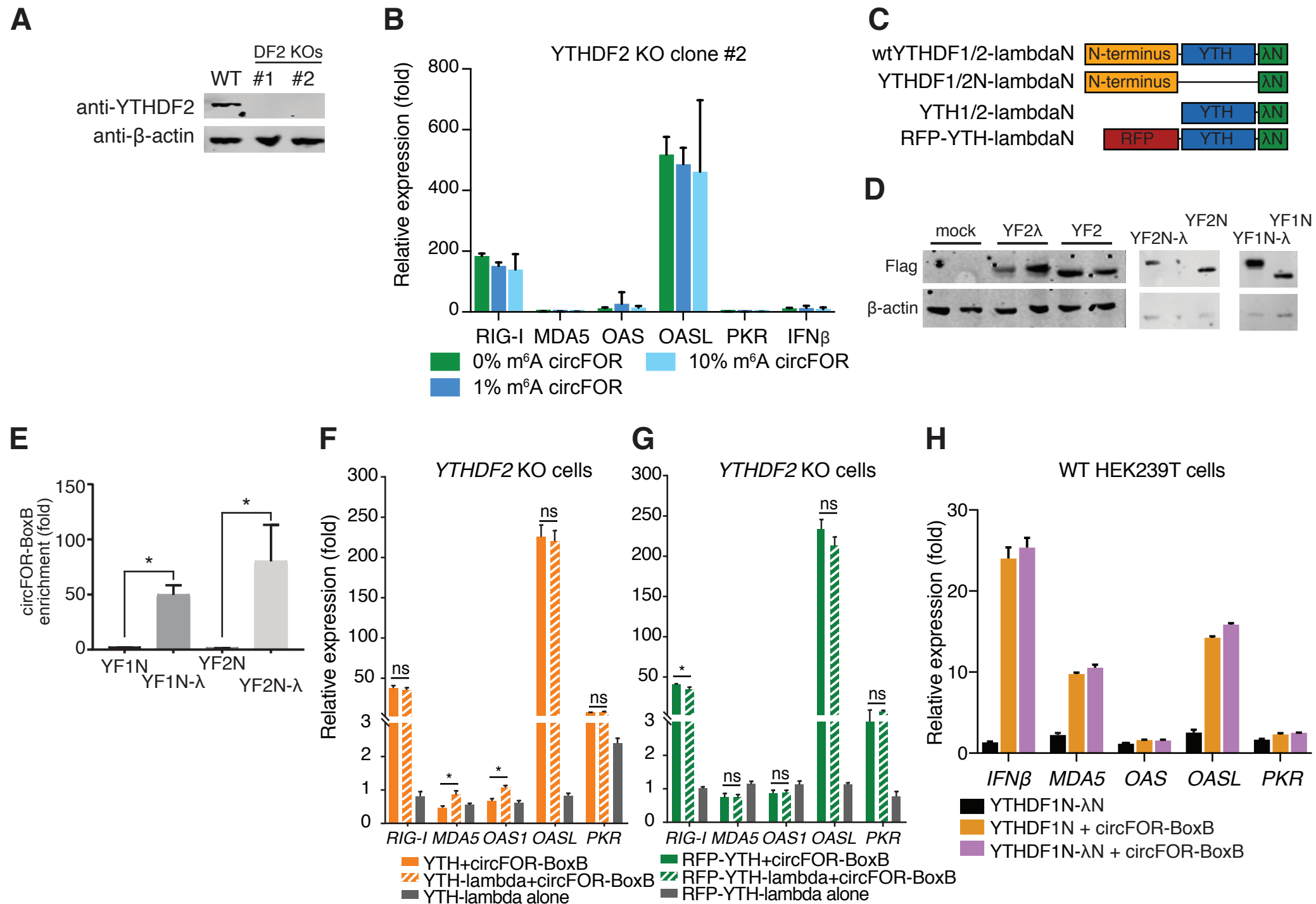
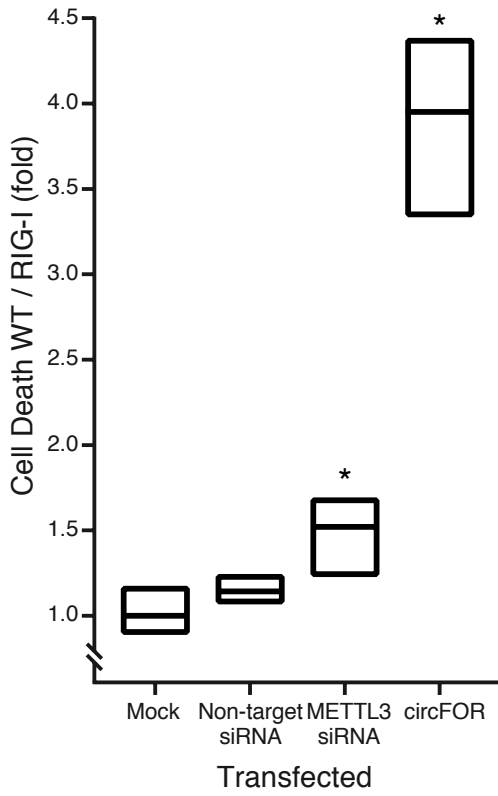


Figure S5. m⁶A reader proteins are not sufficient to block circRNA immunity, related to Figure 4.

- A. Western blot of HeLa wild-type and two YTHDF2 KO clones.
- B. Gene expression of innate immune genes 24 hours following RNA transfection into HeLa YTHDF2^{-/-} clone #2. Relative expression of the indicated mRNA and transfected RNA are measured by qRT-PCR, results normalized to expression following mock transfection. Means \pm SEM are shown (n = 3).
- C. Schematic of YTHDF1/2 constructs used.
- D. Western blots of YTHDF2- λ , YTHDF2, YTHDF2N, YTHDF2N- λ , YTHDF1N, and YTHDF1N- λ .
- E. RIP-qPCR enrichment of indicated YTH protein followed by qRT-PCR of circRNA-BoxB or control actin RNA. Means \pm SEM are shown (n = 3). *p<0.05, Student's t-test.
- F. Transfection of unmodified circBoxB tethered to C-terminal YTH domain of YTHDF2 into YTHDF2 KO cells is insufficient to attenuate immune response. Relative expression of the indicated mRNA and transfected RNA are measured by qRT-PCR, results normalized to expression following mock transfection. Means \pm SEM are shown (n = 3). *p < 0.05, Student's t-test, comparing cells receiving +/- YTHDF2 transfection.
- G. Transfection of unmodified circBoxB tethered to RFP-YTH domain protein fusion into YTHDF2 KO cells is insufficient to attenuate immune response. Relative expression of the indicated mRNA and transfected RNA are measured by qRT-PCR, results normalized to expression following mock transfection. Means \pm SEM are shown (n = 3). *p < 0.05, Student's t-test, comparing cells receiving +/- YTHDF2 transfection.
- H. Transfection of unmodified circBoxB tethered to YTHDF1 is insufficient to attenuate immune response. Gene expression of innate immune genes 24 hours following RNA transfection into wild-type HEK 293T cells. Relative expression of the indicated mRNA and transfected RNA are measured by qRT-PCR, results normalized to expression following transfection of plasmid expressing YTHDF1N- λ N. Means \pm SEM are shown (n = 3).

A**B**

	Mock		Mock siRNA		METTL3 siRNA		circFOREIGN	
	Live	Dead	Live	Dead	Live	Dead	Live	Dead
Wild type	47958	226	48297	184	47447	266	8393	7033
	47801	180	48209	192	67073	282	9046	7153
	47931	172	47780	211	47469	274	8936	5705
RIG-I KO	39397	376	39124	316	48627	348	15429	5353
	39334	259	38775	218	48705	242	16622	6367
	39161	209	38876	206	48588	297	16574	4818

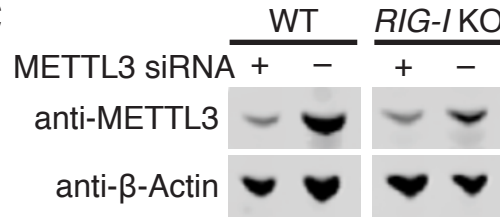
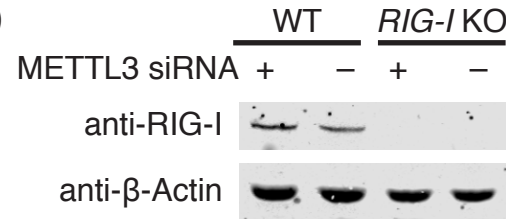
C**D**

Figure S6. m⁶A knockdown increases cell death, related to Figure 4.

- A. RIG-I KO rescues cell death induced by depletion of m⁶A writer METTL3. Graph showing the fold change of cell death in wild-type or RIG-I KO HeLa cells following transfection of indicated RNA. Means \pm SEM are shown (n~50,000 cells analyzed). *p < 0.05, ***p<0.001, Student's t-test, comparing mock transfection to indicated RNA transfection.
- B. Raw cell counts from FACS analysis in A.
- C. Western blot validation of METTL3 knockdown efficiency in HeLa wild-type or RIG-I KO cells with METTL3 siRNA or non-targeting control siRNA transfection.
- D. Western blot validation of RIG-I protein expression in HeLa wild-type and RIG-I KO cells. Cells were transfected with METTL3 siRNA or non-targeting siRNA under comparable conditions to FACS experiment.

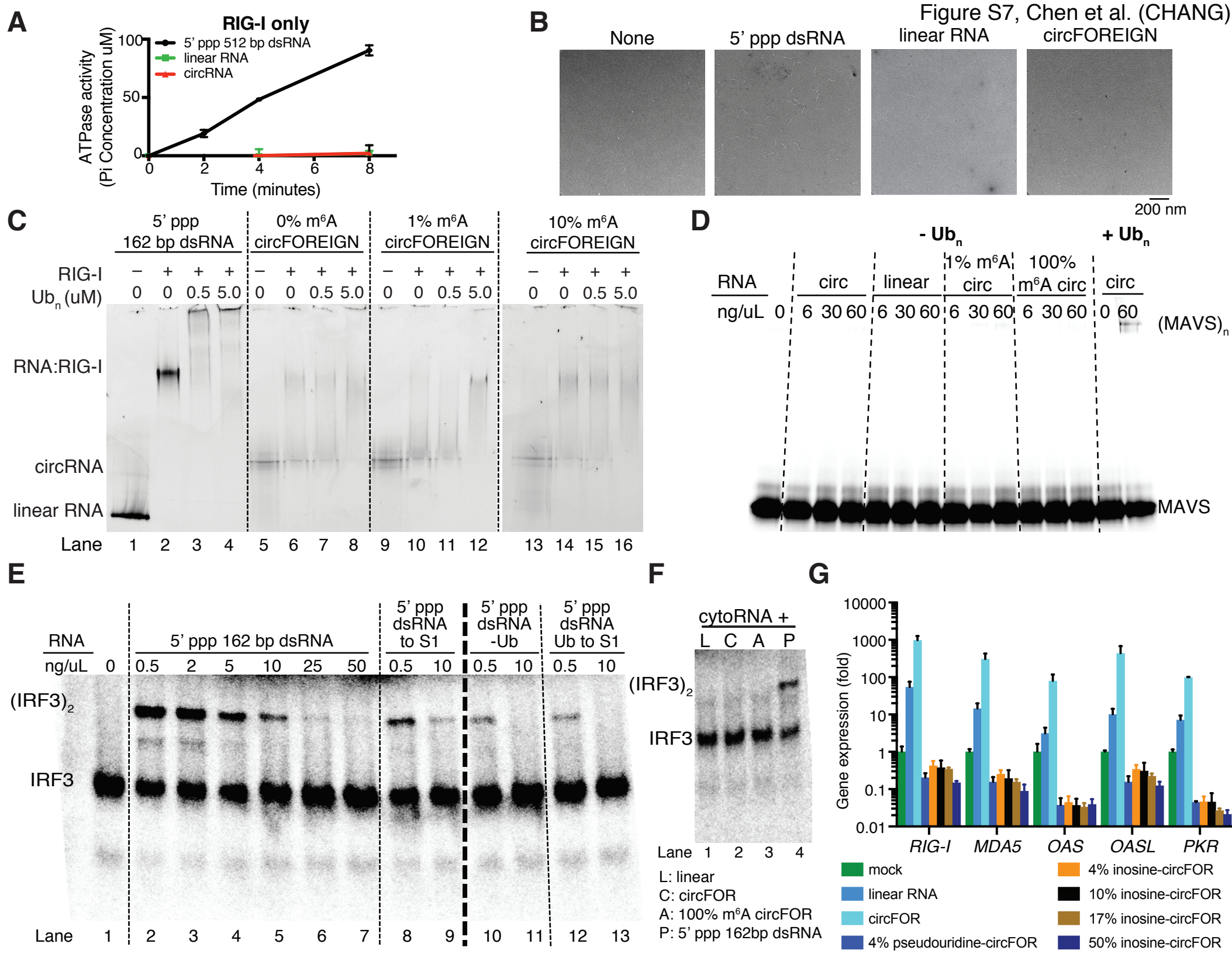


Figure S7. Regulation of circFOREIGN activation of innate immune signaling, related to Figure 5.

- A. CircFOREIGN does not induce ATPase activity of RIG-I. RIG-I and RNA were incubated, and ATP added. Reaction quenched at indicated time points and Pi concentration measured. Means \pm SEM are shown (n = 2).
- B. Representative electron microscopy images of RIG-I filaments after RIG-I is incubated with indicated RNA.
- C. *In vitro* RIG-I binding assay with purified RIG-I, K63-polyubiquitin the indicated RNA ligands. Native electrophoretic gel shift assay shows that RIG-I binding does not distinguish between unmodified and m⁶A-modified circFOREIGN.
- D. *In vitro* reconstitution with purified RIG-I, MAVS, the indicated RNA ligands, and the absence or presence of K63-polyubiquitin. Native gel of fluorescently-labeled MAVS 2CARD domain shows that circFOREIGN-initiated MAVS filamentation is dependent on K63-polyubiquitin.
- E. *In vitro* reconstitution of the circRNA-mediated induction of IRF3 dimerization. RIG-I, IRF3, and the indicated RNA ligands were incubated. Native gel of radiolabeled-IRF3 with the indicated RNA ligands is shown.
- F. Native gel of radiolabeled-IRF3 with the indicated RNA ligands is shown. Cytoplasmic RNA (cytoRNA) and indicated RNAs were each added at 0.5 ng/uL.
- G. Transfection of unmodified circRNAs into wild-type HeLa cells stimulates immune response. Graph showing gene expression of innate immune genes 24 hours following RNA transfection. Relative expression of the indicated mRNA and transfected RNA are measured by qRT-PCR, results normalized to expression following mock transfection. Means \pm SEM are shown (n = 3).