

## Supporting Online Material for

### **A novel lncRNA regulates HCV infection through IFI6**

Xiao Liu<sup>1,3,4\*</sup>, Xiaoqiong Duan<sup>2,3\*</sup>, Jacinta A. Holmes<sup>3</sup>, Wenting Li<sup>3, 5</sup>, Sae Hwan Lee<sup>3,6</sup>, Zeng Tu<sup>3,7</sup>, Chuanlong Zhu<sup>3,8</sup>, Shadi Salloum<sup>3</sup>, Anna Lidofsky<sup>3</sup>, Esperance A. Schaefer<sup>3</sup>, Dachuan Cai<sup>3,9</sup>, Shilin Li<sup>2</sup>, Haoju Wang<sup>1</sup>, Yongfu Huang<sup>1</sup>, Yongju Zhao<sup>1</sup>, Ming-Lung Yu<sup>3,10</sup>, Zhiwen Xu<sup>4</sup>, Limin Chen<sup>2</sup>, Jian Hong<sup>3</sup>, Wenyu Lin<sup>2,3†</sup>, Raymond T. Chung<sup>3†</sup>

<sup>1</sup>Southwest University, College of Animal Science and technology, 400715 Chongqing, China

<sup>2</sup>Institute of Blood Transfusion, Chinese Academy of Medical Sciences and Peking Union Medical College, 610052 Chengdu, China

<sup>3</sup>Liver Center and Gastrointestinal Division, Department of Medicine, Massachusetts General Hospital, Harvard Medical School, Boston, MA 02114, USA

<sup>4</sup>Animal Biotechnology Center, College of Veterinary Medicine, Sichuan Agricultural University, 610052 Chengdu, China

<sup>5</sup>Department of Infectious Disease, Anhui Provincial Hospital, Anhui Medical University, Hefei, China

<sup>6</sup>Soonchunhyang University College of Medicine, Cheonan Hospital, 330721 Dongnamgu Cheonan, Republic of Korea

<sup>7</sup>Department of microbiology, College of Basic Medical Science, Chongqing Medical University, 400715 Chongqing, China

<sup>8</sup>Department of Infectious Disease, the First Affiliated Hospital of Nanjing Medical University, Nanjing 210029, China

<sup>9</sup>Department of Infectious Disease, Chongqing Medical University, 400715 Chongqing, China

<sup>10</sup>Division of Hepatobiliary, Department of Internal Medicine and Hepatitis Center, Kaohsiung Medical University Hospital, Kaohsiung, Kaohsiung Medical University, Taiwan

\*These two authors (Liu X and Duan X co-1<sup>st</sup> author) contributed equally to this work.

**†Corresponding authors**

Correspondence address: Gastrointestinal Unit, Warren 1007, Massachusetts General Hospital, Harvard Medical School, Boston, MA 02114, USA;

Tel.: +1 617 726 2061; fax: +1 617 643 0446.

E-mail: [wlin1@mgh.harvard.edu](mailto:wlin1@mgh.harvard.edu), or [rtchung@partners.org](mailto:rtchung@partners.org)

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## **Supplemental Materials and Methods**

### **Cells and virus**

Huh7.5.1, HepG2, LX2, TWNT4 and Huh7 cells were grown in DMEM (Thermo Fisher Scientific, Waltham, UK) supplemented with 10% fetal bovine serum (FBS) (GIBCO, city, state) and 1% penicillin/streptomycin (Invitrogen, city, state) at 37°C with 5% CO<sub>2</sub>. Huh7.5.1 cells were infected with genotype 2a JFH1 HCV virus at a multiplicity of infection of 0.2 (JFH1 cells) as previously described. Primary human hepatocytes (PHHs) were purchased from TRIANGLE Research Laboratories (Durham, NC), and cultured according to the manufacturer's instructions. In brief, PHHs were seeded onto matrix-coated plates and cultured with Hepatocyte Plating Medium (Durham, NC, USA). Cell viability was determined using a Cell Titer-Glo luminescent cell viability assay kit (Promega, Madison, WI) according to the manufacturer's protocol.

### **Long non-coding RNA high-throughput sequencing and data analysis**

Total RNA from control Huh7.5.1 cells and IFN $\alpha$ -treated (30 IU/mL) Huh7.5.1 cells were used to prepare the lncRNA sequencing library. Oligo dT beads were used to select mRNA from the total RNA. The Illumina library preparation was performed by using broadly designed indexed adapters after cDNA was synthesized with RT primers. The samples were quantified by qPCR after enrichment, followed by lncRNA high-throughput sequencing performed at the Broad Institute (Cambridge, MA, USA) on the Illumina

HiSeq2000 platform using the Illumina Tru Seq™ Rapid SBS kit (#FC-402-4002, Illumina) according to the manufacturer's instructions. The significantly differentially expressed lncRNAs for the IFN $\alpha$  treated sample vs. control sample were determined by fold-change value (see Bioinformatic analysis below), where  $\geq 2.0$  fold-change differential gene expression indicates up-regulation of lncRNA expression in that the lncRNA in IFN $\alpha$ -treated samples, while a fold-change value  $\leq 0.5$  indicates down-regulation of lncRNA gene expression in IFN $\alpha$  treated samples. We then chose 5 up-regulated and 5 down-regulated IFN-induced lncRNAs from our RNAseq bioinformatic analysis for further validation.

### **RNA extraction and quantitative RT-PCR**

Total cellular RNA from cells was harvested using the QIAshredder and RNeasy mini kits (QIAGEN, Valencia, CA) according to the manufacturer's instructions. RNA concentrations were determined using the NanoDrop ND-1000 spectrophotometer (NanoDrop Inc., DE, USA). cDNA was synthesized by reverse transcription using the High-Capacity cDNA Kit (Invitrogen, Carlsbad, CA). Quantitative PCR (qPCR) was performed using Power Up SYBR Green Master Mix (Thermo Fisher Scientific, MA, USA) using the QuantStudio3 platform (Thermo Fisher Scientific, MA, USA). The mRNA expression level of target genes was normalized to GAPDH by using the  $2^{-\Delta\Delta Ct}$  method to obtain mRNA arbitrary units (fold-change). Primer sequences are listed in Supplemental Table (STab 2).

## **Bioinformatics Analysis**

The sequences of lncRNAs were obtained from NCBI and UCSC Genome Bioinformatics (<http://genome.ucsc.edu/index.html>). Novel human-encoded lncRNAs were analyzed using ChIPBase v2.0 (<http://rna.sysu.edu.cn/chipbase/>). The NCBI ORF Finder (<http://www.ncbi.nlm.nih.gov/gorf/gorf.html>) and coding potential calculator (<http://cpc.cbi.pku.edu.cn>) were used to predict the protein coding potential of lncRNAs. The RNAfold web server (<http://rna.tbi.univie.ac.at/cgi-bin/RNAfold.cgi>) was used to predict the secondary structure of lncRNAs and mutated lncRNAs. The precursor mRNAs of ISGs were predicted by using the UCSC genome browser (<http://genome.ucsc.edu/index.html>) and the NCBI Genome database (<http://www.ncbi.nlm.nih.gov/genome/>). The promoters of ISGs were predicted using Softberry (<http://www.softberry.com/>). The UCSC genome browser database (<http://genome.ucsc.edu/index.html>) was used to predict CpG islands.

## **CRISPR/Cas9 guide RNA (gRNA) editing**

In order to study the biological function of lncRNA-IFI6, we used 3 CRISPR/Cas9 guide RNAs (gRNAs) (pSpCas9 BB-2A-Puro PX459 all-in-one system, GenScript Corporation, NJ, USA) to knock out lncRNA-IFI6. We tested 3 lncRNA-IFI6 gRNAs: CRISPR/Cas9 gRNA lncRNA-IFI6 #1 (5'-GTGCGGATTCGCACGGTGTT-3') which targets lncRNA-IFI6 (91-110

basepairs, bp), gRNA IncRNA-IFI6 #2 (5'-GGATTCTGTGCGGATTCGCA-3') which targets IncRNA-IFI6 (185-166 bp), and gRNA IncRNA-IFI6 #3 (5'-CAGAAGCCTCTCGTACGGTG-3') which targets IncRNA-IFI6 (84-103 bp). We selected gRNA #1 for further study based on the knockout effect. We also used 3 CRISPR/Cas9 guide RNAs (gRNAs) (pSpCas9 BB-2A-Puro PX459 all-in-one system, GenScript Corporation, NJ, USA) to knock out IFI6, CRISPR/Cas9 gRNA IFI6 #1 (5'- GCAGCGAGTAAACGGTTCTC-3') which targets IFI6 (155-174 bp), CRISPR/Cas9 gRNA IFI6 #2 (5'- AGATCCTAACTGGAAGAGTT-3') which targets IFI6 (158-177 bp), CRISPR/Cas9 gRNA IFI6 #3 (5'- GCATGCTTGTAATCCTACTT-3') which targets IFI6 (151-170 bp).

### **Plasmid information and cell transfections**

Full-length IncRNA-IFI6 and truncated mutants of IncRNA-IFI6 (mutants 1-4) were synthesized and cloned into a pcDNA3.1(+) vector, carrying a neomycin resistance gene (GenScript corporation). Truncated IncRNA-IFI6 mutant domains were determined based on their secondary structure. Mutant 1 included IncRNA-IFI6 1-282 bp and 471-489 bp (large left arm and central circle structure), mutant 2 contained IncRNA-IFI6 261-489 bp (large right arm and central circle structure), mutant 3 contained IncRNA-IFI6 16-181 bp (small left arm), and mutant 4 contained IncRNA-IFI6 1-15 bp, 182-282 bp and 471-489 bp (central circle structure). IFI6 and OAS3 Gluc-On promoter reporter clones (pEZX-PG04-IFI6 and pEZX-PG04-OAS3) carrying the Gaussia luciferase (Gluc) and Secreted Alkaline Phosphatase (SEAP) were obtained

from GeneCopoeia (San Diego, USA). IFI6 expression, OAS3 expression and pcDNA3.1(+) empty vectors were purchased from GenScript Corporation. The pISRE-luc (expressing firefly luciferase) and pRL-TK (expressing *renilla* luciferase) were obtained from Promega (Madison, WI). The plasmids were transfected into cells using Lipofectamine LTX&PLUS Reagent (Invitrogen, MA, USA.) according to the manufacturer's instructions. Total RNA or protein was harvested at 72 hrs post vector transfection, 48 hrs post JFH1 HCV infection and 24 hrs post IFN $\alpha$  treatment at 30 IU/mL (PBL assay science, MA, USA).

### **Western Blot**

Cells were washed with PBS and lysed using protein RIPA Lysis Buffer containing protease inhibitor cocktail (Sigma Life Science and Biochemicals, St. Louis, MO). Equal quantities of protein (20  $\mu$ g) were loaded into each lane. Protein samples were separated by SDS-PAGE gel electrophoresis with NuPAGE Novex pre-cast 4-12% Bis-Tris gradient gels (Invitrogen, Carlsbad, CA) and blotted onto nitrocellulose membranes. The membranes were blocked with 5% bovine serum albumin (BSA). Targeted proteins were detected with specific primary antibodies including rabbit polyclonal antibody to IFI6 (Abcam, Cambridge, USA), mouse anti- $\beta$ -Actin (Sigma Life Science and Biochemicals, St. Louis, MO), goat anti-OAS3 (Santa Cruz Biotechnology, USA), mouse anti-STAT1 (Cell signaling, USA) and mouse anti-HCV core C7-50 (Fisher Scientific, Pittsburgh, PA). The secondary antibodies were

horseradish peroxidase (HRP)-conjugated ECL donkey anti-rabbit IgG and HRP-conjugated ECL sheep anti-mouse IgG (GE Healthcare Biosciences, Pittsburgh, PA). The blots were detected by chemiluminescence using the Amersham ECL Western blotting detection kit (GE Healthcare Biosciences, Pittsburgh, PA).

### **Chromatin Immunoprecipitation (ChIP) assay**

plncRNA-IFI6-overexpression, lncRNA-IFI6 gRNA, or negative control transfected Huh7.5.1 cells were selected for ChIP assays using the EZ-Magna ChIP A/G chromatin immunoprecipitation kit (Millipore, USA) according to the manufacturer's instructions. Briefly, cells were fixed with 1% formaldehyde for 10 minutes followed by quenching of the formaldehyde by rinsing with 10x glycine. The cells were then lysed in lysis buffer. The nuclear fraction of cells was pelleted in nucleus lysis buffer. The chromatin was ultrasonically treated and immunoprecipitated with the following antibodies: anti-H3K4me3 (Cat# 17-614), anti-H3K27me3 (Cat# 07-449), anti-RNA Polymerase II (Cat# 05-623B) and IgG control (Cat# 12-371B) (Millipore, MA). Elution of protein/DNA complexes and reverse cross-links of protein/DNA complexes to free DNA were performed using the ChIP Elution Buffer mixed with proteinase K, and the Magna Chip magnetic device. The DNA was purified for qRT-PCR to assess the level of IFI6 promoter and GAPDH promoter.

### **Generation of lncRNA CRISPR/Cas9 knockout stable cell lines**

The CRISPR wild-type SpCas9 (WT SpCas9) system and pSpCas9 BB-2A-Puro (PX459) all-in-one vector driven by CBh promoter (drives expression of gRNA and Cas9 in a 1:1 ratio) were purchased from GenScript Corporation. The gRNAs (lncRNA-IFI6 gRNA and Neg gRNA) were transfected into cells by using Lipofectamine LTX&PLUS™ reagent, in accordance with the manufacturer's instructions. Puromycin (Cell culture gibco, MA, USA) was used to select CRISPR/Cas9 stably transfected cell lines.

### **Small interfering RNA (siRNA) and transfection**

The Dharmacon ON-TARGET plus SMART pool Human siRNAs (Fisher Scientific Life Science Research, Pittsburgh, PA) used for gene knock down were as follows: IFI6, STAT1, STAT2, JAK1, and non-target negative control siRNA (Neg-siRNA). The siRNAs were transfected into cells by using Lipofectamine RNAiMAX reagent (Invitrogen, MA, USA.), in accordance with the manufacturer's instructions. At 24 hrs post siRNA transfection, the cells were infected with HCV (JFH1) at 0.2 multiplicity of infection (MOI). At 48 hrs post siRNA transfection, human IFN $\alpha$  was added at a final concentration of 30 (IU/mL). The total RNA or protein lysates were harvested at 72 hrs post siRNAs transfection.

### **ISRE-luciferase reporter assay.**

IFN-induced ISRE signaling was monitored using a luciferase reporter assay system driven by ISRE. pISRE-luc (expressing firefly luciferase) and pRL-TK (expressing *renilla* luciferase) were co-transfected into lncRNA-IFI6 gRNA, Neg gRNA, plncRNA-IFI6 and pEmpty stably expressing Huh 7.5.1 cells, respectively. The luciferase lysates were harvested at 72 hrs post vector transfection, 48 hrs post JFH1 HCV (JFH1 at 0.2 MOI) infection, and 24 hrs post IFN $\alpha$  treatment. IFN $\alpha$ -stimulated ISRE luciferase levels were normalized to RL-TK luciferase levels yielding the relative luciferase unit (RLU).

### **Subcellular fractionation**

Cytoplasmic and nuclear fractions of the cells were separated by using the SurePre™ Nuclear or Cytoplasmic RNA purification kit (Fisher scientific, Canada), in accordance with the manufacturer's instructions. In brief, Huh7.5.1 cells were treated with IFN $\alpha$  30 IU/mL for 24 hours. After washing the cells with PBS, cells were lysed with ice-cold Lysis Solution, and the cell lysates were centrifuged at 13,000 RPM for 15 min at 4°C, after which the cytoplasmic RNA was located in the supernatant, and the nuclear RNA located within the pellets. The cytoplasmic RNA fraction and nuclear RNA fraction were individually bound to a column using a binding solution and washed three times. The cytoplasmic RNA and nuclear RNA were eluted in RNA elution solution.

### **5-Aza-2'-deoxycytidine treatment**

Cells overexpressing lncRNA-IFI6 gRNA, Neg gRNA, plncRNA-IFI6, pEmpty were treated with or without 10  $\mu$ M 5-Aza-2'-deoxycytidine (DAC) (methyltransferase inhibitor decitabine) (Sigma, USA) for 48 hours. Total RNA was isolated using the Total RNA kit (Qiagen, MA, USA). The mRNA level of each sample was detected by qRT-PCR.

### **RNA stabilization assays**

lncRNA-IFI6 gRNA or plncRNA-IFI6 stably transfected Huh7.5.1 cells were treated with actinomycin D (ActD, Sigma, USA) at 1  $\mu$ g/mL, cells were harvested at 0, 5, 10 and 15 hours post-treatment. The mRNA level was detected by qRT-PCR.

The value of fraction of RNA remained at 0 hr is taken as 100%, and the values of 5 hrs, 10 hrs and 15 hrs time points are normalized to 0 hr to calculate the RNA degradation rate.

### **Secreted-Pair Dual Luminescence analysis (Detection of ISGs promoter activity)**

The Secreted-Pair Dual Luminescence Assay Kit for parallel bioluminescence assays of Gaussia luciferase (Gluc) and secreted Alkaline Phosphatase (SEAP) were provided by GeneCopoeia Inc (USA). Cells overexpressing plncRNA-IFI6 and lncRNA-IFI6 gRNA were transfected with a pEZX-PG04-IFI6-promoter and pEZX-PG04-OAS3-promoter, respectively. Gaussia

luciferase (Gluc) assay and secreted Alkaline Phosphatase (SEAP) assays were performed to detect the IFI6 and OAS3 promoter activity.

**Supplemental Table 1. List of identified long non-coding RNA from RNA-Seq**

Supplemental Table 1 can be obtained online by link:

<https://drive.google.com/file/d/0B5t4LtawAMViZWRHRUVpZmVlcTA/view?usp=sharing>

## Supplemental Table 2. List of used primer sequences

| Stable 2. List of used primer sequence |                  |                           |                           |
|--|------------------|---------------------------|---------------------------|
| LncRNA name                            | Accession number | Forward primer            | Reverse primer            |
| RP11-288L9.4 (lncRNA-IFI6)             | HG491811.1       | GAATCCGTTTCCTCTCCGCA      | CTTTCACGTGCCAAACACCG      |
| AP001610.5                             | HG511840.2       | ATCAGCCTTGGGGGAGTGAA      | GAGCTGGAGAAGCACATGTCA     |
| RP11-670E13.5                          | HG509260.1       | TCAAACCTTCTAAGAGGAATCGG   | GTGGGAGGTGGGATTTAGCC      |
| RP1-71H24.1                            | HG505187.1       | TCCTGGATGAACCTCCCCCG      | TGGTTGTCTTCTCAGTCTC       |
| RP11-395B7.7                           | HG500454.1       | GAAAGCTCTGGAACACCCGA      | GCTCAGGTCAGCAACCTCAT      |
| RP11-168P16.2                          | HG508507.1       | GTAAGGGCTCTGCGTGTCTT      | CCAGGGTCCATGCAGTCAA       |
| RP11-717D12.1                          | HG495646.1       | AAGGTTGGGGAAGTGTGAG       | AATAGAGGCATGCACGCAGT      |
| RP11-502N13.2                          | HG504542.1       | CACCACCTGTGAGTATGTT       | AGCTGTGAGTCCAGAACAA       |
| RP11-366L20.3                          | HG504909.1       | TGGAAAGCTTTTTGGACGCC      | CGCCTGTATGGCTTTGCATC      |
| RP11-326L2.1                           | HG500922.1       | TCCCAGCACTTGGCAAAGA       | CACTGGCATACCAGGCAT        |
| Gene name                              | Accession number | Forward primer            | Reverse primer            |
| Human IFI6                             | NM_022873.2      | GGTCTGCGATCCTGAATGGG      | TCACTATCGAGATACTTGTGGGT   |
| Human OAS3                             | NM_006187.3      | GCTTCAAGAGCTATGTGGACC     | GGAAACGTGAGTCTCAGACCA     |
| Human IFIT1                            | NM_001270930.1   | TTGATGACGATGAAATGCCTGA    | CAGGTCACCAGACTCCTCAC      |
| Human IFIT5                            | NM_012420.2      | GGCCAAAATAAAGACGCCCTT     | GACCAGGCTTCGTACTIONTTC    |
| Human MX1                              | NM_001144925.2   | GTTTCCGAAAGTGACATCGCA     | GAAGGGCAACTCCTGACAGT      |
| Human ZAP                              | XM_011516412.2   | CCGGTGCAACTATTCGCAGT      | TCAGTCCAGAGATTCTGTATTT    |
| Human IRF7                             | NM_004031.2      | GCTGGACGTGACCATCATGTA     | GGGCCGTATAGGAACGTGC       |
| Human ISG15                            | NM_005101.3      | TCCTGGTGAGGAATAACAAGGG    | GTCAGCCAGAACAGGTCGTC      |
| Human ISG20                            | NM_001303234.1   | CTCGTTGCAGCCTCGTGAA       | CGGGTTCTGTAATCGGTGATCTC   |
| Human STAT1                            | NM_007315.3      | GAGAGCTGTCTAGGTTAACGTTCCG | AGTCAAGCTGCTGAAAGTTCTGACC |
| Human JAK1                             | NM_001321857.1   | GTGCTCCGCGGCTCTTGAC       | CTTCTTTGGAGATGACGCC       |
| JFH1-HCV                               | AB047639.1       | TCTGCGGAACCGGTGAGTA       | TCAGGCAGTACCACAAGGC       |
| Human GAPDH                            | BC026907.1       | ACCTTCCCCTGCTGTCTGA       | GCTCCTCCTGTTCCGACAGTCA    |
| Human U6                               | NR_004394.1      | CTCGCTTCGGCAGCACA         | AACGCTTACGAATTTGCGT       |
| IF6 promoter                           | NM_022873.2      | GCTGGTGATCAGGCTTCACT      | AGCTTGATGCCACACTTCA       |
| GAPDH promoter                         | BC026907.1       | TACTAGCGGTTTTACGGGCG      | TCGAACAGGAGGAGCAGAGAGCGA  |
| pcDNA3.1(+)                            | EF550208.1       | CTAGAGAACCCACTGCTTAC      | TAGAAGGCACAGTCGAGG        |
| LncRNA name                            | Accession number | Forward primer            | Reverse primer            |
| IFI6-Intron1 (pre-IFI6-1)              | U22970.1         | TGATCCCTGGCTTGTGAACC      | GATGTCTGCCATGGAACCGC      |
| IFI6-Intron2 (pre-IFI6-2)              | U22970.1         | GTCTGGAGGGCGAGGATCT       | GAGGAACAGGAGCAGGTGAG      |
| IFI6-Intron3 (pre-IFI6-3)              | U22970.1         | GTCGCCAGAGTCCCAGATTC      | ACAAAAGCGTAGTGGGGTTGT     |
| IFI6-Intron4 (pre-IFI6-4)              | U22970.1         | TGACATCTGCGGACGTTACC      | GAATCCGTTTCTCTCCGCA       |

## Supplemental Figure

**Supplemental Figure 1. IFN $\alpha$ -induced lncRNAs expression.** We selected genes identified by RNAseq for further characterization. Each selected gene mRNA levels were normalized to GAPDH mRNA yielding arbitrary units (fold-change). \* P < 0.05, \*\* P < 0.01, and # P < 0.001 for comparison between without or with IFN, respectively.

**(A) The Venn distribution diagram of IFN $\alpha$ -induced lncRNAs.** We identified 7901 lncRNAs by RNAseq in Huh7.5.1 cells. There were 495 downregulated and 567 upregulated IFN $\alpha$ -induced lncRNAs.

**(B-F) The selected 5 IFN upregulated lncRNAs.** We confirmed by qRT-PCR 5 IFN-induced lncRNAs including **(B)** lncRNA RP11-288L9.4, **(C)** lncRNA AP001610.5, **(D)** lncRNA RP11-670E13.5, **(E)** lncRNA RP11-473C18.3, **(F)** lncRNA RP11-395B7.7.

**(G-K) The selected 5 IFN downregulated lncRNAs.** **(G)** lncRNA RP1-168P16.2, **(H)** lncRNA RP11-717D12.1, **(I)** lncRNA RP11-502N13.2, **(J)** lncRNA RP11-366L20.3, and **(K)** lncRNA RP11-326L2.1.

**(L) Paradigm of the genomic location of lncRNA gene RP11-288L9.4 (yellow arrow) and the relationship with the coding gene IFI6 (blue arrow).**

**(M) – (R) IFN $\alpha$ -induced lncRNA RP11-288L9.4 expression in several tested cells** including **(M)** Huh7.5.1, **(N)** HepG2, **(O)** LX2, **(P)** TWNT4, **(Q)** Huh7, and **(R)** in human primary hepatocytes (PHH).

**Supplemental Figure 2. lncRNA-IFI6 gRNA or plncRNA-IFI6**

**overexpression did not affect cell viability.** Huh7.5.1 cells line stably expressing specific lncRNA-IFI6 gRNA, Neg gRNA, plncRNA-IFI6 and pEmpty were generated. Cells were then inoculated with JFH1 HCV for 48 hrs. At 24 hrs post infection, human IFN $\alpha$  was added at a final concentration of 30 IU/mL. Total RNA or protein lysates were harvested at 48 hrs post infection. Cell viability was monitored using the Cell Titer-Glo luminescent cell viability assay kit. Data are shown as means  $\pm$  standard deviation of three replicates. \* P < 0.05; \*\* P < 0.01; \*\*\* P < 0.001.

**(A) Paradigm of the lncRNA-IFI6 gRNA targeting sites.**

**(B) lncRNA-IFI6 gRNA did not affect Huh7.5.1 cell viability.** Relative cell viability in Neg gRNA treatment was normalized to 100%.

**(C) Over-expression of plncRNA-IFI6 did not affect Huh7.5.1 cell viability.** Relative cell viability in pEmpty vector treatment was normalized to 100%.

**Supplemental Figure 3. lncRNA-IFI6 regulation on HCV infection through**

**IFI6 expression.** JFH1 HCV was inoculated to the cells for 48 hrs. At 24 hrs post infection, human IFN $\alpha$  was added to a final concentration of 30 IU/ mL. The total RNA or protein lysates were harvested at 48 hrs post infection.

**(A) lncRNA-IFI6 gRNA reduced HCV infection level in JFH1-infected Huh7.5.1 cells at 0, 12, 24, 36, 48, 72 hours post-infection compared to Neg gRNA respectively.**

- (B) Overexpression plncRNA-IFI6 increased lncRNA-IFI6 RNA level in Huh7.5.1 or JFH1 cells compared to pcDNA Empty with or without IFN respectively.**
- (C) Overexpression of plncRNA-IFI6 increased HCV RNA levels in JFH1-infected Huh7.5.1 cells at 0, 12, 24, 36, 48, 72 hours post-infection compared to pEmpty respectively.**
- (D) Overexpression of plncRNA-IFI6 rescued IFN-induced inhibition of HCV RNA in JFH1-infected Huh7.5.1 cells compared to pEmpty respectively.**
- (E) plncRNA-IFI6 overexpression reduced IFN-induced IFI6 mRNA levels compared to pEmpty.**
- (F) Overexpression of lncRNA-IFI6 increased HCV core protein levels and reduced IFI6 protein levels in JFH1-infected Huh7.5.1 cells.**
- (G) lncRNA-IFI6 gRNA decreased lncRNA-IFI6 levels in PHH and JFH1-infected PHH cells compared to Neg gRNA with or without IFN respectively.**
- (H) plncRNA-IFI6 overexpression increased lncRNA-IFI6 RNA levels in PHH or JFH1-infected PHH cells compared to pEmpty with or without IFN respectively.**
- (I) plncRNA-IFI6 overexpression rescued IFN-induced inhibition of HCV RNA in JFH1-infected PHH cells compared to pEmpty.**

**(J) The plncRNA-IFI6 overexpression reduced IFN-induced IFI6 mRNA levels compared to pEmpty in PHH cells.**

**Supplemental Figure 4. lncRNA-IFI6 specifically regulates IFI6.** Huh7.5.1 cells stably expressing lncRNA-IFI6 gRNA, Neg gRNA, plncRNA-IFI6 and pEmpty were generated. Cells were then inoculated with JFH1 HCV for 48 hrs. At 24 hrs post infection, human IFN $\alpha$  was added to a final concentration of 30 IU/mL. Total RNA or protein lysates were harvested at 48 hrs post infection. IFI6 and the selected ISG mRNAs were assessed by qRT-PCR. Data are shown as means  $\pm$  standard deviation of three replicates. \* P < 0.05; \*\* P < 0.01; \*\*\* P < 0.001.

**(A) lncRNA-IFI6 gRNA significantly increased IFI6 mRNA expression** in JFH1 cells (48 hrs post infection) compared to Neg gRNA with or without IFN $\alpha$ , respectively.

**(B)-(I) lncRNA-IFI6 gRNA did not affect several ISGs** including **(B) OAS3, (C) IFIT1, (D) MX1, (E) IFIT5, (F) ZAP, (G) IRF7, (H) ISG15, (I) ISG20.**

**(J) plncRNA-IFI6 overexpression reduced IFN $\alpha$ -induced IFI6 mRNA levels compared to pEmpty.**

**(K)-(R) plncRNA-IFI6 overexpression did not affect several ISGs** including **(K) OAS3, (L) IFIT1, (M) MX1, (N) IFIT5, (O) ZAP, (P) IRF7, (Q) ISG15, (R) ISG20.**

**Supplemental Figure 5. lncRNA-IFI6 did not affect OAS3 mRNA and protein expression.** Huh7.5.1 cells stably expressing specific lncRNA-IFI6 gRNA, Neg gRNA, plncRNA-IFI6 and pEmpty were generated. Cells were inoculated with JFH1 HCV for 48 hrs. At 24 hrs post infection, human IFN $\alpha$  was added to a final concentration of 30 IU/mL. Total RNA or protein lysates were harvested at 48 hrs post infection. OAS3 mRNA was assessed by qRT-PCR. OAS3 and  $\beta$ -actin protein levels were detected by Western blot.

**(A) lncRNA-IFI6 gRNA did not affect mRNA expression levels of OAS3.**

**(B) lncRNA-IFI6 gRNA did not affect OAS3 protein levels.**

**(C) plncRNA-IFI6 overexpression did not affect OAS3 mRNA expression levels.**

**(D) plncRNA-IFI6 overexpression did not affect OAS3 protein levels.**

**Supplemental Figure 6. IFI6 siRNA or pIFI6, lncRNA-IFI6 gRNA and plncRNA-IFI6 overexpression did not affect cell viability.** Huh7.5.1 cells stably expressing lncRNA-IFI6 gRNA, Neg gRNA, plncRNA-IFI6 and pEmpty were generated. IFI6 siRNA, Neg siRNA, pIFI6 and pEmpty were transfected into these Huh7.5.1 cells. Total RNA was harvested at 72 hr post vector transfection, 48 hr post JFH1 HCV infection (JFH1 at 0.2MOI), and 24 hr post IFN $\alpha$  treatment. Cell viability was monitored using the Cell Titer-Glo luminescent cell viability assay kit. Relative cell viability in Neg siRNA or pEmpty treatments was normalized to 100% respectively. Data are shown as

the mean  $\pm$  standard deviation of three replicates. \* P < 0.05; \*\* P < 0.01; \*\*\* P < 0.001.

**(A) IFI6 siRNA did not affect JFH1 cell viability.**

**(B) Overexpression of pIFI6 did not affect JFH1 cell viability.**

**(C) IFI6 siRNA significantly increased HCV RNA levels in JFH1 infected Huh7.5.1 cells compared to Neg siRNA with or without IFN respectively.**

**(D) IFI6 siRNA reduced IFI6 mRNA levels compared to Neg siRNA.**

**(E) IFI6 siRNA increased HCV core protein levels and reduced IFI6 protein expression compared to Neg siRNA.**

**(F) IFI6 siRNA in lncRNA-IFI6 gRNA stably transfected cells did not affect cell viability.**

**(G) Overexpression of pIFI6 in cells overexpressing plncRNA-IFI6 did not affect cell viability.**

**(H) IFI6 siRNA rescued the reduction in HCV RNA mediated by lncRNA-IFI6 gRNA in JFH1 infected Huh7.5.1 cells compared to Neg siRNA.**

**(I) IFI6 siRNA blocked IFI6 mRNA enhancement in lncRNA-IFI6 gRNA treated JFH1 infected Huh7.5.1 cells compared to Neg siRNA.**

**(J) IFI6 siRNA rescued HCV core protein reduction and reversed IFI6 protein enhancement mediated by lncRNA-IFI6 gRNA in JFH1 infected Huh7.5.1 cells compared to Neg siRNA.**

**(K) Overexpression of pIFI6 rescued plncRNA-IFI6 inhibition of IFI6 mRNA expression in JFH1 cells compared to pEmpty.**

**(L) IFI6 siRNA rescued HCV RNA reduction mediated by lncRNA-IFI6 gRNA in JFH1-infected PHH cells compared to Neg siRNA.**

**(M) IFI6 siRNA blocked IFI6 mRNA enhancement in lncRNA-IFI6 gRNA treated JFH1 infected PHH cells compared to Neg siRNA.**

**(N) Overexpression of pIFI6 inhibited plncRNA-IFI6 induction of HCV RNA compared to pEmpty in JFH1-infected PHH cells.**

**(O) Overexpression of pIFI6 rescued plncRNA-IFI6 inhibition of IFI6 mRNA expression in JFH1-infected PHH cells compared to pEmpty.**

**(P) Knock down of IFI6 did not affect lncRNA-IFI6 RNA expression.**

**(Q) Overexpression of pIFI6 did not affect lncRNA-IFI6 RNA levels.**

**Supplemental Figure 7. Cell viability of siRNAs to STAT1, STAT2, JAK1.**

The siRNAs to STAT1, STAT2, JAK1 were transfected into Huh7.5.1 cell for 24 hrs. IFN $\alpha$  (30 IU/mL) was added to the appropriate wells for 24 hrs. Cell viability was monitored using the Cell Titer-Glo luminescent cell viability assay kit. Relative cell viability in Neg siRNA or pEmpty treatment was normalized to 100% respectively. Data are shown as the mean  $\pm$  standard deviation of three replicates. \* P < 0.05; \*\* P < 0.01; \*\*\* P < 0.001.

**(A) lncRNA-IFI6 gRNA did not significantly affect STAT1 mRNA levels compared to Neg gRNA in Huh7.5.1 or JFH1 cells with or without IFN respectively.**

**(B) lncRNA-IFI6 gRNA did not significantly affect STAT1 protein expression compared to Neg gRNA in Huh7.5.1 or JFH1 cells with or without IFN respectively.**

**(C) Overexpression of plncRNA-IFI6 did not significantly affect STAT1 mRNA expression compared to pEmpty in Huh7.5.1 or JFH1 cells with or without IFN respectively.**

**(D) Overexpression of plncRNA-IFI6 did not significantly affect STAT1 protein levels compared to pEmpty in Huh7.5.1 or JFH1 cells with or without IFN respectively.**

**(E) The siRNAs to STAT1, STAT2 or JAK1 did not significantly affect lncRNA-IFI6 mRNA levels in Huh7.5.1 cells with or without IFN respectively.**

**(F) JAK1 siRNA reduced JAK1 mRNA expression compared to Neg siRNA in Huh7.5.1 cells.**

**(G) STAT1 siRNA reduced STAT1 mRNA expression compared to Neg siRNA in Huh7.5.1 cells.**

**(H) STAT2 siRNA reduced STAT2 mRNA expression compared to Neg siRNA in Huh7.5.1 cells.**

**(I) siRNA targeting STAT1, STAT2, JAK1 did not affect Huh7.5.1 cell viability.**

**Supplemental Figure 8. Cell viability for supernatant incubation.** pISRE-luc (expressing firefly luciferase) and pRL-TK (expressing *renilla* luciferase) were co-transfected in to lncRNA-IFI6 gRNA, Neg gRNA, plncRNA-IFI6 and pEmpty stably expressing Huh 7.5.1 cells, respectively. IFN $\alpha$ -stimulated ISRE luciferase levels were normalized to RL-TK luciferase levels yielding the relative luciferase unit (RLU).

Huh7.5.1 cells stably expressing specific lncRNA-IFI6 gRNA, Neg gRNA, plncRNA-IFI6 and pEmpty were generated, respectively. JFH1 HCV was inoculated to the cells for 48 hrs. At 24 hrs post infection, human IFN $\alpha$  was added to a final concentration of 30 IU/ mL. The supernatants of cells were harvested at 48 hrs post infection. The supernatants of these cells were used to incubate the fresh Huh7.5.1 cells.

**(A) lncRNA-IFI6 gRNA did not significantly affect IFN $\alpha$  stimulated ISRE signaling compared to Neg gRNA in Huh7.5.1 and JFH1 cells.**

**(B) Overexpression of plncRNA-IFI6 did not significantly affect IFN $\alpha$  stimulated ISRE signaling compared to pEmpty in Huh7.5.1 and JFH1 cells.**

**(C) lncRNA-IFI6 gRNA or the ISRE-luciferase reporter assay did not affect Huh7.5.1 cell viability.**

**(D) plncRNA-IFI6 overexpression or the ISRE-luciferase reporter assay did not affect Huh7.5.1 cell viability.**

**(E) Experimental schematic of supernatant incubation assay.** To test whether lncRNA-IFI6 affects the total cytokine levels secreted by cells, fresh untreated Huh7.5.1 cells were incubated with the supernatant collected from Huh7.5.1 cells expressing lncRNA-IFI6 gRNA, Neg gRNA, plncRNA-IFI6 or pEmpty for 24 hrs. Cell viability was monitored using the Cell Titer-Glo luminescent cell viability assay kit. Relative cell viability in Neg siRNA or pEmpty treatment was normalized to 100% respectively.

**(F) Incubation of supernatants from lncRNA-IFI6 gRNA did not significantly affect IFI6 mRNA expression compared to Neg gRNA in Huh7.5.1 or JFH1 with or without IFN respectively.**

**(G) Incubation of supernatants from transfected cells overexpressing plncRNA-IFI6 did not significantly affect IFI6 mRNA expression compared to pEmpty in Huh7.5.1 or JFH1 with or without IFN respectively.**

**(H) Supernatants from lncRNA-IFI6 gRNA transfected cells did not affect cell viability.**

**(I) Supernatants from transfected cells overexpressing plncRNA-IFI6 did not affect cell viability.**

**Supplemental Figure 9. lncRNA-IFI6 regulates the initial transcription of IFI6.** Cells stably over expressing lncRNA-IFI6 gRNA, Neg gRNA, plncRNA-IFI6 and pEmpty were treated with or without 10  $\mu$ M 5-Aza-2'-deoxycytidineDNA (DAC) (methyltransferase inhibitor decitabine) (Sigma, USA) for 48 hours. Relative cell viability in Neg gRNA or pEmpty treatment was normalized to 100% respectively.

**(A) Paradigms of IFI6 pre-mRNA structures.** IFI6 has 5 exons (Blue boxes) and 4 introns (Black lines). The CpG island (Green box) was located between exon 2 and intron 2 (4242-4545 bp) of the IFI6 gene.

**(B) lncRNA-IFI6 gRNA and DAC treatment did not affect Huh7.5.1 cell viability.**

**(C) Overexpression of plncRNA-IFI6 and DAC treatment did not affect Huh7.5.1 cell viability.**

**(D) lncRNA-IFI6 gRNA significantly increased IFI6 pre-mRNA (pre-IFI6-2) levels compared to Neg gRNA in Huh7.5.1 or JFH1 cells with or without IFN respectively.**

**(E) Overexpression of plncRNA-IFI6 significantly reduced IFI6 pre-mRNA (pre-IFI6-2) levels compared to pEmpty in Huh7.5.1 or JFH1 cells with or without IFN respectively.**

**(F) ActD treatment inhibited IFI6 pre-mRNA expression levels in lncRNA-IFI6 gRNA stably transfected Huh7.5.1 cells. The IFI6 pre-mRNA values**

were normalized to GAPDH.

**(G) lncRNA-IFI6 gRNA did not significantly affect IFI6 pre-mRNA half-life compared to Neg gRNA in Huh7.5.1 cells.** The pre-mRNA level at 0 hrs in each treatment in SFig 9F was set to 100% of the fraction value. The relative fraction values of each treatment at 5 hrs, 10 hrs or 15 hrs was obtained by normalizing to the value at 0 hr for each time point. The IFI6 pre-mRNA degradation half-life of Neg gRNA+ ActD is relatively equal to lncRNA-IFI6 gRNA+ ActD.

**(H) ActD treatment reduced IFI6 pre-mRNA expression levels in plncRNA-IFI6 stably transfected Huh7.5.1 cells.** The values were normalized to GAPDH.

**(I) Overexpression of plncRNA-IFI6 did not significantly affect IFI6 pre-mRNA half-life compared to pEmpty in Huh7.5.1 cells.** The pre-mRNA level at 0 hrs in each treatment in SFig 9H was set to 100% of the fraction value. The relative fraction values of each treatment at 5 hrs, 10 hrs or 15 hrs was obtained by normalizing to the value at 0 hr for each time point. The IFI6 pre-mRNA degradation half-life of plncRNA-IFI6 + ActD is relatively equal to pEmpty+ ActD.

**Supplemental Figure 10. lncRNA-IFI6 regulates IFI6 through its promoter.**

Cells overexpressing lncRNA-IFI6 gRNA, Neg gRNA, plncRNA-IFI6 or pEmpty were co-transfected with pEZX-PG04-IFI6-promoter or pEZX-PG04-OAS3-promoter, respectively. Guassia luciferase (Gluc) assay and secreted Alkaline Phosphatase (SEAP) assay were performed to detect promoter

activity. Relative cell viability in Neg gRNA or pEmpty treatments was normalized to 100% respectively.

plncRNA-IFI6 overexpression, pEmpty, lncRNA-IFI6 gRNA, or Neg gRNA transfected Huh7.5.1 cells were subjected to ChIP. The relative amounts of IFI6 DNA immunoprecipitated by the H3K4me3 or H3K27me3 antibody were normalized to IFI6 DNA isolated by the control IgG. Data are shown as means  $\pm$  standard deviation of three replicates. \* P < 0.05; \*\* P < 0.01; \*\*\* P < 0.001.

**(A) lncRNA-IFI6 gRNA did not affect pEZX-PG04-OAS3-promoter induced Gaussia luciferase (Gluc) / alkaline phosphatase (SEAP) activity compared to Neg gRNA in Huh7.5.1 or JFH1 cells with or without IFN $\alpha$  treatment.**

**(B) Overexpression of plncRNA-IFI6 did not affect pEZX-PG04-OAS3-promoter induced Gaussia luciferase (Gluc) / alkaline phosphatase (SEAP) activity compared to pEmpty in Huh7.5.1 or JFH1 cells with or without IFN $\alpha$  treatment.**

**(C) lncRNA-IFI6 gRNA and the IFI6 promoter reporter did not affect Huh7.5.1 cell viability.**

**(D) Overexpression of plncRNA-IFI6 and the IFI6 promoter reporter did not affect Huh7.5.1 cell viability.**

**(E) lncRNA-IFI6 gRNA and the OAS3 promoter reporter did not affect Huh7.5.1 cell viability.**

**(F) Overexpression of plncRNA-IFI6 and the OAS3 promoter reporter did not affect Huh7.5.1 cell viability.**

**(G)-(H) ChIP analysis of H3K4me3 (G) and H3K27me3 (H) levels at the IFI6 locus in lncRNA-IFI6 overexpressing and control cells.** The relative amounts of IFI6 DNA immunoprecipitated by the H3K4me3 or H3K27me3 antibody were normalized to IFI6 DNA isolated by the control IgG.

**(I) ChIP analysis of H3K4me3 levels at the GAPDH locus in lncRNA-IFI6 overexpressing and control cells.**

**(J) ChIP analysis of H3K27me3 levels at the GAPDH locus in lncRNA-IFI6 overexpressing and control cells.**

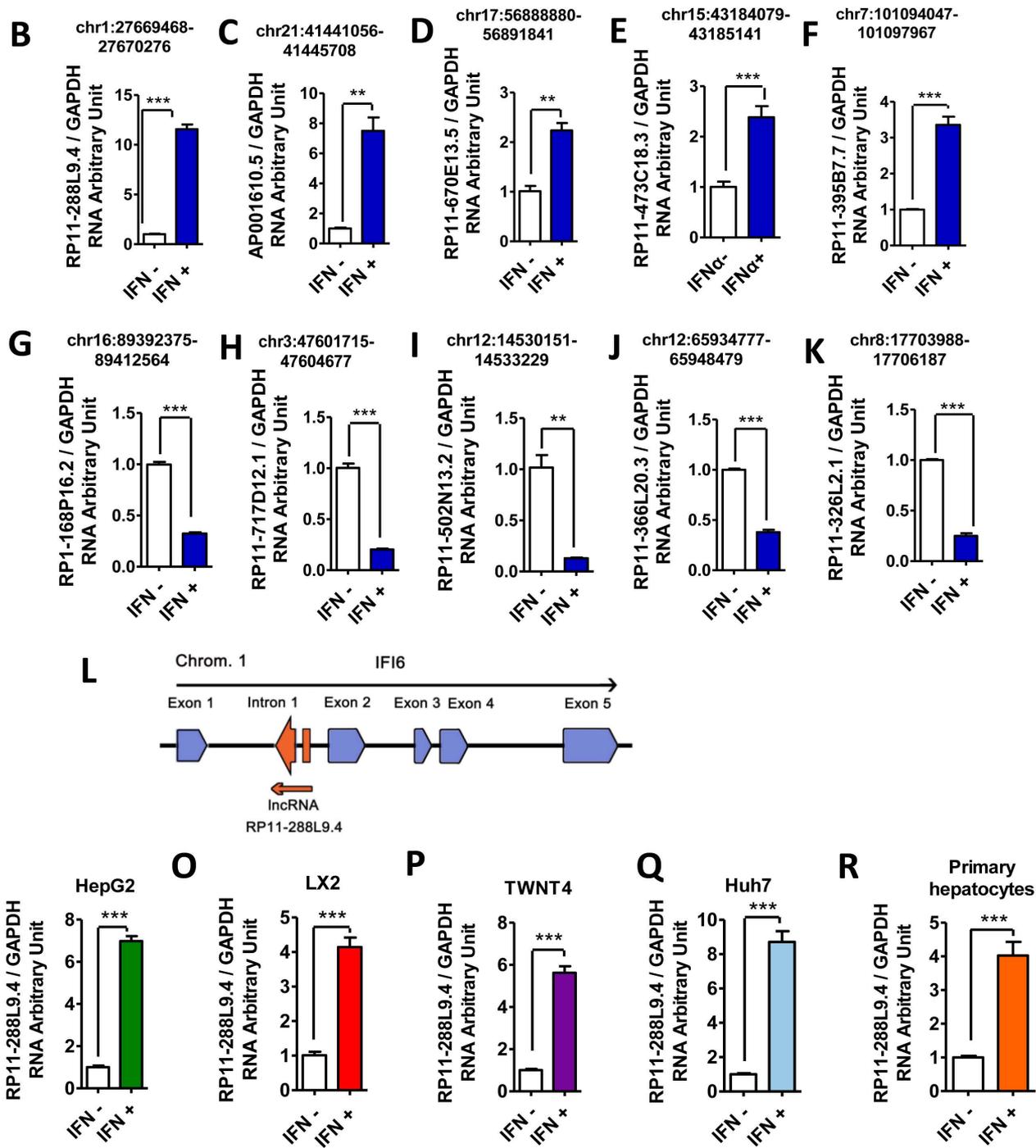
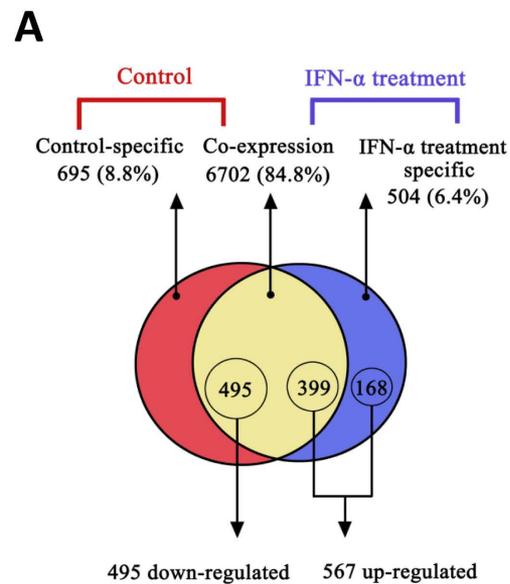
**(K) lncRNA IFI6 gRNA or overexpression of plncRNA-IFI6 did not affect Huh7.5.1 cell viability.**

**Supplemental Figure 11. Overexpression of wild type or mutant lncRNA-IFI6 did not affect cell viability.** Huh7.5.1 cells stably expressing full-length plncRNA-IFI6, pMutants 1-4 and pEmpty were generated. Cells were inoculated with JFH1 HCV for 48 hrs. At 24 hrs post infection, human IFN $\alpha$  was added at final concentration of 30 IU/mL.

**(A) Cell viability was monitored by Cell Titer-Glo luminescent cell viability assay kit.** Relative cell viability in pEmpty treatment was normalized to 100% respectively.

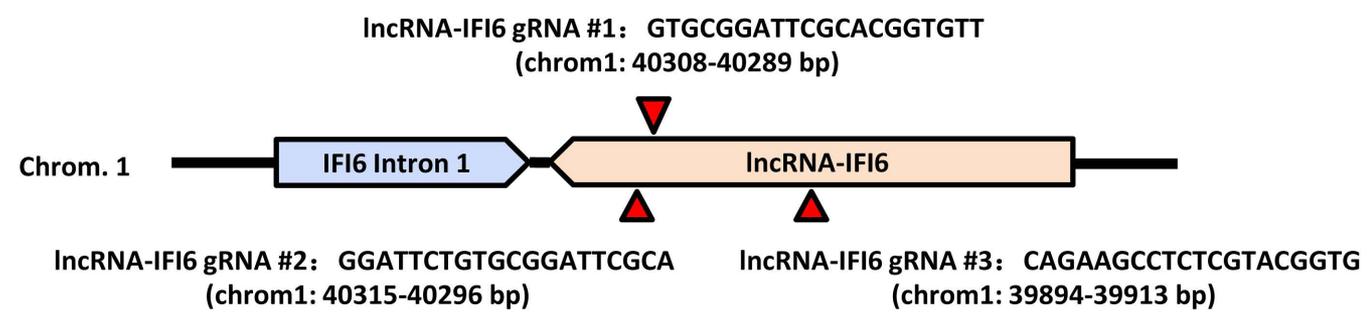
**(B) Overexpression wild type or mutant 2 lncRNA-IFI6 significantly increased HCV RNA levels compared to pEmpty in JFH1 infected PHH cells with or without IFN respectively.**

**(C) Overexpression wild type or mutant 2 lncRNA-IFI6 significantly reduced IFI6 RNA level compared to pEmpty in JFH1 infected PHH cells with or without IFN respectively.**

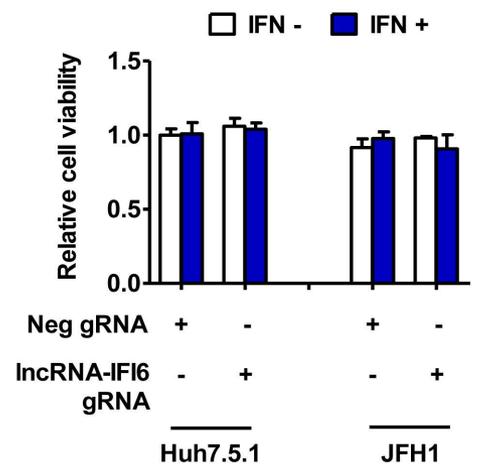
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SFig 2.

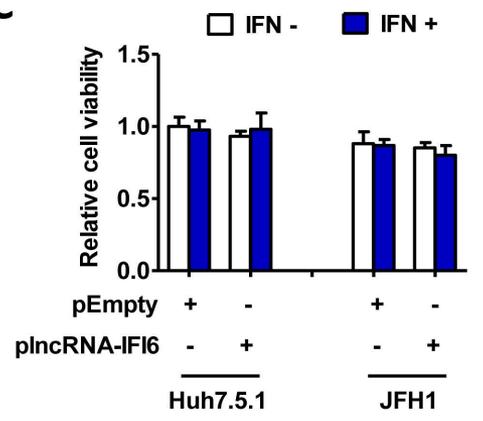
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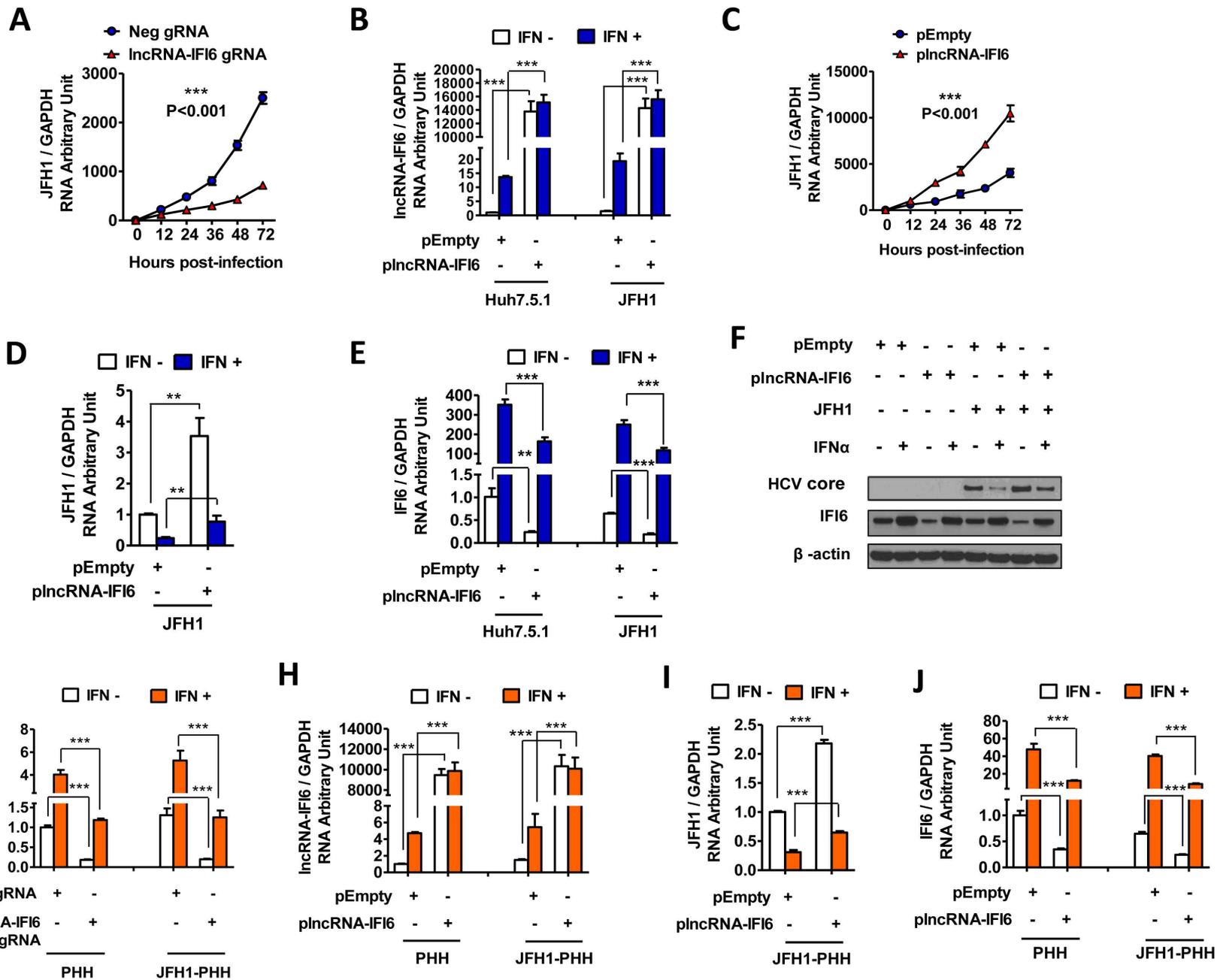
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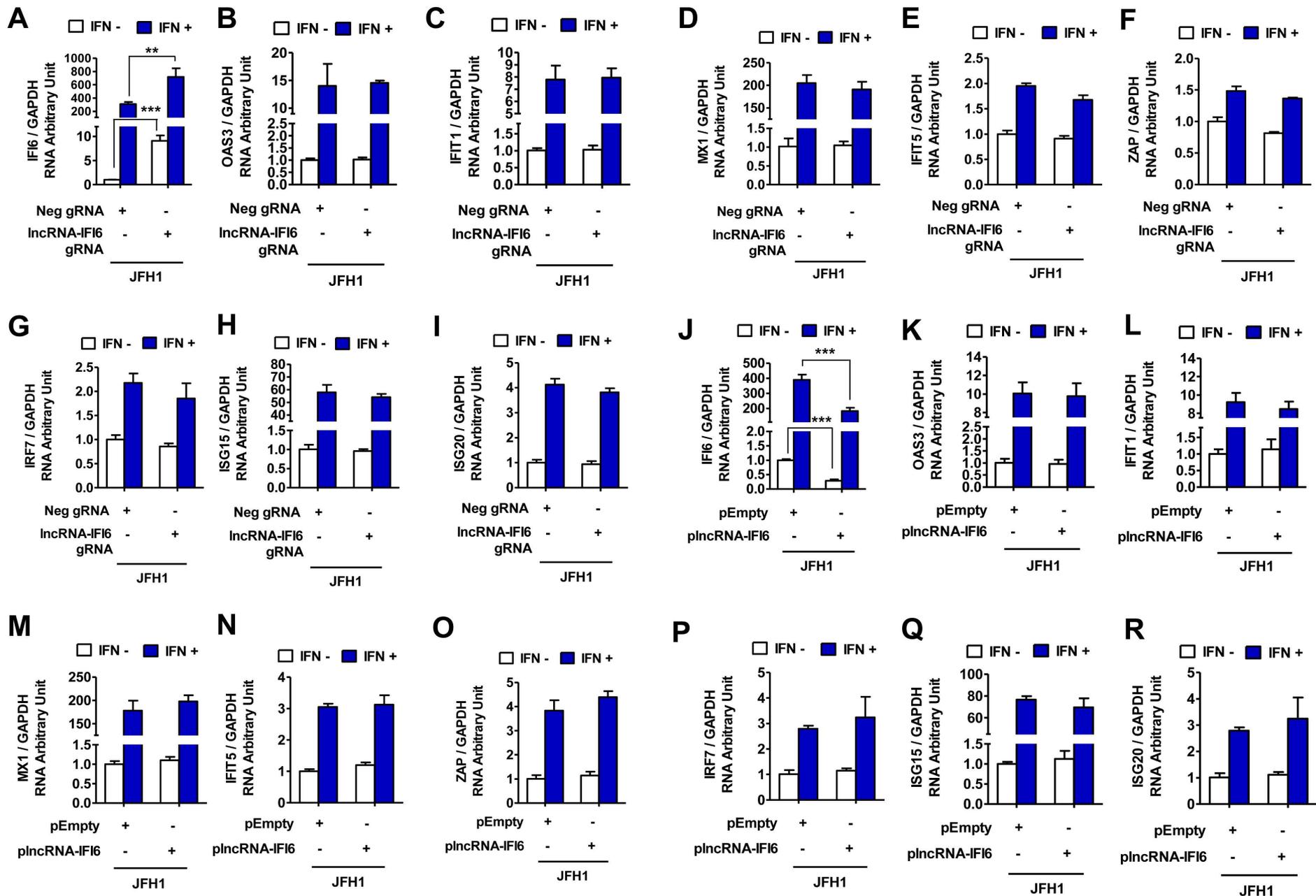
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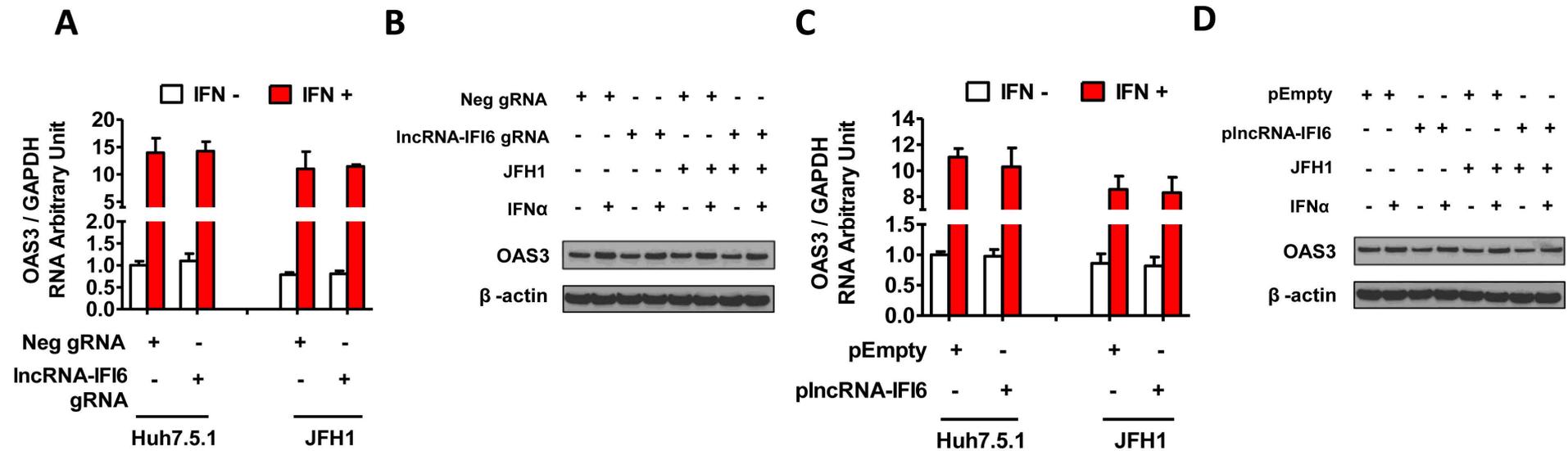
SFig 3.



# SFig 4.

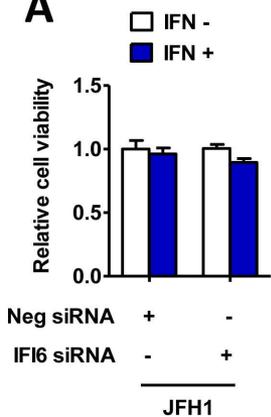


SFig 5.

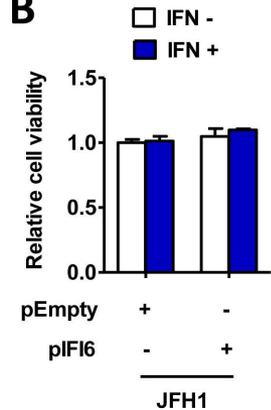


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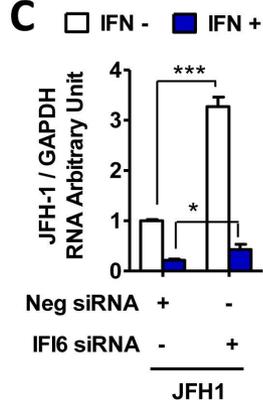
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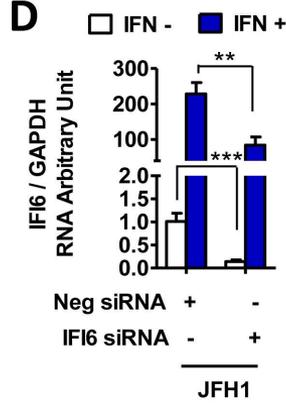
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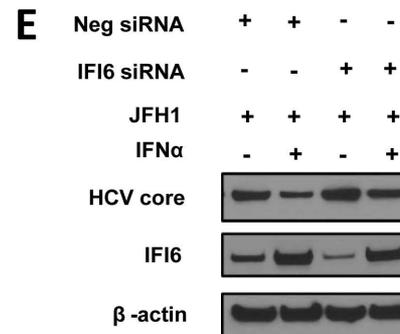
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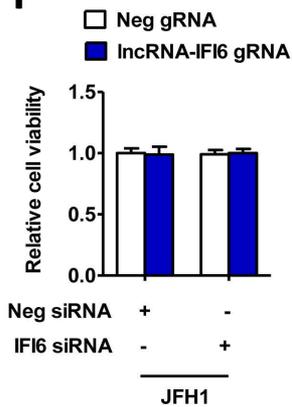
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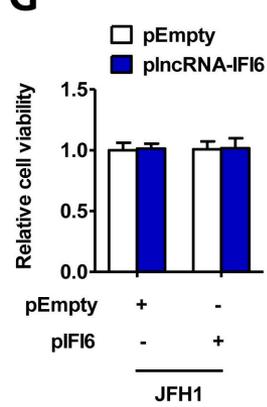
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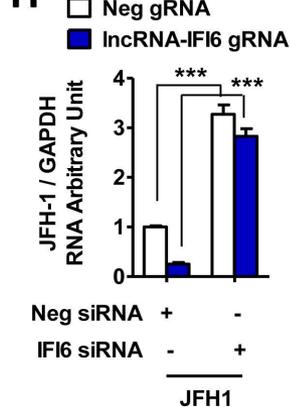
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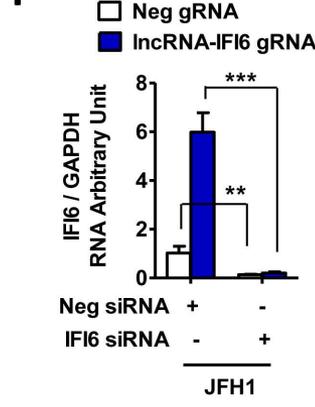
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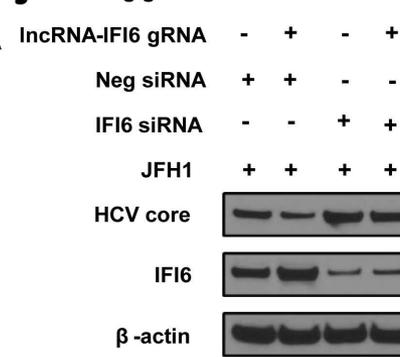
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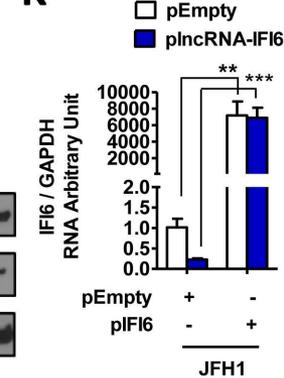
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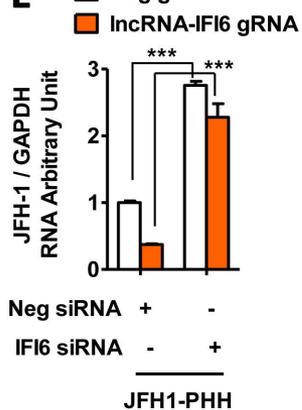
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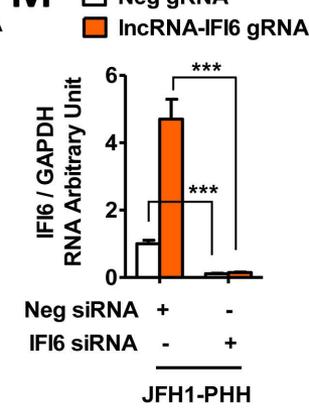
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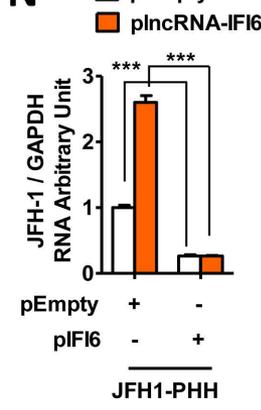
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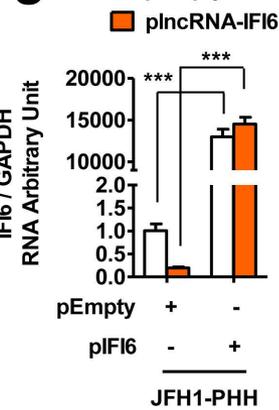
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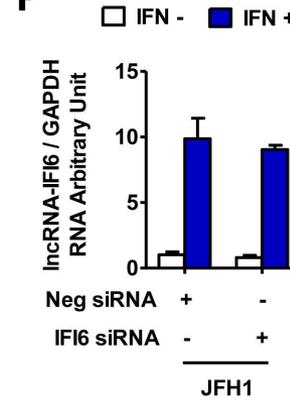
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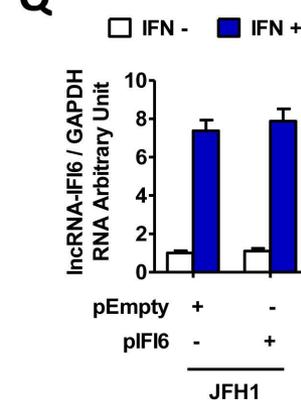
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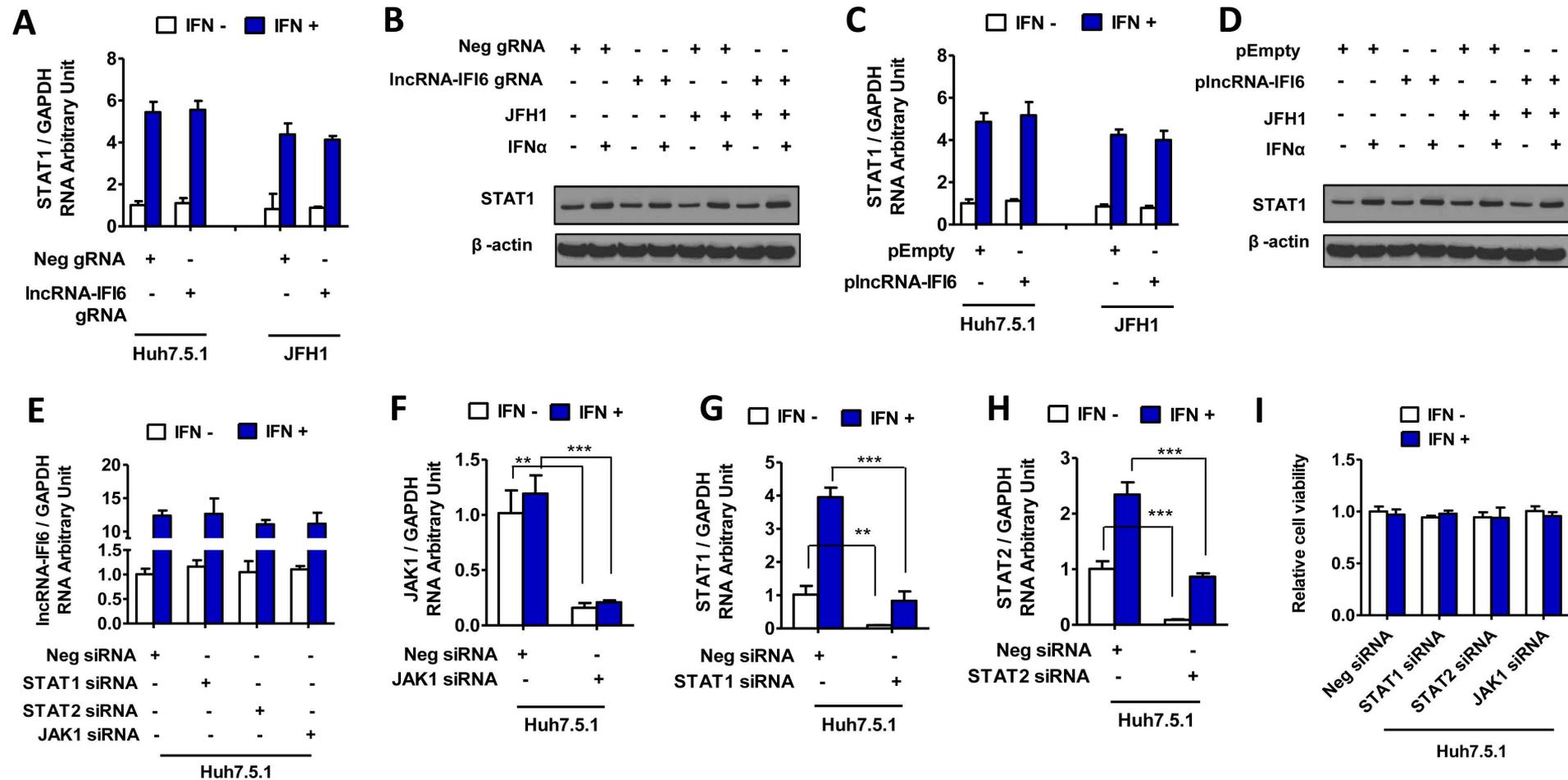
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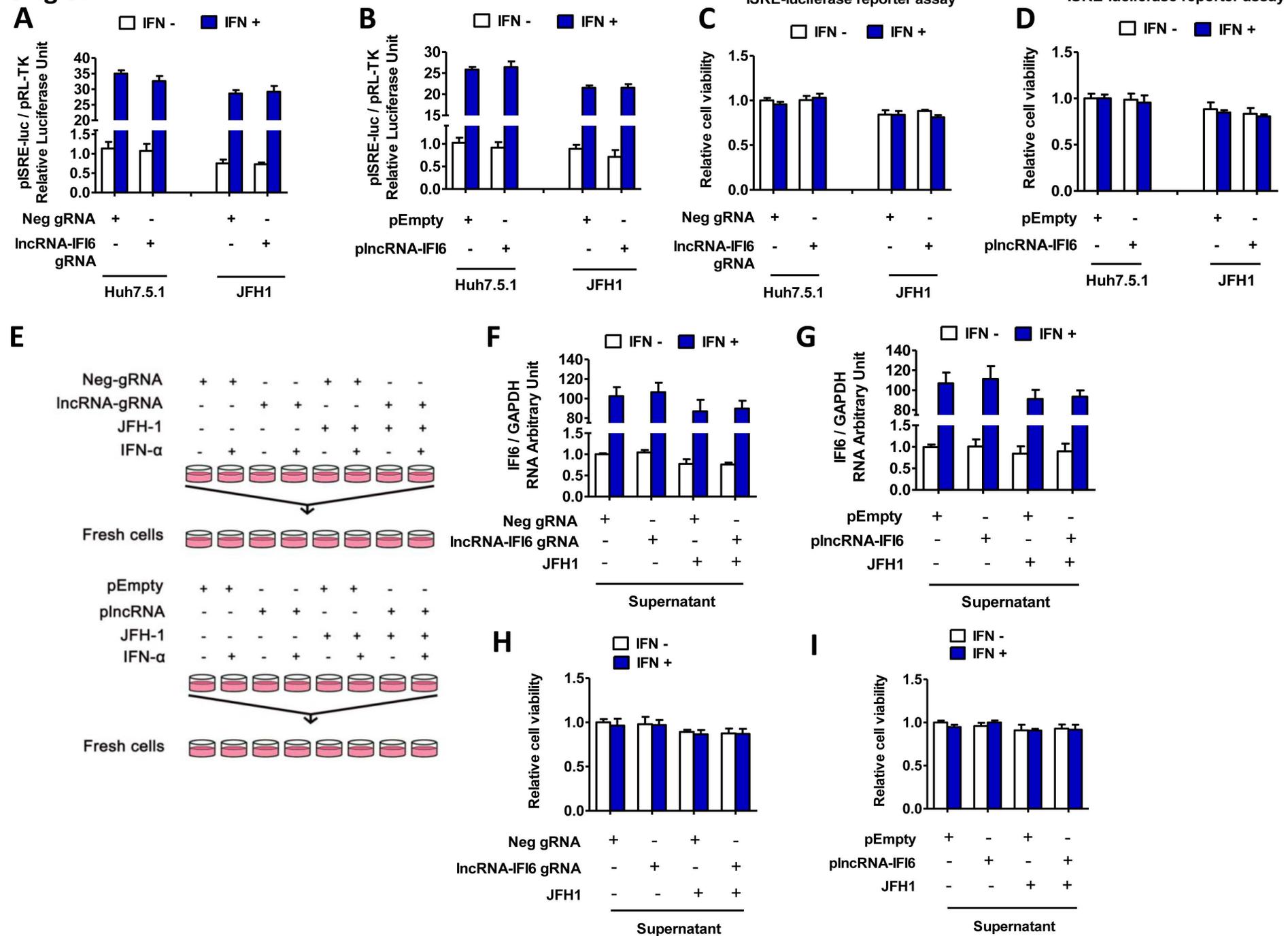
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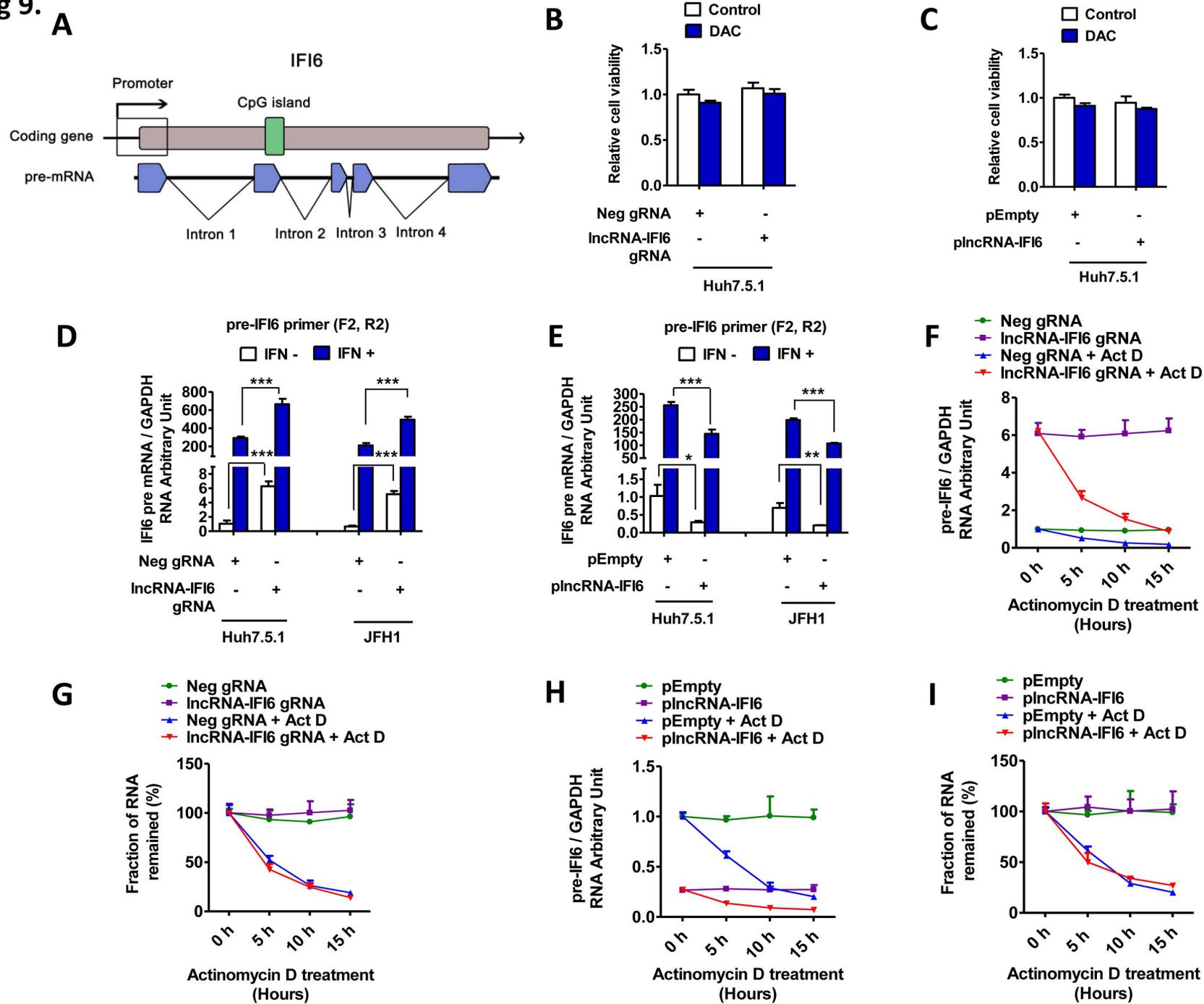
SFig 7.



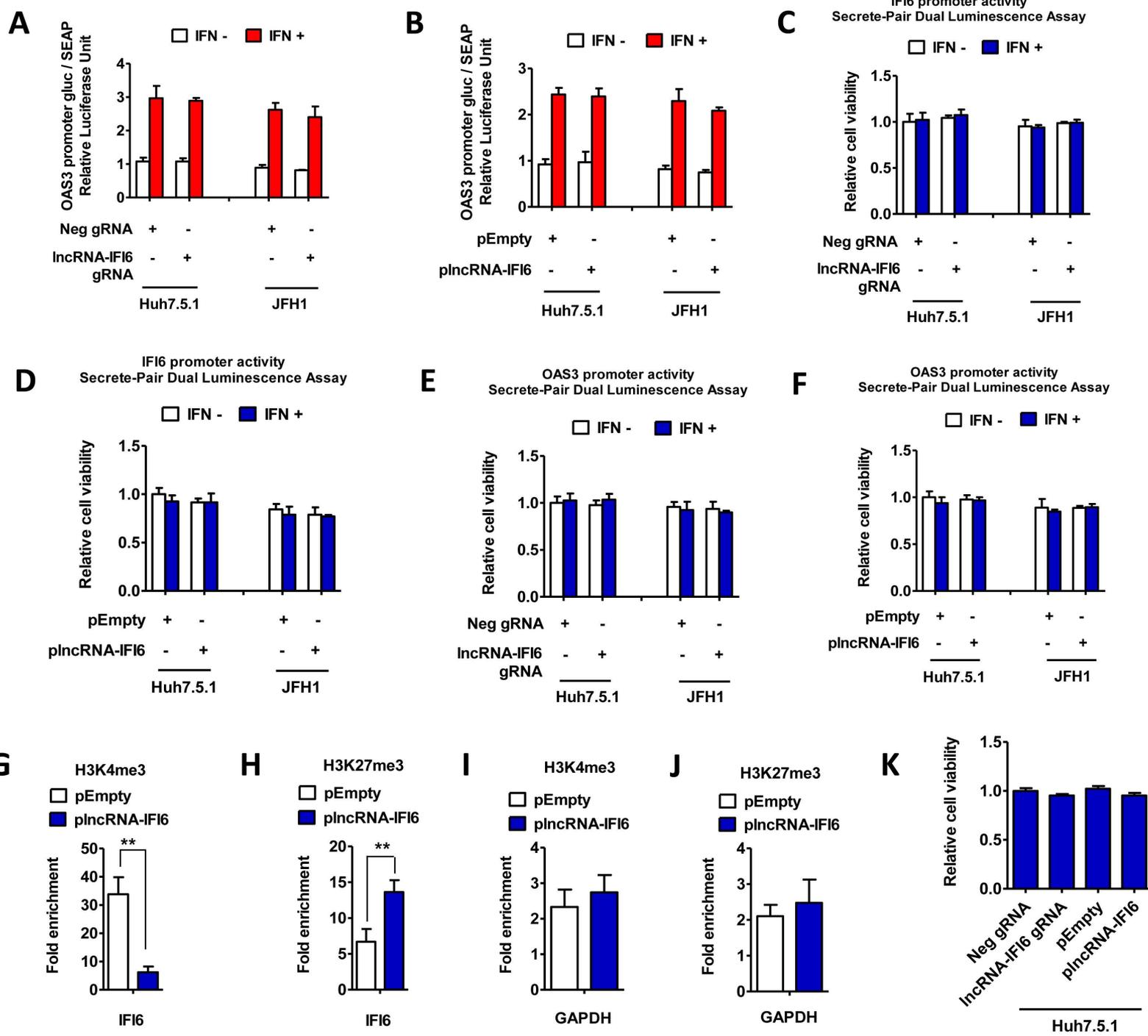
# SFig 8.



SFig 9.

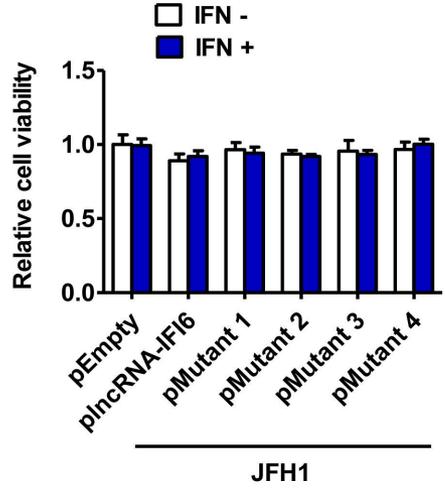


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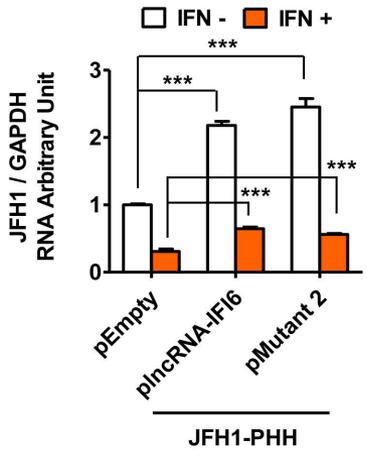


SFig 11.

**A**



**B**



**C**

