# Supporting Information

## Lin et al. 10.1073/pnas.1408759111

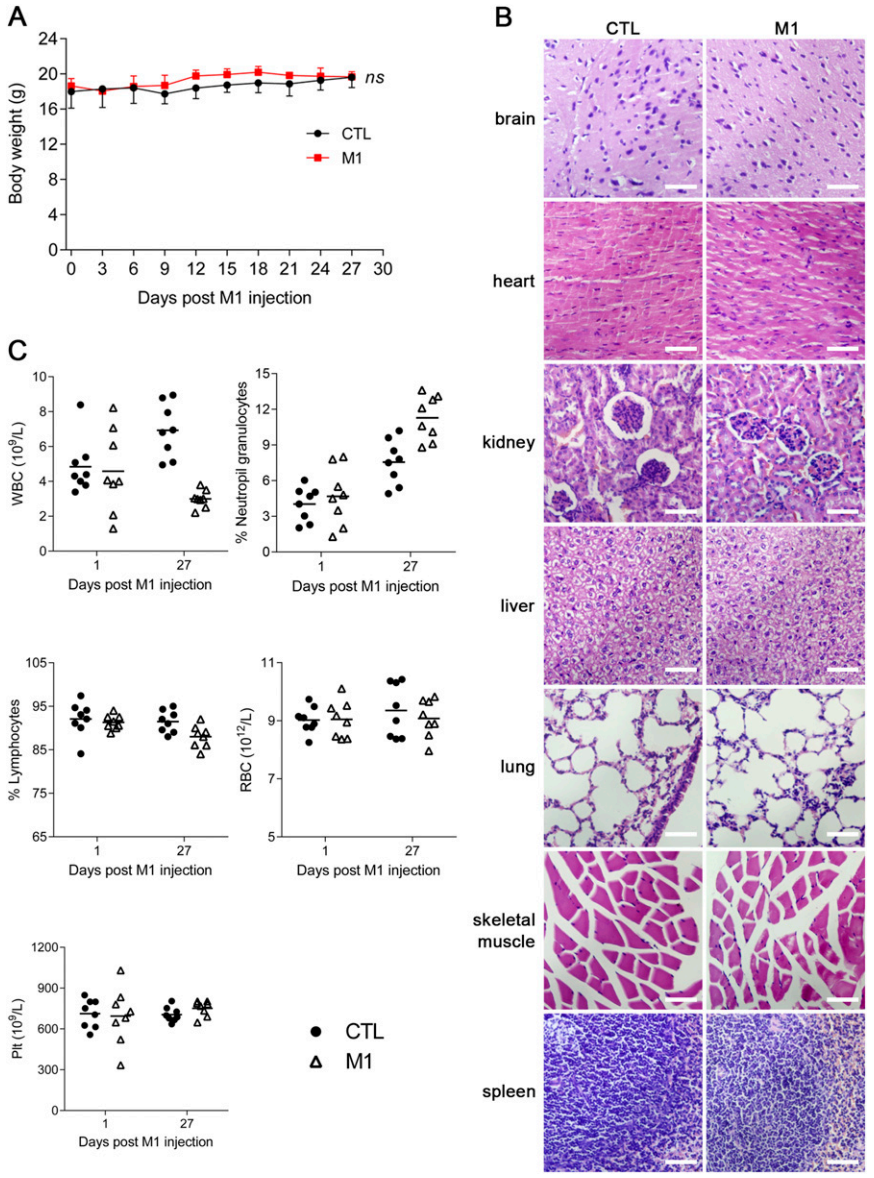



**Fig. S1.** Safety and potential toxicity evaluation of M1 in immunocompetent mice. Immunocompetent BALB/c mice received two doses of i.v. infusion of either M1 ($3 \times 10^7$ pfu per dose) or vehicle. (*A*) Body weight was measured every 3 d. Means ± SDs are shown. $n = 8$ per group. (*B*) H&E staining of vital tissues. (Scale bars: 50 μm.) (*C*) CBC analysis. $n = 8$ per group. CTL, control; ns, not significant; Plt, platelet.

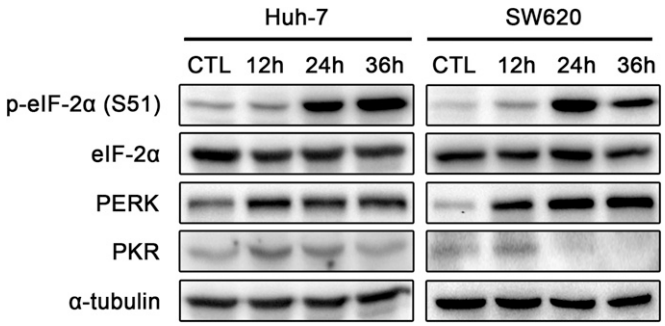



**Fig. S2.** Protein kinase R-like ER kinase (PERK), but not protein kinase R (PKR), is significantly induced by M1 infection. Sensitive cancer cells were treated with M1 (multiplicity of infection = 1) for 12, 24, or 36 h. Protein levels of eIF-2α (eukaryotic translation initiation factor 2, subunit alpha) phosphorylation, PERK, and PKR were determined by Western blot, and α-tubulin served as a loading control. CTL, control.

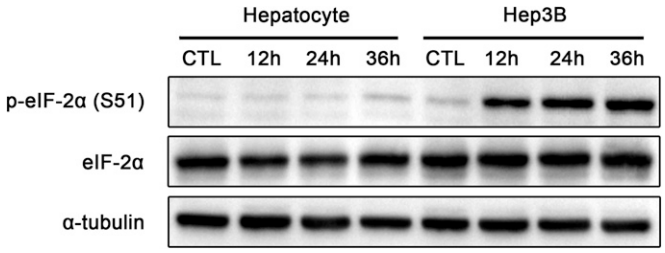



**Fig. S3.** Phosphorylation of eIF-2α is slightly induced by M1 infection in primary human hepatocytes. Primary human hepatocytes and Hep3B cells were infected with M1 (multiplicity of infection = 10), and phosphorylation of eIF-2α was determined by Western blot. Hep3B cells were used as a positive control of M1-induced phosphorylation of eIF-2α. CTL, control.

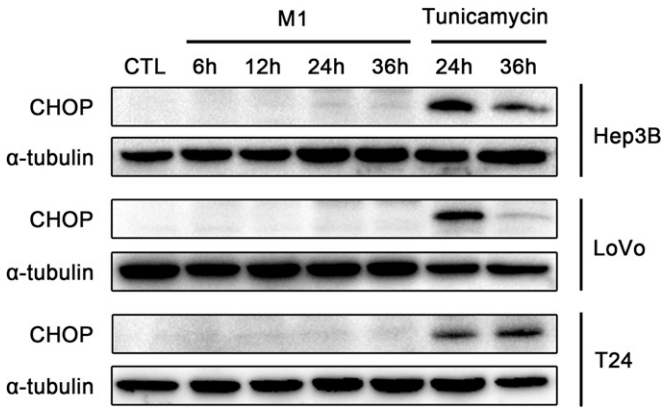
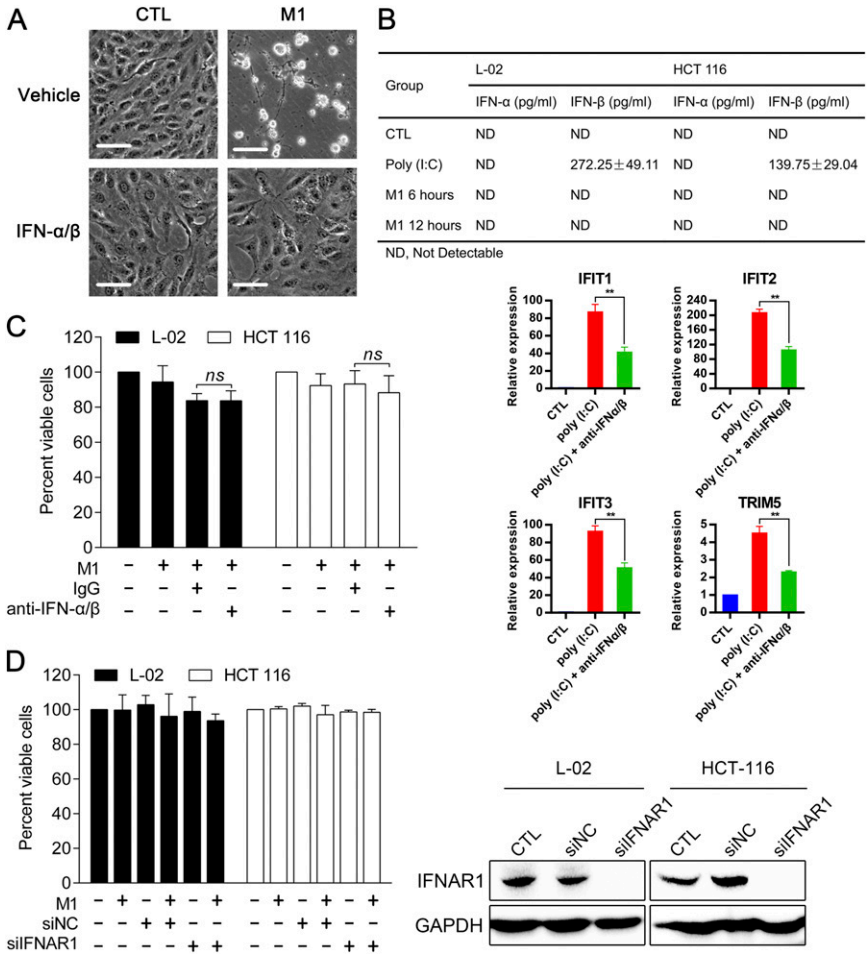



**Fig. S4.** CCAAT-enhancer–binding protein homologous protein (CHOP) is not induced by M1 infection. Sensitive cancer cells were treated with M1 (multiplicity of infection = 1) or tunicamycin (0.5 μg/mL; positive control) for 6–36 h. Protein level of CHOP was determined by Western blot, and α-tubulin served as a loading control. CTL, control.




| Group | L-02 | | HCT 116 | |
|---|---|---|---|---|
| | IFN-α (pg/ml) | IFN-β (pg/ml) | IFN-α (pg/ml) | IFN-β (pg/ml) |
| CTL | ND | ND | ND | ND |
| Poly (I:C) | ND | 272.25±49.11 | ND | 139.75±29.04 |
| M1 6 hours | ND | ND | ND | ND |
| M1 12 hours | ND | ND | ND | ND |

ND, Not Detectable

**Fig. S5.** M1 infection does not induce type I IFNs, and inhibition of type I IFN signal does not lead to M1 susceptibility in resistant cells. (*A*) T24 cells were pretreated with or without IFN-α/β (combination of 10,000 U/mL IFN-α and 30 ng/mL IFN-β) for 6 h before M1 infection [multiplicity of infection (MOI) = 1, 48 h]. Phase–contrast microscopy images were captured after infection. (Scale bars: 100 μm.) (*B*) L-02 and HCT 116 cells were stimulated with poly(I:C) (5 mg/mL; positive control) or infected with M1 (MOI = 10). Supernatants were collected, and secreted IFN-α or IFN-β was detected by ELISA. ND, not detectable. (*C*, *Left*) Cell viability in resistant cells infected with M1 (MOI = 10, 48 h) after 2 h of pretreatment with IFN-α and IFN-β antibodies (800 ng/mL each). (*C*, *Right*) mRNA expression of IFN-stimulated genes. $^{**}P < 0.01$. (*D*, *Left*) Resistant cells were transfected with a nontargeting siRNA or an IFNAR1-specific siRNA for 48 h before M1 infection. After 48 h of infection (MOI = 10), cell viability assays were performed. (*D*, *Right*) Detection of silencing efficiency. (*C* and *D*) Means ± SDs from three independent experiments are shown. CTL, control; IFIT, interferon-induced protein with tetratricopeptide repeats; ns, not significant; siIFNAR1, IFN-α receptor subunit 1 siRNA; siNC, negative control siRNA; TRIM, tripartite motif-containing protein.

**Table S1. Human cell line screening for M1 anticancer efficacy**

| Cell line | Disease | Viability (%) | Cell line | Disease | Viability (%) |
|---|---|---|---|---|---|
| Hep3B | Hepatocellular carcinoma | 3.8 | Ca Ski | Cervix epidermoid carcinoma | 87.0 |
| Huh-7 | Hepatocellular carcinoma | 52.2 | SiHa | Cervix squamous cell carcinoma | 99.6 |
| Huh-6 | Hepatoblastoma | 59.0 | ME-180 | Cervix epidermoid carcinoma | 103.2 |
| SK-HEP-1 | Liver adenocarcinoma | 71.2 | 22Rv1 | Prostate carcinoma | 39.1 |
| Li-7 | Hepatoma | 72.1 | PC-3 | Prostate adenocarcinoma | 72.7 |
| PLC | Hepatoma | 80.5 | DU 145 | Prostate carcinoma | 91.4 |
| HepG2 | Hepatocellular carcinoma | 88.6 | A-375 | Skin malignant melanoma | 47.3 |
| Bel-7402 | Hepatocellular carcinoma | 99.6 | M14 | Melanoma | 92.1 |
| L-02 | Normal liver | 100.3 | MV3 | Melanoma | 114.0 |
| LoVo | Colorectal adenocarcinoma | 6.9 | U-87 MG | Glioblastoma | 32.4 |
| HCT-8 | Colorectal adenocarcinoma | 35.2 | U-251 | Glioblastoma | 34.7 |
| SW620 | Colorectal adenocarcinoma | 43.7 | T98G | Glioblastoma multiforme | 38.2 |
| SW480 | Colorectal adenocarcinoma | 53.8 | U-138 MG | Glioblastoma | 40.1 |
| HCT 116 | Colorectal carcinoma | 81.3 | MGR2 | Glioma | 63.2 |
| SCaBER | Bladder squamous cell carcinoma | 11.5 | DBTRG-05MG | Glioblastoma | 83.3 |
| T24 | Bladder transitional cell carcinoma | 21.1 | LN-229 | Glioblastoma | 98.6 |
| UM-UC-3 | Bladder transitional cell carcinoma | 39.8 | SF-767 | Glioblastoma | 98.6 |
| 5637 | Bladder carcinoma | 50.2 | A-172 | Glioblastoma | 98.7 |
| SW780 | Bladder transitional cell carcinoma | 88.0 | HEB | Glia | 98.8 |
| EJ | Bladder transitional cell carcinoma | 95.3 | Capan-1 | Pancreas adenocarcinoma | 40.4 |
| J82 | Bladder transitional cell carcinoma | 96.8 | PANC-1 | Pancreas epithelioid carcinoma | 49.3 |
| SV-HUC-1 | Immortalized uroepithelial | 97.2 | SW1990 | Pancreas adenocarcinoma | 45.6 |
| A549 | Lung carcinoma | 68.2 | MIA PaCa-2 | Pancreas carcinoma | 49.1 |
| NCI-H358 | Nonsmall cell lung cancer | 87.8 | BxPC-3 | Pancreas adenocarcinoma | 98.8 |
| H1299 | Nonsmall cell lung cancer | 96.3 | NCI-N87 | Gastric carcinoma | 76.4 |
| NCI-H460 | Large cell lung cancer | 99.5 | HGC-27 | Gastric carcinoma | 79.2 |
| HCC827 | Lung adenocarcinoma | 103.0 | AGS | Gastric adenocarcinoma | 92.3 |
| MRC-5 | Lung fibroblast | 76.1 | CNE-2 | Nasopharyngeal carcinoma | 24.5 |
| MDA-MB-468 | Breast adenocarcinoma | 43.7 | CNE-1 | Nasopharyngeal carcinoma | 48.2 |
| MDA-MB-231 | Breast adenocarcinoma | 58.9 | HNE-1 | Nasopharyngeal carcinoma | 76.5 |
| T-47D | Mammary ductal carcinoma | 86.5 | HL-60 | Acute promyelocytic leukemia | 85.2 |
| SK-BR-3 | Breast adenocarcinoma | 89.6 | K-562 | Chronic myelogenous leukemia | 95.1 |
| MCF7 | Breast adenocarcinoma | 95.2 | CCRF-CEM | Acute lymphoblastic leukemia | 110.3 |
| C-33 A | Cervix carcinoma | 14.8 | HEL | Erythroleukemia | 112.0 |
| HeLa | Cervix adenocarcinoma | 66.0 | Reh | Acute lymphocytic leukemia | 113.1 |

Different cells were treated with M1 (multiplicity of infection = 10) for 48 h, and cell viability was detected by 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide assay.

**Table S2. Cancer specificity of M1 in primary human cells**

| | | | | Viability (%) | | | | |
|---|---|---|---|---|---|---|---|---|
| Name | Tissue | Source | Time (hpi) | 0.01 | 0.1 | 1 | 10 | 100 |
| HAEC | Human aortic endothelial cell | ScienCell* | 96 | 101.4 | 99.9 | 95.3 | 98.5 | 96.7 |
| HSkMC | Human skeletal muscle cell | ScienCell | 96 | 103.4 | 101.2 | 99.3 | 95.7 | 95.5 |
| HCM | Human cardiac myocyte | ScienCell | 96 | 104.9 | 95.7 | 94.0 | 89.6 | 88.5 |
| HBdSMC | Human bladder smooth muscle cell | ScienCell | 96 | 102.7 | 116.4 | 115.4 | 112.1 | 113.6 |
| HRGEC | Human renal glomerular endothelial cell | ScienCell | 96 | 101.8 | 101.4 | 110.2 | 104.8 | 108.1 |
| HH | Human hepatocyte | ScienCell | 96 | 103.5 | 107.6 | 104.3 | 91.7 | 103.7 |
| HCEpiC | Human colorectal epithelial cell | Isolated | 96 | 101.9 | 109.6 | 109.0 | 104.6 | 104.1 |
| HCRC1 | Human colorectal carcinoma cell | Isolated | 72 | 93.3 | 106.6 | 100.6 | 87.2 | 67.0 |
| HCC1 | Human hepatocellular carcinoma cell | Isolated | 72 | 77.8 | 44.2 | 34.7 | 27.5 | 23.1 |
| HCC2 | Human hepatocellular carcinoma cell | Isolated | 72 | 101.2 | 85.8 | 89.6 | 73.6 | 66.4 |
| HCC3 | Human hepatocellular carcinoma cell | Isolated | 72 | 99.8 | 100.6 | 87.9 | 79.5 | 68.6 |

Primary human cells were treated with M1 (MOI = 0.01~100), and cell viability was detected by 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide assay. hpi, hours postinfection.
*ScienCell Research Laboratories.

**Table S3. Inclusion criteria for IFN-related genes**

| Database or reference | Inclusion criteria |
|---|---|
| Interferome (http://interferome.its.monash.edu.au/interferome/) | ISGs reported in two or more of these three sets of ISGs were included in our study (type I IFN only) |
| ISG Database (http://lerner.ccf.org/labs/williams/) | |
| 1 | |
| 2 | Genes reported in TLR-dependent and -independent pathways of type I IFN induction were included |

ISG, IFN-stimulated gene; TLR, toll-like receptor.

1. Schoggins JW, et al. (2011) A diverse range of gene products are effectors of the type I interferon antiviral response. *Nature* 472(7344):481–485.
2. Baccala R, Hoebe K, Kono DH, Beutler B, Theofilopoulos AN (2007) TLR-dependent and TLR-independent pathways of type I interferon induction in systemic autoimmunity. *Nat Med* 13(5):543–551.

**Table S4. Expression of IFN-related genes in L-02 and Hep3B cells**

| Gene symbol | Fold change in L-02/Hep3B cells |
|---|---|
| GBP3 | 71.39 |
| CHMP5 | 53.12 |
| SCARB2 | 49.01 |
| IFI16 | 48.52 |
| ODC1 | 45.88 |
| SEPHS2 | 45.06 |
| EPAS1 | 42.49 |
| GNAI1 | 42.34 |
| ZC3HAV1 | 40.40 |
| PNPT1 | 39.24 |
| MAFF | 39.17 |
| EIF2AK2 | 37.96 |
| ADAR | 37.94 |
| SLC1A1 | 37.87 |
| CYP1B1 | 37.72 |
| GCH1 | 35.75 |
| FAM46A | 35.11 |
| HIST1H2AC | 34.63 |
| CRY1 | 33.73 |
| STAT3 | 33.71 |
| TBK1 | 29.20 |
| TICAM2 | 28.77 |
| RECQL | 26.16 |
| MICB | 25.66 |
| PMAIP1 | 25.03 |
| OPTN | 23.80 |
| IMPA2 | 21.74 |
| CLEC2B | 21.50 |
| UCP2 | 20.80 |
| ADM | 20.42 |
| DYNLT1 | 19.94 |
| IFIT3 | 19.87 |
| LIPA | 19.55 |
| PDGFA | 19.41 |
| STAT1 | 18.69 |
| NMI | 17.72 |
| UBE2N | 16.98 |
| TRIM5 | 16.76 |
| NAMPT | 16.52 |
| SAMHD1 | 16.49 |
| DDIT4 | 16.48 |
| NET1 | 15.26 |
| VEGFC | 15.04 |
| BST2 | 14.73 |
| HLA-A | 14.06 |
| IFITM2 | 13.97 |

**Table S4. Cont.**

| Gene symbol | Fold change in L-02/Hep3B cells |
|---|---|
| TAP2 | 13.56 |
| MN1 | 13.33 |
| ATP10D | 12.92 |
| IFITM3 | 12.91 |
| ANKFY1 | 12.81 |
| JAK1 | 12.26 |
| NT5C3 | 11.55 |
| RBCK1 | 11.44 |
| WARS | 11.44 |
| DDX60 | 11.27 |
| SCO2 | 10.56 |
| SQLE | 10.14 |
| LGMN | 9.63 |
| ELF1 | 9.63 |
| GBP1 | 9.49 |
| ATF2 | 8.98 |
| RNF114 | 8.74 |
| LAP3 | 8.73 |
| IER3 | 8.62 |
| LGALS3BP | 8.40 |
| STAT2 | 8.25 |
| ACSL1 | 7.95 |
| DTX3L | 7.75 |
| BLZF1 | 7.24 |
| HEG1 | 7.22 |
| IL8 | 7.00 |
| BAG1 | 6.83 |
| CDK17 | 6.80 |
| PARP12 | 6.73 |
| IFI6 | 6.58 |
| IFIH1 | 6.46 |
| IFIT1 | 6.32 |
| ETS2 | 5.76 |
| FKBP5 | 5.73 |
| IFIT2 | 5.56 |
| HERC6 | 5.37 |
| MYD88 | 5.22 |
| TRAF3 | 5.10 |
| RAB27A | 5.10 |
| NCOA3 | 5.09 |
| EHHADH | 4.84 |
| PHLDA1 | 4.65 |
| IFI30 | 4.62 |
| TAB2 | 4.47 |
| TRIM25 | 4.12 |
| GCA | 3.94 |
| CASP7 | 3.92 |
| MARCKS | 3.85 |
| TLR3 | 3.79 |
| HLA-C | 3.74 |
| TRIM22 | 3.73 |
| IFIT5 | 3.72 |
| FAS | 3.68 |
| PSME1 | 3.60 |
| PSMB8 | 3.58 |
| MCL1 | 3.43 |
| PRKRA | 3.28 |
| MAFB | 3.26 |
| C9orf91 | 3.18 |
| B2M | 3.06 |
| LAMP3 | 2.98 |
| PHF15 | 2.73 |

**Table S4. Cont.**

| Gene symbol | Fold change in L-02/Hep3B cells |
|---|---|
| BTN3A3 | 2.69 |
| HK2 | 2.64 |
| GK | 2.63 |
| TRAFD1 | 2.61 |
| ISG15 | 2.57 |
| MAVS | 2.56 |
| TAP1 | 2.55 |
| TDRD7 | 2.55 |
| TRIM38 | 2.43 |
| PFKFB3 | 2.41 |
| USP4 | 2.37 |
| PNRC1 | 2.31 |
| HLA-E | 2.30 |
| ICAM1 | 2.25 |
| SP110 | 2.22 |
| UBE2E2 | 2.16 |
| APOL2 | 2.10 |
| PRKD2 | 2.04 |
| C22orf28 | 2.04 |
| OAS1 | 2.00 |
| PSMB9 | 1.94 |
| MAP3K7 | 1.80 |
| TXNIP | 1.79 |
| IFNGR1 | 1.71 |
| RNF24 | 1.71 |
| ETV6 | 1.69 |
| MYOM2 | 1.68 |
| IL15 | 1.66 |
| IFI44L | 1.59 |
| NFKB1 | 1.56 |
| OASL | 1.53 |
| ID1 | 1.51 |
| RIPK1 | 1.51 |
| SPTLC2 | 1.49 |
| PRAME | 1.48 |
| CCDC109B | 1.48 |
| IRAK4 | 1.46 |
| GTPBP1 | 1.44 |
| SLC25A28 | 1.44 |
| PTGS1 | 1.43 |
| JUNB | 1.42 |
| NR4A3 | 1.41 |
| C1S | 1.41 |
| RBMS1 | 1.36 |
| RIPK2 | 1.35 |
| PHF11 | 1.35 |
| FTSJD2 | 1.34 |
| SOCS2 | 1.34 |
| CYTH1 | 1.31 |
| USP18 | 1.28 |
| SMAD3 | 1.28 |
| DDX58 | 1.27 |
| GTPBP2 | 1.24 |
| TEAD4 | 1.24 |
| IFI35 | 1.20 |
| CASP4 | 1.13 |
| CEBPD | 1.12 |
| ABTB2 | 1.10 |
| THBD | 1.07 |
| GBP2 | 1.07 |
| TNFAIP3 | 1.07 |
| TNFAIP6 | 1.07 |

**Table S4. Cont.**

| Gene symbol | Fold change in L-02/Hep3B cells |
|---|---|
| IRF9 | 1.07 |
| UBE2L6 | 1.05 |
| TRIM21 | 1.00 |
| MT1X | 1.00 |
| CCL2 | 0.98 |
| PLAUR | 0.98 |
| OAS3 | 0.97 |
| PSMB10 | 0.96 |
| MAX | 0.95 |
| TRAF6 | 0.94 |
| TYK2 | 0.94 |
| BTG1 | 0.92 |
| IRF2 | 0.91 |
| IRF3 | 0.90 |
| PLSCR1 | 0.88 |
| IFI44 | 0.87 |
| FUT4 | 0.87 |
| BAK1 | 0.85 |
| ARNTL | 0.83 |
| DDX3X | 0.83 |
| PRIC285 | 0.83 |
| RNF213 | 0.83 |
| SAMD4A | 0.82 |
| IL6 | 0.81 |
| MX2 | 0.80 |
| LMO2 | 0.78 |
| IFITM1 | 0.78 |
| UBE2V1 | 0.78 |
| SECTM1 | 0.78 |
| JAK2 | 0.76 |
| GEM | 0.76 |
| TLK2 | 0.75 |
| RNF19B | 0.75 |
| OGFR | 0.75 |
| CD47 | 0.74 |
| MX1 | 0.74 |
| CXCL11 | 0.74 |
| TLR7 | 0.71 |
| TREX1 | 0.71 |
| MT1M | 0.70 |
| TNFSF10 | 0.69 |
| TRADD | 0.68 |
| IRF1 | 0.68 |
| PPM1K | 0.66 |
| IL1B | 0.65 |
| HESX1 | 0.64 |
| IKBKB | 0.64 |
| PDGFRL | 0.63 |
| TICAM1 | 0.63 |
| MAPK1 | 0.63 |
| CD58 | 0.63 |
| TYMP | 0.62 |
| PIM1 | 0.61 |
| CCNA1 | 0.60 |
| STARD5 | 0.60 |
| RNASEL | 0.60 |
| MAP3K14 | 0.60 |
| IRF7 | 0.57 |
| LY6E | 0.56 |
| TRIM14 | 0.56 |
| MT1H | 0.56 |
| N4BP1 | 0.55 |

**Table S4. Cont.**

| Gene symbol | Fold change in L-02/Hep3B cells |
|---|---|
| ISG20 | 0.54 |
| TIRAP | 0.54 |
| DUSP5 | 0.54 |
| TNFSF13B | 0.54 |
| THBS1 | 0.53 |
| FAM46C | 0.53 |
| CDK18 | 0.53 |
| APOL6 | 0.52 |
| GBP4 | 0.51 |
| CCL8 | 0.51 |
| IRAK1 | 0.51 |
| SERPINE1 | 0.51 |
| CD69 | 0.50 |
| TMEM140 | 0.49 |
| VEGFA | 0.48 |
| HLA-F | 0.48 |
| BRF2 | 0.48 |
| PML | 0.48 |
| IKBKE | 0.47 |
| CCR1 | 0.47 |
| GMPR | 0.45 |
| CD163 | 0.44 |
| OAS2 | 0.44 |
| IFI27 | 0.44 |
| SERPINB3 | 0.43 |
| AIM2 | 0.42 |
| SERPING1 | 0.42 |
| IL15RA | 0.42 |
| C4BPA | 0.42 |
| FUT2 | 0.41 |
| HSH2D | 0.41 |
| ATF3 | 0.40 |
| RELA | 0.39 |
| NAPA | 0.39 |
| AXL | 0.39 |
| TLR8 | 0.38 |
| APOL3 | 0.37 |
| SHMT2 | 0.37 |
| CD274 | 0.37 |
| HBEGF | 0.36 |
| DHX58 | 0.36 |
| C10orf10 | 0.36 |
| PLEKHA4 | 0.36 |
| SPATS2L | 0.36 |
| HLA-G | 0.35 |
| RTP4 | 0.35 |
| FZD5 | 0.34 |
| MAZ | 0.34 |
| BCL2L14 | 0.34 |
| EGR1 | 0.34 |
| APOL1 | 0.34 |
| EHD4 | 0.33 |
| CD38 | 0.33 |
| CX3CL1 | 0.32 |
| MAPK3 | 0.31 |
| EPSTI1 | 0.31 |
| SLC15A3 | 0.31 |
| ADAM11 | 0.31 |
| CXCL10 | 0.31 |
| CDKN1A | 0.30 |
| LGALS9 | 0.29 |
| SERPINB9 | 0.29 |

**Table S4. Cont.**

| Gene symbol | Fold change in L-02/Hep3B cells |
|---|---|
| MYC | 0.29 |
| IRF5 | 0.29 |
| RARRES3 | 0.28 |
| UBA7 | 0.28 |
| XAF1 | 0.28 |
| CCL5 | 0.27 |
| IL1RN | 0.27 |
| RSAD2 | 0.27 |
| CD74 | 0.27 |
| ETV7 | 0.26 |
| BATF2 | 0.25 |
| P2RY6 | 0.25 |
| TAB1 | 0.25 |
| CXCL9 | 0.24 |
| TNF | 0.24 |
| SAT1 | 0.23 |
| IDO1 | 0.22 |
| JUN | 0.21 |
| INHBA | 0.20 |
| TAGAP | 0.19 |
| SOCS1 | 0.19 |
| VAMP5 | 0.18 |
| FST | 0.16 |

**Table S5. RNAi screening of IFN-related genes**

| Gene | (siX + M1)/siX | *z* Score | Gene | (siX + M1)/siX | *z* score |
|---|---|---|---|---|---|
| ZC3HAV1 | 0.71 | −0.40 | DDIT4 | 1.20 | 0.01 |
| IFIT2 | 0.87 | −0.26 | IFIH1 | 1.21 | 0.02 |
| IFI6 | 0.90 | −0.24 | IFI16 | 1.22 | 0.03 |
| RNF114 | 0.91 | −0.23 | TLR3 | 1.23 | 0.04 |
| GBP3 | 0.94 | −0.20 | NC | 1.23 | 0.04 |
| IL8 | 0.94 | −0.20 | IFIT3 | 1.24 | 0.04 |
| UBE2N | 0.97 | −0.18 | RBCK1 | 1.25 | 0.05 |
| ADAR | 0.98 | −0.17 | ISG15 | 1.26 | 0.07 |
| IFIT1 | 1.01 | −0.15 | WARS | 1.26 | 0.07 |
| MAVS | 1.01 | −0.15 | NT | 1.26 | 0.07 |
| MYD88 | 1.01 | −0.14 | USP4 | 1.27 | 0.07 |
| PSME1 | 1.01 | −0.14 | NMI | 1.28 | 0.08 |
| IFIT5 | 1.02 | −0.14 | TRAF3 | 1.31 | 0.11 |
| STAT1 | 1.02 | −0.14 | TRIM25 | 1.34 | 0.13 |
| JAK1 | 1.03 | −0.13 | IFI30 | 1.34 | 0.13 |
| STAT2 | 1.03 | −0.13 | TAP1 | 1.34 | 0.13 |
| EIF2AK2 | 1.05 | −0.11 | BST2 | 1.35 | 0.14 |
| PNPT1 | 1.06 | −0.11 | OAS1 | 1.37 | 0.16 |
| TAB2 | 1.06 | −0.10 | TBK1 | 1.39 | 0.17 |
| IER3 | 1.07 | −0.10 | TRIM5 | 1.40 | 0.18 |
| PSMB8 | 1.08 | −0.09 | TRIM22 | 1.40 | 0.19 |
| PMAIP1 | 1.09 | −0.08 | NAMPT | 1.43 | 0.21 |
| PRKRA | 1.09 | −0.08 | SAMHD1 | 1.43 | 0.21 |
| PARP12 | 1.14 | −0.04 | GBP1 | 1.49 | 0.26 |
| IFITM3 | 1.15 | −0.03 | TICAM2 | 1.50 | 0.26 |
| TAP2 | 1.15 | −0.03 | IFITM2 | 1.55 | 0.31 |
| ATF2 | 1.15 | −0.03 | BTN3A3 | 1.94 | 0.64 |
| DDX60 | 1.17 | −0.01 | | | |

Data are ranked by relative cell count (siX + M1/siX). *z* Scores are included to show distribution. NC, scramble siRNA; NT, nontransfected.