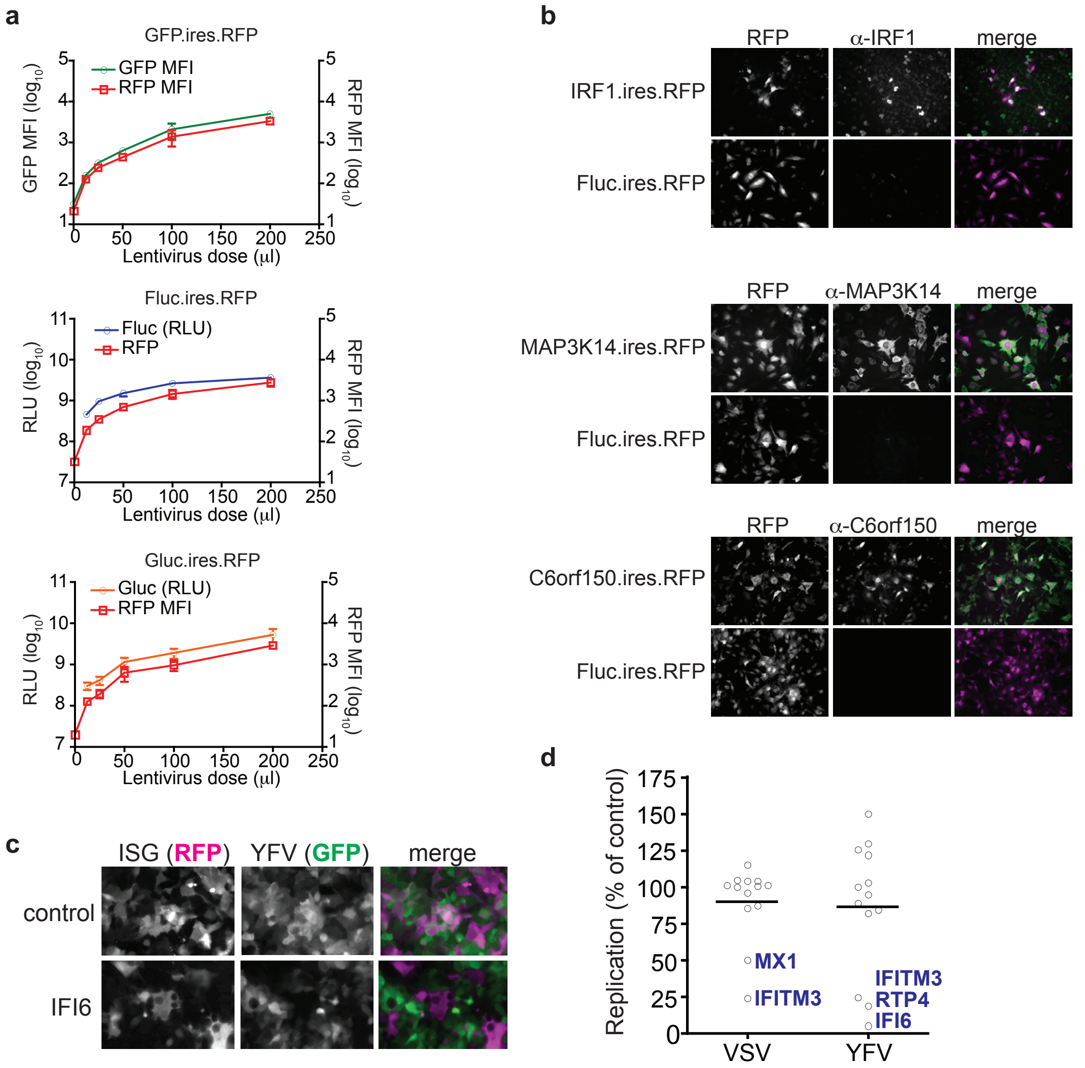
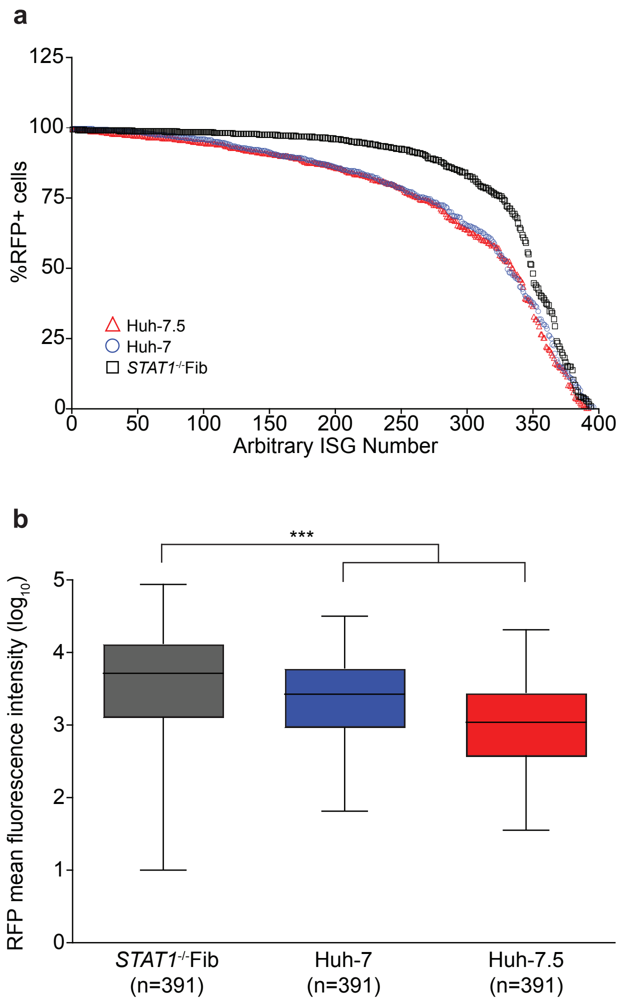
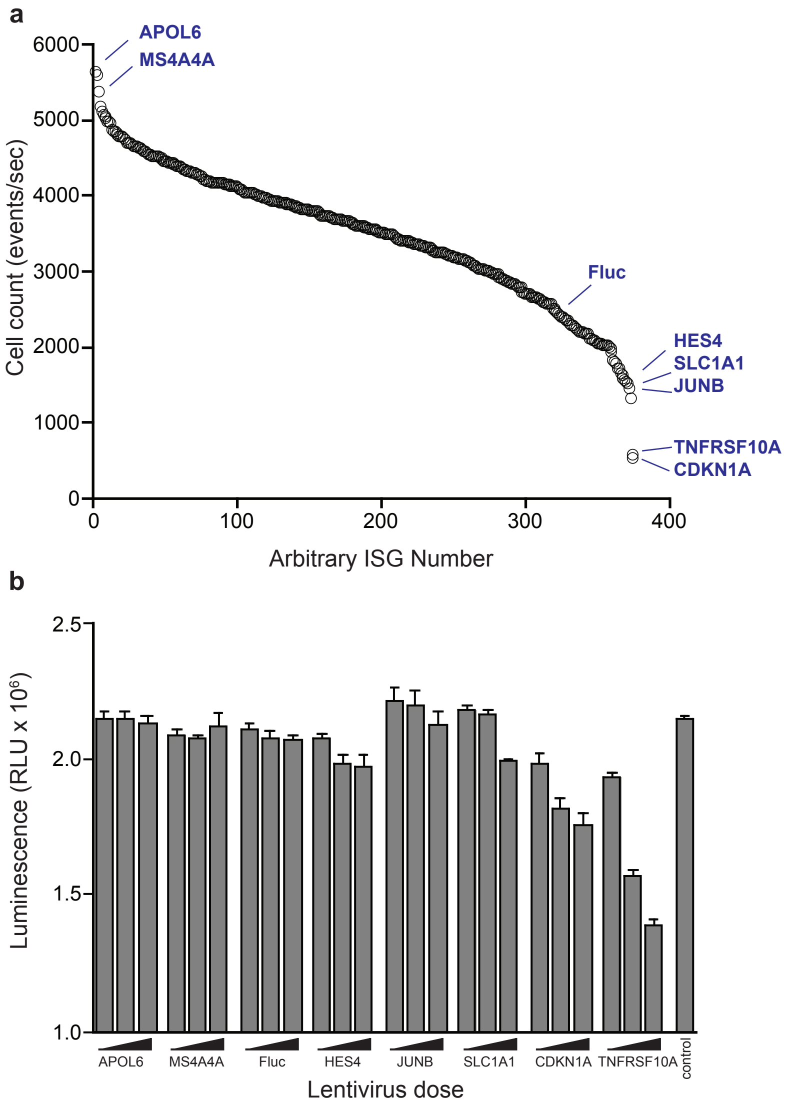


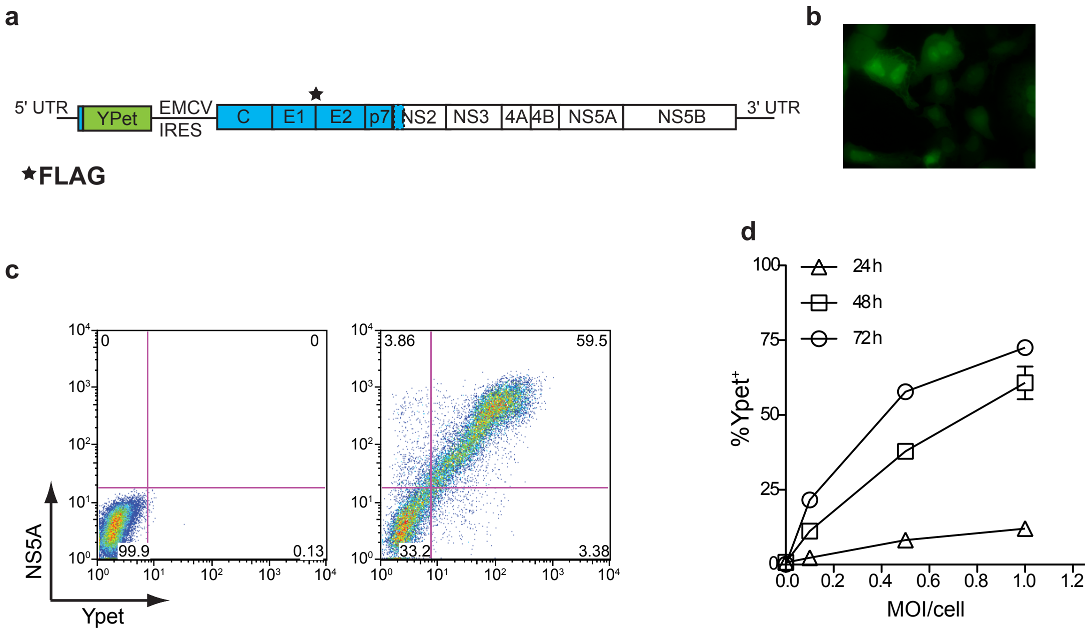
Supplementary Figure 1. Characterization of bicistronic lentivirus construct. **a.** Three reporter genes (GFP, Fluc, Gluc) were inserted into the bicistronic lentiviral construct shown in Fig 1a. Lentiviral stocks were generated as described in Supplementary Methods and used to transduce 7 x 10^4 *STAT1*$^{-/-}$Fib in 24 well plates at the indicated doses. Transduced cells were harvested 48 h later and processed for FACS analysis as described in Supplemental Methods. The mean fluorescence intensities of GFP and RFP were quantified by FACS. Fluc and Gluc were measured by commercially available kits (Promega). First cistron genes (GFP, Fluc, Gluc) are plotted on the left y-axis and the second cistron gene (RFP) is plotted on the right y-axis. The data show that, for all three constructs, both cistrons express well and levels are approximately 1:1. Results are mean ± s.d. from a representative experiment performed with n=3 (Gluc, GFP) or n=4 (Fluc). **b.** Three ISG-expressing lentiviral preps (IRF1.ires.RFP, MAP3K14.ires.RFP, C6orf150.ires.RFP) were used to transduce *STAT1*$^{-/-}$Fib as above. Cells were processed for immunofluorescence as described in Supplementary Methods. Single channel red and green images are shown in black and white. Merged images are shown in magenta and green, with overlap depicted as white. **c.** Representative microscopy images showing IFI6-mediated inhibition of YFV as compared to Fluc control in Huh-7 cells. Images were processed with Adobe Photoshop with minor adjustments to contrast. **d.** Small-scale screen testing the antiviral potential of eleven ISGs (described in text) and two controls (Fluc, Gluc) against VSV and YFV. Replication represents the percentage of GFP$^+$ cells in the RFP$^+$ population normalized to Fluc control. Black line indicates population mean.



Supplementary Figure 2. RFP levels from TRIP.CMV.IVSb.ISG.ires.TagRFP lentiviruses. **a.** The percentage of RFP$^+$ cells in Huh-7.5, Huh-7, and *STAT1*$^{-/-}$Fib during HCV and YFV large-scale screens was quantified by FACS. Data points were ranked numerically from high to low. Transduction efficiency as measured by % RFP$^+$ cells was higher in *STAT1*$^{-/-}$Fib compared to Huh-7 or Huh-7.5 cells. Approximately 12% of genes exhibited poor transduction (less than 30% RFP$^+$) and were excluded from subsequent analyses or assayed for inhibitory activity by transient transfection (see Supplementary Figure 4). **b.** The average RFP mean fluorescence intensity (a surrogate for ISG expression levels) from all samples in **(a)** was quantified by FACS and depicted as box and whisker plots. Data represent n=391. Statistical significance was determined by one-way ANOVA. (***,P<0.001, **,P<0.01, *,P<0.05, ns-not significant).



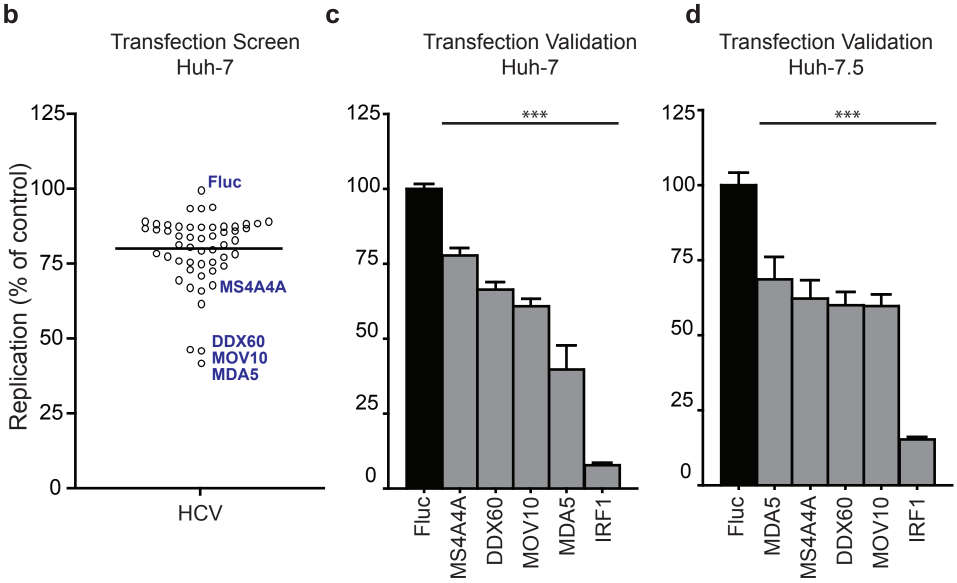
Supplementary Figure 3. Cell viability in ISG-transduced cells. **a.** Cell count data from the VEEV screen was obtained during flow cytometry acquisition. Two genes (*TNFRSF10A* and *CDKN1A*) were identified as potentially toxic based on low cell numbers. **b.** *STAT1*$^{-/-}$Fib were plated at a density of 10^4 cells/well in 96 well plates and transduced with 5, 10, or 20 µl of indicated ISG-expressing lentiviral stocks. Cells were incubated for 48 h and tested for viability using Cell-titer Glo luminescence-based assay (Promega). The data show that increased doses of lentiviral preparations lead to decreased cell counts for *TNFRSF10A* and *CDKN1A*, whereas several other genes tested had little to no impact on cell viability. Results are mean ± s.d. from a representative experiment, n=8.



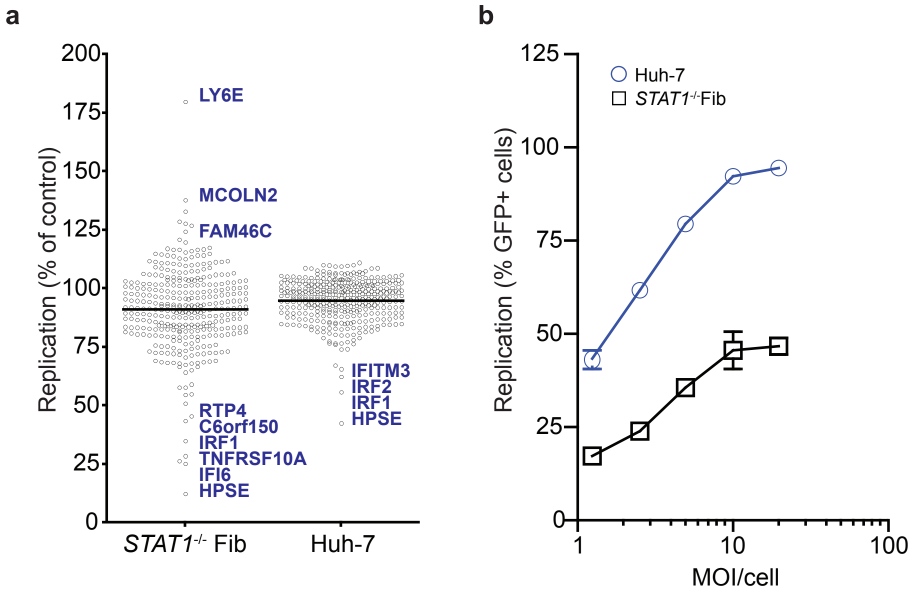
Supplementary Figure 4. Characterization of HCV expressing Ypet. **a.** Diagram of Bi-Ypet-Jc1FLAG2 molecular clone. The HCV IRES drives Ypet expression in the first cistron and the EMCV IRES drives expression of the Jc1 HCV polyprotein in the second cistron. **b.** Fluorescence microscopy image of Huh-7.5 at 48 h post-infection with HCV-Ypet. **c.** Co-staining of Ypet and NS5A. Huh-7.5 cells infected with HCV-Ypet were harvested in 200 µl Accumax, washed in 1X PBS, and processed with Cytofix/Cytoperm kit (BD Biosciences) to stain for NS5A expression using the 9E10 monoclonal antibody. **d.** Dose and time dependency of HCV-Ypet replication. Huh-7 cells were infected with varying doses of HCV-Ypet, harvested 24 h, 48 h, or 72 h post-infection, and analyzed for Ypet expression by FACS. Results are mean ± s.d. from a representative experiment, n=3.

a

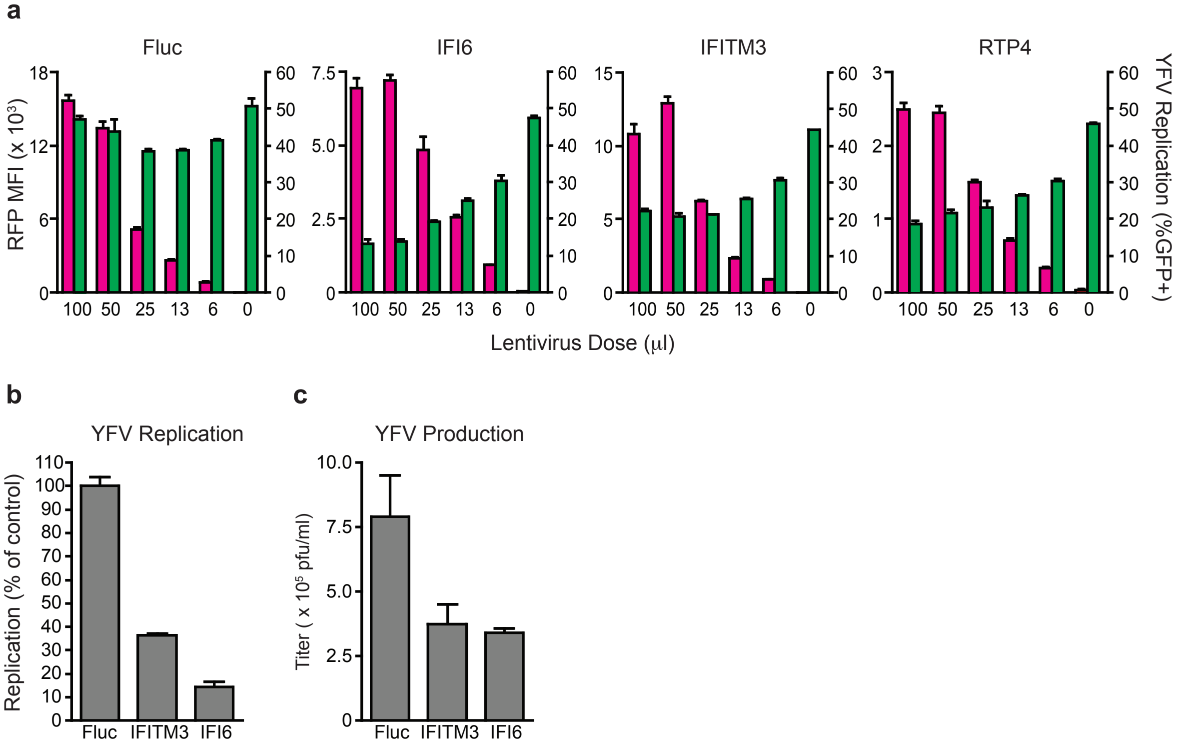
Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score
IFIH1/MDA5	42.3	-3.22	**ABCA9**	78.7	-0.13	**B4GALT5**	87.2	0.59
MOV10	46.4	-2.87	**SAT1**	79.0	-0.10	**IFITM1**	87.7	0.64
DDX60	46.7	-2.85	**DDX3X**	79.8	-0.04	**RNF24**	87.7	0.64
UBA7	62.0	-1.55	**SLFN12**	80.3	0.01	**ZNF107**	87.7	0.64
FLJ11286	66.4	-1.17	**APOL6**	81.1	0.08	**CCL2**	88.0	0.66
NOS2A	67.5	-1.08	**TRIM56**	81.7	0.13	**BUB1**	88.0	0.66
MS4A4A	68.3	-1.01	**C9orf19**	82.0	0.15	**ZNF295**	88.0	0.66
PABPC4	69.9	-0.87	**ADAR**	83.3	0.27	**DTX3L**	88.5	0.71
N4BP1	71.6	-0.73	**PLEKHA4**	83.9	0.31	**BST2**	88.8	0.73
APOBEC3G	73.2	-0.59	**CEACAM1**	84.4	0.36	**TLR7**	88.8	0.73
OAS3	73.5	-0.57	**ANKFY1**	84.7	0.38	**TFEC**	89.1	0.75
CNP	74.9	-0.45	**RAB27A**	85.0	0.41	**EIF2AK2**	89.6	0.80
BLZF1	75.4	-0.41	**APOL3**	86.1	0.50	**FLT1**	89.6	0.80
TLK2	76.0	-0.36	**VEGFC**	86.3	0.52	**RASGEF1**	94.0	1.17
PCTK3	76.0	-0.36	**ZNF313**	86.6	0.55	**ZAP**	94.0	1.17
CASP1	76.5	-0.31	**OAS1**	86.9	0.57	**RBM25**	94.5	1.22
MX2	77.6	-0.22	**RARRES3**	87.2	0.59	**Fluc**	100.0	1.68
FNDC3B	77.9	-0.20						



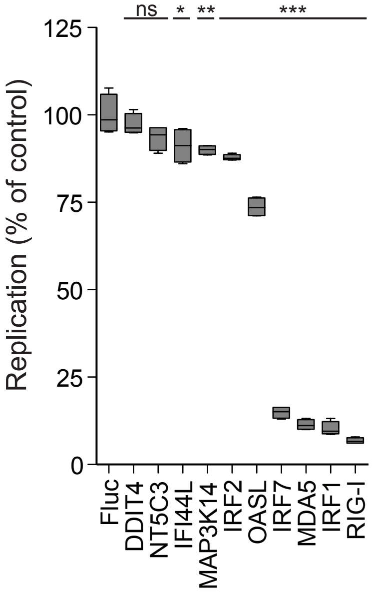
Supplementary Figure 5. Transient transfection-based screen of 50 ISGs against HCV. Fifty ISGs that failed to mediate high-level RFP expression in lentiviral assays were screened by transient transfection in Huh-7 cells as described in Supplementary Methods. **a.** Table showing HCV inhibition by fifty genes with infectivity and Z-scores. **b.** Dot plot of data in **(a)**. Replication levels were normalized to Fluc control. Select ISGs are denoted in blue. Black line indicates population mean. **c, d.** Validation assays of selected genes in Huh-7 **(c)** and Huh-7.5 **(d)**. Results are mean ± s.d. from a representative experiment, n=3.



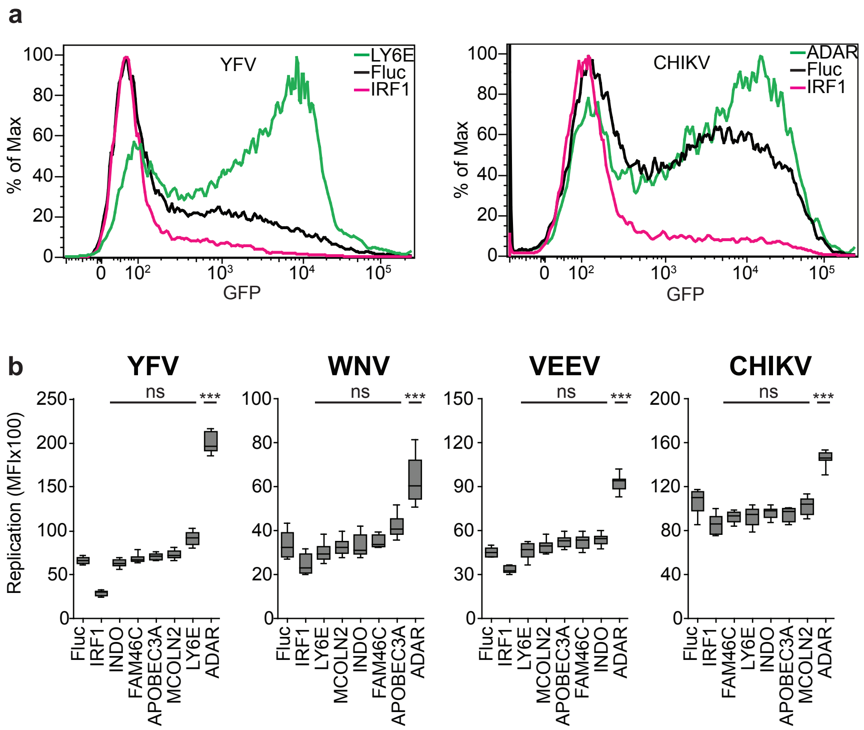
Supplementary Figure 6. Large-scale ISG screens against YFV in *STAT1*$^{-/-}$Fib and Huh-7. **a.** Dot plots of YFV replication in *STAT1*$^{-/-}$Fib or Huh-7 normalized to Fluc control. Select ISGs are denoted in blue. Black line indicates population mean. *STAT1*$^{-/-}$Fib data is identical to screening data in Fig 2 and is shown here for comparison to Huh-7. **b.** Differential YFV replication levels in *STAT1*$^{-/-}$Fib and Huh-7. Cells were infected with varying doses of YFV, harvested 24 h post-infection, and replication levels were quantified by FACS. Results are mean ± s.d. from a representative experiment, n=3.



Supplementary Figure 7. Validation of *IFI6*, *IFITM3*, and *RTP4* as anti-YFV hits in *STAT1*$^{-/-}$Fib. **a.** Lentiviruses expressing *IFI6*, *IFITM3*, or *RTP4* were tested for dose-dependent inhibition of YFV. RFP mean fluorescence (magenta bars) is plotted on the left y-axis and YFV replication (green bars) is plotted in the right y-axis. **b.** Inhibition of YFV expressing GFP by *IFITM3* and *IFI6* as measured in by FACS. **c.** Inhibition of YFV-17D (non-GFP) by *IFITM3* and *IFI6* as measured by plaque assay on BHK-J cells. For all panels, results are mean ± s.d. from a representative experiment, n=3.



Supplementary Figure 8. Anti-HCV effect of ISGs post-infection. Huh-7 cells were infected with HCV-Ypet for 12 hours, followed by transduction with ISG-expressing lentiviruses as described above. 48 hours post transduction, cells were harvested and replication levels were quantified by FACS. Data are depicted as box and whisker plots. Data are from a representative experiment with n=4. Statistical significance was determined by one-way ANOVA. (***,P<0.001, **,P<0.01, *,P<0.05, ns-not significant).

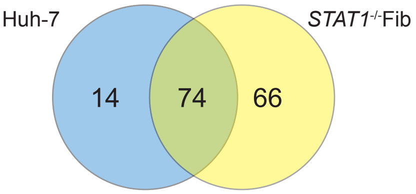


Supplementary Figure 9. Identification of ISGs that enhance replication of YFV, WNV, VEEV, and CHIKV. **a.** Representative FACS plots showing impact of *LY6E* on YFV (left panel) and *ADAR* on CHIKV (right panel). **b.** Validation assays of selected enhancing ISGs. Independent lentiviral preparations were generated and tested for replication enhancement. Replication levels were plotted as GFP mean fluorescence intensity in the RFP^+GFP^+ population. Data are represented by box and whisker plots with n=9. Statistical significance was determined by one-way ANOVA. (***,$P<0.001$, **,$P<0.01$, *,$P<0.05$, ns-not significant)

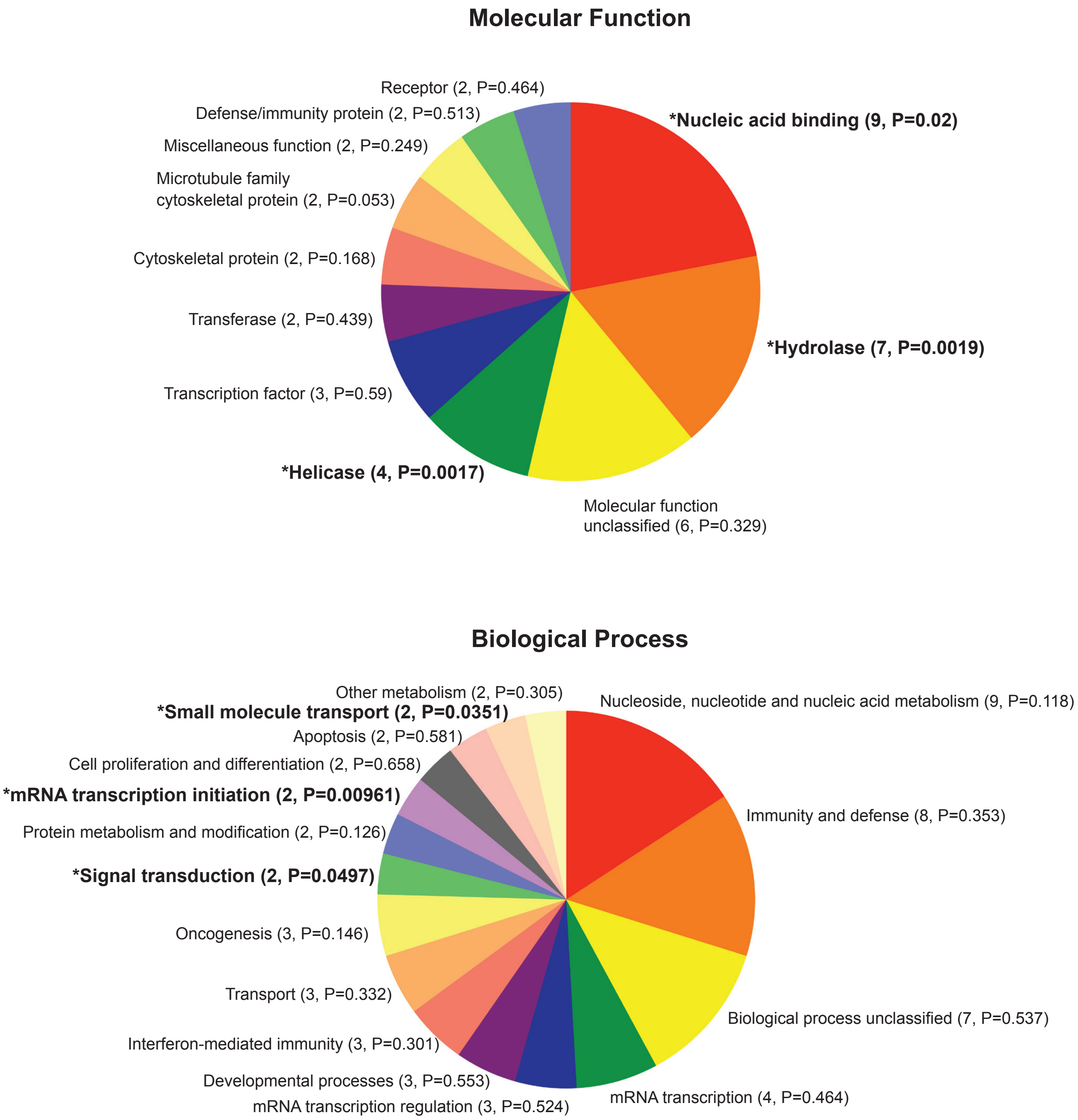
a

	Gene	FC (Huh-7)	FC ($STAT1^{-/-}$Fib)	Accession	Gene	FC (Huh-7)	FC ($STAT1^{-/-}$Fib)	Accession	Gene	FC (Huh-7)	FC ($STAT1^{-/-}$Fib)	Accession
Huh-7	CXCL11	10.3		NM_005409.3								
	IFITM3	7.7		NM_021034.2								
	IFITM2	6.5		NM_006435.2								
	CXCL10	6.0		NM_001565.2								
	OAS1	5.3		NM_002534.2								
	MT2A	4.5		NM_005953.2								
	SERPINA7	4.0		NM_000354.3								
	STAT1	3.6		NM_139266.1								
	EIF2AK2	3.5		NM_002759.1								
	STAT1	3.4		NM_007315.2								
	LOC441019	3.1		XM_498969.2								
	MLKL	3.1		NM_152649.1								
	MT1A	3.1		NM_005946.2								
	LCN2	3.0		NM_005564.3								
Huh-7 and *STAT1*$^{-/-}$Fib	RARRES3	91.7	13.9	NM_004585.3	LGALS3BP	8.8	3.8	NM_005567.2	GBP3	4.5	6.4	NM_018284.2
	MX1	68.1	32.5	NM_002462.2	PSMB8	8.7	5.2	NM_148919.3	TAP2	4.4	3.7	NM_018833.2
	IFI6	30.7	12.3	NM_022872.2	PSMB9	8.5	7.9	NM_002800.4	KIAA1618	4.2	4.3	NM_020954.2
	SLC15A3	27.5	7.8	NM_016582.1	DDX60	7.6	5.0	NM_017631.4	BIRC3	4.1	3.7	NM_001165.3
	OAS2	25.7	50.5	NM_016817.2	IFI44L	7.3	11.8	NM_006820.1	PARP9	4.0	6.5	NM_031458.1
	OAS3	20.4	8.8	NM_006187.2	IRF9	6.8	3.6	NM_006084.4	TAPBP	3.9	3.3	NM_003190.3
	EPSTI1	19.0	9.0	NM_033255.2	IFIT2	6.7	6.0	NM_001547.4	HERC5	3.9	4.2	NM_016323.2
	IFIT1	18.3	12.4	NM_001548.3	PARP14	6.7	8.5	NM_017554.1	XAF1	3.9	7.6	NM_199139.1
	TAP1	17.7	5.1	NM_000593.5	IFI35	6.6	6.3	NM_005533.2	PARP9	3.9	7.2	NM_031458.1
	ISG15	16.9	7.6	NM_005101.1	HERC6	6.5	7.1	NM_017912.3	IL15	3.9	3.6	NM_000585.2
	IFIH1	16.1	10.4	NM_022168.2	UBE2L6	6.1	4.9	NM_004223.3	PARP10	3.7	3.5	XM_001127571.1
	GBP4	16.0	10.7	NM_052941.3	HLA-F	5.7	10.6	NM_018950.1	PSME2	3.6	4.7	NM_002818.2
	IFI27	15.0	59.3	NM_005532.3	TAP2	5.6	4.3	NM_000544.3	RTP4	3.6	4.1	NM_022147.2
	IFI44	14.4	15.5	NM_006417.3	LOC400759	5.5	5.6	NR_003133.1	PSME1	3.6	3.3	NM_006263.2
	CASP1	13.4	7.1	NM_033294.2	PRIC285	5.5	6.0	NM_033405.2	ISG20	3.5	14.6	NM_002201.4
	LOC100129681	13.2	9.6	XM_001726834.1	PSMB8	5.3	5.5	NM_148919.3	OAS2	3.5	6.2	NM_002535.2
	IFIT3	12.8	13.3	NM_001031683.1	UBE2L6	5.2	4.2	NM_004223.3	PARP12	3.5	5.3	NM_022750.2
	GBP1	12.5	10.9	NM_002053.1	HLA-H	5.2	10.1	NR_001434.1	TNFSF10	3.4	8.7	NM_003810.2
	PSMB8	11.3	5.3	NM_004159.4	SAMD9	5.0	5.6	NM_017654.2	PARP10	3.4	3.9	XM_001127571.1
	OAS1	11.2	5.5	NM_001032409.1	TNFRSF14	5.0	4.8	NM_003820.2	APOL3	3.3	10.5	NM_145641.1
	HLA-B	10.8	14.1	NM_005514.5	HLA-A	4.8	3.2	NM_002116.5	IFIT3	3.3	7.4	NM_001549.2
	BST2	10.6	9.5	NM_004335.2	PARP10	4.8	4.4	NM_032789.1	IFI30	3.3	3.1	NM_006332.3
	IFI6	10.2	3.3	NM_022873.2	USP18	4.7	14.4	NM_017414.3	LOC389386	3.0	3.5	XR_037483.1
	OAS2	8.9	8.1	NM_001032731.1	PSMB10	4.7	6.7	NM_002801.2	SP110	3.0	3.1	NM_004510.2
	CASP1	8.8	5.9	NM_033294.2	UBA7	4.7	5.9	NM_003335.2				
STAT1$^{-/-}$Fib	CD74		32.5	NM_001025159.1	WARS		4.5	NM_173701.1	BTN3A2		3.4	NM_007047.3
	CD74		17.7	NM_004355.2	HLA-C		4.5	NM_002117.4	APOL2		3.4	NM_145637.1
	SAMD9L		13.7	NM_152703.2	DHX58		4.4	NM_024119.2	ZC3HAV1		3.3	NM_024625.3
	IDO1		12.8	NM_002164.4	IRF7		4.3	NM_004029.2	PAGE2B		3.3	NM_001015038.1
	INDO		12.5	NM_002164.3	IRF7		4.2	NM_004029.2	GJD3		3.3	NM_152219.3
	CCL5		10.1	NM_002985.2	LAP3		4.2	NM_015907.2	C19orf66		3.3	NM_018381.2
	XAF1		9.9	NM_199139.1	IFIT5		4.0	NM_012420.1	BTN3A1		3.2	NM_007048.4
	CCL5		9.7	NM_002985.2	UBD		4.0	NM_006398.2			3.2	BF674170
	TRIM22		7.9	NM_006074.3	BTN3A3		4.0	NM_197974.1	ACSL5		3.2	NM_203379.1
	APOBEC3G		7.6	NM_021822.1	OAS3		3.9	NM_006187.2	STAT2		3.2	NM_005419.2
	PZP		6.3	NM_002864.1	APOL2		3.9	NM_145637.1	NMI		3.2	NM_004688.1
	IFITM1		6.2	NM_003641.3	RSAD2		3.9	NM_080657.4	IL18BP		3.2	NM_173042.2
	MX2		6.1	NM_002463.1	CENTA1		3.8	NM_006869.1	DTX3L		3.2	NM_138287.2
	SPTA1		6.0	NM_003126.2	ARL9		3.8	NM_206919.1	FCRLA		3.2	NM_032738.3
	ACSL5		5.7	NM_016234.3	ZNFX1		3.7	NM_021035.2	OASL		3.2	NM_198213.1
	HLA-DRA		5.5	NM_019111.3	HLA-G		3.7	NM_002127.3	CD74		3.1	NM_001025159.1
	GZMA		5.4	NM_006144.2	CD40		3.7	NM_001250.4	TLR3		3.1	NM_003265.2
	CEACAM1		4.9	NM_001024912.1	TMEM62		3.7	NM_024956.3	LGALS9		3.1	NM_009587.2
	HLA-A29.1		4.7	NM_001080840.1	WARS		3.7	NM_004184.3	NFE2L3		3.0	NM_004289.5
	HLA-H		4.7	NR_001434.1	ERAP2		3.5	NM_022350.2	TDRD7		3.0	NM_014290.1
	HLA-F		4.6	NM_001098479.1	CFB		3.5	NM_001710.4	BATF2		3.0	NM_138456.3
	DDX58		4.6	NM_014314.3	MMP9		3.4	NM_004994.2	APOBEC3F		3.0	NM_145298.5

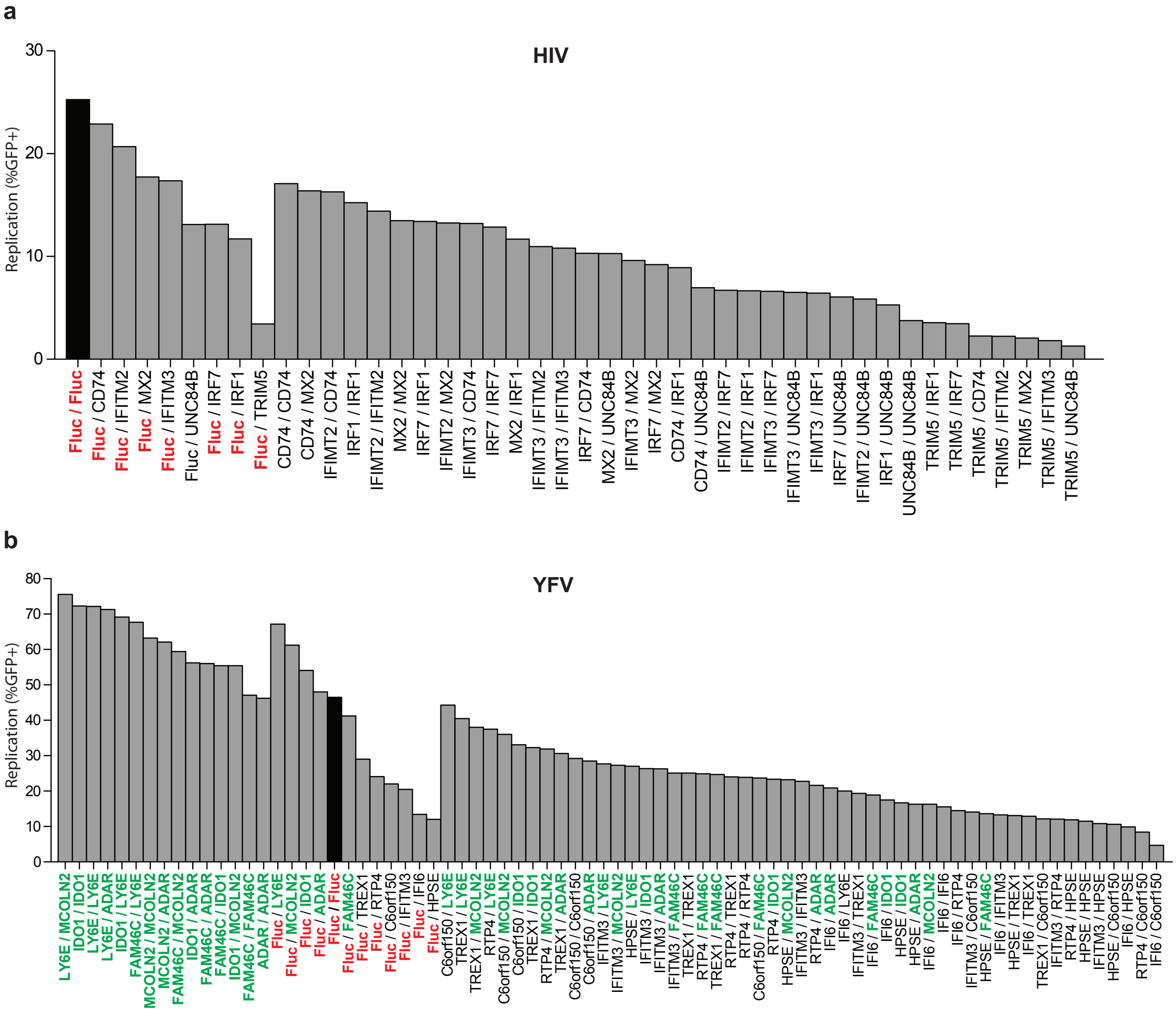
b



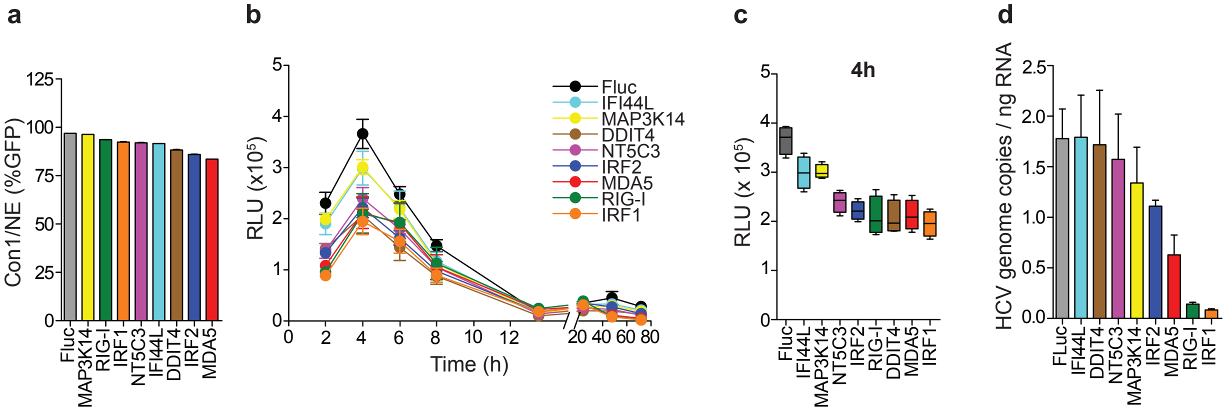
Supplementary Figure 10. Microarray analysis of *IRF*1-expressing cells. Huh-7 and *STAT1*$^{-/-}$Fib were transduced with lentiviruses expressing *IRF1* or Fluc as a control. Total RNA was harvested at 48 h and processed for Illumina BeadArray. Data was analyzed with GeneSpring Software. Genes shown were induced at least 3-fold by IRF1 compared to Fluc ($p<0.05$, $n=3$). Data represent one of two experiments.



Supplementary Figure 11. Gene ontology analysis classifying validated hits by molecular function (top panel) and biological process (bottom panel). The 389 ISG list was used as a reference. Only categories with two or more genes were charted. * denotes enriched categories ($P<0.05$).



Supplementary Figure 12. Combinatorial action of inhibitory and enhancing ISGs. Select ISGs were tested in all 2-gene combinations for inhibition of HIV in MT-4 cells **(a)** or YFV in *STAT1*$^{-/-}$Fib **(b)**. Data are represented as %GFP-expressing cells. ISGs are color-coded: control (red), inhibitory (black), enhancing (green).



Supplementary Figure 13. ISG antiviral effects in the HCV life cycle. **a.** ISG-expressing Huh-7 cells were infected with genotype 1b-Con1 HCV pseudoparticles expressing GFP or Gluc. 48 h post-infection HCVpp entry was assessed by quantitation of GFP by FACS or Gluc by reporter gene assay of cell supernatants. The fold increase of HCVpp infection over a non-enveloped (NE) pseudoparticle expressing a homologous reporter is reported. Data are from one of three experiments with n=3. **b.** ISG-expressing Huh-7 cells were transfected with in vitro transcribed replication-defective HCV subgenomic replicon RNA (SG-GNN) expressing Gluc. Reporter gene activity was measured in cell supernatants at 2, 4, 6, 8, 13.5, 24, 48, and 72 h post-transfection. **c.** ISG-mediated inhibition of primary translation (from panel **b**) was inferred from Gluc levels at 4 h. Data represent one of three independent experiments with n=4. Fluc-GNN data in this figure is identical to Fluc-GNN data in Figure 3a and is shown in both graphs for comparison. **d.** ISG-expressing Huh-7 cells were transfected with in vitro transcribed HCV subgenomic replicon RNA expressing Gluc. Total RNA was harvested 72 h post-transfection and HCV genome copy number was assessed by real time RT-PCR. Data are represented as genome copies per ng input RNA.

Supplementary Table 1: ISG microarray data sets and inclusion criteria for screening

Reference	***IFN***[1]	***Tissue/cell type***	***Time pt.***	***Inclusion Criteria (FC – fold change)***[2,3]
Brodsky LI et al. *PLoS One*. 2007;2(7):e584.	IFNα	PBMCs from HCV-infected patients	0, 1, 2, 7, 14, 28 d	included 36 gene associated with early decrease in HCV titers
de Veer MJ et al. *J Leukoc Biol.* 2001;69(6):912-20.	IFNα, IFNβ	HT1080, MEFs, human dendritic cells	1, 3, 6, 18, 24 h	FC>2.0 (IFNα), FC>1.5 (IFNβ)
He XS et al. *Hepatology.* 2006;44(2):352-9.	IFNα	PBMCs from HCV-infected patients (treated ex vivo)	5 h	FC>2
Hilkens CM, *J Immunol*. 2003;171(10):5255-63.	IFNα	human T cells and dendritic cells	6, 8 h	FC>2 at 6h
Hultcrantz M et al. *Virology.* 2007;367(1):92-101.	IFNα	human pancreatic islet cells	6 h	FC>2.0
Indraccolo S et al. *J Immunol.* 2007;178(2):1122-35	IFNα, IFNβ	HUVEC	5 h	FC>2.0
Lanford RE et al. *Hepatology.* 2006;43(5):961-72.	pIFNα	chimpanzee liver biopsies/PBMC	4, 8, 24 h	FC>2 at 4 h, FC>4 at 8 h, in liver only FC>4 at 4 h in PBMC only FC>2 at 4 h and 8 h in liver and PBMC FC>4 at 4 h in primary hepatocytes
Leaman D et al. *J Interferon Cytokine Res.* 2003;23(12):745-56.	IFNα, IFNβ	human melanoma cell lines	2, 8, 18 h	FC>2.3
Rani MR et al. *J Leukoc Biol*. 2007;82(5):1353-60.	IFNβ	human PBMCs	2, 6, 12 h	FC>2 at 6 h
Sarasin-Filipowicz M et al. *PNAS.* 2008;105(19):7034-9.	pIFNα	human liver biopsies/PBMC	4 h	FC>2 in liver from rapid responders

[1] pIFNα denotes pegylated IFNα

[2] For liver and PBMC data sets, only genes appearing in 2 or more studies were included

[3] A total of 444 genes were compiled, of which 387 were available as sequence-validated Gateway-ready clones

Supplementary Table 1. ISG microarray data sets and inclusion criteria for screening. Ten publications with microarray data sets from various IFN-treated cell types or tissues were analyzed. Inclusion criteria: 1) only type I IFN-treated cells or tissues were included (type II IFN excluded), 2) only data from early time points (4, 6, or 8 h) were included, 3) for liver and PBMC data sets, only genes that appear in at least two or more studies were included, 4) only genes with fold changes greater than 2 or 4 were included (last column). With these inclusion criteria, a list of 444 genes were compiled, and 387 were available as sequence-validated Gateway-ready clones.

Supplementary Tables 2-10. Large scale ISG screens for viruses. Each table shows complete data sets from large scale screens for HCV, HIV, YFV, WNV, VEEV, and CHIKV in the indicated cell line. Data are ranked by percent infection normalized to Fluc or Gluc control starting with the strongest inhibitors in the first column. Z scores are included to show distribution. For WNV, VEEV, and CHIKV screens, the 100% normalization value was determined from the average of 3 independent preparations of Fluc.ires.TagRFP lentiviral pseudoparticles. Common ISG aliases: BST2 - tetherin, C19orf66 - FLJ11286, DDX58 - RIG-I, DDX60 - FLJ20035, DHX58 - LGP2, EIF2AK2 - PKR, IDO1 - INDO, IFI6 - G1P3 / 6-16, IFIH1 - MDA5, IFIT1 - ISG56, IFIT2 - ISG54, IFIT3 - ISG50, IFIT5 - ISG58, IFITM1 - 9-27, IFITM2 - 1-8D, IFITM3 - 1-8U, PSMB8 - LMP7, PSMB9 - LMP2, PSMB10 - MECL1, NAMPT - PBEF1, RSAD2 - viperin, ZBP1 - DAI, ZC3HAV1- ZAP.

Supplementary Table 2. Large scale ISG screen: HCV in Huh-7.5 cells at 48 h (page 1 of 2)

Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score
IFIH1	22.8	-4.36	**CXCL9**	66.9	-0.97	**CREB3L3**	73.5	-0.46	**GTPBP1**	77.7	-0.13
DDX58	24.2	-4.25	**G6PC**	66.9	-0.97	**VAMP5**	73.6	-0.45	**CTCFL**	77.9	-0.12
IRF1	30.9	-3.74	**IGFBP2**	67.0	-0.96	**B2M**	73.6	-0.45	**SPTLC2**	77.9	-0.12
IRF7	35.0	-3.42	**OASL**	67.0	-0.96	**CD69**	73.8	-0.44	**IFI44L**	78.0	-0.11
CCL2	51.4	-2.16	**PDGFRL**	67.0	-0.96	**IRF9**	73.9	-0.43	**MT1X**	78.1	-0.10
MKX	52.8	-2.05	**CCL19**	67.1	-0.95	**SOCS1**	73.9	-0.43	**CCL4**	78.2	-0.09
HSH2D	52.8	-2.05	**GEM**	67.6	-0.91	**SOCS2**	74.3	-0.39	**IL28RA**	78.3	-0.09
SLC1A1	54.5	-1.92	**XAF1**	68.0	-0.88	**DEFB1**	74.4	-0.39	**CD9**	78.3	-0.09
LRG1	54.6	-1.91	**HLA-G**	68.2	-0.87	**CFB**	74.5	-0.38	**ZNF313**	78.4	-0.08
SLFN5	55.6	-1.83	**C5orf39**	68.3	-0.86	**IFI35**	74.6	-0.37	**FAM46C**	78.5	-0.07
APOL2	56.1	-1.80	**USP18**	68.5	-0.84	**APOL1**	74.7	-0.36	**RPL22**	78.5	-0.07
FBXO6	56.3	-1.78	**JUNB**	68.6	-0.84	**SLC25A28**	74.9	-0.35	**HLA-E**	78.6	-0.06
MAB21L2	56.6	-1.76	**C4orf33**	68.6	-0.84	**WARS**	75.1	-0.34	**NDC80**	78.7	-0.06
IRF2	56.6	-1.76	**SAT3**	68.6	-0.84	**CCL5**	75.1	-0.34	**RNASE4**	78.8	-0.05
C22orf28	56.9	-1.74	**TNFSF10**	68.6	-0.83	**C10orf10**	75.1	-0.33	**LINCR**	78.9	-0.04
GZMB	57.4	-1.70	**VEGFC**	68.8	-0.82	**IFITM2**	75.1	-0.33	**TRIM21**	79.0	-0.03
TNFAIP6	58.3	-1.63	**CD80**	69.6	-0.76	**IFIT1**	75.1	-0.33	**ADAMDEC1**	79.1	-0.02
PI4K2B	58.4	-1.62	**CCDC92**	69.6	-0.76	**FLJ39739**	75.3	-0.32	**HK2**	79.2	-0.02
PBEF1	58.7	-1.60	**C5orf27**	69.7	-0.75	**NUP50**	75.3	-0.32	**IFITM3**	79.3	-0.01
CCDC109B	59.3	-1.56	**THBD**	70.0	-0.73	**MYD88**	75.4	-0.31	**GAK**	79.4	0.00
GK	59.5	-1.54	**CCL8**	70.0	-0.73	**DYNLT1**	75.5	-0.30	**SP110**	79.5	0.00
IFIT5	59.6	-1.53	**ETV7**	70.3	-0.70	**DTX3L**	75.5	-0.30	**ANKRD22**	79.5	0.00
ARG2	60.4	-1.47	**MT1H**	70.3	-0.70	**NAPA**	75.6	-0.30	**SAA1**	79.5	0.01
MAFB	60.4	-1.46	**NRN1**	70.4	-0.70	**CSDA**	75.6	-0.30	**CXCL10**	79.6	0.01
SIRPA	60.5	-1.46	**C15orf48**	70.4	-0.69	**NOD2**	75.6	-0.30	**MT1G**	79.7	0.02
UPP2	60.8	-1.44	**ADFP**	70.5	-0.69	**NT5C3**	75.6	-0.29	**C2orf31**	79.8	0.03
EIF2AK2	61.2	-1.40	**DDIT4**	70.8	-0.67	**PMM2**	75.6	-0.29	**HESX1**	79.9	0.04
LAP3	61.5	-1.39	**LY6E**	70.9	-0.66	**MT1F**	75.7	-0.29	**ABTB2**	80.0	0.04
GTPBP2	61.5	-1.38	**TLR3**	70.9	-0.66	**S100A8**	75.8	-0.28	**GMPR**	80.0	0.05
BATF2	61.8	-1.36	**P2RY6**	71.0	-0.65	**ISG15**	75.8	-0.28	**TNFRSF10A**	80.1	0.05
GCH1	62.6	-1.30	**GBP2**	71.0	-0.65	**CES1**	75.9	-0.27	**EIF3L**	80.1	0.05
SERPINE1	63.0	-1.27	**AGPAT9**	71.0	-0.65	**IL17RB**	75.9	-0.27	**DCP1A**	80.2	0.05
PUS1	63.1	-1.26	**NCF1**	71.4	-0.62	**FNDC4**	76.0	-0.27	**SMAD3**	80.2	0.06
PFKFB3	63.2	-1.25	**EPSTI1**	71.5	-0.61	**MT1M**	76.0	-0.27	**BUB1**	80.2	0.06
MAP3K14	63.6	-1.22	**AIM2**	71.7	-0.60	**NFIL3**	76.1	-0.25	**BTN3A3**	80.3	0.07
BCL2L14	63.7	-1.21	**PNRC1**	72.0	-0.58	**PXK**	76.2	-0.25	**KIAA0040**	80.3	0.07
ANGPTL1	63.7	-1.21	**STEAP4**	72.1	-0.57	**ENPP1**	76.3	-0.25	**PML**	80.3	0.07
PDK1	64.5	-1.15	**LGALS9**	72.1	-0.57	**CASP7**	76.4	-0.23	**MAP3K5**	80.5	0.08
LGALS3	64.6	-1.14	**PARP12**	72.2	-0.56	**HES4**	76.4	-0.23	**OAS2**	80.6	0.09
IFNGR1	65.1	-1.10	**IFI44**	72.3	-0.55	**IFI30**	76.4	-0.23	**TRIM5**	80.6	0.09
SERPING1	65.3	-1.09	**CMAH**	72.4	-0.54	**EPAS1**	76.5	-0.23	**MAFF**	80.6	0.09
CRP	65.3	-1.09	**PRAME**	72.4	-0.54	**LGMN**	76.5	-0.23	**UBE2L6**	81.0	0.12
IMPA2	65.4	-1.08	**CEBPD**	72.4	-0.54	**SSBP3**	76.6	-0.22	**RASSF4**	81.0	0.12
CYP1B1	65.5	-1.08	**SECTM1**	72.7	-0.52	**PADI2**	76.7	-0.21	**TAP2**	81.2	0.13
ALDH1A1	65.5	-1.07	**COMMD3**	72.8	-0.51	**PMAIP1**	76.8	-0.20	**CXCL11**	81.2	0.13
TMEM49	65.5	-1.07	**TMEM51**	73.1	-0.49	**FLJ23556**	76.8	-0.20	**CDKN1A**	81.3	0.14
TNFSF13B	65.6	-1.07	**PCTK2**	73.1	-0.49	**EXT1**	76.9	-0.20	**ZBP1**	81.3	0.14
HPSE	65.7	-1.06	**FAM125B**	73.1	-0.49	**KIAA1618**	76.9	-0.19	**CCDC75**	81.4	0.15
TYMP	66.5	-1.00	**BLVRA**	73.2	-0.48	**MAX**	77.2	-0.17	**TREX1**	81.5	0.15
TRIM14	66.7	-0.98	**FUT4**	73.2	-0.48	**SCARB2**	77.6	-0.14	**CCND3**	81.5	0.16
FAM70A	66.9	-0.97	**TRIM38**	73.3	-0.47	**MTHFD2L**	77.7	-0.14	**CPT1A**	81.5	0.16

Supplementary Table 2. Large scale ISG screen: HCV in Huh-7.5 cells at 48 h (page 2 of 2)

Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score
CCR1	81.6	0.17	**TBX3**	86.7	0.56	**SLC15A3**	93.7	1.10			
CD74	81.7	0.17	**ISG20**	86.8	0.56	**MX1**	93.7	1.10			
DHX58	81.7	0.17	**CHMP5**	86.9	0.57	**BCL3**	94.4	1.16			
MSR1	81.7	0.18	**LAMP3**	86.9	0.58	**EHD4**	94.6	1.17			
TDRD7	81.8	0.18	**BAG1**	87.0	0.58	**DUSP5**	94.7	1.17			
HLA-C	81.9	0.19	**SNN**	87.0	0.58	**AQP9**	94.8	1.18			
THOC4	81.9	0.19	**IL6ST**	87.3	0.60	**GBP4**	94.8	1.19			
GLRX	82.1	0.20	**PHF11**	87.5	0.62	**MCOLN2**	95.0	1.20			
TLK2	82.1	0.20	**IFI6**	87.6	0.63	**PPM1K**	95.1	1.21			
STAP1	82.1	0.21	**UNC84B**	87.7	0.63	**NCOA3**	95.4	1.23			
ATP10D	82.3	0.22	**GBP5**	87.8	0.64	**WHDC1**	95.8	1.26			
SERPINB9	82.4	0.23	**PTMA**	87.9	0.65	**BST2**	95.9	1.27			
AMPH	82.4	0.23	**RARRES3**	88.1	0.67	**CX3CL1**	95.9	1.27			
SCO2	82.6	0.25	**MARCKS**	88.2	0.67	**STARD5**	96.2	1.29			
ADM	82.7	0.25	**ETV6**	88.2	0.68	**TRIM34**	96.4	1.30			
PHF15	82.8	0.26	**IL1RN**	88.3	0.68	**TAGAP**	96.9	1.35			
GPX2	82.9	0.26	**PPM1K**	88.8	0.72	**ARNTL**	97.1	1.36			
MX1	83.1	0.28	**FKBP5**	89.0	0.74	**UNC93B1**	97.4	1.38			
IFI27	83.2	0.29	**GBP1**	89.1	0.74	**CLEC4D**	97.5	1.39			
AXUD1	83.3	0.30	**MCL1**	89.2	0.75	**C6orf150**	97.5	1.39			
ANKFY1	83.4	0.30	**FFAR2**	89.2	0.75	**SAMD4A**	97.9	1.42			
CLEC2B	83.4	0.31	**IL1R**	89.3	0.76	**SLC16A1**	98.0	1.43			
IFIT3	83.8	0.33	**AKT3**	89.4	0.77	**FAM134B**	98.3	1.45			
IFI16	83.8	0.34	**AHNAK2**	89.5	0.77	**HLA-F**	98.7	1.48			
FNDC3B	84.0	0.35	**NPAS2**	89.7	0.79	**FER1L3**	98.7	1.48			
LMO2	84.1	0.36	**RNF19B**	89.7	0.79	**IFITM3**	98.7	1.48			
Gluc	84.1	0.36	**HEG1**	89.7	0.79	**PRKD2**	98.9	1.50			
PSCD1	84.2	0.37	**CCNA1**	89.8	0.80	**PSMB9**	98.9	1.50			
LIPA	84.3	0.37	**C1S**	90.0	0.81	**OPTN**	99.6	1.55			
PRIC285	84.4	0.38	**NMI**	90.3	0.83	**ADAR**	99.7	1.56			
IDO1	84.4	0.39	**DDX3X**	90.4	0.84	**TNFAIP3**	99.8	1.57			
TIMP1	84.5	0.39	**CLEC4E**	90.5	0.85	**Fluc**	100.0	1.58			
IFIT2	84.5	0.39	**ODC1**	90.7	0.87	**ABLIM3**	100.3	1.61			
RGS1	84.6	0.40	**JAK2**	91.0	0.89	**STAT2**	101.2	1.68			
ATF3	84.6	0.40	**PSMB8**	91.1	0.90	**ARHGEF3**	101.4	1.69			
HERC6	84.9	0.42	**ERLIN1**	91.4	0.92	**MICB**	101.7	1.72			
GCA	84.9	0.42	**GJA4**	91.5	0.93	**RBCK1**	102.5	1.78			
PIM3	85.0	0.43	**GBP3**	91.5	0.93	**OGFR**	102.6	1.79			
SAMHD1	85.1	0.43	**IL15**	92.2	0.98	**ELF1**	103.7	1.87			
PNPT1	85.3	0.45	**RIPK2**	92.2	0.98	**CRY1**	103.9	1.88			
SLC25A30	85.6	0.48	**ULK4**	92.3	0.99	**DNAPTP6**	104.1	1.90			
IFI6	85.8	0.49	**IL15RA**	92.6	1.02	**TRAFD1**	104.4	1.92			
CD38	85.8	0.49	**CD274**	92.7	1.02	**FAM46A**	104.7	1.95			
SPSB1	85.9	0.50	**PLSCR1**	92.7	1.02	**TRIM25**	104.9	1.96			
STAT1	86.0	0.51	**MASTL**	92.9	1.03	**GALNT2**	106.1	2.05			
TMEM140	86.4	0.53	**C9orf91**	93.0	1.04	**CD163**	106.4	2.08			
ZNF385B	86.4	0.54	**TXNIP**	93.2	1.06	**LEPR**	108.2	2.22			
APOBEC3A	86.5	0.55	**RTP4**	93.2	1.06	**B4GALT5**	109.6	2.32			
TCF7L2	86.6	0.55	**ACSL1**	93.5	1.08						
TAP1	86.6	0.55	**KIAA0082**	93.5	1.08						
FCGR1A	86.6	0.55	**C4orf32**	93.5	1.08						

Supplementary Table 3. Large scale ISG screen: HCV in Huh-7.5 cells at 72 h (page 1 of 2)

Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score
IRF1	27.8	-7.08	**IFI30**	85.5	-0.83	**ARNTL**	89.5	-0.39	**MCOLN2**	92.8	-0.03
IFIH1	42.1	-5.53	**TNFAIP6**	85.5	-0.82	**NPAS2**	89.6	-0.39	**CLEC4E**	92.8	-0.03
DDX58	43.1	-5.43	**SIRPA**	85.5	-0.82	**PDK1**	89.6	-0.38	**EHD4**	93.0	-0.01
IRF7	65.3	-3.02	**SERPINE1**	85.5	-0.82	**THOC4**	89.7	-0.38	**PCTK2**	93.0	-0.01
CCL2	65.8	-2.96	**PSCD1**	85.7	-0.81	**MCL1**	89.7	-0.38	**STEAP4**	93.1	-0.01
IRF2	65.9	-2.95	**SSBP3**	85.7	-0.80	**SLFN5**	89.7	-0.37	**ACSL1**	93.1	0.00
MKX	72.1	-2.28	**CCL19**	85.9	-0.78	**BAG1**	89.7	-0.37	**KIAA1618**	93.1	0.00
JUNB	72.2	-2.27	**ALDH1A1**	85.9	-0.78	**CCNA1**	89.7	-0.37	**PMAIP1**	93.2	0.01
TNFRSF10A	73.0	-2.18	**IL28RA**	86.2	-0.75	**APOBEC3A**	89.9	-0.35	**IFI6**	93.3	0.02
HSH2D	73.3	-2.15	**IMPA2**	86.3	-0.74	**TMEM49**	89.9	-0.34	**IFIT1**	93.3	0.02
SERPINB9	74.3	-2.04	**ADAMDEC1**	86.4	-0.73	**TCF7L2**	90.0	-0.34	**CLEC4D**	93.4	0.03
MTHFD2L	76.4	-1.81	**TAP1**	86.4	-0.73	**AKT3**	90.0	-0.34	**KIAA0082**	93.4	0.03
NCF1	78.0	-1.64	**CRP**	86.5	-0.72	**PPM1K**	90.0	-0.33	**PUS1**	93.4	0.03
C5orf39	78.0	-1.64	**PFKFB3**	86.7	-0.69	**BLVRA**	90.1	-0.33	**HERC6**	93.4	0.03
MT1H	79.0	-1.54	**MAP3K14**	86.9	-0.68	**GBP3**	90.3	-0.31	**HLA-G**	93.5	0.04
MT1F	79.3	-1.50	**UNC84B**	86.9	-0.67	**C1S**	90.3	-0.30	**GLRX**	93.8	0.07
MT1M	79.6	-1.46	**CXCL9**	86.9	-0.67	**FNDC3B**	90.4	-0.30	**G6PC**	93.8	0.07
C5orf27	79.7	-1.45	**LGMN**	87.0	-0.67	**MYD88**	90.5	-0.28	**NDC80**	93.8	0.08
C22orf28	80.2	-1.40	**FAM70A**	87.0	-0.66	**DYNLT1**	90.6	-0.28	**P2RY6**	93.9	0.09
FLJ23556	80.3	-1.40	**ZBP1**	87.1	-0.66	**IFI35**	90.6	-0.27	**FUT4**	94.1	0.11
NT5C3	80.4	-1.38	**CASP7**	87.1	-0.65	**GBP2**	90.8	-0.26	**TAGAP**	94.2	0.11
ARG2	80.4	-1.38	**MT1G**	87.1	-0.65	**IGFBP2**	90.8	-0.25	**SOCS2**	94.2	0.12
SLC1A1	80.9	-1.33	**SLC25A30**	87.3	-0.63	**AGPAT9**	90.9	-0.24	**IL15**	94.2	0.12
IRF9	81.0	-1.31	**ZNF385B**	87.4	-0.62	**JAK2**	91.1	-0.22	**TMEM51**	94.4	0.14
TLR3	81.1	-1.30	**CLEC2B**	87.4	-0.62	**GCH1**	91.1	-0.22	**TAP2**	94.6	0.16
UPP2	81.4	-1.27	**CCL8**	87.4	-0.62	**HPSE**	91.1	-0.22	**TREX1**	94.6	0.16
IFIT5	81.5	-1.26	**TIMP1**	87.5	-0.61	**PNRC1**	91.2	-0.21	**NAPA**	94.6	0.16
LGALS3	81.6	-1.25	**HLA-C**	87.5	-0.61	**BATF2**	91.3	-0.20	**CD274**	94.8	0.18
FNDC4	81.7	-1.24	**IFIT2**	87.6	-0.60	**AHNAK2**	91.3	-0.20	**TRIM34**	94.9	0.19
CEBPD	81.7	-1.24	**RASSF4**	88.0	-0.56	**B2M**	91.3	-0.20	**CCL4**	94.9	0.19
CCND3	82.0	-1.20	**Gluc**	88.0	-0.55	**CCL5**	91.4	-0.19	**TRIM14**	94.9	0.19
PBEF1	82.1	-1.19	**GZMB**	88.1	-0.54	**SAT3**	91.4	-0.19	**PPM1K**	94.9	0.20
MAX	82.9	-1.10	**C15orf48**	88.2	-0.54	**PDGFRL**	91.5	-0.17	**HK2**	95.0	0.20
PI4K2B	83.5	-1.04	**TYMP**	88.2	-0.53	**USP18**	91.6	-0.17	**IFITM2**	95.0	0.20
NRN1	83.6	-1.03	**ATP10D**	88.3	-0.52	**FBXO6**	91.6	-0.17	**C4orf33**	95.0	0.20
GK	83.8	-1.01	**TNFSF10**	88.4	-0.52	**IFNGR1**	91.6	-0.17	**TNFSF13B**	95.0	0.20
HLA-E	84.4	-0.95	**SLC15A3**	88.4	-0.51	**DEFB1**	91.7	-0.15	**FLJ39739**	95.1	0.21
MAB21L2	84.4	-0.94	**AIM2**	88.4	-0.51	**PTMA**	91.7	-0.15	**ETV6**	95.1	0.22
PNPT1	84.5	-0.93	**STAP1**	88.5	-0.50	**BCL2L14**	91.8	-0.14	**CXCL11**	95.2	0.23
HES4	84.5	-0.93	**CREB3L3**	88.6	-0.49	**GBP4**	91.9	-0.14	**MARCKS**	95.2	0.23
NMI	84.7	-0.91	**IFITM3**	88.7	-0.48	**CCDC109B**	92.0	-0.13	**ANGPTL1**	95.2	0.23
LIPA	84.8	-0.91	**RARRES3**	88.7	-0.47	**MT1X**	92.1	-0.11	**IFI44**	95.2	0.23
GTPBP2	85.0	-0.88	**IL1R**	88.8	-0.47	**CMAH**	92.2	-0.10	**ERLIN1**	95.3	0.24
STAT1	85.0	-0.88	**GCA**	88.8	-0.47	**VAMP5**	92.4	-0.08	**PRAME**	95.5	0.25
LRG1	85.1	-0.87	**APOL2**	88.8	-0.47	**C6orf150**	92.4	-0.08	**GTPBP1**	95.6	0.27
DDIT4	85.2	-0.86	**IL1RN**	89.0	-0.44	**DUSP5**	92.6	-0.06	**NCOA3**	95.7	0.28
LAP3	85.2	-0.85	**MAFB**	89.0	-0.44	**TBX3**	92.6	-0.05	**IFI44L**	95.8	0.29
NOD2	85.3	-0.85	**CYP1B1**	89.1	-0.44	**FER1L3**	92.7	-0.04	**IFI27**	95.8	0.29
GAK	85.3	-0.85	**ADFP**	89.2	-0.43	**C2orf31**	92.8	-0.04	**TRIM38**	95.9	0.30
ADM	85.3	-0.85	**MX1**	89.3	-0.42	**C10orf10**	92.8	-0.04	**WHDC1**	96.0	0.31
SLC25A28	85.4	-0.83	**IL6ST**	89.3	-0.41	**ATF3**	92.8	-0.03	**VEGFC**	96.0	0.31

Supplementary Table 3. Large scale ISG screen: HCV in Huh-7.5 cells at 72 h (page 2 of 2)

	Percent			Percent			Percent			Percent	
Gene	Infected	Z score	Gene	Infected	Z score	Gene	Infected	Z score	Gene	Infected	Z score
CRY1	96.0	0.31	**TRIM5**	99.0	0.64	**CD74**	101.6	0.92			
CXCL10	96.1	0.32	**ARHGEF3**	99.2	0.66	**SOCS1**	101.7	0.93			
AQP9	96.1	0.32	**DTX3L**	99.2	0.66	**C4orf32**	101.8	0.94			
EPSTI1	96.3	0.34	**TFEC**	99.3	0.67	**NFIL3**	101.8	0.94			
PADI2	96.4	0.36	**SAMD4A**	99.4	0.68	**TNFAIP3**	101.8	0.94			
FAM125B	96.5	0.36	**RBM25**	99.4	0.68	**AMPH**	101.8	0.94			
PRIC285	96.5	0.37	**OGFR**	99.5	0.69	**ULK4**	101.9	0.95			
CCDC92	96.5	0.37	**TRAFD1**	99.5	0.69	**PHF15**	102.1	0.97			
PXK	96.5	0.37	**SAA1**	99.7	0.71	**MAP3K5**	102.3	0.99			
GJA4	96.6	0.38	**DDX3X**	99.7	0.71	**SCO2**	102.4	1.01			
LINCR	96.6	0.38	**HESX1**	99.7	0.72	**CD9**	102.5	1.01			
SECTM1	96.6	0.38	**MAFF**	99.8	0.72	**BUB1**	102.6	1.03			
ISG15	96.7	0.39	**CDKN1A**	99.8	0.73	**DHX58**	102.7	1.04			
EIF3L	96.8	0.40	**EXT1**	99.9	0.73	**LMO2**	102.7	1.04			
DCP1A	96.8	0.40	**MASTL**	100.0	0.74	**CD38**	102.8	1.05			
UNC93B1	96.9	0.41	**GBP1**	100.0	0.74	**FAM134B**	102.8	1.05			
IL15RA	96.9	0.41	**DNAPTP6**	100.0	0.74	**SP110**	102.8	1.05			
XAF1	97.0	0.42	**Fluc**	100.0	0.75	**BCL3**	102.9	1.06			
UBE2L6	97.0	0.42	**IFIT3**	100.0	0.75	**ADAR**	102.9	1.06			
LY6E	97.1	0.43	**GEM**	100.1	0.75	**PSMB8**	102.9	1.06			
HLA-F	97.2	0.44	**SLC16A1**	100.1	0.75	**AXUD1**	103.0	1.07			
CFB	97.4	0.47	**ETV7**	100.1	0.76	**PSMB9**	103.8	1.15			
ODC1	97.4	0.47	**ABLIM3**	100.2	0.76	**SAMHD1**	103.8	1.15			
RBCK1	97.5	0.47	**TRIM21**	100.2	0.77	**ANKFY1**	103.8	1.16			
ANKRD22	97.5	0.47	**PARP12**	100.3	0.78	**TRIM25**	103.8	1.16			
PMM2	97.5	0.48	**BTN3A3**	100.3	0.78	**TMEM140**	103.9	1.17			
CX3CL1	97.6	0.48	**FFAR2**	100.3	0.78	**ZNF313**	104.0	1.18			
KIAA0040	97.6	0.49	**CD80**	100.4	0.79	**GBP5**	104.1	1.19			
S100A8	97.7	0.49	**STARD5**	100.4	0.79	**TLK2**	104.2	1.20			
CPT1A	97.7	0.49	**SMAD3**	100.4	0.79	**IFITM3**	104.2	1.20			
IL17RB	97.8	0.51	**RNF19B**	100.5	0.79	**LAMP3**	104.2	1.20			
SERPING1	97.8	0.51	**HEG1**	100.5	0.80	**B4GALT5**	104.2	1.20			
GMPR	97.9	0.51	**ABTB2**	100.5	0.80	**FCGR1A**	104.3	1.21			
ENPP1	98.0	0.53	**NUP50**	100.6	0.81	**PHF11**	104.3	1.21			
MICB	98.0	0.53	**STAT2**	100.7	0.82	**CCR1**	104.4	1.22			
OASL	98.2	0.55	**CCDC75**	100.7	0.82	**GPX2**	104.5	1.24			
TDRD7	98.2	0.55	**EPAS1**	100.7	0.82	**CD163**	104.7	1.25			
THBD	98.2	0.55	**RIPK2**	100.8	0.83	**MX1**	104.8	1.27			
COMMD3	98.3	0.56	**LGALS9**	100.8	0.83	**FAM46A**	104.8	1.27			
CTCFL	98.3	0.56	**RPL22**	100.9	0.84	**CSDA**	105.4	1.33			
SPSB1	98.3	0.56	**IFI6**	100.9	0.84	**FAM46C**	105.5	1.34			
C9orf91	98.3	0.56	**MSR1**	100.9	0.85	**CHMP5**	105.6	1.35			
CES1	98.3	0.56	**GALNT2**	101.0	0.85	**PML**	105.7	1.36			
ELF1	98.4	0.57	**CD69**	101.0	0.85	**ISG20**	105.7	1.36			
OPTN	98.4	0.57	**IFI16**	101.1	0.86	**SPTLC2**	105.9	1.39			
APOL1	98.6	0.59	**PIM3**	101.2	0.87	**PLSCR1**	106.7	1.48			
RGS1	98.6	0.60	**SCARB2**	101.2	0.87	**RTP4**	108.0	1.61			
WARS	98.7	0.61	**RNASE4**	101.3	0.89	**IDO1**	108.1	1.62			
LEPR	98.8	0.61	**PRKD2**	101.4	0.90	**BST2**	108.9	1.71			
FKBP5	98.9	0.62	**SNN**	101.4	0.90						
OAS2	98.9	0.63	**TXNIP**	101.4	0.90						

Supplementary Table 4. Large scale ISG screen: HCV in Huh-7 cells at 48 h (page 1 of 2)

Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score
IRF1	36.1	-3.24	**PADI2**	75.2	-0.95	**PRIC285**	81.9	-0.56	**MASTL**	87.4	-0.24
IRF2	39.4	-3.05	**BCL2L14**	75.2	-0.95	**PLEKHA4**	81.9	-0.56	**FAM125B**	87.8	-0.22
SLC1A1	44.5	-2.75	**SAT3**	75.2	-0.95	**TIMP1**	82.3	-0.54	**FNDC3B**	87.8	-0.22
DDX58	49.2	-2.47	**TAP2**	75.2	-0.95	**PNPT1**	82.3	-0.54	**HPSE**	88.2	-0.19
MAP3K14	53.9	-2.20	**TLR3**	75.2	-0.95	**TYMP**	82.7	-0.52	**CCL19**	88.2	-0.19
IRF7	55.1	-2.13	**UNC84B**	75.6	-0.93	**THOC4**	82.7	-0.52	**RARRES3**	88.2	-0.19
TRIM14	58.3	-1.94	**BTN3A3**	75.6	-0.93	**CD69**	82.7	-0.52	**FBXO6**	88.2	-0.19
DDIT4	61.0	-1.78	**IFNGR1**	75.6	-0.93	**IFI30**	83.1	-0.49	**SLFN5**	88.2	-0.19
NT5C3	61.8	-1.74	**CTCFL**	76.0	-0.91	**SERPING1**	83.1	-0.49	**MCL1**	88.6	-0.17
SSBP3	63.8	-1.62	**PCTK2**	76.0	-0.91	**PUS1**	83.1	-0.49	**IFI6**	88.6	-0.17
IFIH1	64.6	-1.58	**BUB1**	76.0	-0.91	**SAMHD1**	83.1	-0.49	**IRF9**	89.0	-0.15
LGMN	66.1	-1.48	**LGALS3**	76.4	-0.88	**EXT1**	83.1	-0.49	**ACSL1**	89.0	-0.15
GBP2	66.5	-1.46	**CEBPD**	76.8	-0.86	**CFB**	83.1	-0.49	**MAX**	89.4	-0.12
ZBP1	67.3	-1.41	**IFIT5**	76.8	-0.86	**UBE2L6**	83.5	-0.47	**MICB**	89.4	-0.12
TREX1	67.7	-1.39	**PBEF1**	76.8	-0.86	**IL28RA**	83.5	-0.47	**DEFB1**	89.4	-0.12
SOCS2	67.7	-1.39	**BAG1**	77.2	-0.84	**IFI27**	83.5	-0.47	**FCGR1A**	89.4	-0.12
BLVRA	68.1	-1.37	**BATF2**	77.2	-0.84	**IFI6**	83.5	-0.47	**CD274**	89.4	-0.12
PPM1K	68.1	-1.37	**MS4A4A**	77.2	-0.84	**ENPP1**	83.5	-0.47	**GEM**	89.4	-0.12
PARP12	68.1	-1.37	**MAB21L2**	77.6	-0.82	**DDX3X**	83.5	-0.47	**RIPK2**	89.4	-0.12
IFI44L	68.1	-1.37	**FLJ23556**	77.6	-0.82	**APOL2**	83.9	-0.45	**SERPINB9**	90.2	-0.08
MT1H	68.9	-1.32	**MTHFD2L**	77.6	-0.82	**NMI**	83.9	-0.45	**HSH2D**	90.2	-0.08
FNDC4	68.9	-1.32	**PDK1**	77.6	-0.82	**HLA-F**	84.3	-0.42	**ANKRD22**	90.2	-0.08
NPAS2	68.9	-1.32	**LRG1**	78.0	-0.79	**B2M**	84.3	-0.42	**CXCL10**	90.6	-0.05
NOD2	69.3	-1.30	**GTPBP2**	78.0	-0.79	**CPT1A**	84.3	-0.42	**STAT1**	90.6	-0.05
MKX	69.3	-1.30	**ARG2**	78.0	-0.79	**STAP1**	84.6	-0.40	**CCL4**	90.6	-0.05
OASL	69.3	-1.30	**AKT3**	78.3	-0.77	**ATF3**	84.6	-0.40	**CLEC2B**	90.6	-0.05
MT1F	69.7	-1.28	**GTPBP1**	78.7	-0.75	**CRP**	84.6	-0.40	**TMEM49**	90.6	-0.05
ADM	70.1	-1.25	**PPM1K**	78.7	-0.75	**NCF1**	85.0	-0.38	**RNF19B**	90.6	-0.05
C5orf27	70.5	-1.23	**GZMB**	78.7	-0.75	**MX1**	85.0	-0.38	**CASP7**	90.6	-0.05
ZNF385B	70.5	-1.23	**NAPA**	78.7	-0.75	**UPP2**	85.0	-0.38	**WHDC1**	90.6	-0.05
PSCD1	70.5	-1.23	**CCL2**	79.1	-0.72	**AMPH**	85.0	-0.38	**DNAPTP6**	90.6	-0.05
DCP1A	70.5	-1.23	**SIRPA**	79.1	-0.72	**TAP1**	85.0	-0.38	**RASSF4**	90.9	-0.03
ALDH1A1	70.9	-1.21	**CLEC4E**	79.1	-0.72	**IL1RN**	85.4	-0.35	**IFIT2**	90.9	-0.03
LIPA	71.3	-1.18	**TDRD7**	79.1	-0.72	**CCL8**	85.4	-0.35	**IFI16**	90.9	-0.03
NDC80	71.3	-1.18	**ISG15**	79.5	-0.70	**DTX3L**	85.4	-0.35	**USP18**	91.3	-0.01
CYP1B1	71.7	-1.16	**C2orf31**	79.5	-0.70	**LINCR**	85.8	-0.33	**IL17RB**	91.3	-0.01
ADFP	71.7	-1.16	**COMMD3**	79.5	-0.70	**TAGAP**	85.8	-0.33	**CX3CL1**	91.3	-0.01
C22orf28	72.4	-1.11	**OAS2**	79.9	-0.68	**PHF15**	85.8	-0.33	**ZNF313**	91.3	-0.01
TNFSF10	72.4	-1.11	**CXCL11**	79.9	-0.68	**TNFRSF10A**	85.8	-0.33	**ANGPTL1**	91.7	0.01
S100A8	72.8	-1.09	**C10orf10**	80.3	-0.65	**GPX2**	86.2	-0.31	**CD9**	92.1	0.04
MT1M	73.2	-1.07	**C4orf33**	80.3	-0.65	**GCH1**	86.2	-0.31	**HERC6**	92.1	0.04
DYNLT1	73.2	-1.07	**PFKFB3**	80.7	-0.63	**ABTB2**	86.2	-0.31	**IFITM3**	92.5	0.06
PI4K2B	73.2	-1.07	**SAA1**	80.7	-0.63	**EPAS1**	86.2	-0.31	**RTP4**	92.5	0.06
DUSP5	73.2	-1.07	**SP110**	80.7	-0.63	**IFITM3**	86.6	-0.28	**Gluc**	92.9	0.08
SMAD3	73.6	-1.05	**PMAIP1**	81.1	-0.61	**G6PC**	86.6	-0.28	**PHF11**	92.9	0.08
MYD88	74.0	-1.02	**CCNA1**	81.1	-0.61	**TNFSF13B**	86.6	-0.28	**MT1X**	93.3	0.11
GK	74.0	-1.02	**LAP3**	81.5	-0.58	**GBP5**	86.6	-0.28	**SLC15A3**	93.3	0.11
KIAA1618	74.4	-1.00	**CDKN1A**	81.5	-0.58	**TRIM34**	86.6	-0.28	**RSAD2**	93.3	0.11
SLC25A28	74.8	-0.98	**SOCS1**	81.5	-0.58	**UNC93B1**	87.4	-0.24	**C15orf48**	93.7	0.13
CCDC109B	74.8	-0.98	**KIAA0040**	81.5	-0.58	**LY6E**	87.4	-0.24	**ULK4**	93.7	0.13
MT1G	75.2	-0.95	**HLA-E**	81.9	-0.56	**HK2**	87.4	-0.24	**DHX58**	94.1	0.15

Supplementary Table 4. Large scale ISG screen: HCV in Huh-7 cells at 48 h (page 2 of 2)

Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score
AXUD1	94.1	0.15	**CLEC4D**	99.2	0.45	**TRIM5**	107.1	0.91	**FFAR2**	135.0	2.55
FAM46C	94.1	0.15	**STEAP4**	99.2	0.45	**HEG1**	107.5	0.94	**SAMD4A**	135.4	2.57
FER1L3	94.1	0.15	**JUNB**	99.6	0.48	**XAF1**	107.5	0.94	**SPSB1**	137.8	2.71
TLR7	94.1	0.15	**IL6ST**	99.6	0.48	**CMAH**	107.9	0.96			
EIF3L	94.5	0.18	**Fluc**	100.0	0.50	**C6orf150**	107.9	0.96			
IMPA2	94.5	0.18	**PXK**	100.4	0.52	**IL15RA**	107.9	0.96			
KIAA0082	94.5	0.18	**ETV7**	100.4	0.52	**PMM2**	108.3	0.98			
CCL5	94.9	0.20	**HLA-C**	100.8	0.54	**WARS**	108.3	0.98			
PRAME	95.3	0.22	**ERLIN1**	100.8	0.54	**P2RY6**	108.3	0.98			
GBP4	95.3	0.22	**NUP50**	100.8	0.54	**MSR1**	109.8	1.07			
ABLIM3	95.3	0.22	**GBP1**	100.8	0.54	**LMO2**	111.0	1.14			
AHNAK2	95.3	0.22	**MX1**	100.8	0.54	**RBCK1**	111.0	1.14			
IGFBP2	95.7	0.25	**ATP10D**	101.6	0.59	**FAM134B**	111.0	1.14			
FUT4	95.7	0.25	**SLC16A1**	101.6	0.59	**TRIM25**	111.0	1.14			
IFITM2	95.7	0.25	**TRIM38**	101.6	0.59	**IDO1**	112.2	1.21			
THBD	95.7	0.25	**PLSCR1**	101.6	0.59	**TBX3**	112.6	1.24			
AGPAT9	95.7	0.25	**MAFB**	102.0	0.61	**BCL3**	113.4	1.28			
CCDC92	95.7	0.25	**GLRX**	102.0	0.61	**GALNT2**	113.8	1.31			
IL1R	95.7	0.25	**JAK2**	102.0	0.61	**SPTLC2**	113.8	1.31			
NFIL3	95.7	0.25	**IL15**	102.0	0.61	**APOL6**	113.8	1.31			
B4GALT5	95.7	0.25	**OPTN**	102.4	0.64	**APOBEC3A**	114.2	1.33			
HES4	96.1	0.27	**ANKFY1**	102.4	0.64	**FAM46A**	115.0	1.37			
CRY1	96.1	0.27	**EHD4**	102.8	0.66	**FKBP5**	115.7	1.42			
TNFAIP6	96.1	0.27	**HLA-G**	102.8	0.66	**CCDC75**	116.9	1.49			
VEGFC	96.5	0.29	**LEPR**	102.8	0.66	**GBP3**	117.3	1.51			
ADAMDEC1	96.5	0.29	**CD74**	103.1	0.68	**MAFF**	117.3	1.51			
ARNTL	96.5	0.29	**CREB3L3**	103.1	0.68	**GCA**	117.7	1.54			
GJA4	96.5	0.29	**C1S**	103.1	0.68	**C4orf32**	117.7	1.54			
CES1	96.9	0.31	**C9orf91**	103.1	0.68	**RAB27A**	117.7	1.54			
LAMP3	97.2	0.34	**PSMB8**	103.1	0.68	**PSMB9**	118.5	1.58			
CXCL9	97.6	0.36	**SCO2**	103.5	0.71	**STARD5**	118.9	1.60			
GAK	97.6	0.36	**SCARB2**	103.5	0.71	**CSDA**	119.3	1.63			
AQP9	97.6	0.36	**AIM2**	103.5	0.71	**CD163**	120.5	1.70			
PTMA	97.6	0.36	**EPSTI1**	103.5	0.71	**RNF24**	120.5	1.70			
SNN	97.6	0.36	**IFI44**	103.5	0.71	**TMEM140**	120.9	1.72			
MAP3K5	97.6	0.36	**CHMP5**	103.5	0.71	**TNFAIP3**	121.3	1.74			
SERPINE1	98.0	0.38	**NRN1**	103.9	0.73	**GMPR**	121.7	1.77			
VAMP5	98.0	0.38	**OGFR**	104.3	0.75	**ISG20**	122.8	1.84			
TMEM51	98.0	0.38	**LGALS9**	104.7	0.78	**CCR1**	123.6	1.88			
ARHGEF3	98.0	0.38	**IFIT3**	104.7	0.78	**IFITM1**	124.8	1.95			
PML	98.0	0.38	**RGS1**	105.1	0.80	**NCOA3**	125.2	1.97			
MX2	98.0	0.38	**CD80**	105.1	0.80	**TXNIP**	127.6	2.11			
ODC1	98.0	0.38	**FLJ39739**	105.5	0.82	**TRIM21**	127.6	2.11			
TCF7L2	98.0	0.38	**APOL1**	105.5	0.82	**ADAR**	128.7	2.18			
IFIT1	98.4	0.41	**TRAFD1**	105.5	0.82	**RPL22**	129.5	2.23			
MCOLN2	98.4	0.41	**PDGFRL**	106.3	0.87	**ETV6**	129.9	2.25			
RNASE4	98.4	0.41	**STAT2**	106.3	0.87	**TFEC**	129.9	2.25			
FAM70A	98.4	0.41	**PNRC1**	106.7	0.89	**MARCKS**	130.3	2.27			
IFI35	98.4	0.41	**PRKD2**	106.7	0.89	**CD38**	131.5	2.34			
SLC25A30	98.8	0.43	**HESX1**	106.7	0.89	**PIM3**	131.9	2.37			
SECTM1	99.2	0.45	**CCND3**	107.1	0.91	**C9orf19**	132.3	2.39			

Supplementary Table 5. Large scale ISG screen: YFV in *STAT1* $^{-/-}$ fibroblasts at 24 h (page 1 of 2)

Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score
HPSE	12.3	-4.56	**C4orf33**	76.2	-0.87	**GBP3**	83.9	-0.42	**PRKD2**	89.9	-0.08
IFI6	25.2	-3.81	**CCDC92**	76.4	-0.85	**PLSCR1**	83.9	-0.42	**IFIT2**	89.9	-0.08
TNFRSF10A	26.4	-3.74	**GZMB**	76.7	-0.84	**MX1**	83.9	-0.42	**FKBP5**	89.9	-0.08
IFI6	28.5	-3.62	**MT1M**	77.7	-0.78	**CCL8**	84.2	-0.41	**BAG1**	90.2	-0.06
IRF1	35.0	-3.25	**IFITM2**	78.0	-0.76	**DYNLT1**	84.2	-0.41	**PBEF1**	90.4	-0.05
C6orf150	43.5	-2.75	**PSMB9**	78.0	-0.76	**LMO2**	84.2	-0.41	**FAM125B**	90.4	-0.05
RTP4	45.6	-2.63	**LRG1**	79.3	-0.69	**UBE2L6**	84.5	-0.39	**TMEM140**	90.4	-0.05
IFITM3	51.0	-2.32	**TNFSF10**	79.3	-0.69	**C4orf32**	84.5	-0.39	**DDX58**	90.4	-0.05
IRF2	54.7	-2.11	**UPP2**	79.5	-0.68	**NRN1**	84.7	-0.38	**B2M**	90.7	-0.03
IFITM3	54.9	-2.10	**ETV7**	79.5	-0.68	**TNFSF13B**	84.7	-0.38	**IMPA2**	90.7	-0.03
IRF7	57.8	-1.93	**CD9**	79.5	-0.68	**RASSF4**	84.7	-0.38	**RGS1**	90.9	-0.02
TREX1	57.8	-1.93	**TXNIP**	79.5	-0.68	**FAM134B**	84.7	-0.38	**CHMP5**	90.9	-0.02
ZBP1	59.1	-1.86	**ANKRD22**	79.5	-0.68	**GBP1**	84.7	-0.38	**HLA-G**	91.2	0.00
TRIM25	64.2	-1.56	**PPM1K**	79.8	-0.66	**CRP**	85.0	-0.36	**FNDC4**	91.5	0.01
GCH1	65.3	-1.50	**HLA-E**	80.1	-0.65	**APOBEC3A**	85.2	-0.35	**TMEM49**	91.5	0.01
CCL5	66.6	-1.42	**CCDC109B**	80.1	-0.65	**CCL19**	85.5	-0.33	**MICB**	91.5	0.01
IL28RA	66.6	-1.42	**CREB3L3**	80.1	-0.65	**IFI30**	85.5	-0.33	**AIM2**	91.5	0.01
CYP1B1	67.6	-1.36	**CLEC2B**	80.1	-0.65	**GTPBP1**	85.8	-0.32	**STARD5**	91.5	0.01
CCL2	68.1	-1.33	**MKX**	80.1	-0.65	**MS4A4A**	86.0	-0.30	**MTHFD2L**	91.7	0.03
SOCS2	68.1	-1.33	**CLEC4D**	80.6	-0.62	**CEBPD**	86.3	-0.29	**PRIC285**	91.7	0.03
HSH2D	68.4	-1.32	**STAT1**	80.6	-0.62	**FBXO6**	86.3	-0.29	**PDK1**	92.0	0.04
C5orf39	68.4	-1.32	**COMMD3**	80.6	-0.62	**GTPBP2**	86.8	-0.26	**HLA-F**	92.2	0.06
GALNT2	68.4	-1.32	**TAGAP**	80.8	-0.60	**CD74**	86.8	-0.26	**TMEM51**	92.2	0.06
THOC4	68.7	-1.30	**SERPINB9**	81.1	-0.59	**SLC25A30**	86.8	-0.26	**IGFBP2**	92.5	0.07
SLC25A28	68.7	-1.30	**C1S**	81.3	-0.57	**IFI27**	87.3	-0.23	**FLJ39739**	92.5	0.07
ARG2	68.9	-1.29	**GK**	81.6	-0.56	**TNFAIP6**	87.3	-0.23	**MAFF**	92.5	0.07
PMAIP1	69.2	-1.27	**BCL2L14**	81.6	-0.56	**NMI**	87.3	-0.23	**ATP10D**	92.5	0.07
CXCL9	69.2	-1.27	**OPTN**	81.6	-0.56	**PHF11**	87.3	-0.23	**CD80**	92.5	0.07
IL1RN	70.7	-1.18	**ADFP**	81.9	-0.54	**MT1H**	87.6	-0.21	**PADI2**	92.7	0.09
ISG20	71.5	-1.14	**STAP1**	81.9	-0.54	**ISG15**	87.6	-0.21	**TRIM38**	92.7	0.09
P2RY6	71.8	-1.12	**MT1F**	82.1	-0.53	**GCA**	87.8	-0.20	**ARHGEF3**	92.7	0.09
TBX3	72.0	-1.11	**G6PC**	82.1	-0.53	**WARS**	87.8	-0.20	**PI4K2B**	93.0	0.10
SAMD4A	72.3	-1.09	**ZNF313**	82.4	-0.51	**CD69**	87.8	-0.20	**ABLIM3**	93.0	0.10
CXCL10	72.5	-1.08	**MT1G**	82.6	-0.50	**FAM70A**	88.1	-0.18	**JAK2**	93.0	0.10
FLJ23556	72.8	-1.06	**BATF2**	82.6	-0.50	**TAP1**	88.1	-0.18	**LIPA**	93.3	0.12
MAB21L2	72.8	-1.06	**GPX2**	82.6	-0.50	**PFKFB3**	88.3	-0.17	**LAP3**	93.3	0.12
C10orf10	72.8	-1.06	**CCNA1**	82.6	-0.50	**HK2**	88.3	-0.17	**GJA4**	93.3	0.12
EPSTI1	72.8	-1.06	**PSMB8**	82.6	-0.50	**SPTLC2**	88.3	-0.17	**MAX**	93.5	0.13
MYD88	73.1	-1.05	**AKT3**	82.6	-0.50	**SSBP3**	88.6	-0.15	**ALDH1A1**	93.5	0.13
TIMP1	73.3	-1.03	**LINCR**	82.9	-0.48	**DUSP5**	88.6	-0.15	**TRIM5**	93.5	0.13
C2orf31	73.3	-1.03	**LGMN**	82.9	-0.48	**APOL2**	88.9	-0.14	**CCND3**	93.8	0.15
ADM	73.6	-1.02	**BLVRA**	83.2	-0.47	**CDKN1A**	89.1	-0.12	**ULK4**	93.8	0.15
MARCKS	73.6	-1.02	**GLRX**	83.2	-0.47	**CES1**	89.4	-0.11	**OGFR**	94.0	0.16
LGALS3	74.4	-0.97	**ZNF385B**	83.4	-0.45	**IFIT1**	89.4	-0.11	**IL6ST**	94.3	0.18
EHD4	74.6	-0.96	**NCF1**	83.4	-0.45	**IL1R**	89.4	-0.11	**TNFAIP3**	94.6	0.19
HES4	74.9	-0.94	**MT1X**	83.4	-0.45	**C15orf48**	89.6	-0.09	**TLR3**	94.6	0.19
C5orf27	75.4	-0.91	**MAFB**	83.4	-0.45	**PTMA**	89.6	-0.09	**S100A8**	94.8	0.21
PPM1K	75.4	-0.91	**CCL4**	83.7	-0.44	**NT5C3**	89.6	-0.09	**CCDC75**	94.8	0.21
BCL3	75.4	-0.91	**FUT4**	83.7	-0.44	**EIF3L**	89.6	-0.09	**CSDA**	94.8	0.21
SLFN5	75.6	-0.90	**CXCL11**	83.7	-0.44	**GEM**	89.6	-0.09	**APOL6**	95.1	0.22
DEFB1	75.9	-0.88	**PIM3**	83.9	-0.42	**UNC84B**	89.9	-0.08	**LGALS9**	95.6	0.25

Supplementary Table 5. Large scale ISG screen: YFV in *STAT1* $^{-/-}$ fibroblasts at 24 h (page 2 of 2)

Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score
CMAH	95.6	0.25	**ENPP1**	101.8	0.61	**RAB27A**	110.6	1.12			
NPAS2	95.6	0.25	**HERC6**	101.8	0.61	**STEAP4**	110.9	1.13			
AGPAT9	95.9	0.27	**AHNAK2**	101.8	0.61	**ATF3**	110.9	1.13			
TRAFD1	95.9	0.27	**C9orf19**	101.8	0.61	**SLC16A1**	110.9	1.13			
HLA-C	96.1	0.28	**SAT3**	102.1	0.63	**CD163**	111.4	1.16			
SERPING1	96.1	0.28	**ANGPTL1**	102.1	0.63	**SOCS1**	111.7	1.18			
CX3CL1	96.1	0.28	**KIAA0040**	102.1	0.63	**KIAA0082**	111.7	1.18			
SAA1	96.4	0.30	**IRF9**	102.6	0.66	**RIPK2**	111.9	1.19			
RBCK1	96.4	0.30	**KIAA1618**	102.6	0.66	**IFI44L**	111.9	1.19			
NCOA3	96.4	0.30	**IFNGR1**	102.6	0.66	**TCF7L2**	112.7	1.24			
VEGFC	96.6	0.31	**TRIM34**	102.6	0.66	**SIRPA**	113.0	1.25			
HEG1	96.6	0.31	**PMM2**	103.4	0.70	**OAS2**	113.5	1.28			
ACSL1	96.6	0.31	**MCL1**	103.4	0.70	**CTCFL**	114.0	1.31			
PSCD1	97.2	0.34	**PLEKHA4**	103.6	0.72	**NUP50**	114.2	1.33			
OASL	97.4	0.36	**NOD2**	103.6	0.72	**PNPT1**	114.2	1.33			
TRIM21	97.4	0.36	**IFI44**	103.6	0.72	**TDRD7**	114.2	1.33			
JUNB	97.7	0.37	**IFIT3**	103.6	0.72	**DTX3L**	114.8	1.36			
RARRES3	97.7	0.37	**RPL22**	103.6	0.72	**CRY1**	115.0	1.37			
USP18	97.9	0.39	**SCARB2**	103.9	0.73	**MX2**	115.0	1.37			
STAT2	97.9	0.39	**LEPR**	103.9	0.73	**AXUD1**	115.5	1.40			
SECTM1	98.2	0.40	**DDIT4**	104.1	0.75	**TAP2**	116.1	1.43			
CLEC4E	98.2	0.40	**FAM46A**	104.1	0.75	**AQP9**	116.6	1.46			
IL15	98.2	0.40	**TRIM14**	104.7	0.78	**CFB**	116.6	1.46			
CPT1A	98.4	0.42	**CD274**	104.7	0.78	**BUB1**	116.6	1.46			
GBP5	98.4	0.42	**HESX1**	104.9	0.79	**IFI16**	116.8	1.48			
XAF1	98.4	0.42	**DNAPTP6**	104.9	0.79	**FAM46C**	117.1	1.49			
EPAS1	98.4	0.42	**ODC1**	104.9	0.79	**ARNTL**	117.6	1.52			
MAP3K14	98.4	0.42	**PML**	105.2	0.81	**PARP12**	119.9	1.66			
C9orf91	98.7	0.43	**UNC93B1**	105.7	0.84	**APOL1**	121.0	1.72			
PCTK2	99.0	0.45	**MX1**	106.0	0.85	**MAP3K5**	124.4	1.91			
IL15RA	99.0	0.45	**MASTL**	106.0	0.85	**SP110**	126.9	2.06			
NAPA	99.2	0.46	**SERPINE1**	106.2	0.87	**DDX3X**	127.7	2.11			
IFITM1	99.2	0.46	**DHX58**	106.2	0.87	**RNF19B**	128.8	2.17			
PUS1	99.5	0.48	**ADAMDEC1**	106.2	0.87	**FNDC3B**	132.9	2.41			
ERLIN1	99.5	0.48	**EXT1**	106.5	0.88	**MCOLN2**	137.8	2.69			
SLC15A3	99.7	0.49	**SCO2**	106.7	0.90	**LY6E**	179.8	5.11			
Gluc	100.0	0.51	**SNN**	107.0	0.91						
CCR1	100.0	0.51	**IDO1**	107.0	0.91						
NDC80	100.3	0.52	**PNRC1**	107.5	0.94						
WHDC1	100.3	0.52	**PDGFRL**	107.5	0.94						
RNASE4	100.5	0.54	**ABTB2**	107.5	0.94						
SPSB1	100.8	0.55	**DCP1A**	108.0	0.97						
BTN3A3	100.8	0.55	**FCGR1A**	108.3	0.99						
MSR1	101.0	0.57	**CASP7**	108.8	1.01						
GMPR	101.3	0.58	**CD38**	109.1	1.03						
GBP4	101.3	0.58	**IFI35**	109.3	1.04						
VAMP5	101.6	0.60	**AMPH**	109.8	1.07						
B4GALT5	101.6	0.60	**SAMHD1**	110.1	1.09						
FFAR2	101.6	0.60	**IL17RB**	110.4	1.10						
GBP2	101.8	0.61	**ANKFY1**	110.4	1.10						
PHF15	101.8	0.61	**GAK**	110.6	1.12						

Supplementary Table 6. Large scale ISG screen: YFV in Huh-7 cells at 24 h (page 1 of 2)

Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score
HPSE	42.5	-5.08	**FNDC4**	85.1	0.30	**CCL8**	90.7	1.01	**GBP4**	94.6	1.50
IRF1	55.7	-3.41	**CCND3**	85.3	0.33	**STAP1**	90.8	1.03	**RNASE4**	94.7	1.52
IRF2	62.3	-2.57	**TIMP1**	85.3	0.33	**FAM70A**	90.9	1.04	**CRP**	94.8	1.53
IFITM3	65.7	-2.15	**FCGR1A**	85.4	0.34	**NUP50**	90.9	1.04	**GALNT2**	94.9	1.55
ETV6	67.3	-1.95	**ZNF385B**	85.4	0.34	**C4orf33**	91.0	1.05	**CRY1**	95.1	1.56
TRIM14	74.2	-1.08	**MAP3K14**	85.6	0.37	**EHD4**	91.2	1.07	**NRN1**	95.3	1.59
IRF7	74.3	-1.06	**PRIC285**	85.8	0.39	**AKT3**	91.2	1.07	**RTP4**	95.4	1.61
IFITM3	76.1	-0.83	**PFKFB3**	85.8	0.39	**GPX2**	91.7	1.14	**UNC84B**	95.5	1.62
NT5C3	76.3	-0.80	**IL17RB**	86.0	0.42	**ISG15**	91.8	1.16	**HLA-C**	95.5	1.62
IFI6	76.7	-0.76	**ANGPTL1**	86.0	0.42	**MCL1**	91.8	1.16	**HLA-F**	95.5	1.62
PI4K2B	76.8	-0.74	**CCL2**	86.2	0.45	**ERLIN1**	92.0	1.17	**PNPT1**	95.5	1.62
PBEF1	76.8	-0.74	**PCTK2**	86.5	0.47	**RASSF4**	92.0	1.17	**LINCR**	95.6	1.63
C2orf31	77.2	-0.70	**SIRPA**	86.6	0.49	**GZMB**	92.0	1.17	**SLC15A3**	95.6	1.63
C5orf39	77.5	-0.66	**THOC4**	86.6	0.49	**MAX**	92.0	1.17	**GCA**	95.6	1.63
MYD88	78.2	-0.57	**BATF2**	86.9	0.53	**IFI6**	92.0	1.17	**CD69**	95.8	1.65
ADFP	79.0	-0.47	**LGMN**	86.9	0.53	**PADI2**	92.1	1.18	**GEM**	95.8	1.65
SSBP3	79.0	-0.47	**FAM46C**	86.9	0.53	**BCL2L14**	92.1	1.18	**FBXO6**	95.9	1.66
C22orf28	80.1	-0.32	**JUNB**	87.0	0.55	**CXCL11**	92.2	1.20	**PHF15**	95.9	1.66
LAP3	80.1	-0.32	**TREX1**	87.1	0.56	**HSH2D**	92.2	1.20	**TAP1**	96.0	1.68
ZBP1	80.4	-0.29	**PSCD1**	87.7	0.63	**PPM1K**	92.2	1.20	**RARRES3**	96.1	1.69
GK	80.5	-0.28	**NCF1**	87.8	0.65	**PMAIP1**	92.3	1.21	**RNF19B**	96.1	1.69
MT1F	80.9	-0.22	**SERPING1**	87.9	0.66	**OASL**	92.4	1.23	**TMEM51**	96.1	1.69
CCNA1	81.2	-0.19	**LGALS3**	87.9	0.66	**UPP2**	92.5	1.24	**SPTLC2**	96.1	1.69
CYP1B1	81.6	-0.14	**NDC80**	88.1	0.68	**CLEC2B**	92.7	1.26	**COMMD3**	96.1	1.69
ADM	81.6	-0.14	**LAMP3**	88.2	0.69	**CES1**	92.7	1.26	**PTMA**	96.3	1.72
GTPBP2	81.6	-0.14	**SERPINB9**	88.2	0.69	**GTPBP1**	92.7	1.26	**CCL5**	96.3	1.72
ALDH1A1	82.0	-0.09	**GBP2**	88.3	0.71	**CXCL10**	92.9	1.29	**CCDC92**	96.3	1.72
FLJ23556	82.5	-0.02	**PPM1K**	88.3	0.71	**OAS2**	92.9	1.29	**IFIT2**	96.4	1.74
PUS1	82.7	0.00	**DEFB1**	88.4	0.72	**LIPA**	92.9	1.29	**TNFAIP6**	96.4	1.74
FUT4	82.8	0.01	**G6PC**	88.6	0.75	**CCL19**	93.0	1.30	**IL15**	96.4	1.74
C5orf27	82.9	0.02	**PXK**	88.7	0.76	**SCARB2**	93.1	1.32	**APOBEC3A**	96.4	1.74
PDK1	82.9	0.02	**IL28RA**	89.0	0.79	**BTN3A3**	93.2	1.33	**SLFN5**	96.6	1.75
IFITM2	83.1	0.05	**MT1G**	89.0	0.79	**UBE2L6**	93.3	1.34	**SECTM1**	96.7	1.77
IFNGR1	83.4	0.08	**IFI30**	89.4	0.85	**SLC25A30**	93.3	1.34	**ADAMDEC1**	96.7	1.77
IFIT5	83.4	0.08	**HLA-E**	89.4	0.85	**B2M**	93.3	1.34	**OPTN**	96.7	1.77
LRG1	83.4	0.08	**ETV7**	89.6	0.87	**C10orf10**	93.3	1.34	**PRKD2**	96.8	1.78
MTHFD2L	83.5	0.10	**NFIL3**	89.6	0.87	**CLEC4E**	93.7	1.39	**CD274**	96.9	1.79
DDX58	83.7	0.13	**APOL2**	89.6	0.87	**SAA1**	93.7	1.39	**Fluc**	97.0	1.81
CEBPD	83.8	0.14	**EIF3L**	89.6	0.87	**GCH1**	93.7	1.39	**RIPK2**	97.0	1.81
SLC1A1	83.9	0.16	**TNFSF10**	89.6	0.87	**SOCS2**	93.7	1.39	**IFI27**	97.2	1.84
TYMP	84.0	0.17	**NAPA**	89.9	0.91	**CASP7**	93.7	1.39	**CCL4**	97.4	1.85
CCDC109B	84.2	0.18	**DDIT4**	89.9	0.91	**KIAA1618**	93.9	1.42	**CXCL9**	97.5	1.87
MT1M	84.5	0.23	**STAT1**	89.9	0.91	**C1S**	93.9	1.42	**CPT1A**	97.6	1.88
SMAD3	84.6	0.24	**NOD2**	89.9	0.91	**BAG1**	94.0	1.43	**NPAS2**	97.6	1.88
IDO1	84.7	0.26	**HK2**	89.9	0.91	**DCP1A**	94.0	1.43	**DUSP5**	97.7	1.90
IL1RN	84.7	0.26	**PRAME**	90.0	0.92	**VAMP5**	94.1	1.45	**AMPH**	97.8	1.91
ARG2	84.7	0.26	**S100A8**	90.0	0.92	**TAP2**	94.3	1.46	**CD9**	97.8	1.91
MT1H	84.8	0.27	**IFI44L**	90.1	0.94	**IRF9**	94.5	1.49	**C4orf32**	97.8	1.91
MAB21L2	85.0	0.29	**NMI**	90.2	0.95	**TNFSF13B**	94.5	1.49	**DDX3X**	97.8	1.91
SLC25A28	85.0	0.29	**DYNLT1**	90.4	0.97	**SNN**	94.5	1.49	**MASTL**	97.9	1.92
BLVRA	85.1	0.30	**MKX**	90.7	1.01	**STAT2**	94.6	1.50	**FAM134B**	98.0	1.94

Supplementary Table 6. Large scale ISG screen: YFV in Huh-7 cells at 24 h (page 2 of 2)

Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score
FAM125B	98.2	1.95	**LMO2**	100.7	2.27	**HLA-G**	103.8	2.66	**TXNIP**	110.1	3.46
ABTB2	98.2	1.95	**GLRX**	100.7	2.27	**IL15RA**	103.8	2.66	**STARD5**	110.2	3.48
SAT3	98.3	1.97	**EPAS1**	100.8	2.29	**PARP12**	103.8	2.66	**TRIM21**	111.1	3.59
GBP5	98.3	1.97	**TCF7L2**	100.8	2.29	**MX2**	103.8	2.66			
ULK4	98.4	1.98	**C6orf150**	100.9	2.30	**ANKFY1**	103.9	2.68			
GAK	98.5	2.00	**CMAH**	100.9	2.30	**CDKN1A**	104.0	2.69			
VEGFC	98.5	2.00	**MAFB**	101.0	2.32	**ATF3**	104.1	2.71			
EPSTI1	98.5	2.00	**ODC1**	101.0	2.32	**ELF1**	104.1	2.71			
TRAFD1	98.5	2.00	**DHX58**	101.1	2.33	**IGFBP2**	104.2	2.72			
CLEC4D	98.6	2.01	**CREB3L3**	101.1	2.33	**TFEC**	104.4	2.74			
C15orf48	98.6	2.01	**MS4A4A**	101.1	2.33	**PML**	104.5	2.75			
WHDC1	98.6	2.01	**PHF11**	101.4	2.36	**FAM46A**	104.6	2.77			
GBP1	98.6	2.01	**ZNF313**	101.4	2.36	**NCOA3**	104.6	2.77			
DTX3L	98.6	2.01	**MCOLN2**	101.6	2.39	**IFIT1**	104.7	2.78			
FER1L3	98.6	2.01	**IL1R**	101.7	2.40	**BUB1**	104.7	2.78			
SAMHD1	98.7	2.03	**KIAA0082**	101.7	2.40	**TLR3**	104.8	2.80			
SOCS1	98.7	2.03	**PSMB9**	101.8	2.42	**CX3CL1**	104.9	2.81			
MT1X	98.9	2.04	**CCR1**	101.8	2.42	**RPL22**	104.9	2.81			
CTCFL	98.9	2.04	**MAP3K5**	101.8	2.42	**MARCKS**	105.1	2.82			
KIAA0040	98.9	2.04	**PLSCR1**	101.8	2.42	**TLR7**	105.1	2.82			
IL6ST	98.9	2.04	**FNDC3B**	101.8	2.42	**BCL3**	105.2	2.84			
CFB	98.9	2.04	**RBCK1**	102.0	2.43	**ABLIM3**	105.2	2.84			
TAGAP	98.9	2.04	**TMEM49**	102.1	2.45	**C9orf19**	105.2	2.84			
AIM2	99.0	2.06	**ENPP1**	102.1	2.45	**PNRC1**	105.4	2.87			
HES4	99.1	2.07	**CD80**	102.1	2.45	**IFIT3**	105.5	2.88			
THBD	99.1	2.07	**MAFF**	102.2	2.46	**IMPA2**	105.9	2.93			
RGS1	99.1	2.07	**SP110**	102.3	2.48	**ISG20**	106.0	2.94			
ANKRD22	99.1	2.07	**AXUD1**	102.3	2.48	**LY6E**	106.1	2.95			
PMM2	99.2	2.08	**LGALS9**	102.4	2.49	**IFI35**	106.2	2.97			
PLEKHA4	99.2	2.08	**SERPINE1**	102.5	2.51	**TNFAIP3**	106.2	2.97			
CSDA	99.3	2.10	**USP18**	102.5	2.51	**IFITM1**	106.2	2.97			
HEG1	99.3	2.10	**SAMD4A**	102.6	2.52	**TRIM38**	106.3	2.98			
PSMB8	99.4	2.11	**AGPAT9**	102.6	2.52	**STEAP4**	106.4	3.00			
MX1	99.5	2.13	**WARS**	102.8	2.53	**TRIM5**	106.5	3.01			
ARHGEF3	99.7	2.14	**C9orf91**	102.8	2.53	**XAF1**	106.7	3.03			
APOL6	99.7	2.14	**AHNAK2**	102.8	2.53	**ADAR**	106.7	3.03			
AQP9	99.8	2.16	**CD163**	102.8	2.53	**CD38**	106.8	3.04			
ARNTL	99.8	2.16	**EXT1**	102.9	2.55	**TBX3**	107.0	3.07			
FLJ39739	99.9	2.17	**TRIM34**	102.9	2.55	**MICB**	107.1	3.09			
SCO2	99.9	2.17	**RSAD2**	103.1	2.58	**FKBP5**	107.2	3.10			
Gluc	100.0	2.19	**SLC16A1**	103.1	2.58	**GMPR**	107.5	3.13			
IFI16	100.0	2.19	**LEPR**	103.1	2.58	**PIM3**	107.6	3.14			
HERC6	100.1	2.20	**MX1**	103.1	2.58	**APOL1**	107.8	3.17			
JAK2	100.1	2.20	**GBP3**	103.2	2.59	**SPSB1**	108.6	3.27			
GJA4	100.2	2.21	**RNF24**	103.2	2.59	**DNAPTP6**	108.7	3.29			
TDRD7	100.2	2.21	**DDX60**	103.2	2.59	**B4GALT5**	108.8	3.30			
ACSL1	100.3	2.23	**TRIM25**	103.3	2.61	**FFAR2**	108.8	3.30			
HESX1	100.5	2.24	**CCDC75**	103.4	2.62	**PDGFRL**	109.5	3.39			
TMEM140	100.6	2.26	**CHMP5**	103.4	2.62	**P2RY6**	109.5	3.39			
CD74	100.7	2.27	**UNC93B1**	103.6	2.64	**RAB27A**	109.9	3.43			
ATP10D	100.7	2.27	**OGFR**	103.7	2.65	**IFI44**	110.0	3.45			

Supplementary Table 7. Large scale ISG screen: HIV in T cells at 48 h (page 1 of 2)

Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score
TNFRSF10A	20.5	-5.01	**PMAIP1**	91.8	-0.64	**MKX**	96.7	-0.34	**GBP1**	101.2	-0.07
IFITM3	21.5	-4.94	**IFI27**	92.0	-0.63	**GCA**	96.9	-0.33	**PLEKHA4**	101.4	-0.05
IRF1	45.3	-3.49	**STEAP4**	92.0	-0.63	**GBP2**	97.2	-0.31	**PPM1K**	101.4	-0.05
CD74	46.5	-3.41	**CCDC75**	92.3	-0.61	**MT1F**	97.2	-0.31	**LMO2**	101.4	-0.05
IFITM2	49.5	-3.23	**THBD**	92.3	-0.61	**MT1M**	97.4	-0.30	**AMPH**	101.6	-0.04
BCL3	49.8	-3.21	**GTPBP1**	92.3	-0.61	**HLA-F**	97.4	-0.30	**AIM2**	101.6	-0.04
MX2	64.3	-2.32	**C9orf91**	92.3	-0.61	**EPSTI1**	97.4	-0.30	**CCDC92**	101.6	-0.04
UNC84B	66.7	-2.18	**HESX1**	92.3	-0.61	**PSMB8**	97.7	-0.28	**C22orf28**	101.9	-0.02
MICB	68.3	-2.08	**VEGFC**	92.5	-0.60	**FLJ23556**	97.7	-0.28	**HEG1**	101.9	-0.02
ATF3	69.0	-2.04	**CXCL9**	93.0	-0.57	**FAM70A**	97.7	-0.28	**IMPA2**	101.9	-0.02
IRF7	70.4	-1.95	**C4orf33**	93.0	-0.57	**SPSB1**	97.9	-0.27	**ULK4**	101.9	-0.02
NFIL3	75.6	-1.63	**PI4K2B**	93.2	-0.56	**TRIM21**	97.9	-0.27	**TFEC**	102.1	-0.01
STARD5	77.5	-1.52	**BTN3A3**	93.2	-0.56	**STAT1**	97.9	-0.27	**TAGAP**	102.3	0.00
IRF2	78.6	-1.45	**UNC93B1**	93.2	-0.56	**PFKFB3**	98.1	-0.25	**ANKRD22**	102.3	0.00
SNN	79.3	-1.40	**CDKN1A**	93.4	-0.54	**TMEM49**	98.1	-0.25	**MS4A4A**	102.3	0.00
TREX1	81.5	-1.27	**NRN1**	93.7	-0.53	**NMI**	98.1	-0.25	**ARHGEF3**	102.6	0.02
MCOLN2	82.4	-1.22	**PRAME**	93.9	-0.51	**PSCD1**	98.1	-0.25	**IRF9**	102.6	0.02
CREB3L3	82.9	-1.19	**HSH2D**	93.9	-0.51	**GBP4**	98.4	-0.24	**SLC16A1**	102.6	0.02
TRIM14	83.1	-1.17	**MAFF**	94.1	-0.50	**OASL**	98.6	-0.23	**CLEC4D**	102.6	0.02
CD274	84.0	-1.12	**MT1H**	94.4	-0.48	**RNF19B**	98.6	-0.23	**TNFAIP6**	102.6	0.02
TRIM5	84.3	-1.10	**JUNB**	94.6	-0.47	**LRG1**	98.6	-0.23	**SERPINE1**	102.8	0.03
CLEC4E	84.3	-1.10	**SLC15A3**	94.8	-0.46	**PDK1**	98.8	-0.21	**GJA4**	102.8	0.03
SECTM1	84.5	-1.09	**SLC1A1**	95.1	-0.44	**IGFBP2**	98.8	-0.21	**MAB21L2**	102.8	0.03
IDO1	84.7	-1.07	**DHX58**	95.1	-0.44	**TAP2**	98.8	-0.21	**NT5C3**	103.1	0.05
SQLE	85.2	-1.04	**CMAH**	95.1	-0.44	**MT1G**	98.8	-0.21	**NCF1**	103.1	0.05
SOCS2	85.7	-1.02	**FLJ39739**	95.1	-0.44	**PTMA**	98.8	-0.21	**IL28RA**	103.1	0.05
SCARB2	87.3	-0.91	**PNRC1**	95.1	-0.44	**ISG20**	99.1	-0.20	**STAT3**	103.3	0.06
CD69	87.8	-0.89	**IFIT3**	95.3	-0.43	**SERPINB9**	99.1	-0.20	**XAF1**	103.3	0.06
TMEM51	87.8	-0.89	**RASSF4**	95.3	-0.43	**FNDC4**	99.1	-0.20	**MX1**	103.3	0.06
GEM	88.3	-0.86	**C5orf27**	95.3	-0.43	**RASGEF1B**	99.3	-0.18	**PRIC285**	103.3	0.06
AKT3	88.5	-0.84	**PBEF1**	95.5	-0.41	**PML**	99.8	-0.15	**IFI30**	103.8	0.09
AQP9	88.7	-0.83	**C15orf48**	95.5	-0.41	**TAP1**	99.8	-0.15	**RBCK1**	103.8	0.09
TYMP	89.0	-0.81	**GMPR**	95.5	-0.41	**NOD2**	99.8	-0.15	**DYNLT1**	104.0	0.11
HK2	89.0	-0.81	**CCND3**	95.5	-0.41	**PLSCR1**	99.8	-0.15	**CCL5**	104.0	0.11
GAK	89.2	-0.80	**BATF2**	95.5	-0.41	**IFNGR1**	100.0	-0.14	**TRIM38**	104.0	0.11
FAM125B	89.4	-0.79	**TNFSF13B**	95.5	-0.41	**PCTK2**	100.0	-0.14	**CRY1**	104.0	0.11
CD9	89.7	-0.77	**DEFB1**	95.8	-0.40	**PXK**	100.0	-0.14	**TIMP1**	104.0	0.11
PMM2	89.9	-0.76	**SERPING1**	96.0	-0.38	**Fluc**	100.0	-0.14	**CFB**	104.2	0.12
SSBP3	89.9	-0.76	**RPL22**	96.0	-0.38	**IFI35**	100.0	-0.14	**LIPA**	104.2	0.12
SAMD4A	89.9	-0.76	**IFIT2**	96.0	-0.38	**KIAA1618**	100.0	-0.14	**STAT2**	104.2	0.12
WHDC1	90.1	-0.74	**GZMB**	96.0	-0.38	**SMAD3**	100.2	-0.12	**ABTB2**	104.5	0.13
NUP50	90.4	-0.73	**GK**	96.2	-0.37	**UBE2L6**	100.5	-0.11	**IFIT1**	104.5	0.13
IFI44	90.4	-0.73	**EIF3L**	96.2	-0.37	**USP18**	100.5	-0.11	**EXT1**	104.7	0.15
RGS1	90.6	-0.71	**GTPBP2**	96.5	-0.35	**THOC4**	100.5	-0.11	**KIAA0040**	104.7	0.15
RAB27A	91.1	-0.68	**MTHFD2L**	96.5	-0.35	**MCL1**	100.7	-0.10	**C10orf10**	104.7	0.15
GCH1	91.1	-0.68	**IFIT5**	96.7	-0.34	**COMMD3**	100.7	-0.10	**APOL2**	104.7	0.15
ADFP	91.3	-0.67	**ARNTL**	96.7	-0.34	**PNPT1**	100.9	-0.08	**P2RY6**	104.9	0.16
CASP7	91.3	-0.67	**HES4**	96.7	-0.34	**BLVRA**	100.9	-0.08	**TNFAIP3**	104.9	0.16
ALDH1A1	91.5	-0.66	**ZNF313**	96.7	-0.34	**CEBPD**	100.9	-0.08	**CCL4**	105.2	0.18
LGALS9	91.5	-0.66	**UPP2**	96.7	-0.34	**FBXO6**	100.9	-0.08	**AGPAT9**	105.2	0.18
NAPA	91.5	-0.66	**BCL2L14**	96.7	-0.34	**ADM**	101.2	-0.07	**TBX3**	105.2	0.18

Supplementary Table 7. Large scale ISG screen: HIV in T cells at 48 h (page 2 of 2)

Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score
CHMP5	105.4	0.19	**S100A8**	111.3	0.55	**DDX3X**	122.5	1.24			
DUSP5	105.4	0.19	**PPM1K**	111.3	0.55	**SLFN5**	122.8	1.25			
ABLIM3	105.4	0.19	**ANGPTL1**	111.5	0.56	**WARS**	123.0	1.27			
PUS1	105.6	0.21	**TRIM34**	111.5	0.56	**AHNAK2**	123.7	1.31			
FCGR1A	105.6	0.21	**SAA1**	111.7	0.58	**EPAS1**	124.2	1.34			
HPSE	105.9	0.22	**LAP3**	112.0	0.59	**PABPC4**	126.1	1.46			
GBP5	105.9	0.22	**RSAD2**	112.0	0.59	**CCR1**	126.3	1.47			
MYD88	105.9	0.22	**TRAFD1**	112.4	0.62	**TRIM25**	127.2	1.53			
ZNF385B	105.9	0.22	**G6PC**	112.4	0.62	**CSDA**	128.2	1.58			
HLA-C	105.9	0.22	**ARG2**	112.7	0.64	**IL1R**	131.0	1.76			
CRP	105.9	0.22	**MAP3K5**	112.9	0.65	**IL6ST**	132.4	1.84			
IL17RB	106.1	0.23	**OPTN**	112.9	0.65	**ETV6**	132.6	1.86			
PIM3	106.1	0.23	**SLC25A30**	113.1	0.67	**ATP10D**	132.6	1.86			
STAP1	106.1	0.23	**BST2**	113.1	0.67	**GALNT2**	132.9	1.87			
ADAMDEC1	106.1	0.23	**APOL1**	113.4	0.68	**TMEM140**	133.1	1.89			
AXUD1	106.3	0.25	**ZBP1**	113.6	0.69	**ELF1**	133.6	1.92			
DDIT4	106.6	0.26	**RNASE4**	113.6	0.69	**MAFB**	133.8	1.93			
ENPP1	106.8	0.28	**SAMHD1**	113.8	0.71	**MASTL**	135.4	2.03			
HLA-G	106.8	0.28	**LAMP3**	114.1	0.72	**MSR1**	135.7	2.04			
RARRES3	106.8	0.28	**OAS1**	114.3	0.74	**IFI16**	137.3	2.15			
MARCKS	106.8	0.28	**FUT4**	114.3	0.74	**DNAPTP6**	139.2	2.26			
TNFSF10	106.8	0.28	**CYP1B1**	115.0	0.78	**TLR3**	144.6	2.59			
MAX	107.0	0.29	**KIAA0082**	115.0	0.78	**CD163**	148.6	2.83			
BAG1	107.3	0.31	**SOCS1**	115.3	0.79	**LEPR**	156.3	3.31			
C4orf32	107.5	0.32	**NDC80**	115.5	0.81	**ADAR**	162.9	3.71			
C9orf19	107.5	0.32	**DTX3L**	115.5	0.81						
CCDC109B	107.5	0.32	**FAM134B**	115.5	0.81						
PDGFRL	107.7	0.34	**C1S**	115.5	0.81						
IFI6	108.5	0.38	**GBP3**	115.5	0.81						
ERLIN1	108.7	0.39	**B4GALT5**	115.7	0.82						
SIRPA	108.9	0.41	**C2orf31**	116.0	0.84						
MT1X	109.2	0.42	**IL15RA**	116.0	0.84						
RNF24	109.2	0.42	**PADI2**	116.2	0.85						
CD38	109.4	0.44	**HLA-E**	116.4	0.87						
FKBP5	109.4	0.44	**SP110**	117.1	0.91						
IL15	109.4	0.44	**GPX2**	117.4	0.92						
LGALS3	109.4	0.44	**EHD4**	117.6	0.94						
IL1RN	109.6	0.45	**PHF15**	117.8	0.95						
CCNA1	109.6	0.45	**HERC6**	118.1	0.97						
CX3CL1	109.6	0.45	**NPAS2**	118.5	1.00						
OGFR	109.6	0.45	**PSMB9**	119.0	1.02						
CD80	109.6	0.45	**CPT1A**	119.0	1.02						
LINCR	109.9	0.46	**ISG15**	119.2	1.04						
SLC25A28	109.9	0.46	**ETV7**	119.2	1.04						
PHF11	109.9	0.46	**LY6E**	119.7	1.07						
C6orf150	110.1	0.48	**TXNIP**	120.7	1.13						
CTCFL	110.3	0.49	**OAS2**	120.9	1.14						
RTP4	110.3	0.49	**PARP12**	121.6	1.18						
LGMN	110.6	0.51	**ANKFY1**	121.6	1.18						
PRKD2	110.6	0.51	**FAM46A**	121.8	1.20						
CLEC2B	110.8	0.52	**RIPK2**	122.1	1.21						

Supplementary Table 8. Large scale ISG screen: WNV in *STAT1*$^{-/-}$ fibroblasts at 6 h (page 1 of 2)

Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score
IRF1	15.1	-4.60	**FBXO6**	80.2	-0.95	**IL17RB**	88.5	-0.49	**TRIM25**	93.9	-0.19
HPSE	20.3	-4.31	**ATF3**	80.2	-0.95	**STEAP4**	88.5	-0.49	**TREX1**	94.3	-0.17
UNC93B1	30.0	-3.76	**IFNGR1**	80.2	-0.95	**CCL19**	88.8	-0.48	**TRIM38**	94.3	-0.17
C6orf150	30.4	-3.74	**IFI27**	80.9	-0.92	**MICB**	88.8	-0.48	**ACSL1**	94.3	-0.17
DDX58	41.1	-3.14	**TRIM14**	80.9	-0.92	**B2M**	89.1	-0.46	**CXCL9**	94.6	-0.15
IFIH1	49.0	-2.70	**IFITM2**	81.6	-0.88	**FAM70A**	89.1	-0.46	**GTPBP1**	94.6	-0.15
IRF7	53.5	-2.45	**CCDC75**	81.6	-0.88	**RPL22**	89.1	-0.46	**GCA**	94.6	-0.15
PBEF1	58.3	-2.18	**LRG1**	81.9	-0.86	**GBP4**	89.1	-0.46	**GBP5**	94.6	-0.15
BCL2L14	59.0	-2.14	**TNFAIP6**	81.9	-0.86	**RNF24**	89.1	-0.46	**IFI6**	95.0	-0.13
PHF15	60.7	-2.05	**THBD**	81.9	-0.86	**HK2**	89.5	-0.44	**FCGR1A**	95.0	-0.13
SAA1	61.7	-1.99	**IMPA2**	82.3	-0.84	**DCP1A**	89.5	-0.44	**TCF7L2**	95.0	-0.13
GJA4	63.8	-1.88	**TRAFD1**	82.3	-0.84	**MKX**	89.8	-0.42	**GZMB**	95.3	-0.11
C5orf39	64.1	-1.86	**IFI44**	82.6	-0.82	**MCOLN2**	90.2	-0.40	**ANGPTL1**	95.3	-0.11
TNFSF13B	65.8	-1.76	**CHMP5**	82.6	-0.82	**PCTK2**	90.2	-0.40	**CXCL10**	95.7	-0.09
CCL8	67.2	-1.68	**TFEC**	82.6	-0.82	**XAF1**	90.2	-0.40	**WARS**	95.7	-0.09
PLSCR1	67.2	-1.68	**USP18**	83.0	-0.80	**CCL5**	90.5	-0.38	**PNPT1**	95.7	-0.09
CXCL11	67.9	-1.65	**NUP50**	83.0	-0.80	**TNFSF10**	90.5	-0.38	**SPTLC2**	96.0	-0.07
P2RY6	68.2	-1.63	**CD274**	83.3	-0.78	**ELF1**	90.5	-0.38	**OPTN**	96.0	-0.07
IFI16	68.2	-1.63	**NAPA**	83.7	-0.76	**NRN1**	90.9	-0.36	**SERPINE1**	96.7	-0.03
C15orf48	69.3	-1.57	**EPSTI1**	83.7	-0.76	**UPP2**	90.9	-0.36	**COMMD3**	96.7	-0.03
CD9	70.3	-1.51	**PML**	84.3	-0.72	**IFI44L**	90.9	-0.36	**IFIT2**	96.7	-0.03
MCL1	70.6	-1.49	**EPAS1**	84.3	-0.72	**DDX3X**	90.9	-0.36	**Fluc**	97.0	-0.01
PMAIP1	71.0	-1.47	**LGALS9**	84.7	-0.71	**PUS1**	91.2	-0.34	**ARNTL**	97.0	-0.01
EHD4	71.0	-1.47	**CPT1A**	84.7	-0.71	**FAM125B**	91.2	-0.34	**IFI35**	97.4	0.00
ABTB2	72.0	-1.41	**PDGFRL**	84.7	-0.71	**FUT4**	91.5	-0.32	**MTHFD2L**	97.4	0.00
IFITM3	72.3	-1.40	**GEM**	85.0	-0.69	**DEFB1**	91.5	-0.32	**MX1**	97.4	0.00
SAMD4A	73.0	-1.36	**KIAA0082**	85.0	-0.69	**CCDC109B**	91.5	-0.32	**FFAR2**	97.4	0.00
MAP3K14	73.4	-1.34	**GPX2**	85.4	-0.67	**PNRC1**	91.5	-0.32	**MS4A4A**	97.7	0.02
IFIT3	73.7	-1.32	**CCL4**	85.7	-0.65	**ALDH1A1**	91.5	-0.32	**C10orf10**	98.4	0.06
SLC15A3	74.1	-1.30	**SIRPA**	85.7	-0.65	**CSDA**	91.5	-0.32	**ADFP**	98.4	0.06
STARD5	74.1	-1.30	**SLFN5**	85.7	-0.65	**ISG20**	91.5	-0.32	**CLEC2B**	98.4	0.06
RARRES3	74.7	-1.26	**DTX3L**	85.7	-0.65	**BUB1**	91.5	-0.32	**BTN3A3**	98.4	0.06
IFITM3	75.4	-1.22	**CRP**	86.1	-0.63	**PSMB8**	91.9	-0.30	**Fluc**	98.4	0.06
TNFRSF10A	75.8	-1.20	**THOC4**	86.1	-0.63	**TBX3**	91.9	-0.30	**PFKFB3**	98.7	0.08
SCARB2	76.1	-1.18	**EXT1**	86.1	-0.63	**TLR3**	91.9	-0.30	**NOD2**	98.7	0.08
NDC80	76.8	-1.15	**LAMP3**	86.1	-0.63	**AQP9**	92.2	-0.28	**GBP3**	98.7	0.08
BLVRA	77.1	-1.13	**PSCD1**	86.1	-0.63	**GBP1**	92.2	-0.28	**MARCKS**	98.7	0.08
OASL	77.5	-1.11	**GALNT2**	86.4	-0.61	**NFIL3**	92.2	-0.28	**TMEM51**	99.1	0.10
BCL3	77.8	-1.09	**RSAD2**	86.7	-0.59	**JUNB**	92.9	-0.24	**CES1**	99.1	0.10
TMEM49	77.8	-1.09	**SLC25A28**	86.7	-0.59	**SECTM1**	92.9	-0.24	**IFIT5**	99.4	0.12
KIAA1618	77.8	-1.09	**TDRD7**	86.7	-0.59	**SERPING1**	92.9	-0.24	**ZBP1**	99.4	0.12
TAP1	78.2	-1.07	**CTCFL**	87.1	-0.57	**MT1X**	93.3	-0.23	**ANKRD22**	99.4	0.12
AMPH	78.2	-1.07	**MSR1**	87.1	-0.57	**BATF2**	93.3	-0.23	**TRIM5**	99.4	0.12
ETV7	78.5	-1.05	**PSMB9**	87.4	-0.55	**PRIC285**	93.6	-0.21	**STAT2**	99.4	0.12
AGPAT9	78.5	-1.05	**AIM2**	87.4	-0.55	**DYNLT1**	93.6	-0.21	**MX2**	99.4	0.12
CLEC4E	78.9	-1.03	**RNASE4**	87.8	-0.53	**DHX58**	93.6	-0.21	**LIPA**	99.8	0.14
CMAH	79.2	-1.01	**MYD88**	88.1	-0.51	**TNFAIP3**	93.6	-0.21	**PI4K2B**	99.8	0.14
MAFB	79.2	-1.01	**RTP4**	88.1	-0.51	**PHF11**	93.6	-0.21	**PTMA**	99.8	0.14
IFIT1	79.2	-1.01	**SOCS2**	88.5	-0.49	**ARHGEF3**	93.6	-0.21	**C4orf33**	100.1	0.16
LGALS3	79.5	-0.99	**HLA-G**	88.5	-0.49	**ARG2**	93.9	-0.19	**HSH2D**	100.1	0.16
APOL1	79.5	-0.99	**SSBP3**	88.5	-0.49	**OGFR**	93.9	-0.19	**APOL2**	100.1	0.16

Supplementary Table 8. Large scale ISG screen: WNV in *STAT1*$^{-/-}$ fibroblasts at 6 h (page 2 of 2)

Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score
FAM134B	100.1	0.16	AXUD1	105.6	0.46	WHDC1	113.5	0.91	PXK	125.5	1.58
GTPBP2	100.5	0.18	ADAR	105.6	0.46	ZNF385B	113.8	0.93	PPM1K	125.5	1.58
C2orf31	100.5	0.18	PRAME	105.9	0.48	GAK	113.8	0.93	SAMHD1	125.5	1.58
RAB27A	100.5	0.18	VAMP5	106.3	0.50	TRIM34	113.8	0.93	PCTK3	125.8	1.60
SPSB1	100.8	0.20	IGFBP2	106.3	0.50	AHNAK2	113.8	0.93	ERLIN1	127.2	1.67
TAP2	100.8	0.20	HLA-C	106.3	0.50	C9orf19	113.8	0.93	TYMP	127.9	1.71
IFITM1	100.8	0.20	TXNIP	106.3	0.50	LAP3	114.2	0.94	MT1M	128.6	1.75
CYP1B1	101.1	0.22	FLJ39739	106.6	0.52	CD74	114.2	0.94	FNDC3B	128.9	1.77
GLRX	101.1	0.22	CDKN1A	107.0	0.54	RASSF4	114.2	0.94	ODC1	129.6	1.81
HEG1	101.1	0.22	G6PC	107.0	0.54	MT1G	114.5	0.96	FLT1	129.6	1.81
NMI	101.5	0.23	ZAP	107.0	0.54	MT1H	114.5	0.96	TIMP1	131.3	1.90
CX3CL1	101.5	0.23	NCF1	107.3	0.56	CREB3L3	114.5	0.96	MAP3K5	138.2	2.29
PLEKHA4	101.8	0.25	RNF19B	107.3	0.56	RBCK1	114.9	0.98	TAGAP	139.5	2.36
GCH1	101.8	0.25	ULK4	107.3	0.56	CCNA1	114.9	0.98	APOBEC3A	143.3	2.57
CCDC92	101.8	0.25	MX1	107.7	0.58	IL15RA	114.9	0.98	IDO1	144.7	2.65
ATP10D	101.8	0.25	C22orf28	108.0	0.60	HESX1	115.2	1.00			
CFB	102.2	0.27	FKBP5	108.0	0.60	FER1L3	115.2	1.00			
OAS2	102.2	0.27	ABLIM3	108.0	0.60	MASTL	115.5	1.02			
IRF2	102.2	0.27	PDK1	108.3	0.62	NPAS2	115.9	1.04			
UNC84B	102.5	0.29	ENPP1	108.3	0.62	B4GALT5	115.9	1.04			
HERC6	102.5	0.29	CCR1	108.3	0.62	ZNF313	116.2	1.06			
IL6ST	102.5	0.29	SAT3	108.7	0.64	LEPR	116.2	1.06			
APOL6	102.5	0.29	S100A8	109.0	0.66	NCOA3	116.2	1.06			
Gluc	102.9	0.31	PPM1K	109.0	0.66	GBP2	116.6	1.08			
CLEC4D	102.9	0.31	CCL2	109.4	0.68	FAM46C	116.6	1.08			
DNAPTP6	102.9	0.31	NOS2A	109.4	0.68	NT5C3	117.3	1.12			
ETV6	103.2	0.33	LGMN	109.7	0.69	AKT3	117.3	1.12			
RGS1	103.2	0.33	GMPR	109.7	0.69	MAX	117.9	1.16			
SNN	103.5	0.35	PMM2	110.1	0.71	SCO2	117.9	1.16			
JAK2	103.5	0.35	SLC1A1	110.1	0.71	TLK2	118.3	1.17			
CASP7	103.5	0.35	PRKD2	110.4	0.73	ANKFY1	118.6	1.19			
HES4	103.9	0.37	LY6E	110.4	0.73	BST2	118.6	1.19			
SERPINB9	103.9	0.37	SLC16A1	110.4	0.73	MT1F	119.3	1.23			
SLC25A30	103.9	0.37	C1S	110.7	0.75	HLA-F	119.7	1.25			
PARP12	103.9	0.37	TRIM21	111.1	0.77	IL15	119.7	1.25			
CD38	103.9	0.37	HLA-E	111.4	0.79	CD69	120.0	1.27			
PADI2	104.2	0.39	LMO2	111.4	0.79	BAG1	120.7	1.31			
EIF3L	104.2	0.39	PIM3	111.4	0.79	FAM46A	121.7	1.37			
UBE2L6	104.6	0.41	GK	111.4	0.79	STAT1	122.1	1.39			
Fluc	104.6	0.41	OAS1	111.4	0.79	SMAD3	122.7	1.42			
STAP1	104.6	0.41	ISG15	111.8	0.81	MAFF	123.1	1.44			
IL1R	104.6	0.41	KIAA0040	111.8	0.81	RIPK2	123.1	1.44			
RBM25	104.6	0.41	C9orf91	111.8	0.81	DDX60	123.4	1.46			
LINCR	104.9	0.43	SP110	112.1	0.83	CEBPD	123.8	1.48			
MAB21L2	104.9	0.43	CD80	112.1	0.83	C5orf27	123.8	1.48			
CRY1	104.9	0.43	TMEM140	112.1	0.83	CCND3	124.1	1.50			
VEGFC	105.3	0.45	ADM	112.5	0.85	IL1RN	124.1	1.50			
C4orf32	105.3	0.45	IL28RA	112.8	0.87	DDIT4	124.1	1.50			
IFI6	105.6	0.46	CD163	113.1	0.89	IRF9	124.1	1.50			
SOCS1	105.6	0.46	FLJ23556	113.5	0.91	DUSP5	124.5	1.52			
ADAMDEC1	105.6	0.46	FNDC4	113.5	0.91	IFI30	125.1	1.56			

Supplementary Table 9. Large scale ISG screen: VEEV in *STAT1*$^{-/-}$ fibroblasts at 5.5 h (page 1 of 2)

Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score
IRF1	10.0	-4.23	**MAFB**	69.1	-0.99	**OAS2**	75.3	-0.64	**CHMP5**	82.4	-0.26
UNC93B1	18.9	-3.74	**SLFN5**	69.4	-0.97	**CCL19**	75.6	-0.63	**CASP7**	83.0	-0.23
C6orf150	31.8	-3.03	**PCTK2**	69.4	-0.97	**NUP50**	75.9	-0.61	**FAM70A**	83.2	-0.21
DDX58	32.1	-3.02	**IFI44**	69.6	-0.96	**ANGPTL1**	75.9	-0.61	**IL17RB**	83.2	-0.21
HPSE	37.8	-2.70	**ADAMDEC1**	69.6	-0.96	**APOL6**	75.9	-0.61	**GTPBP2**	83.5	-0.20
PBEF1	43.5	-2.39	**MAP3K14**	69.6	-0.96	**TFEC**	76.2	-0.60	**TRIM5**	83.5	-0.20
IFIH1	51.1	-1.97	**TMEM51**	69.9	-0.94	**CLEC4D**	76.7	-0.57	**TCF7L2**	83.5	-0.20
PHF15	51.4	-1.96	**FNDC4**	70.2	-0.93	**MT1H**	77.0	-0.56	**CCL2**	84.0	-0.17
IRF7	52.8	-1.88	**ALDH1A1**	70.2	-0.93	**SLC1A1**	77.0	-0.56	**TRIM14**	84.0	-0.17
IL15RA	52.8	-1.88	**UPP2**	70.4	-0.91	**PLSCR1**	77.2	-0.54	**PSMB8**	84.0	-0.17
SAMD4A	54.1	-1.81	**SNN**	70.4	-0.91	**MARCKS**	77.5	-0.53	**C15orf48**	84.9	-0.12
ABTB2	54.1	-1.81	**XAF1**	70.4	-0.91	**MYD88**	77.8	-0.51	**CCDC92**	84.9	-0.12
P2RY6	54.1	-1.81	**USP18**	70.7	-0.90	**NAPA**	77.8	-0.51	**PMAIP1**	85.4	-0.09
SIRPA	54.7	-1.78	**BLVRA**	71.0	-0.88	**TAP1**	78.3	-0.48	**LIPA**	85.7	-0.08
AQP9	54.7	-1.78	**TDRD7**	71.0	-0.88	**STARD5**	78.3	-0.48	**MCOLN2**	85.7	-0.08
SCARB2	57.4	-1.63	**TNFAIP6**	71.3	-0.87	**RPL22**	78.3	-0.48	**RGS1**	85.7	-0.08
EPSTI1	58.5	-1.57	**TREX1**	71.3	-0.87	**IFITM1**	78.3	-0.48	**ANKRD22**	85.9	-0.06
LGALS9	58.7	-1.55	**CMAH**	71.5	-0.85	**PSCD1**	78.6	-0.47	**EIF3L**	86.2	-0.05
ACSL1	58.7	-1.55	**ABLIM3**	71.5	-0.85	**B2M**	78.9	-0.45	**NPAS2**	86.2	-0.05
TLR3	59.0	-1.54	**MSR1**	71.5	-0.85	**IGFBP2**	78.9	-0.45	**UBE2L6**	86.5	-0.03
APOL1	59.3	-1.52	**DEFB1**	71.8	-0.84	**SSBP3**	79.1	-0.44	**TAP2**	86.5	-0.03
IFIT2	59.6	-1.51	**RNASE4**	71.8	-0.84	**MAX**	79.4	-0.42	**UNC84B**	87.0	0.00
SECTM1	60.7	-1.45	**CXCL10**	72.3	-0.81	**FBXO6**	79.4	-0.42	**SERPING1**	87.0	0.00
PDGFRL	60.7	-1.45	**EXT1**	72.3	-0.81	**CTCFL**	79.4	-0.42	**PSMB9**	87.3	0.01
GJA4	60.7	-1.45	**CD274**	72.3	-0.81	**NT5C3**	79.4	-0.42	**GK**	87.3	0.01
MCL1	60.9	-1.43	**SAT3**	72.6	-0.79	**FAM125B**	79.4	-0.42	**RSAD2**	87.3	0.01
CFB	61.2	-1.42	**VEGFC**	72.6	-0.79	**CD9**	79.7	-0.41	**KIAA0082**	87.3	0.01
AIM2	61.5	-1.40	**CLEC2B**	72.6	-0.79	**CCL8**	80.0	-0.39	**MICB**	87.3	0.01
NRN1	61.7	-1.39	**IFI30**	72.9	-0.78	**ATP10D**	80.0	-0.39	**HSH2D**	87.6	0.03
IMPA2	62.3	-1.36	**C9orf91**	72.9	-0.78	**IFNGR1**	80.2	-0.38	**HES4**	87.9	0.04
IFI27	62.6	-1.35	**DTX3L**	73.2	-0.76	**TRIM34**	80.2	-0.38	**HLA-F**	87.9	0.04
C4orf32	62.8	-1.33	**PTMA**	73.7	-0.73	**CXCL11**	80.5	-0.36	**CSDA**	87.9	0.04
EPAS1	63.6	-1.29	**SLC15A3**	73.7	-0.73	**C10orf10**	80.5	-0.36	**TRIM38**	88.1	0.06
EHD4	64.2	-1.26	**SAA1**	74.0	-0.72	**WARS**	80.5	-0.36	**PHF11**	88.1	0.06
GLRX	64.5	-1.24	**IFI35**	74.0	-0.72	**IFIT5**	80.8	-0.35	**BST2**	88.1	0.06
ENPP1	65.3	-1.20	**WHDC1**	74.0	-0.72	**OGFR**	80.8	-0.35	**THOC4**	88.4	0.07
HLA-G	65.8	-1.17	**STEAP4**	74.0	-0.72	**C22orf28**	81.1	-0.33	**HK2**	88.7	0.09
AMPH	65.8	-1.17	**KIAA1618**	74.0	-0.72	**BCL2L14**	81.1	-0.33	**C5orf39**	88.7	0.09
RARRES3	66.4	-1.14	**NOD2**	74.3	-0.70	**AHNAK2**	81.1	-0.33	**CES1**	88.9	0.10
CCL5	66.6	-1.12	**PNRC1**	74.3	-0.70	**CXCL9**	81.3	-0.32	**PARP12**	88.9	0.10
THBD	66.6	-1.12	**BCL3**	74.3	-0.70	**SERPINE1**	81.3	-0.32	**TNFAIP3**	88.9	0.10
CCL4	66.9	-1.11	**BAG1**	74.3	-0.70	**NDC80**	81.3	-0.32	**TRAFD1**	88.9	0.10
SLC16A1	66.9	-1.11	**TBX3**	74.3	-0.70	**FNDC3B**	81.3	-0.32	**NOS2A**	88.9	0.10
AGPAT9	67.2	-1.09	**TMEM49**	74.3	-0.70	**GCH1**	81.6	-0.30	**PLEKHA4**	89.2	0.12
IFIT1	67.2	-1.09	**MT1X**	74.5	-0.69	**PML**	81.9	-0.29	**GBP5**	89.2	0.12
CLEC4E	67.5	-1.08	**NCF1**	74.5	-0.69	**OAS1**	81.9	-0.29	**MTHFD2L**	89.5	0.13
CX3CL1	67.7	-1.06	**ANKFY1**	74.5	-0.69	**BATF2**	82.1	-0.27	**GPX2**	89.5	0.13
IFI16	68.0	-1.05	**IFITM3**	74.8	-0.67	**PUS1**	82.1	-0.27	**TNFSF13B**	89.5	0.13
OASL	68.5	-1.02	**PI4K2B**	74.8	-0.67	**CD163**	82.1	-0.27	**ZNF313**	89.5	0.13
VAMP5	68.8	-1.00	**IFITM3**	75.3	-0.64	**CCDC75**	82.4	-0.26	**CRP**	90.0	0.16
DHX58	68.8	-1.00	**APOL2**	75.3	-0.64	**ODC1**	82.4	-0.26	**DDX3X**	90.0	0.16

Supplementary Table 9. Large scale ISG screen: VEEV in *STAT1*$^{-/-}$ fibroblasts at 5.5 h (page 2 of 2)

Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score
MX2	90.0	0.16	**RAB27A**	96.6	0.52	**PDK1**	104.2	0.94	**PPM1K**	116.7	1.62
RASSF4	90.3	0.18	**OPTN**	96.6	0.52	**MS4A4A**	104.2	0.94	**ERLIN1**	116.7	1.62
MKX	90.3	0.18	**JUNB**	96.8	0.53	**ETV7**	104.4	0.95	**ADM**	117.2	1.65
GEM	90.3	0.18	**GZMB**	96.8	0.53	**ZBP1**	104.4	0.95	**LEPR**	118.3	1.71
TNFSF10	90.6	0.19	**IRF2**	96.8	0.53	**DCP1A**	104.7	0.97	**SOCS1**	118.6	1.73
G6PC	90.6	0.19	**HERC6**	97.4	0.56	**TRIM21**	104.7	0.97	**PPM1K**	119.1	1.76
MASTL	90.8	0.21	**TAGAP**	97.4	0.56	**RTP4**	105.0	0.98	**TLK2**	120.2	1.82
CCND3	91.4	0.24	**ULK4**	97.6	0.58	**NCOA3**	105.8	1.03	**TIMP1**	121.0	1.86
SPSB1	91.4	0.24	**SP110**	97.9	0.59	**TRIM25**	106.1	1.04	**FKBP5**	121.3	1.88
GMPR	91.7	0.25	**PRKD2**	97.9	0.59	**LINCR**	106.6	1.07	**SMAD3**	122.7	1.95
CD80	91.7	0.25	**LAMP3**	97.9	0.59	**CCDC109B**	106.6	1.07	**IDO1**	123.2	1.98
SLC25A28	91.9	0.26	**BUB1**	97.9	0.59	**ATF3**	106.6	1.07	**IL1RN**	125.4	2.10
STAT2	91.9	0.26	**GCA**	98.2	0.61	**FUT4**	106.9	1.08	**CCNA1**	125.7	2.11
CEBPD	92.2	0.28	**IL6ST**	98.2	0.61	**IL1R**	106.9	1.08	**DDX60**	129.5	2.32
AKT3	92.2	0.28	**HESX1**	98.5	0.62	**MT1G**	107.2	1.10	**APOBEC3A**	138.2	2.80
AXUD1	92.2	0.28	**CCR1**	98.5	0.62	**TXNIP**	107.2	1.10			
ADFP	92.5	0.29	**IRF9**	98.7	0.64	**SLC25A30**	107.4	1.11			
CPT1A	92.5	0.29	**DNAPTP6**	98.7	0.64	**C2orf31**	108.0	1.14			
MX1	92.5	0.29	**LRG1**	99.0	0.65	**CDKN1A**	108.0	1.14			
TMEM140	92.5	0.29	**BTN3A3**	99.0	0.65	**ARG2**	108.3	1.16			
SOCS2	92.7	0.31	**SPTLC2**	99.0	0.65	**FLT1**	108.3	1.16			
Fluc	92.7	0.31	**FAM134B**	99.3	0.67	**GALNT2**	108.5	1.17			
FFAR2	92.7	0.31	**ARNTL**	99.5	0.68	**HLA-E**	108.8	1.19			
IFITM2	93.0	0.32	**ELF1**	99.5	0.68	**IL15**	108.8	1.19			
PMM2	93.0	0.32	**DDIT4**	99.8	0.70	**ETV6**	109.1	1.20			
Fluc	93.3	0.34	**C1S**	99.8	0.70	**PXK**	109.1	1.20			
FCGR1A	93.3	0.34	**CD74**	100.1	0.71	**ADAR**	109.1	1.20			
GBP4	93.3	0.34	**MT1M**	100.4	0.73	**JAK2**	109.6	1.23			
B4GALT5	93.3	0.34	**C4orf33**	100.4	0.73	**C9orf19**	109.6	1.23			
LGALS3	93.6	0.35	**PIM3**	100.6	0.74	**IFI6**	109.9	1.25			
FLJ39739	93.6	0.35	**GBP2**	100.6	0.74	**SCO2**	110.7	1.29			
PRAME	93.6	0.35	**GAK**	100.9	0.76	**GBP1**	111.2	1.32			
ZAP	93.6	0.35	**Gluc**	101.2	0.77	**SAMHD1**	111.8	1.35			
NMI	93.8	0.37	**CD38**	101.2	0.77	**CREB3L3**	112.3	1.38			
PNPT1	93.8	0.37	**SERPINB9**	101.5	0.79	**MAP3K5**	113.1	1.43			
MAB21L2	94.1	0.38	**CD69**	101.7	0.80	**GBP3**	113.1	1.43			
FLJ23556	94.1	0.38	**DUSP5**	101.7	0.80	**HLA-C**	113.4	1.44			
IFI6	94.1	0.38	**C5orf27**	102.0	0.82	**MAFF**	113.4	1.44			
IFI44L	94.1	0.38	**CRY1**	102.0	0.82	**RIPK2**	113.7	1.46			
LAP3	94.7	0.41	**KIAA0040**	102.0	0.82	**Fluc**	114.0	1.47			
ISG20	94.7	0.41	**PFKFB3**	102.3	0.83	**TNFRSF10A**	114.5	1.50			
ARHGEF3	94.7	0.41	**LY6E**	102.3	0.83	**FAM46C**	114.5	1.50			
STAP1	94.9	0.43	**PADI2**	102.5	0.85	**ISG15**	115.0	1.53			
IFIT3	94.9	0.43	**HEG1**	102.5	0.85	**TYMP**	115.3	1.55			
LMO2	95.5	0.46	**MX1**	102.8	0.86	**IL28RA**	115.6	1.56			
DYNLT1	95.5	0.46	**S100A8**	103.1	0.88	**FAM46A**	115.6	1.56			
STAT1	95.5	0.46	**LGMN**	103.4	0.89	**ZNF385B**	115.9	1.58			
NFIL3	95.5	0.46	**RNF19B**	103.6	0.91	**GTPBP1**	115.9	1.58			
PRIC285	95.7	0.47	**RBM25**	103.6	0.91	**CYP1B1**	116.1	1.59			
COMMD3	96.0	0.49	**RNF24**	103.6	0.91	**PCTK3**	116.1	1.59			
RBCK1	96.6	0.52	**FER1L3**	103.9	0.92	**MT1F**	116.7	1.62			

Supplementary Table 10. Large scale ISG screen: CHIKV in *STAT1*$^{-/-}$ fibroblasts at 10 h (page 1 of 2)

Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score
IRF1	3.8	-4.20	**CCL2**	77.8	-0.83	**G6PC**	87.3	-0.40	**PML**	94.5	-0.07
UNC93B1	13.6	-3.75	**BLVRA**	78.4	-0.80	**PCTK2**	87.5	-0.38	**PRIC285**	94.8	-0.05
C6orf150	21.5	-3.40	**SPSB1**	78.4	-0.80	**SAA1**	87.8	-0.37	**IFI6**	94.8	-0.05
SLC25A28	28.5	-3.07	**FLJ39739**	78.4	-0.80	**PMM2**	88.1	-0.36	**NUP50**	94.8	-0.05
SLC15A3	28.8	-3.06	**RSAD2**	78.4	-0.80	**DDIT4**	88.3	-0.35	**TLR3**	94.8	-0.05
P2RY6	35.5	-2.75	**SCO2**	78.6	-0.79	**USP18**	88.3	-0.35	**TCF7L2**	95.3	-0.03
CDKN1A	38.2	-2.63	**STAP1**	79.7	-0.74	**CCL5**	88.3	-0.35	**FLJ23556**	95.6	-0.02
TNFRSF10A	39.3	-2.58	**B2M**	80.0	-0.73	**ANKRD22**	88.3	-0.35	**HEG1**	95.6	-0.02
IFIH1	43.4	-2.40	**RAB27A**	80.0	-0.73	**IFI6**	88.6	-0.34	**UBE2L6**	95.6	-0.02
EHD4	43.6	-2.38	**PI4K2B**	80.3	-0.72	**RARRES3**	88.9	-0.32	**ACSL1**	95.6	-0.02
C5orf39	49.3	-2.13	**CD74**	80.3	-0.72	**RIPK2**	89.1	-0.31	**MAB21L2**	95.9	0.00
IRF2	49.6	-2.11	**C15orf48**	80.5	-0.70	**CSDA**	89.4	-0.30	**BATF2**	95.9	0.00
IFITM3	52.0	-2.00	**PSMB9**	80.8	-0.69	**TAP2**	89.7	-0.29	**IFI44**	96.1	0.01
GJA4	53.9	-1.92	**AKT3**	81.1	-0.68	**TMEM49**	89.9	-0.27	**CASP7**	96.4	0.02
FAM134B	55.7	-1.83	**HLA-G**	81.1	-0.68	**KIAA1618**	89.9	-0.27	**SLFN5**	96.4	0.02
MAP3K14	55.7	-1.83	**CCL4**	81.1	-0.68	**C4orf32**	89.9	-0.27	**NAPA**	96.4	0.02
DDX58	56.6	-1.80	**TNFSF10**	81.3	-0.67	**RASSF4**	90.2	-0.26	**DDX3X**	96.4	0.02
IFITM1	56.8	-1.78	**THOC4**	81.6	-0.65	**BAG1**	90.8	-0.24	**GMPR**	96.7	0.03
TRIM14	57.4	-1.76	**HPSE**	81.6	-0.65	**GK**	91.0	-0.22	**FFAR2**	96.7	0.03
ZBP1	58.2	-1.72	**HES4**	82.1	-0.63	**APOL2**	91.3	-0.21	**Fluc**	96.9	0.05
IRF7	58.2	-1.72	**TNFAIP6**	82.1	-0.63	**C5orf27**	91.6	-0.20	**CXCL11**	96.9	0.05
SAMD4A	58.2	-1.72	**GCH1**	82.1	-0.63	**GPX2**	91.6	-0.20	**PNPT1**	97.2	0.06
STARD5	58.7	-1.70	**RNF19B**	82.4	-0.62	**PSMB8**	91.6	-0.20	**SNN**	97.2	0.06
NRN1	60.6	-1.61	**VAMP5**	82.7	-0.61	**XAF1**	91.8	-0.19	**IGFBP2**	97.5	0.07
BCL3	62.7	-1.51	**NCF1**	82.9	-0.59	**C10orf10**	92.1	-0.18	**TNFSF13B**	97.5	0.07
IFIT1	62.7	-1.51	**STEAP4**	83.2	-0.58	**ALDH1A1**	92.1	-0.18	**IL15RA**	97.5	0.07
MYD88	63.3	-1.49	**PHF15**	83.2	-0.58	**CCDC109B**	92.1	-0.18	**IMPA2**	97.8	0.08
SECTM1	63.3	-1.49	**EPAS1**	83.2	-0.58	**GZMB**	92.1	-0.18	**CEBPD**	97.8	0.08
IFITM3	64.6	-1.43	**AIM2**	84.0	-0.54	**PDGFRL**	92.1	-0.18	**TRIM38**	97.8	0.08
IFI27	65.7	-1.38	**SSBP3**	84.0	-0.54	**TFEC**	92.1	-0.18	**DYNLT1**	98.0	0.09
ARHGEF3	66.0	-1.37	**LGALS9**	84.0	-0.54	**CYP1B1**	92.4	-0.16	**EIF3L**	98.0	0.09
JUNB	66.2	-1.35	**CX3CL1**	84.0	-0.54	**MT1X**	92.4	-0.16	**IL1RN**	98.3	0.11
IFITM2	67.1	-1.32	**IFI35**	84.3	-0.53	**RPL22**	92.4	-0.16	**MKX**	98.3	0.11
PLSCR1	67.1	-1.32	**CXCL9**	84.3	-0.53	**MT1F**	92.6	-0.15	**CCDC75**	98.3	0.11
EPSTI1	67.3	-1.30	**CCL8**	84.6	-0.52	**HSH2D**	92.6	-0.15	**TRAFD1**	98.3	0.11
CD9	68.1	-1.27	**CCL19**	84.6	-0.52	**CXCL10**	92.6	-0.15	**PIM3**	98.6	0.12
ATF3	68.7	-1.24	**CCDC92**	84.8	-0.51	**ARNTL**	92.6	-0.15	**UNC84B**	98.6	0.12
TAP1	68.7	-1.24	**FNDC4**	85.1	-0.49	**GBP1**	92.9	-0.14	**PDK1**	98.6	0.12
ISG20	68.9	-1.23	**ADFP**	85.4	-0.48	**GLRX**	92.9	-0.14	**MX1**	98.6	0.12
FAM70A	69.5	-1.21	**DHX58**	85.4	-0.48	**CHMP5**	92.9	-0.14	**PPM1K**	98.8	0.13
PBEF1	69.7	-1.19	**CMAH**	85.4	-0.48	**IFIT3**	92.9	-0.14	**LGMN**	98.8	0.13
C9orf91	70.0	-1.18	**CRP**	85.6	-0.47	**MTHFD2L**	93.2	-0.13	**LINCR**	99.1	0.14
DEFB1	70.6	-1.16	**LGALS3**	86.2	-0.45	**LMO2**	93.2	-0.13	**IFIT2**	99.1	0.14
BST2	71.1	-1.13	**FBXO6**	86.4	-0.43	**ABTB2**	93.2	-0.13	**CLEC4E**	99.1	0.14
CES1	72.7	-1.06	**OASL**	86.4	-0.43	**HLA-F**	93.4	-0.11	**C2orf31**	99.4	0.16
MICB	74.3	-0.99	**ARG2**	86.7	-0.42	**TREX1**	93.4	-0.11	**Gluc**	99.4	0.16
AGPAT9	74.6	-0.97	**TBX3**	86.7	-0.42	**IFI44L**	93.7	-0.10	**MSR1**	99.6	0.17
PUS1	75.1	-0.95	**SIRPA**	87.0	-0.41	**SCARB2**	93.7	-0.10	**COMMD3**	99.9	0.18
SERPINE1	76.8	-0.88	**STAT2**	87.3	-0.40	**RNASE4**	94.0	-0.09	**MAFB**	99.9	0.18
BCL2L14	77.0	-0.86	**NOD2**	87.3	-0.40	**RGS1**	94.3	-0.08	**NDC80**	99.9	0.18
MCOLN2	77.6	-0.84	**PMAIP1**	87.3	-0.40	**MT1H**	94.5	-0.07	**ETV7**	100.2	0.19

Supplementary Table 10. Large scale ISG screen: CHIKV in *STAT1*$^{-/-}$ fibroblasts at 10 h (page 2 of 2)

Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score	Gene	Percent Infected	Z score
Fluc11/17	100.2	0.19	IL28RA	106.9	0.50	HERC6	114.2	0.83	ODC1	133.6	1.71
PLEKHA4	100.4	0.20	IFI30	106.9	0.50	AQP9	114.2	0.83	LY6E	134.6	1.76
ELF1	100.4	0.20	LRG1	106.9	0.50	SERPING1	114.2	0.83	OAS3	136.0	1.83
TRIM25	100.7	0.22	SOCS1	106.9	0.50	MX2	114.2	0.83	FAM46A	137.1	1.87
MCL1	100.7	0.22	IL17RB	106.9	0.50	RTP4	114.7	0.86	MARCKS	137.6	1.90
LIPA	101.0	0.23	ZNF313	106.9	0.50	CFB	115.0	0.87	GALNT2	138.2	1.92
GTPBP2	101.3	0.24	GEM	106.9	0.50	RBCK1	116.3	0.93	N4BP1	138.7	1.95
SERPINB9	101.3	0.24	MT1M	107.2	0.51	DNAPTP6	116.6	0.94	DDX60	140.6	2.03
TIMP1	101.8	0.27	PADI2	107.5	0.52	IL15	116.9	0.95	IDO1	147.3	2.34
GCA	101.8	0.27	NMI	107.5	0.52	WHDC1	117.1	0.97	ADAR	157.3	2.79
CD38	101.8	0.27	GBP5	107.5	0.52	FAM46C	117.1	0.97			
PNRC1	102.1	0.28	C9orf19	107.5	0.52	CCR1	117.1	0.97			
VEGFC	102.3	0.29	CD274	107.5	0.52	GBP3	117.7	0.99			
ISG15	102.3	0.29	KIAA0040	108.0	0.55	AHNAK2	117.7	0.99			
TMEM51	102.3	0.29	KIAA0082	108.0	0.55	FCGR1A	117.7	0.99			
ATP10D	102.3	0.29	IL6ST	108.3	0.56	NPAS2	118.0	1.00			
CPT1A	102.3	0.29	OPTN	108.3	0.56	CRY1	118.2	1.02			
OAS1	102.3	0.29	DTX3L	108.3	0.56	NT5C3	118.8	1.04			
ULK4	102.6	0.30	PPM1K	108.5	0.57	C1S	119.3	1.06			
LAP3	102.9	0.32	S100A8	108.5	0.57	SLC25A30	119.3	1.06			
GBP2	102.9	0.32	CCNA1	108.8	0.59	ANGPTL1	120.4	1.11			
C4orf33	102.9	0.32	GTPBP1	108.8	0.59	SLC16A1	120.4	1.11			
Fluc	102.9	0.32	MAFF	108.8	0.59	PTMA	120.6	1.13			
NOS2A	102.9	0.32	CTCFL	109.1	0.60	JAK2	121.2	1.15			
UPP2	103.1	0.33	HESX1	109.1	0.60	PABPC4	121.5	1.16			
MX1	103.1	0.33	ZNF385B	109.6	0.62	DCP1A	121.7	1.17			
PSCD1	103.1	0.33	PHF11	109.6	0.62	MASTL	121.7	1.17			
TRIM5	103.4	0.34	RNF24	109.9	0.63	EXT1	121.7	1.17			
APOL6	103.7	0.35	SOCS2	110.1	0.65	PRKD2	122.0	1.19			
SAT3	103.9	0.36	SP110	110.1	0.65	BUB1	123.1	1.24			
TMEM140	103.9	0.36	STAT1	110.4	0.66	SAMHD1	123.3	1.25			
OAS2	104.2	0.38	APOL3	110.4	0.66	HK2	123.6	1.26			
CD80	104.5	0.39	ADAMDEC1	110.7	0.67	AXUD1	123.6	1.26			
CLEC2B	104.8	0.40	WARS	110.7	0.67	CD163	125.0	1.32			
TNFAIP3	104.8	0.40	IFNGR1	111.0	0.68	TLR7	125.5	1.35			
CD69	104.8	0.40	TDRD7	111.0	0.68	ZNF295	125.8	1.36			
CLEC4D	105.0	0.41	HLA-E	111.2	0.70	BLZF1	126.0	1.37			
ENPP1	105.0	0.41	APOBEC3A	112.0	0.73	ANKFY1	126.0	1.37			
TRIM34	105.0	0.41	CREB3L3	112.3	0.75	SPTLC2	126.0	1.37			
ZAP	105.0	0.41	MS4A4A	112.3	0.75	FNDC3B	126.8	1.41			
ADM	105.3	0.43	FAM125B	112.3	0.75	TAGAP	127.1	1.42			
MAP3K5	105.6	0.44	ERLIN1	112.6	0.76	HLA-C	127.4	1.43			
APOL1	105.6	0.44	IL1R	112.8	0.77	BTN3A3	127.9	1.46			
GAK	105.8	0.45	AMPH	112.8	0.77	DUSP5	128.2	1.47			
TRIM21	105.8	0.45	IFI16	112.8	0.77	TXNIP	129.5	1.53			
FKBP5	106.1	0.46	PCTK3	113.4	0.79	B4GALT5	129.5	1.53			
ABLIM3	106.1	0.46	FER1L3	113.4	0.79	NCOA3	131.7	1.63			
MT1G	106.4	0.48	RBM25	113.4	0.79	FLT1	132.5	1.67			
OGFR	106.4	0.48	PFKFB3	113.6	0.81	TLK2	133.3	1.70			
GBP4	106.4	0.48	PARP12	113.6	0.81	LEPR	133.3	1.70			
MAX	106.9	0.50	CCND3	113.9	0.82	IRF9	133.6	1.71			

Supplementary Table 11: Gene ontology analysis of validated antiviral ISGs

Gene ID	Gene Symbol	Gene Name	Panther Molecular Function	Panther Biological Process	Chromosome
115004	C6orf150	chromosome 6 open reading frame 150	Molecular function unclassified	Biological process unclassified	6
972	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	Major histocompatibility complex antigen	MHCII-mediated immunity	5
54541	DDIT4	DNA-damage-inducible transcript 4	Molecular function unclassified	Biological process unclassified	10
23586	DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	Helicase;Hydrolase	Nucleoside, nucleotide and nucleic acid metabolism;Apoptosis	9
55601	DDX60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	Helicase;Hydrolase	Nucleoside, nucleotide and nucleic acid metabolism;Meiosis	4
10855	HPSE	heparanase	Glycosidase	Developmental processes	4
10964	IFI44L	interferon-induced protein 44-like	Molecular function unclassified	Biological process unclassified	1
2537	IFI6	interferon, alpha-inducible protein 6	Molecular function unclassified	Immunity and defense	1
64135	IFIH1	interferon induced with helicase C domain 1	Helicase;Hydrolase	Nucleoside, nucleotide and nucleic acid metabolism;Apoptosis	2
10581	IFITM2	interferon induced transmembrane protein 2 (1-8D)	Other miscellaneous function protein	Immunity and defense;Cell proliferation and differentiation	11
10410	IFITM3	interferon induced transmembrane protein 3 (1-8U)	Other miscellaneous function protein	Immunity and defense;Cell proliferation and differentiation	11
3659	IRF1	interferon regulatory factor 1	Other transcription factor;Nucleic acid binding	mRNA transcription regulation;Interferon-mediated immunity;Oncogenesis	5
3665	IRF7	interferon regulatory factor 7	Other transcription factor;Nucleic acid binding	mRNA transcription regulation;Interferon-mediated immunity;Oncogenesis	11
9020	MAP3K14	mitogen-activated protein kinase kinase kinase 14	Protein kinase;Transferase	Protein phosphorylation;Phosphate metabolism;Other metabolism	17
4343	MOV10	Mov10, Moloney leukemia virus 10, homolog (mouse)	Helicase;Hydrolase	Other nucleoside, nucleotide and nucleic acid metabolism;Translational regulation;Developmental processes	1
51338	MS4A4A	membrane-spanning 4-domains, subfamily A, member 4	Receptor	Biological process unclassified	11
4600	MX2	myxovirus (influenza virus) resistance 2 (mouse)	Microtubule family cytoskeletal protein;Small GTPase;Other hydrolase	Endocytosis;Transport;Cell structure	21
51251	NT5C3	5'-nucleotidase, cytosolic III	Esterase	Biological process unclassified	7
8638	OASL	2'-5'-oligoadenylate synthetase-like	Nucleic acid binding;Synthetase;Nucleotidyltransferase;Defense/immunity protein	Nucleoside, nucleotide and nucleic acid metabolism;Interferon-mediated immunity;Other metabolism	12
5031	P2RY6	pyrimidinergic receptor P2Y, G-protein coupled, 6	G-protein coupled receptor	G-protein mediated signaling	11
10135	PBEF1	pre-B-cell colony enhancing factor 1	Other cytokine	Ligand-mediated signaling;Immunity and defense	7
23338	PHF15	PHD finger protein 15	Other zinc finger transcription factor;Nucleic acid binding	mRNA transcription initiation;Oncogenesis	5
64108	RTP4	receptor (chemosensory) transporter protein 4	Molecular function unclassified	Biological process unclassified	3
51296	SLC15A3	solute carrier family 15, member 3	Other transporter	Small molecule transport;Other transport	11
81894	SLC25A28	solute carrier family 25, member 28	Mitochondrial carrier protein	Small molecule transport	10
23648	SSBP3	single stranded DNA binding protein 3	Single-stranded DNA-binding protein	mRNA transcription initiation;mRNA transcription regulation	1
11277	TREX1	three prime repair exonuclease 1	Molecular function unclassified	Biological process unclassified	3
25777	UNC84B	unc-84 homolog B (C. elegans)	Non-motor microtubule binding protein	Mitosis	22

Supplementary Table 11. Gene ontology analysis of validated antiviral ISGs. The PANTHER Classification System was used to classify validated antiviral ISGs by molecular function or biological process. Table shows GeneID, gene symbol, gene name, molecular function, biological process, and chromosome location.