

SUPPLEMENTARY MATERIAL

Supplementary Experimental Procedures

IFN α /STAT2 array design. Aiming at designing an oligonucleotide-based array containing a large repertoire of genes targeted by IFN- α/β , but not IFN- γ , we included: a) the few genes already confirmed by ChIP to be direct targets of STAT2 at the time this study was designed (*PKR* and *OAS1*); b) 32 genes identified by ChIP-chip on a DNA microarray of human chromosome 22 as bound by STAT2 and induced by IFN α but not IFN γ (18); c) genes whose expression is modulated in response to IFN- α/β in microarray-based expression profiling studies (a complete list of references is included in Table S2). The resulting > 300 genes were analyzed by bioinformatics tools (UCSC Genome Browser, Transfac and MacVector) to identify the presence of predicted ISRE binding sequences (consensus: AGTTTN3TTTCC, with >80% conservation) either in their promoter or in the first intron (i.e. a region spanning from -2500 to +1000 respect to tss). After this analysis, a total of 113 putative direct STAT2 target genes were selected for the array design. Selection criteria favored first those promoters confirmed by classical ChIP or ChIP-chip, and then, to those genes that were not ChIP validated we applied a ranking score based on the percentage of ISRE conservation, the position of the ISRE elements (core promoter preferred to upstream regions and upstream regions preferred to first intron), the number of ISRE sites (additional sites in the upstream/intron region besides the core promoter ISRE were preferred). Gene Ontology analysis of the 113 selected genes revealed that many putative IFN α direct target are involved in cellular activities well beyond innate immunity and inflammation with several genes belonging to the GO categories Transcription Regulation and Apoptosis/Proliferation (see Table S2). For each target gene, three different 50mer long oligos were designed (using PrimerQuest <http://eu.idtdna.com/Scitools/Applications/Primerquest/default.aspx>): the first one mapping in the upstream promoter (between -1500 and -500 from tss - Oligo 1), the second one in the proximal promoter (between -500 and +0 - Oligo 2) and the third downstream (between +0 and +1000 - Oligo 3) of the transcription start site (see Table S3). This design allows to have an internal control for every promoter represented. All oligos were spotted in triplicate and the resulting array was printed 4 times on the same slide for a total of 4068 spots. Moreover, 96 positive control and 120 negative control spots were added. Spotting sessions were performed at the Rome Oncogenomic Centre consortium using a MicroGrid II Plus Compact (Genomic Solutions), UltraGAPSTM Coated Slides (Corning) covalently bound coating of Gamma Amino Propyl Silane, Pronto!™ Universal Spotting Solution (Corning, #40025) and MWG 50mer oligonucleotides at 500ng/ μ l (M-Medical). After crosslinking of the oligos to the slide surface via exposure to UV energy (600mJ), the slides were maintained at room temperature in dry atmosphere.

Probe generation and microarray hybridization. Probe generation was done essentially as previously described in the Whole Genome Amplification Method (25) using 10ng of the Input and the whole ChIP samples. After checking that the specific enrichment on a control promoter was not affected by the amplification step (see Figure S3), ChIP and Input amplicons (1 μ g each) were labelled with amino-allyl dUTP by random priming using the BioPrime DNA labelling system (Invitrogen, #18094-011) and subsequently coupled to Post Labelling Reactive Dyes (GE Healthcare, #RPN5661). Microarrays were prehybridized for 2 h at 55°C with 100 μ l of Genisphere Hybridization Buffer (Labogen, #C600V600S25) supplemented with 100 ng/ μ l Salmon Sperm DNA (Sigma Aldrich). After washing, each array was cohybridized at 55°C for 16 hours with denaturated ChIP Cy5 and Input Cy3 labelled amplicons in a final volume of 110 μ l of hybridization buffer. Slides were washed twice in 0,1% SDS, 1X SSC (at 55°C and after at room temperature) for 5' shaking, once in 0.2X SSC for 5' at room temperature shaking and, finally, briefly rinsed in H₂O. Slides were spun dry, scanned and analyzed with a Genepix Professional 4200a Microarray Scanner (Axon Instruments). Each set of hybridizations was repeated three times with different ChIP materials.

SUPPLEMENTARY FIGURES

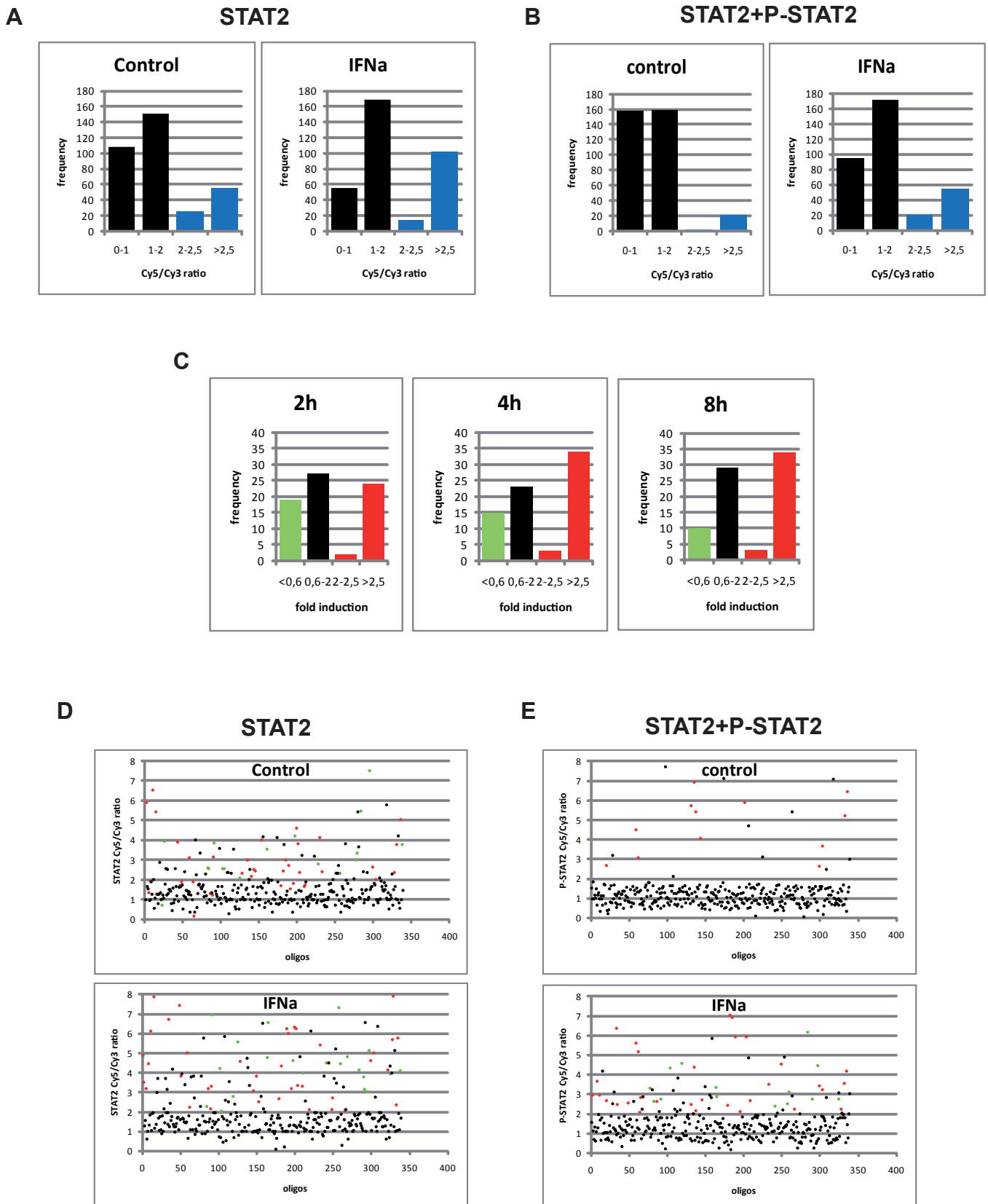
Fig. S1. *A.* and *B.* Histograms represent how the 339 oligonucleotides divide into Cy5/Cy3 ratio enrichment classes before (left panel) and after IFN α treatment (1000 IU/ml for 1h in Huh7 cells) (right panel). In *A*) STAT2 hybridization data, while in *B*) P-STAT2 hybridization data are shown. Blue column indicate enrichment classes scored as “positive” in our analysis.

C. Histogram representation of Huh7 cells gene expression results at 2, 4 and 8 hours of IFN α treatment (1000 IU/ml) for the 76 TLDA genes divided into classes as indicated. Green columns indicate repressed genes; red columns indicate activated genes.

D. and E. Scatter plots representing the Cy5/Cy3 ratio of each 339 oligonucleotide present in the array before (upper panel) and after (lower panel) IFN α treatment for STAT2 (D) or P-STAT2 (E) hybridization. Red and green spots indicate enriched oligonucleotides corresponding to activated and repressed genes, respectively.

Fig. S2. Position and nucleotide composition analysis of ISREs derived from activated and repressed IFN α /Stat2 direct target genes. Tables summarize the ISRE position and nucleotide composition of activated and repressed ISGs. The ISREs considered are all bound in vivo by Stat2 in Huh7 cells after 1h of IFN α treatment (1000 IU/ml) The sequence logos are a graphical representation of the ISREs nucleic acid multiple sequence alignment and were created through WebLogo 2.8.2 [<http://weblogo.berkeley.edu/>]

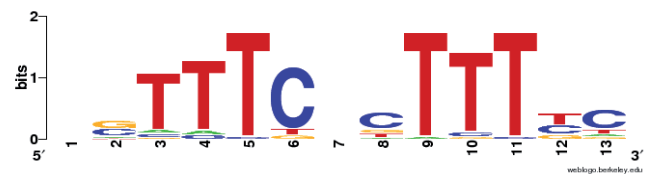
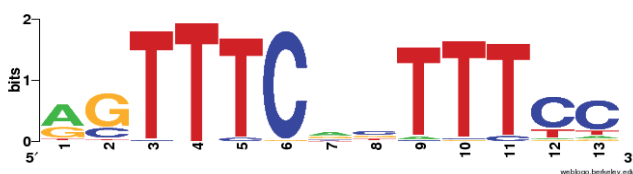
Fig. S3. Whole Genome Amplification quality controls. A. ChIP analysis of *ISG15* promoter in Huh7 cells untreated (K) or treated with IFN α 1000 IU/ml for 1h. B. Amplicons (left panel) and PCR analysis of *ISG15* promoter (right panel) after the Linear Amplification of chromatin derived from Input and STAT2 and NoAb ChIPs in Huh7 cells untreated or after IFN α stimulation. C. Amplicons (left panel) and PCR analysis of *Isg15* promoter (right panel) after the Linear Amplification of chromatin derived from Input and STAT2+P-STAT2 and STAT2+NoAb ChIPs in Huh7 cells untreated or after IFN α stimulation. See Experimental Procedures section for details. Primers used were: ISG15_for aggtgttccagggtgttg ISG15_rev GATGAGTTCGCTGCCTCTCA



ACTIVATED			
GENE NAME ^a	ISRE POSITION RESPECT TO PUTATIVE tss ^b	ISRE SEQUENCE	% ADHERENCE TO MATRICE ^c
A4GALT	-650	ggtttcattttt	83,6
ADAR	0	gctttcgtttct	83,6
ATF5	-370	tctttcccttcc	86,8
BAG3	-220	ggtttcggcttc	85,9
BST2	-170	agtttcagttcc	96,7
CAV1	-680	gatttgactttc	85,5
CXCL10	-200	ggtttcactttcc	97,5
CXCL11	-100	agtttcgttttg	85,9
EIF2AK2 (PKR)	-50	agtttcggtttcc	93,4
ISG15	-100	agtttcggtttcc	94,4
		agtttcattttcc	93,4
IFI6 (6-16)	-100	agtttcattttcc	97,4
GBP1	-100	agtttcatattac	80,1
GBP2	-130	ggtttctcttaa	85,4
HERC5	-150	agtttcctttcc	88,7
IFI16	+370 (tra tss e ATG)	gttttcactttc	95
IFI27	-90	agtttcggtttcc	88,3
IFI35	-370	agtttcactcttg	85
IFI44	-50	agtttcagtttcc	88,7
IFIT1 (ISG56)	-100	agtttcactttcc	97,5
IFIT2 (ISG54)	-80	agtttcactttcc	97,5
		agtttcactttcc	90,6
IFIT3 (RIG-G)	-100	ggtttcattttcc	95,6
IFIT5	-100	agtttcagtttct	85,4
		agtttctatttcc	88,3
IFITM1	-150	cgtttcagtttct	84,7
IFITM2	+190 (tra tss e ATG)	gtttcctctcct	83,1
ISGF3G	-70	agtttcagttctc	85,4
MNT	-330	ggttccgctttcc	87,4
LAP3	-270	agtttctatttcc	94
MX1	-180	tgtttctctttcc	87,8
MYD88	-80	gctttcgctttcc	96,2
OAS1	-30	actttcctttgc	78,3
PLEC1	-400	actttccattgc	80,5
PLSCR1	+20	ggtttcctttcc	86,1
PSME2	+10 (tra tss e ATG)	gctttcgctttca	87,4
		agtttcgattttt	80,1
RSAD2	-100	actttcagtttca	82,8
SP110	-50	actttcacttttc	97,5
STAT1	+30	agtttcgctttcc	95
STAT2	+1000	agtttcagtttcc	88,7
TBX1	-1600	agcttcccttttc	83,6
TNFRSF1B	-10	gctttcgctttca	87,4
TNFSF10	-120	tctttcagtttcc	84,9
UBE2L6	-1100	agtttcactgtcg	84,1
		agtttcgctttcc	86,8
USP18	+60	gctttcgctttcc	86,4

RERESSED			
GENE NAME ^a	ISRE POSITION RESPECT TO PUTATIVE tss ^b	ISRE SEQUENCE	% ADHERENCE TO MATRICE ^c
BAX	-350	ggttttgttttt	80,3
BCR	-1000	tgtttcctttcc	86,7
EMID1	+870	ggtttcagtttgc	80,9
GGA1	-500	agtatcactttct	89,2
GHDC	+500 (tra tss e ATG)	aatttcattttc	86,8
GNAZ	-600	cctttctgtttgc	81,1
HIF1A	-300	cctttctctttcc	88,1
HNF1a	+1080	tatttctcttttg	80,8
IL17RA	-670	gctttctctttct	81,3
NDUFA6	-900	actttcccatttc	83
		tctctcactttcc	82,4
PITX2	+60	cctttcgctctcc	83
		tctttccctttc	86,6
POLR3H	+400	agtttccattttt	86,5
		ggtttcgctgtga	80,3
RBX1	+860	aatttgcctttcc	80,5
RFC2	-550	ggtttcagtttcc	89,7
		ccttttcttttc	81,1
SAMM50	-750	gcttcccttttc	84,9
SF3A1	-570	tctttcttttttc	81,8
		ggtttgattttcc	81,7
SGSM3	+440	tctttcactctgc	82,4
SLC2A11	-250	tgtttgacttttg	83,6
		aatttctctttct	82,1
SMARCB1	+110 (tra tss e ATG)	ggcttcggtttcc	80,5
ST13	-1100	tgattcagttttc	80,8
		ggcttcacttttc	90,6
TRMU	+1100	ccattcgatttgc	75,5
		agtttcctctctg	95,3
		agtttctctttcc	82,6
WARS	-650	ctgttcgcttttc	81,1
ZBED4	+2100	gcttttcttttta	85,9

^a according to HUGO
^b tss = transcription start site
^c according to TRANSFAC weight matrices



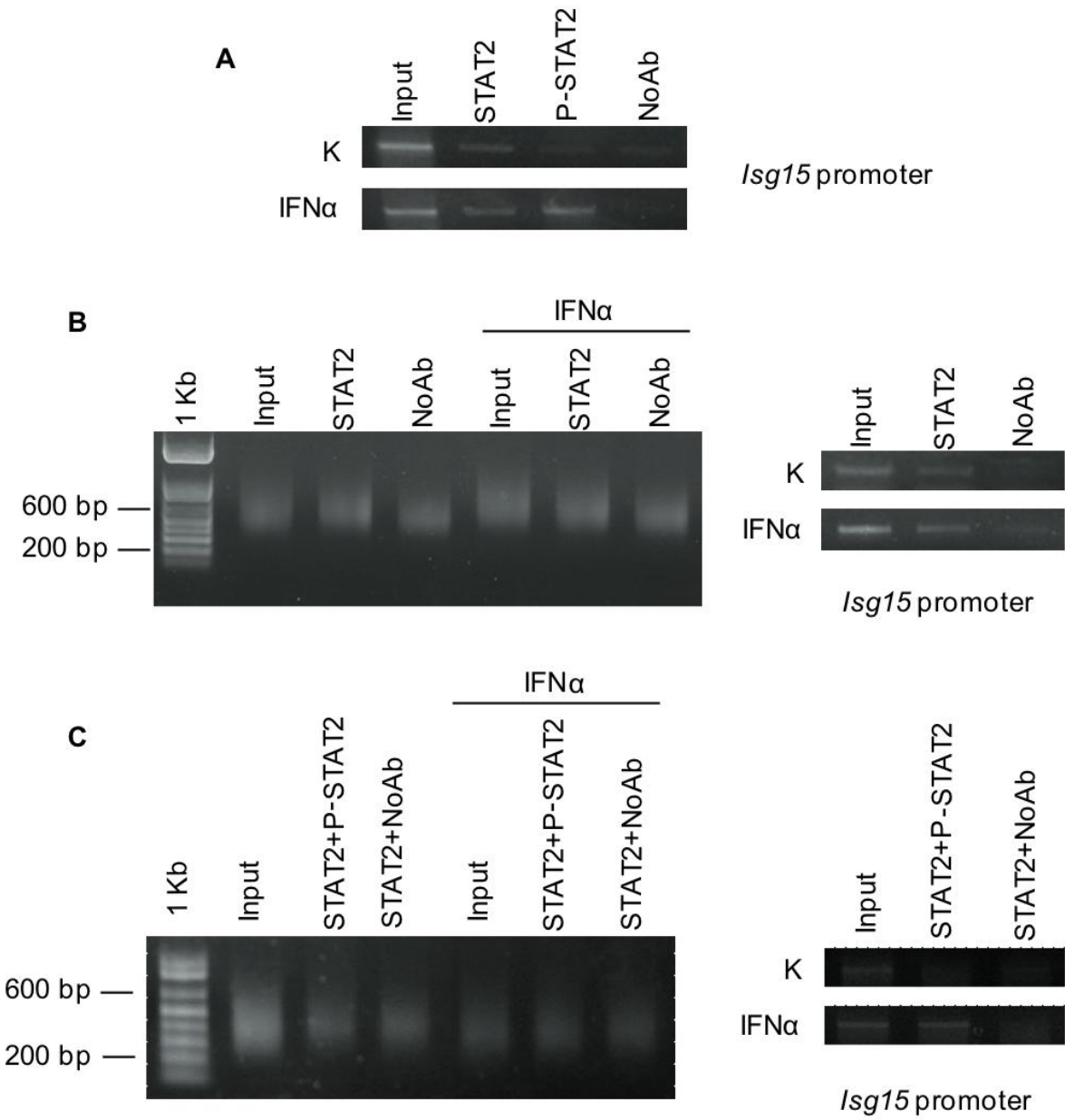


Table S1.

List of primers used for Real time PCR analysis

oligo name	sequence
q6-16_for	TGAGACGTGGGAGGATCCA
q6-16_rev	AACGGTTCTCCGGCTGAAG
qA4GALT_for	GGGCGTCAGCACTCAAGAAG
qA4GALT_rev	CTGGGACAACAAAGACTGCAAA
qAP1G2_for	TCCCTTCCCCCTTTACATCAG
qAP1G2_rev	ATCTTTGATCCCCTCCTTCTGTT
qCAV1_for	CCAGATTCAGGAACAGACAAAATACTT
qCAV1_rev	GGCTGTGAGGAAAGATTTGACTTT
qCXCL10_for	AAGAGGAGCAGAGGGAAATTCC
qCXCL10_rev	CCATGTTGCAGACTCGAAGGT
qHERC5_for	GTGTGTCAGGGTGCCTCCTAGT
qHERC5_rev	TGGACGGAATGGCTTTTCG
qHIF1a_for	CACCCCATCTCCTTTCTCTT
qHIF1a_rev	CGCTCACGTGCTCGTCTGT
qIRF1_for	CCCTTCGCCGCTAGCTCTA
qIRF1_rev	GCTGCGTGCCGTCATTTTC
qISG15_for	AAACCGAAACTGAAGCCAAATTT
qISG15_rev	CCTATTATAAGCCTGAGGCACACA
qLAP3_for	CCCACGTTTCCCAGAATTAAGA
qLAP3_rev	GCGACCTTCGTAATTTTTTTGGA
qLGP1_for	TCCTGCCTTCTTCCCAATTTTC
qLGP1_rev	TTCTCCTCCCACGCTCTACTG
qMX1_for	TCCGTGAATAAAAAGCCAGTGA
qMX1_rev	TGTCCCAGAGCGTAGAAGAG
qOAS1_for	TGAAATTCAGCACTGGGATCAG
qOAS1_rev	GGAGGAGCTGTCTTTGCACTTT
qPITX2_for	ACGCCTCGTCCCAAACAA
qPITX2_rev	GGCCCAAGAGACGGAACAA
qRBX1_for	CGCGGAGTAAAGGGTTTCATT
qRBX1_rev	CCGGCTTCCTTTTCGTGGTA
qRFC2_for	ACTCCTGGGCTTAATCGCTCTT
qRFC2_rev	ACCCCTCTAATCCCAGCACTTT
qSF3A1_for	GGCAGGAGAATCGCTTGAAC
qSF3A1_rev	AGTGGCGCGATCTTGACTCT
qST13_for	CGCCTGCAAGGAAGGTGAT
qST13_rev	GCGAGCAATTAATCTGATGAACAT
qUSP18_for	TCAGTGAGGTTCTGGCAGCTT
qUSP18_rev	CCGTCCCCGCAGCAA
qVIPERIN_for	CCAGGCATCTGCCACAATG
qVIPERIN_rev	CACTCAAGAGCTTCCCAGCAA
qWARS_for	TGACCCCAAGAACTCCTGATCTT
qWARS_rev	AATTCCCCGCATCTGTTTCAC
qZBED4_for	CCCTTCTGCTCCCCACTTTT
qZBED4_rev	GGGATCTGAGGTAAGTGCAGAATG

Table S2.List of the 113 genes comprised in the IFN α /STAT2 array

Gene Symbol^a	Definition^b	Gene Ontology^c	literature source^d
A4GALT	alpha 1,4-galactosyltransferase	cell metabolism	1
ADAR	adenosine deaminase, RNA-specific	mRNA processing	4
AP1G2 G2AD	adaptor-related protein complex 1, gamma 2 subunit	cell metabolism	5,6
ATF5 ATFX	activating transcription factor 5	transcription	3
BAG3	BCL2-associated athanogene 3	apoptosis/proliferation	commercial arrays
BAX	BCL2-associated X protein	apoptosis/proliferation	5
BCR	breakpoint cluster region	apoptosis/proliferation	1
BRCA1	breast cancer 1, early onset	transcription	5
BST1 CD157	bone marrow stromal cell antigen 1	immune modulation/host defense	
BST2 CD137	bone marrow stromal antigen 2	immune modulation/host defense	5
C1QTNF6 CTRP6/ ZACRP6	complement C1q tumor necrosis factor-related 6	immune modulation/host defense	1
CABP7 CALN2	calcium-binding protein 7	cell metabolism	1
CAV1	caveolin 1, caveolae protein, 22kDa	cell metabolism	commercial arrays
CSF2RB CD131/ IL3RB/IL5RB	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	immune modulation/host defense	1
CXCL10 IP-10	chemokine (C-X-C motif) ligand 10	immune modulation/host defense	7
CXCL11 H174/I-TAC/IP-9	chemokine (C-X-C motif) ligand 11	immune modulation/host defense	
CXCL9 mig/CMK/humig	chemokine (C-X-C motif) ligand 9	immune modulation/host defense	6
CYBB gp91-phox/CGD/NOX2	cytochrome b-245, beta polypeptide	immune modulation/host defense	commercial arrays

DAD1 OST2	defender against cell death 1	apoptosis/proliferation	commercial arrays
DNp53	tumor protein P53, N-truncated	transcription	
DNp63	tumor protein P63, N-truncated	transcription	
DNp73	tumor protein P73, N-truncated	transcription	
E2F2	E2F transcription factor 2	transcription	5
EIF2AK2 PKR/EIF2AK1	eukaryotic translation initiation factor 2-alpha kinase 2	immune modulation/host defense	8
EMID1 EMI5/EMU1	EMI domain-containing protein 1	cell metabolism	1
GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	immune modulation/host defense	
GBP2	guanylate binding protein 2, interferon-inducible	immune modulation/host defense	6
GGA1	golgi-associated, gamma adaptin ear containing, ARF binding protein 1	signal transduction	1
GHDC LGP1	GH3 domain containing	chromatin remodelling	3
GNAZ	guanine nucleotide binding protein (G protein), alpha z polypeptide	signal transduction	1
HDAC10	histone deacetylase 10	chromatin remodelling	1
HERC5 CEB1	hect domain and RLD 5	Ubiquitination/protein degradation	3
HIF1A MOP1/PASD8	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	transcription	9
HLA-C	major histocompatibility complex, class I, C	immune modulation/host defense	5
HLA-E	major histocompatibility complex, class I, E	immune modulation/host defense	5
HLA-F CDA12	major histocompatibility complex, class I, F	immune modulation/host defense	6
HLA-G HLA6	major histocompatibility complex, class I, G	immune modulation/host defense	6
HNF1A	HNF1 homeobox A	transcription	commercial arrays
HNF4A	hepatocyte nuclear factor 4, alpha	transcription	

IFI16 PYHIN2/IFNGIP1	interferon gamma inducible protein 16	immune modulation/host defense	10
IFI27 ISG12	interferon, alpha-inducible protein 27	apoptosis/proliferation	5, 11
IFI35	interferon-induced protein 35	immune modulation/host defense	5
IFI44 HCV associated p44	interferon-induced protein 44	immune modulation/host defense	5,6
IFI6 G1P3/6-16	interferon, alpha-inducible protein 6	immune modulation/host defense	2,3
IFIT1 ISG56	interferon-induced protein with tetratricopeptide repeats 1	immune modulation/host defense	3, 12
IFIT2 ISG54/IFI54/isg42/G10P2	interferon-induced protein with tetratricopeptide repeats 2	immune modulation/host defense	13, 14
IFIT3 RIG-G/ISG60/ IRG2/cig49	interferon-induced protein with tetratricopeptide repeats 3	immune modulation/host defense	15
IFIT5 RI58	interferon-induced protein with tetratricopeptide repeats 5	immune modulation/host defense	
IFITM1 9-27/IFI17	interferon induced transmembrane protein 1 (9-27)	immune modulation/host defense	2,3
IFITM2 1-8D	interferon induced transmembrane protein 2(1-8D)	immune modulation/host defense	11
IFITM3 1-8U	interferon induced transmembrane protein 3(1-8U)	immune modulation/host defense	11
IFNA1	interferon, alpha 1	immune modulation/host defense	
IFNA4	interferon, alpha 4	immune modulation/host defense	
IFNB1	interferon, beta 1	immune modulation/host defense	
IL17RA	interleukin-17 receptor A	immune modulation/host defense	1
IL8 CXCL8	interleukin 8	immune modulation/host defense	
IRF1	IFN regulatory factor 1	transcription	
IRF2	IFN regulatory factor 2	transcription	6
IRF3	IFN regulatory factor 3	transcription	
IRF7	IFN regulatory factor 7	transcription	16
IRF9 p48/ISGF3G	interferon regulatory factor 9	transcription	5

ISG15 IFI15/G1P2/UCRP	ISG15 ubiquitin-like modifier	Ubiquitination/protein degradation	3, 17
LAP3 PEPS/LAPEP	leucine aminopeptidase 3	apoptosis/proliferation	3
MET HGFR/RCCP2	met proto-oncogene (hepatocyte growth factor receptor)	apoptosis/proliferation	5
MNT MAD6, MXD6, ROX, bHLHd3	MAX binding protein	apoptosis/proliferation	commercial arrays
MX1 MXA	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	immune modulation/host defense	3, 18
MX2 MXB	myxovirus (influenza virus) resistance 2 (mouse)	immune modulation/host defense	19
MYD88	Myeloid differential primary response gene (88)	immune modulation/host defense	commercial arrays
NCF1 p47(phox)/NOXO2	neutrophil cytosolic factor 1	immune modulation/host defense	commercial arrays
NDUFA6 B14/CI-B14/NADHB14	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa	signal transduction	1
NFAM1	NFAT activating protein with ITAM motif 1	immune modulation/host defense	1
OAS1 IFI4	2'-5' oligoadenylate synthetases (2-5A)	immune modulation/host defense	1
PARVB CGI-56/affixin	parvin, beta	cytoskeleton	1
PITX2	paired-like homeodomain 2	transcription	
PLEC HD1/PCN	plectin	cytoskeleton	5
PLSCR1	phospholipid scramblase 1	cell metabolism	5, 20, 21
PNN PININ/DRS	pinin, desmosome associated protein	mRNA processing	6
POLR3H RPC8	polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)	Transcription	1
PPARA NR1C1	peroxisome proliferator-activated receptor alpha	transcription	1
PSME1 IFI5111/PA28A/MGC8628/REGalpha/PA28alpha	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	cell metabolism	5
PSME2 PA28 beta	proteasome (prosome, macropain) activator subunit 1 (PA28 beta)	Ubiquitination/protein degradation	commercial arrays
PVALB	parvalbumin	cell metabolism	1

RASD2 Rhes/TEM2	RASD family, member 2	signal transduction	1
RBX1 ROC1/DDB/CUL4	RING-box 1	Ubiquitination/protein degradation	1
RFC2 RFC40	replication factor C (activator 1) 2, 40kDa	DNA replication	5
RFPL3	Ret finger protein-like 3	signal transduction	1
RSAD2 VIPERIN/CIG5/vig1	radical S-adenosyl methionine domain containing 2	immune modulation/host defense	6
SAMM50 SAM50	sorting and assembly machinery component 50 homolog (<i>S. cerevisiae</i>)	signal transduction	1
SEC14L4 TAP3	SEC14-like 4 (<i>S. cerevisiae</i>)	cell metabolism	1
SF3A1	splicing factor 3a, subunit 1, 120kDa	mRNA processing	1
SGSM3 RUTBC3	small G protein signaling modulator 3	apoptosis/proliferation	1
SLC25A1 CIC	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	cell metabolism	1
SLC2A11 GLUT11	solute carrier family 2 (facilitated glucose transporter), member 11	cell metabolism	1
SLC5A1 NAGT/SGLT1	solute carrier family 5 (sodium/glucose cotransporter), member 1	cell metabolism	1
SMARCB1 INI1/BAF47	SWI/SNF related, matrix associated, actin dependent regulator of chromatin subfamily B1	chromatin remodelling	1
SP110 IFI75/IFI41	SP110 nuclear body protein	immune modulation/host defense	11
SSTR3	somatostatin receptor 3	signal transduction	1
ST13 HIP/HOP	solute carrier family 5 (sodium/glucose cotransporter), member 1	signal transduction	1
STAT1	transducer and activator of transcription 1, 91kDa	transcription	5,6
STAT2	transducer and activator of transcription 2, 113 kDa	transcription	6
TBX1	T-box 1	Transcription	1
TCN2	transcobalamin II	cell metabolism	commercial arrays
TNFRSF1B CD120b	tumor necrosis factor receptor superfamily, member 1B	immune modulation/host defense	22

TNFSF10 TRAIL/APO2L/CD253	tumor necrosis factor (ligand) superfamily, member 10	apoptosis/proliferation	5
TP53	tumor protein p53	transcription	
TP63	tumor protein p63	transcription	
TP73	tumor protein p73	Transcription	
TRMU TRMT1	tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase	Transcription	1
TUBGCP6	gamma-tubulin complex componenet 6	cytoskeleton	1
UBE2L6 UBCH8/RIG-B	ubiquitin-conjugating enzyme E2L 6	Ubiquitination/protein degradation	5
USP18 UBP43/ISG43	ubiquitin specific peptidase 18	Ubiquitination/protein degradation	1, 3
WARS hWRS/IFI53/IFP53	tryptophanyl-tRNA synthetase	signal transduction	
ZBED4	zinc finger BED domain-containing protein 4	Transcription	1

^{a,b}Gene Symbol and Definition according to HUGO

^cGene Ontology category to which the gene has been assigned

^dList of the source literature references:

- 1) Hartman SE et al, Genes & Dev (2005)19:2953-68
- 2) Imam et al,NAR (1990)18(22):6573
- 3) Chen et al, Gastroenterology (2005)128:1435-54
- 4) Patterson et al, Virol.(1995) 210(2):508-11
- 5) Radaeva et al, Gastroenterology (2002)122:1020-69
- 6) Helbig et al, Hepatology (2005) 42:702-10
- 7) Veckman V et al, Virology (2006)345:96-104
- 8) Ward et al,Virology (2003) 313:553-66
- 9) Der SD et al, PNAS (1998) 95(26):15623-8
- 10) Dawson MJ et al, J.Cell Biochem (1995)57(1):39-51
- 11)Zhu et al, Hepatology (2003) 37:1180-88
- 12) Grandvaux et al, J.Virol (2002) 76(11):5532-9
- 13) Levyet al, PNAS (1986)83:8929-33
- 14) Kessler et al,PNAS(1988)85:8521-25
- 15) Yu Man et al,PNAS(1997)94:7406-11
- 16) Lu R et al, JBC (2000)275:31805-12
- 17) Reich et al,PNAS(1987)84:6394-98
- 18) Ronni T et al, J.Int. Cyt. Res (1998) 18(9):773-8
- 19) Aebi et al, MCB (1989)9(11)5062-72
- 20) Zhou et al,Blood(2000)95(8):2593-9
- 21) Zhao et al,JBC(2005)280(52):42707-14
- 22) Santee et al,JBC (1996)35:21151-59
- 23) Frolova et al, Gene (1993) 128(2):237-45

Table S3.List of the oligonucleotides spotted on the IFN α /STAT2 array

Gene symbol ^a	RefSeq	oligo 1 (-1500 / -500) ^b		oligo 2 (-500 / 0) ^b		oligo 3 (0 / +1000) ^b
A4GALT	NM_017436	from -1170 to -1120	806	from -314 to -268	1137	from +869 to +915
ADAR1	NM_001111	from -1265 to -1215	1110	from -105 to -60	793	from +733 to +783
AP1G2/G2AD	NM_003917	from -825 to -755	596	from -159 to -111	1080	from +969 to +1019
ATF5/ATFX	NM_012068	from -1094 to -1044	741	from -303 to -253	672	from +419 to +469
BAG3	NM_004281	from -1092 to -1042	767	from -275 to -229	659	from +430 to +479
BAX	NM_004324	from -905 to -859	634	from -225 to -175	934	from +759 to +809
BCR	NM_004327	from -1083 to -1033	900	from -133 to -83	1145	from +1062 to +1112
BRCA1	NM_007295	from -990 to -940	698	from -242 to -192	984	from +792 to +842
BST1/ CD157	NM_004334	from -1078 to -1028	899	from -129 to -79	887	from +808 to +858
BST2	NM_004335	from -751 to -701	535	from -166 to -116	974	from +858 to +908
C1QTNF6/CTRP6/ ZACRP6	NM_031910	from -1085 to -1035	811	from -224 to -174	798	from -624 to + 674
CABP7	NM_182527	from -798 to -751	830	from +79 to +126	665	from +791 to +834
CAV1	NM_001753	from -1199 to -1149	946	from -203 to -158	945	from +787 to +837
CSF2RB/CD131/ IL3RB/IL5RB	NM_000395	from -1098 to -1048	807	from -241 to -193	552	from +359 to +407
CXCL10/IP-10	NM_001565	from -1138 to -1088	971	from -117 to -67	503	from +436 to +485
CXCL11/H174/I-TAC/IP-9	NM_005409	from -1030 to -980	685	from -295 to -245	1057	from +812 to +862
CXCL9/mig/CMK/humig	NM_002416	from -1072 to -1024	748	from -276 to -228	991	from +763 to +812
CYBB/gp91-phox/CGD/ NOX2	NM_000397	from -978 to -928	868	from -60 to -15	820	from +805 to +855
DAD1	NM_001344	from -897 to -847	587	from -260 to -210	728	from +518 to +568
DNp53	NM_000546	from -1404 to -1354	1140	from -214 to -164	611	from +447 to +497
DNp63	NM_003722	from -1291 to -1241	1063	from -178 to -129	1050	from +921 to +971
DNp73	NM_005427	from -1010 to -960	771	from -189 to -141	881	from +740 to +790
E2F2	NM_004091	from -1063 to -1013	814	from -199 to -148	1140	from +992 to +1042
EIF2AK2/PKR/EIF2AK1/PRKR	NM_002759	from -1460 to -1410	1048	from -362 to -312	1031	from +719 to +769
EMID1/EMI5/EMU1	NM_133455	from -1053 to -1003	715	from -288 to -239	999	from +760 to +810
GBP1	NM_002053	from -1080 to -1030	853	from -177 to -27	692	from +665 to +715
GBP2	NM_004120	from -1018 to -968	728	from -240 to -190	621	from +431 to +480
GGA1	NM_013365	from -967 to -917	667	from -250 to -200	1185	from +985 to +1035
GHDC/LGP1	NM_032484	from -1221 to -1171	1028	from -143 to -84	1289	from +1205 to +1255
GNAZ	NM_002073	from -1191 to -1141	802	from -339 to -291	961	from +670 to +720

HDAC10	NM_032019	from -526 to -476	776	from +300 to +350	788	from +1138 to +1188
HERC5/CEB1	NM_016323	from -1039 to -989	785	from -204 to -154	961	from +807 to +856
HIF-1A/MOP1/ PASD8	NM_001530	from -1356 to -1307	1123	from -184 to -134	1030	from +896 to +942
HLA-C	NM_002117	from -960 to -910	742	from -168 to -118	559	from +441 to +491
HLA-E	NM_005516	from -1049 to -999	862	from -137 to +87	881	from +968 to +1017
HLA-F/CDA12	NM_018950	from -1070 to -1020	837	from -183 to -103	980	from +877 to +927
HLA-G/HLA6	NM_002127	from -1103 to -1054	819	from -235 to -185	1072	from +887 to +937
HNF1A	NM_000545	from -1341 to -1291	1047	from -244 to -194	917	from +723 to +773
HNF4A	NM_000457	from -1080 to -1030	721	from -309 to -259	871	from +612 to +662
IFI16/PYHIN2/ IFNGIP1	NM_005531	from -1304 to -1254	1037	from -217 to -167	748	from +581 to +631
IFI27/ISG12	NM_005532	from -1232 to -1182	1189	from +7 to +57	543	from +600 to +650
IFI35	NM_005533	from -1220 to -1170	902	from -268 to -218	810	from +592 to +642
IFI44/HCV associated p44	NM_006417	from -1088 to -1038	913	from -125 to -75	644	from +569 to +619
IFI6/6-16/G1P3	NM_002038	from -1009 to -959	855	from -104 to -54	943	from +889 to +939
IFI75/IFI41/SP110	NM_004509	from -1132 to -1082	785	from -297 to -247	865	from +618 to +668
IFIT1/ISG56	NM_001001887	from -1057 to -1007	904	from -103 to -53	771	from +718 to +768
IFIT2/ISG54/IFI54/ cig42/GARG39/ G10P2	NM_001547	from -1153 to -1104	926	from -178 to -128	868	from +740 to +788
IFIT3/RIG-GISG60/ IRG2/cig49/GARG49	NM_001031683	from -863 to -816	616	from -200 to -150	779	from +629 to +678
IFIT5/RI58	NM_012420	from -1069 to -1019	831	from -188 to -138	926	from +788 to +838
IFITM1/9-27/IFI17/ CD225/LEU13	NM_003641	from -1190 to -1140	934	from -206 to -156	616	from +460 to +510
IFITM2/1-8D	NM_006435	from -1272 to -1222	992	from -230 to -180	803	from +623 to +672
IFITM3/1-8U	NM_021034	from -1744 to -1699	1417	from -282 to -233	1014	from +781 to +831
IFNA1	NM_024013	from -707 to -657	583	from -74 to -24	562	from +538 to +588
IFNA4	NM_021068	from -856 to -806	605	from -201 to -151	774	from +623 to +673
IFNB1	NM_002176	from -905 to -855	770	from -85 to -35	600	from +565 to +615
IL17R	NM_014339	from -916 to -866	717	from -149 to -99	619	from +520 to +570
IL8	NM_000584	from -1085 to -1035	884	from -151 to -104	960	from +856 to +906
IRF1	NM_002198	from -839 to -789	711	from -78 to -28	877	from +849 to +899
IRF2	NM_002199	from -1038 to -988	831	from -157 to -109	900	from +791 to +841
IRF3	NM_001571	from -1089 to -1039	776	from -263 to -213	971	from +758 to +808
IRF7/IRF7A/IRF-7H	NM_001572	from -1368 to -1318	1223	from -95 to -48	1277	from +1229 to +1274
ISG15/IFI15/G1P2/UCRP	NM_005101	from -1226 to -1181	1024	from -157 to -111	812	from +701 to +751
ISGF3G/p48/IRF9	NM_006084	from -1175 to -1125	929	from -196 to -146	876	from +730 to +780

LAP3/PEPS/LAPEP	NM_015907	from -1123 to -1073	762	from -311 to -266	954	from +688 to +738
MET/HGFR/RCCP2	NM_000245	from -716 to -666	814	from +148 to +198	544	from +742 to +792
MNT	NM_020310	from -1025 to -975	834	from -141 to -93	1022	from +929 to +977
MX1/MXA	NM_002462	from -1066 to -1016	782	from -234 to -185	1075	from +890 to +940
MX2/MXB	NM_002463	from -1020 to -970	825	from -145 to -95	1050	from +955 to +1005
MYD88	NM_002468	from -999 to -949	747	from -202 to -157	864	from +707 to +757
NCF1/p47(phox)/ NOXO2	NM_000265	from -921 to -871	662	from -209 to -160	1031	from +871 to +921
NDUFA6/B14/Ci-B14/ NADHB14	NM_002490	from -1246 to -1196	1097	from -99 to -49	1016	from +967 to +1017
NFAM1	NM_145912	from -1270 to -1220	1047	from -173 to -123	763	from +640 to +690
OAS1/IFI4	NM_001032409	from -1155 to -1105	956	from -149 to -99	725	from +626 to +676
PARVB/CGI-56/affixin	NM_001003828	from -1039 to -990	759	from -231 to -181	787	from +606 to +656
PITX2	NM_153426	from -992 to -942	738	from -204 to -154	991	from +837 to +887
PLEC/HD1/PCN/EBS1/ EBSO/PLTN	NM_000445	from -1180 to -1130	879	from -251 to -202	709	from +507 to +557
PLSCR1	NM_021105	from -853 to -803	623	from -180 to -130	994	from +864 to +914
PNN/PININ/DRS/SDK3	NM_002687	from -989 to -939	711	from -228 to -178	859	from +681 to +731
POLR3H/RPC8	NM_001018050	from -1056 to -1006	761	from -245 to -200	899	from +699 to +744
PPARA/NR1C1	NM_001001928	from -649 to -599	857	from +258 to +308	958	from +1266 to +1316
PSME1/IEFSSP5111/PA28A; IFI5111; MGC8628; REGalpha; PA28alpha	NM_006263	from -1190 to -1140	835	from -305 to -258	1007	from +749 to + 799
PSME2	NM_002818	from -747 to -697	553	from -144 to -94	967	from +873 to +923
PVALB	NM_002854	from -1320 to -1270	1061	from -209 to -159	922	from +763 to +813
RASD2/Rhes/TEM2	NM_014310	from -1302 to -1252	942	from -310 to -260	949	from +689 to +739
RBX1/ROC1/RNF75	NM_014248	from -1366 to -1316	997	from -319 to -270	933	from +663 to +713
RFC2	NM_002914	from -1061 to -1011	765	from -246 to -201	993	from +792 to +842
RFPL3	NM_006604	from -1172 to -1122	825	from -297 to -250	787	from +537 to +587
RSAD2/VIPERIN/CIG5/vig1	NM_080657	from -900 to -850	730	from -120 to -70	974	from +904 to +954
SAMM50/OMP85/TOB55/TRG-3/SAM50	NM_015380	from -1270 to -1220	883	from -337 to -289	1061	from +772 to +822
SEC14L4/TAP3	NM_174977	from -997 to -947	693	from -254 to -206	1069	from +863 to +913
SF3A1/PRP21/ PRPF21/SAP114	NM_001005409	from -1049 to -999	795	from -204 to -160	665	from +505 to +555
SGSM3/RUTBC3/MAP/RUSC3	NM_015705	from -1073 to -1023	807	from -216 to -166	931	from +765 to +815
SLC25A1	NM_005984	from -1119 to -1069	814	from -255 to -205	911	from +706 to +754

SLC2A11	NM_030807	from -1008 to -958	820	from -138 to -88	946	from +858 to +908
SLC5A1/NAGT/SGLT1	NM_000343	from -1187 to -1137	943	from -194 to -144	1006	from +862 to +912
SMARCB1/RDT/INI1/SNF5/Snr1/BAF47/Sfh1p/hSNFS/SNF5L1	NM_001007468	from -1059 to -1009	823	from -186 to -136	852	from +716 to +766
SSTR3	NM_001051	from -862 to -812	719	from -93 to -44	893	from +849 to +899
ST13/HIP7HOP/P48/ AAG2/SNC6/HSPABP	NM_003932	from -859 to -809	649	from -160 to -110	1037	from +927 to +977
STAT1	NM_007315	from -967 to -917	700	from -217 to -167	1203	from +1036 to +1086
STAT2	NM_005419	from -1232 to -1182	878	from -304 to -259	938	from +679 to +729
TAp53	NM_000546	from -1199 to -1149	991	from -158 to -108	888	from +780 to +830
TAp63	NM_003722	from -1185 to -1135	898	from -237 to -187	913	from +726 to +776
TAp73	NM_005427	from -1317 to -1268	1023	from -245 to -195	905	from +710 to +760
TBX1/DGS/TGA/CAFS/CTHM/DGCR/DORV/VCFS/TBX1C	NM_005992	from -937 to -887	702	from -185 to -135	661	from +526 to +576
TCN2/TC2	NM_000355	from -1123 to -1073	907	from -166 to -116	862	from +746 to +796
TNFRSF1B/CD120b/p75/TBPII/TNFBR/TNFR2/ TNFR80/TNF-R75/p75TNFR/TNF-R-II	NM_001066	from -776 to -726	545	from -181 to -131	1030	from +899 to +949
TNFSF10/TRAIL/APO2L/CD253	NM_003810	from -1005 to -955	831	from -124 to -74	613	from +539 to +589
TRMU/TRMT1	NM_017722	from -1266 to -1216	943	from -273 to -225	879	from +654 to +700
TUBGCP6	NM_001008658	from -1277 to -1227	1025	from -202 to -152	880	from +728 to +778
UBE2L6/UBCH8/RIG-B	NM_004223	from -1138 to -1088	772	from -316 to -263	983	from +720 to +770
USP18/UBP43/ISG43	NM_017414	from -1307 to -1257	1034	from -223 to -176	674	from +498 to +543
WARS/WARS/IFI53/ IFP53	NM_004184 NM_173701	from -1123 to -1073	823	from -250 to -200	1071	from +871 to +921
ZBED4	NM_014838	from -1247 to -1197	824	from -373 to -324	1072	from +748 to +798

^aGene Symbol according to HUGO

^bOligonucleotide position respect to transcription start site (indicated with 0)

Table S4.

IFN α /STAT2 array ChIP-chip results

Gene Name ^a	IFN α ^b	STAT2 ^c			P-STAT2 ^c			expression in Huh7 after IFN α ^d		expression in PHH after IFN α ^d	
		oligo n ^o	-	+	oligo n ^o	oligo n ^o	-	+	oligo n ^o		
A4GALT		2	pos	pos	2		neg	pos	2	↑	↑
ADAR		2	pos	pos	2		neg	pos	2	↑	↑
AP1G2		3	pos	pos	3		neg	pos	3	NC	↓
ATF5			neg	pos	2		neg	neg		↑	NC
BAG3		2	pos	pos	1,2	2	pos	pos	2	NC	↓
BAX			neg	neg			neg	neg		↓	NC
BCR		2	pos	neg			neg	neg		↓	↓
BRCA1		1,3	pos	pos	1,3	1	pos	pos	1	NC	↓
BST1			neg	pos	2		neg	neg		NE	↑
BST2			neg	pos	1,2		neg	pos	1,2	↑	↑
C1QTNF6			neg	pos	1		neg	neg			
CABP7		1	pos	pos	1		neg	neg			
CAV1		1	pos	neg			neg	neg		↑	↑
CSF2RB			neg	pos	2		neg	pos	2	NE	↑
CXCL10		2	pos	pos	2	2	pos	pos	2	↑	↑
CXCL11		2	pos	pos	2	2	pos	pos	2	↑	↑
CXCL9			neg	pos	1,2		neg	pos	1,2	NC	↑
CYBB		2	pos	pos	2	2	pos	neg		NE	↑
DAD1		1,2	pos	pos	1,2		neg	pos	1,2	NC	↑
DNp53			neg	neg			neg	neg			
DNp63		1	pos	pos	1		neg	neg			
DNp73			neg	pos	1,2		neg	pos	2		
E2F2		2	pos	pos	2		neg	pos	2	NE	NE
EIF2AK2		1	pos	neg			neg	neg		↑	↑
EMID1		2,3	pos	pos	2,3		neg	pos	2	↓	NC
GBP1			neg	pos	2		neg	pos	2	↑	↑
GBP2		3	pos	pos	2,3		neg	pos	2	↑	↑
GGA1		1,2	pos	pos	2		neg	pos	2	↓	↓
GHDC		2	pos	pos	2		neg	neg		↓	↑
GNAZ			neg	neg			neg	neg		↓	↓
HDAC10		3	pos	pos	3		neg	neg		↓	↑
HERC5			neg	pos	1,3		neg	neg		↑	↑
HIF1a		2	pos	neg			neg	pos	2	↓	↑
HLA-C		3	pos	pos	3	3	pos	pos	3		
HLA-E		2	pos	pos	2		neg	pos	2		
HLA-F		3	pos	pos	2,3		neg	pos	2,3		
HLA-G		3	pos	pos	3		neg	pos	3		
HNF1A			neg	pos	2		neg	pos	2	↓	↓
HNF4a			neg	pos	1		neg	pos	1		
IFI16		2	pos	pos	2		neg	neg		↑	↑
IFI27		2,3	pos	pos	2		neg	pos	2	↑	↑
IFI35		2	pos	pos	2	2	pos	pos	2	↑	↑
IFI44		3	pos	pos	1,3	3	pos	pos	1,3	↑	↑
IFI6/6-16		2	pos	pos	1,2		neg	pos	2	↑	↑
IFI75		2	pos	pos	2		neg	neg		↑	↑

IFIT1			neg	pos	2			neg	pos	2			↑			↑
IFIT2		3	pos	pos	3			neg	pos	3			↑			↑
IFIT3			neg	neg				neg	neg				↑			↑
IFIT5		2	pos	pos	2		2	pos	neg				↑			↑
IFITM1/9-27			neg	pos	2			neg	neg				↑			↑
IFITM2		1	pos	pos	1			neg	pos	1			↑			↑
IFITM3			neg	pos	3			neg	pos	3						
IFNA1		3	pos	pos	3			neg	neg							
IFNA4		2	pos	pos	2,3			neg	pos	2						
IFNB1			neg	pos	2,3			neg	pos	2						
IL17RA		1	pos	pos	1			neg	neg				↓			↓
IL8		3	pos	pos	2,3			neg	pos	2,3			↓			↑
IRF1			neg	neg				neg	neg							
IRF2			neg	neg				neg	neg							
IRF3		3	pos	neg			3	pos	neg							
IRF7			neg	neg				neg	neg							
IRF9			neg	pos	2			neg	pos	2			↑			↑
ISG15		2	pos	pos	2			neg	pos	2			↑			↑
LAP3			neg	pos	3			neg	pos	3			↑			↑
MET		1	pos	pos	1			neg	neg				NC			↑
MNT		1,3	pos	pos	1,3		3	pos	neg				↑			NC
MX1		2	pos	pos	1,2			neg	pos	2			↑			↑
MX2		2	pos	pos	2		2	pos	pos	2			NC			↑
MYD88			neg	pos	2,3			neg	pos	2			↑			↑
NCF1			neg	pos	2			neg	pos	2			NE			↑
NDUFA6			neg	pos	1			neg	pos	1			↓			↑
NFAM1			neg	pos	1			neg	pos	1						
OAS1			neg	pos	2			neg	pos	2			↑			↑
PARVB		1,3	pos	neg			3	pos	neg							
PITX2		3	pos	neg				neg	neg				↓			↓
PLEC		2	pos	pos	2			neg	pos	2			↑			NC
PLSCR1			neg	neg				neg	neg				↑			↑
PNN			neg	pos	1			neg	pos	1			NC			NC
POLR3H			neg	pos	1			neg	pos	1			↓			NC
PPARA			neg	pos	1			neg	pos	1						
PSME1		2,3	pos	pos	2,3		2	pos	pos	2			NC			NC
PSME2		3	pos	pos	2,3			neg	pos	2,3			↑			↑
PVALB		2	pos	pos	2			neg	pos	2						
RASD2		1,2	pos	pos	1,2			neg	pos	1,2			NE			↑
RBX1		1	pos	pos	2			neg	pos	2			↓			↑
RFC2			neg	pos	1			neg	pos	1			↓			↓
RFPL3		2	pos	pos	2		2	pos	pos	2						
RSAD2		3	pos	pos	2		3	pos	pos	2			↑			↑
SAMM50			neg	neg				neg	neg				↓			NC
SEC14L4		2	pos	neg				neg	neg							
SF3A1		2,3	pos	neg				neg	neg				↓			↓
SGSM3			neg	pos	2			neg	pos	2			↓			↑
SLC25A1		1,2	pos	neg				neg	neg				NC			↓
SLC2A11		2	pos	pos	2			neg	pos	2			↓			↑
SLC5A1		2	pos	neg				neg	neg				NE			↓
SMARCB1			neg	pos	2,3			neg	pos	2			↓			NC
SSTR3		1	pos	pos	1			neg	neg							
ST13		1	pos	pos	1,3			neg	pos	3			↓			↓

STAT1		2	pos	pos	2		2	pos	pos	2		↑		↑
STAT2		3	pos	pos	3		3	pos	pos	3		↑		↑
TAp53			neg	pos	3			neg	neg					
TAp63		2	pos	pos	2		2	pos	pos	2				
TAp73			neg	neg				neg	neg					
TBX1			neg	neg				neg	neg			↑		↑
TCN2		2	pos	neg			2	pos	neg					
TNFRSF1B			neg	neg				neg	neg			↑		NC
TNFSF10			neg	pos	3			neg	pos	3		↑		↑
TRMU			neg	pos	3			neg	pos	3		↓		↓
TUBGCP6		1	pos	pos	1,3			neg	pos	1				
UBE2L6		1	pos	pos	1,2			neg	pos	1,2		↑		↑
USP18		1,3	pos	pos	1,3		3	pos	pos	3		↑		↑
WARS		1,2	pos	pos	2			neg	neg			↓		↑
ZBED4		2,3	pos	pos	3		3	pos	pos	3		↓		↓

^aGene Symbol according to HUGO

^bHuh7 cells were left untreated or treated with 1000 IU/ml of IFN α for 1h

^cStat2 or P-Stat2 occupancy on indicated oligonucleotides (see Experimental Procedures for Data Analysis information)

^dGene expression in Huh7 cells or Primary Human Hepatocytes (PHH) after IFN α treatment (see Experimental Procedures and Table S5 for details)

Table S5.

Taqman® Low Density Array analysis results

Gene name ^a	Huh7 ^b				PHH ^b		
	IFN 2h	IFN 4h	IFN 8h		IFN 2h	IFN 4h	IFN 8h
<i>A4galt</i>	2,8	2,2	4,9		1,5	1,6	1,7
<i>Adar</i>	1	1,5	2		1,1	1	2,4
<i>Ap1g2</i>	0,6	0,8	0,7		0,5	0,6	1,3
<i>Atf5</i>	1,3	1,2	2		1,3	0,8	1
<i>Bag3</i>	1,1	2,7	1,5		1	0,7	0,4
<i>Bax</i>	0,6	0,5	1		0,9	1,1	1,3
<i>Bcr</i>	0,5	0,7	0,9		0,8	1	0,4
<i>Brca1</i>	0,7	0,6	1,6		0,7	0,8	0,3
<i>Bst2</i>	42,2	150	139		1,3	1,1	2,9
<i>Cav1</i>	10,3	16,2	32		2,3	3,2	2,5
<i>Cxcl10</i>	12,1	24,5	40		219	351	361
<i>Cxcl11</i>	4,8	5,2	19		2694	2276	3595
<i>Cxcl9</i>	1,4	1,2	1,1		22,5	32,5	29
<i>Dad1</i>	0,9	0,8	0,8		2,3	1,9	1,6
<i>Eif2ak2/Pkr</i>	2,8	7,1	8,7		5,9	6,1	11,6
<i>Emid1</i>	0,4	0,5	0,2		1,1	2,5	0,6
<i>Gbp1</i>	5,7	12,1	13,7		8,4	5,1	13,5
<i>Gbp2</i>	1,8	2,6	1,8		2,6	2,6	1,9
<i>Gga1</i>	0,5	1	0,9		0,6	0,7	0,5
<i>Ghdc/Lgp1</i>	0,4	0,2	0,1		1,7	3,1	2,1
<i>Gnaz</i>	1	0,7	0,5		0,8	1,2	0,4
<i>Hdac10</i>	0,3	0,3	0,4		3,1	4,6	7,7
<i>Herc5/Ceb1</i>	16,9	22,9	47		62,5	41,5	88,5
<i>Hif1a</i>	0,6	0,5	0,6		2,8	5	2,5
<i>Hnf1a</i>	0,7	0,5	0,7		0,5	0,8	1,2
<i>Ifi16</i>	0	0	70		10,5	20,9	18,8
<i>Ifi27</i>	0	28,8	9,1		3,1	1,4	17,9
<i>Ifi35</i>	1,2	4,9	5,7		2,6	1,2	7,2
<i>Ifi44</i>	0	53	28,3		106,3	53,1	187,9
<i>Ifi6/6-16</i>	12,2	44,5	50,6		6,4	3,3	13,6
<i>Ifit1/ISG56</i>	402	1127	710,4		2423	1510	3663
<i>Ifit2/Isq54</i>	124	361	93,6		66,3	70	77
<i>Ifit3/Rig-g</i>	44,7	104,6	69,4		26,1	34,3	33,3
<i>Ifit5</i>	14,1	37,6	22,6		2,8	0,6	2,2
<i>Ifitm1/9-27</i>	44,6	110	138		6	3,3	21
<i>Ifitm2/1-8D</i>	0,9	1,1	1,52		1,7	1,1	2,1
<i>Il17ra</i>	0,3	2,3	1		0,8	0,8	0,6
<i>Il8</i>	0,3	0,6	1,7		0,8	5	6
<i>Irf9</i>	5,5	12,3	8,6		1,9	1	4,6
<i>Isq15</i>	50,5	66,3	108		18,2	15,7	57

<i>Lap3</i>	1,1	2,4	2,9	7	3,1	12,9
<i>Met</i>	0,9	0,7	1	2,6	3,8	3,4
<i>Mnt</i>	6,7	4	4	0,8	1,3	1,7
<i>Mx1</i>	204	527	741	14,2	15	25,9
<i>Mx2</i>	1	0,9	1,2	12,3	12,4	34,7
<i>Myd88</i>	1,5	2,5	1,9	2,8	1,7	4,3
<i>Ndufa6</i>	0,6	0,8	0,7	1	2,2	1
<i>Oas1</i>	90	283	268	9,6	5,4	23,7
<i>Pitx2</i>	0,3	0,2	0,2	0,2	0,006	0,8
<i>Plec</i>	2,2	1,8	1,4	0,7	1,3	1,7
<i>Plscr1</i>	3,7	10,7	11,8	4,6	3,1	9,2
<i>Pnn</i>	0,9	0,9	0,8	0,7	1,4	0,9
<i>Polr3h</i>	0,3	0,8	0,8	1	0,7	1,8
<i>Psme1/Ifi5111</i>	0,8	1,4	1,3	1,2	0,8	1,4
<i>Psme2</i>	1,4	2,6	2	1	1,2	2,2
<i>Rbx1</i>	0,8	0,7	0,8	1,3	1,7	1,7
<i>Rfc2</i>	0,3	1	0,8	0,6	1,3	0,8
<i>Rsad2/Viperin</i>	125	1103	837	453	224	892
<i>Samm50</i>	0,5	0,8	0,5	0,8	1,1	0,9
<i>Sf3a1</i>	0,7	0,6	0,7	0,5	0,6	0,7
<i>Sgsm3/Rutbc3</i>	0,7	0,3	0,7	0,9	2,1	1,6
<i>Slc25a1</i>	1	1,1	1	0,6	0,8	0,7
<i>Slc2a11</i>	1	0,3	0,7	0,9	2,7	7,4
<i>SmarcbB1</i>	0,7	0,7	0,6	1,7	1,5	1,1
<i>Sp110/Ifi75</i>	0,3	15,3	17,2	8	3,8	15,5
<i>St13</i>	0,6	0,6	0,8	0,8	1,5	0,7
<i>Stat1</i>	2,3	4,2	4,8	5,4	4,7	8,7
<i>Stat2</i>	1,4	2,6	3,8	5,7	1,6	6,6
<i>Tbx1</i>	0	174	85,2	43,7	20	16,4
<i>Tnfrsf1b/Cd120b</i>	0,6	1,2	3,6	0,9	1,3	0,8
<i>Tnfsf10/Trail</i>	55,5	162	151,8	49,5	25,2	61,5
<i>Trmu/Trmt1</i>	0,6	0,4	0,3	0,5	0,6	0,7
<i>Ube2l6</i>	10,8	14	14	2,3	0,8	2,1
<i>Usp18</i>	21,8	37,9	83,6	23,4	11	46,8
<i>Wars</i>	0,8	0,6	0,5	9,1	2,2	11,8
<i>Zbed4</i>	0,8	1,5	0,7	0,3	0,1	0,2

^aGene Symbol according to HUGO

^bHuh7 cells and Primary Human Hepatocytes (PHH) were left untreated or treated with 1000 IU/ml of IFN α for the indicated time points. Expression values represent relative enrichment over control untreated cells. 18s was used as internal calibrator for equal loading of samples (see Experimental Procedures for details)