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A variant upstream of *IFNL3* (*IL28B*) creating a novel interferon gene *IFNL4* is associated with impaired clearance of hepatitis C virus

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SUMMARY

Chronic infection with hepatitis C virus (HCV) is a common cause of liver cirrhosis and cancer. We performed RNA-sequencing in primary human hepatocytes activated with synthetic dsRNA to

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COMPETING FINANCIAL INTERESTS

L.P.-O., B. M., R. P. D. and T. R. O'B. are inventors on a patent application filed by the National Cancer Institute on the basis of these findings.

DATA DEPOSITION

Sequences for all novel transcripts JN806234, JN806225, JN806226, JN806232, JN806233, JN806227, JN806228, JN806229, JN806230 and JN806231 are deposited to NCBI database <http://www.ncbi.nlm.nih.gov/>, ss469415590 and ss539198934 are submitted to dbSNP database <http://www.ncbi.nlm.nih.gov/snp/>.

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AUTHOR CONTRIBUTIONS

L. P.-O. and T. R. O'B. conceived and supervised the project, J.A., H. L. B., B. R. E., C. D. H., T. R. M. and D. L. T. performed the clinical and epidemiologic studies that contributed the DNA samples and data; L. P.-O., B. R., R. P. D. designed the experiments, L. P.-O., B. M., W. T., H. P., H. D., D. H., P. P.-G., I. K., A. M., N. B., M. T., L. L., F. S., B. R. and R. P. D. performed experiments and analysis, T. R. O'B., R.M.P and S. C. performed statistical analysis of genetic association; L.P.-O. and T.R.O'B. wrote the manuscript. All authors contributed to scientific discussions and approved the final manuscript.

mimic HCV infection. Upstream of *IFNL3* (*IL28B*) on chromosome 19q13.13, we discovered a novel, transiently induced region that harbors dinucleotide variant ss469415590 (TT/ G), which is in high linkage disequilibrium with rs12979860, a genetic marker strongly associated with HCV clearance. ss469415590- G is a frame-shift variant that creates a novel primate-specific gene, designated interferon lambda 4 (*IFNL4*), which encodes a protein of moderate similarity with IFNL3. Compared to rs12979860, ss469415590 is more strongly associated with HCV clearance in individuals of African ancestry, whereas it provides comparable information in Europeans and Asians. Transient over-expression of IFNL4 in a hepatoma cell line induced STAT1/STAT2 phosphorylation and expression of interferon-stimulated genes. Our findings provide new insights into the genetic regulation of HCV clearance and its clinical management.

More than 3% of the world population is infected with hepatitis C virus (HCV)¹. Up to 80% of acutely-infected individuals fail to clear the virus and develop chronic hepatitis C (CHC)², with as many as 5% eventually progressing to liver cancer³. Success of CHC treatment with pegylated interferon- plus ribavirin (pegIFN- /RBV) depends on HCV genotype and reaches 50–80% in patients of European ancestry, but only 30% in patients of African ancestry. Adding a direct acting antiviral (DAA) agent to this regimen increases the success rate, but is subject to numerous side effects of pegIFN- /RBV⁴ and DAA treatment. If this treatment fails, there is an increased risk of selection of resistant HCV strains that may compromise future treatment options^{5,6}.

Recent genome-wide association studies (GWAS) have identified single nucleotide polymorphisms (SNPs) rs12979860 and rs8099917 on chromosome 19q13.13 near *IFNL3* (*IL28B*) gene as markers associated with both spontaneous HCV clearance^{7,8} and response to pegIFN- /RBV treatment^{7–11}. Within this region reside the three interferon- genes, *IFNL1*, *IFNL2* and *IFNL3* (formerly *IL29*, *IL28A* and *IL28B*, respectively), which encode the type-III IFNs^{12,13}. Type-I IFNs (IFN- and IFN-) and type-III IFNs (IFN- s) induce antiviral activity and suppress HCV replication *in vitro*^{14,15} and *in vivo*¹⁶ by activation of the JAK/STAT pathway and up-regulation of interferon-stimulated genes (ISGs)^{14,17,18}. The molecular phenotype of this genetic association remains unclear. The GWAS markers have not been consistently associated with hepatic *IFNL3* mRNA expression^{19–21} and a non-synonymous *IFNL3* variant, rs8103142 (Arg70Lys), which is in strong linkage disequilibrium (LD) with rs12979860 in all HapMap populations ($r^2=0.8–1.0$), does not seem to affect the function of the IFNL3 protein²².

A genetic variant creates a novel interferon protein (IFNL4) of similarity with IFNL3

We sequenced mRNA (RNA-seq) from primary human hepatocytes (PHH) treated with PolyI:C, which is a synthetic mimic of double-stranded HCV RNA. The PHH sample was from a liver donor who was heterozygous for rs12979860 (C/T) and uninfected with HCV. The hepatocytes were treated with PolyI:C for 0, 1, 2, 4, 8 or 24 hours, and induction of the *IFN-* genes (*IFNL1–3*) was confirmed by TaqMan expression analysis prior to RNA-seq. An analysis of RNA-seq data that focused on a 150-Kb region around rs12979860 showed concordance with the TaqMan expression results – there was no expression of *IFN-* genes without PolyI:C treatment, and these genes were induced after 2–24 hours of PolyI:C activation (Fig. 1a).

We also observed transient activation of a novel transcribed region upstream of *IFNL3*, with the highest levels of expression detected at 2 and 4 hours (Fig. 1b). Analysis of paired-end RNA-seq reads identified one major splice-junction site. Using this common sequence as a starting point for 5' rapid amplification of cDNA ends (5' RACE), we mapped a transcription

start site, followed by a unique protein translation start site 277 bp downstream. Within the first exon (at amino acid 22), we detected a novel compound dinucleotide variant, denoted ss469415590 TT/ G, comprised of a one-base insertion/deletion (indel) polymorphism (T/ , rs67272382) and a one-base substitution variant (T/G, rs74597329). Using PolyI:C-stimulated PHH from 5 additional liver donors and primer presented in Supplementary Table 1, we cloned and annotated ten individual transcripts created by a combination of the ss469415590 alleles and inclusion of several alternative exons (Fig. 1c, d, NCBI accession numbers presented in Supplementary Table 2). The location of these novel transcripts 3 Kb upstream of and in the same orientation as *IFNL3*, raised the possibility that they are alternative splicing forms of *IFNL3* or fusions. However, the presence of a CTCF transcriptional insulator site^{23,24} between the two transcribed regions (Fig. 1b), the results of the RACE experiments and the failure to generate an RT-PCR product between *IFNL3* and the novel transcribed region, confirmed their independence. Despite high overall similarity with a genomic region upstream of *IFNL2*, the novel transcripts and ss469415590 are specific for the region upstream of *IFNL3* (Supplementary Fig. 1).

Of the ten novel transcripts, four were interrupted by premature stop codons and, thus, are likely to be eliminated by nonsense-mediated decay²⁵. The remaining six transcripts were predicted to produce full-length proteins of: 143 amino acids (aa; p143) and 124 aa (p124) from transcripts with the ss469415590-TT allele; 179 aa (p179), 170 aa (p170), 131 aa (p131) and 107 aa (p107) from transcripts with the ss469415590- G allele (Fig. 1c). A global protein BLAST search found homology only for p179, with 29.1% aa identity and 40.8% aa similarity with *IFNL3*. However, the p179 and *IFNL3* cDNA sequences were not similar enough to be aligned using a BLAST bl2seq tool. Based on the protein sequence homology with type-III IFNs (Table 1), we designated p179 as interferon analog protein (IFNL4). *IFNL3* and p179 (IFNL4) proteins are most related within the sequences that correspond to the A and F helices of *IFNL3*, which constitute the core area for interaction of *IFNL3* and other type-III IFNs with their primary receptor, IFNLR1 (IL28R1). However, IFNL4 differs in the area corresponding to the D helix of *IFNL3*, which is the area of interaction of type-III IFNs with the second chain of the IFNL receptor complex, IL10R2 (Fig. 2)²⁶⁻²⁹.

Association of genetic variants within *IFNL4* with HCV clearance

The GWAS markers rs12979860 and rs8099917 are located 367 bp downstream (intron 1) and 4 kb upstream of ss469415590, respectively. Analysis of the HapMap³⁰ (Supplementary Table 3) and the 1000 Genomes project³¹ data (Supplementary Table 4) showed that the *IFNL4*-creating ss469415590- G allele is perfectly correlated with the unfavorable rs12979860-T allele in Asians (CHB+JPT sets, $r^2=1.00$) and well correlated in Europeans (CEU set, HapMap, $r^2=0.92$; 1000 Genomes, $r^2=0.83$). In Africans, however, this correlation is only moderate (YRI set, HapMap, $r^2=0.71$; 1000 Genomes, $r^2=0.65$), even though rs12979860 is the best surrogate for ss469415590 of all markers within the 100-Kb region. Correlation between ss469415590 and rs8099917 is high in Asians ($r^2=0.91$), moderate in Europeans ($r^2=0.44$), but very low in Africans ($r^2=0.008$) (Supplementary Table 3).

We assessed the association of ss469415590 and rs12979860 with HCV clearance in 1,436 African-American and 1,480 European-American individuals from four studies. In VirahepC³² and HALT-C³³, we evaluated response to pegIFN- /RBV therapy in patients with CHC (Supplementary Table 5). There were differences in the rates of sustained virological response (SVR) among the subjects from these studies, which reflect well known racial differences in response to treatment and the differing selection criteria for these clinical trials: Virahep C European-American, 52%; Virahep C African-American, 28%; HALT-C European-American, 18%; African-American, 7%. We evaluated spontaneous

HCV clearance in injection drug users enrolled in two studies, UHS³⁴ and ALIVE³⁵ (Supplementary Table 6). The decrease in HCV RNA during the first 28 days of treatment is a powerful early predictor of ultimate treatment response that is strongly associated with rs12979860 genotype^{36,37}. In African-American Virahep-C participants, the decline in HCV RNA levels after 28 days of treatment was more strongly associated with ss469415590 genotype than with rs12979860 genotype ($p=0.015$, difference in mean values; Fig. 3; Supplementary Table 7). In the same study we observed a stronger association for ss469415590 than for rs12979860 with other measures of treatment response (week 24 response, end-of-treatment response and SVR; Table 2), although these differences did not reach statistical significance. The association pattern was similar in African-American patients from the HALT-C study, with a stronger association for ss469415590 than for rs12979860 (week 20 response, end-of-treatment and SVR, Table 2). Spontaneous HCV clearance among African-Americans was evaluated using the area under the receiver operating curve (AUC). In UHS participants, the AUC value was greater for ss469415590 (0.62) than rs12979860 (0.58) (Table 3). In the ALIVE study, which has higher percentage of HCV/HIV co-infected patients, the AUC values were similar for rs12979860 (0.64) and ss469415590 (0.64; Table 3).

Virahep-C, HALT-C and UHS also enrolled European-American participants. In these subjects, ss469415590 and rs12979860 showed similar associations for both treatment-induced and spontaneous HCV clearance (Supplementary Tables 7, 8, 9, 10). Taken as a whole, our results show that among African-American individuals, ss469415590 is a better marker than rs12979860 for predicting response to pegIFN- α /RBV treatment of CHC and possibly for spontaneous HCV clearance, while these variants are similarly informative in European-Americans.

By sequencing *IFNL4* in 270 HapMap samples we annotated three non-synonymous variants, rs73555604 (Cys17Tyr) in exon 1, rs142981501 (Arg60Pro) and rs117648444 (Pro70Ser) in exon 2, as well as four synonymous variants, rs150891559 (Ala11Ala) and rs4803221 (Ser30Ser) in exon 1, and rs12971396 (Ser149Ser) and rs137902769 (Ser175Ser) in exon 5 (Fig. 2, Supplementary Fig. 2, Supplementary Tables 11, 12). Based on a haplotype analysis of 16 markers from the 8-Kb *IFNL3/IFNL4* region, we identified eight markers that captured all haplotypes present in HapMap sets (Supplementary Table 13). These eight markers were also tested in European-American and African-American patients from Virahep-C. In all populations, the unique favorable haplotype included the ss469415590-TT allele, which abrogates the *IFNL4* protein. The unfavorable ss469415590-G allele was found on a number of haplotypes, including two haplotypes that were reported as being neutral in Europeans despite carrying the unfavorable rs12979860-T allele^{38,39}; these two haplotypes include minor alleles of either non-synonymous variants rs73555604 or rs11764844. It is possible, therefore, that these variants modify the risk in carriers of the unfavorable ss469415590-G allele and are the source of haplotype heterogeneity previously reported in Europeans^{38,39}, however, data from Virahep C are too sparse to confirm this finding (Supplementary Table 13).

IFNL4 induces expression of ISGs

We evaluated functional properties of the 6 novel protein isoforms created by alleles of ss469415590. For an analysis of 45 signaling pathways, HepG2 hepatoma cells were transiently transfected with expression constructs for all 6 isoforms or treated with recombinant IFN- α , IFNL3 and IFNL4 (the latter two produced in the sfs9 baculoviral expression system). Only transfection with IFNL4 expression construct, as well as treatment with IFN- α or IFNL3, induced activation of an interferon stimulated response element reporter (ISRE-Luc), which contains STAT1/STAT2 binding sites responsive to type-I and

type-III IFN signaling, and the IRF1 reporter (Fig. 4a). These results were validated in HepG2 cells transiently (Fig. 4b), as well as stably (Fig. 4c), expressing ISRE-Luc reporter constructs. The effect was comparable when the cells were transfected with IFNL4 expression constructs generating proteins either with a Halo-tag or a FLAG-tag (Supplementary Fig. 3). Similarly, only transient transfection with IFNL4 construct decreased HCV RNA replication in hepatoma cells stably expressing a subgenomic luciferase-expressing hepatitis C virus replicon⁴⁰ (Fig. 4d), and induced STAT1 and STAT2 phosphorylation (Fig 4 e). Transfection with IFNL4 activated the ISRE reporter in HepG2 and HEK-293T cells, but not in HeLa cells (Supplementary Fig. 4).

The recombinant IFNL4 protein expression was detectable in cells and cell lysates of transfected HepG2 and 293T cells, by confocal imaging and Western blots with antibodies specific for IFNL4 and tag proteins (Supplementary Fig. 5, 6). We also detected weak expression of recombinant IFNL4 in media of transfected HepG2 cells, but not of 293T cells (Supplementary Fig. 7). In PolyI:C- stimulated PHH from liver donors not infected with HCV endogenous protein expression of IFNL4 was detected by confocal imaging in carriers of the unfavorable ss469415590- G allele but not in a homozygous carrier of the favorable ss469415590-TT allele (Fig. 5). In hepatocytes from the donor heterozygous for ss469415590- G, we detected endogenous expression of IFNL4 in cells treated with PolyI:C and after *in-vitro* infection with the JFH1HCV strain (Supplementary Fig. 6d). In fact, in hepatocytes from one of these donors (G/TT genotype), we observed low IFNL4 expression even without PolyI:C treatment or *in-vitro* HCV infection (hour 0 time point). Though preliminary, these results suggest that IFNL4 might be expressed in conditions unrelated to HCV infection.

To further explore the functional consequences of IFNL4 expression, we performed RNA-seq in HepG2 cells transiently transfected with IFNL4 or an empty vector (mock) (Supplementary Fig. 8a) and found that the top canonical pathways induced by IFNL4 are related to the activation of interferon signaling (Supplementary Fig. 8b). We validated the RNA-seq results by qRT-PCR analysis and showed that IFNL4 induced expression of many ISGs in a pattern similar to that induced by IFN- and IFNL3 (Supplementary Fig. 8c). Previously, genes in these pathways have been shown to be expressed at higher levels in pre-treatment liver biopsies from HCV-infected patients who do not respond to pegIFN- / RBV treatment; these patients tend to carry the unfavorable genotypes of rs12979860 and rs8099917^{19,41-44} which mark the ss469415590- G allele that produces IFNL4. To mimic this clinical phenotype, we transfected HepG2 cells with mock or IFNL4 expression constructs and/or treated cells with 10 ng/ml of recombinant IFN- or IFNL3. In these samples we validated the RNA-seq data by qRT-PCR analysis and showed that IFNL4 induced expression of selected ISGs (*STAT1*, *ISG15*, *IFIH1/MDA5*, *OAS1*, *MX1*, *DHX58/RIG-I*) in a pattern similar to that induced by IFN- and IFNL3 (Supplementary Fig. 8d). Furthermore, treatment by IFN- or IFNL3 of cells already expressing IFNL4 did not induce additional activation of ISGs (Supplementary Fig. 8d). Some genes known as markers of HCV-induced liver damage, such as chemokine *CCL5 (RANTES)*⁴⁵ and the proto-oncogene *FOS*⁴⁶⁻⁴⁸ were induced by IFNL4 but not by IFNs (Supplementary Fig. 8d), suggesting a functional role for IFNL4 distinct from the roles of IFN- and IFNL3.

Conclusions

We have identified a novel inducible human protein-coding gene, *IFNL4*, which is related to, but distinct from known IFNs and other class-2 cytokines. The 179 aa open-reading frame of *IFNL4* transcript is created by a common deletion frame-shift allele of ss469415590, which is a dinucleotide variant strongly linked with rs12979860. In individuals of African ancestry, the IFNL4-generating ss469415590- G allele is superior to

the rs12979860-T allele for predicting response to pegIFN- α /RBV treatment of CHC. Within *IFNL4* we identified three non-synonymous variants, rs73555604 (Cys17Tyr), rs142981501 (Arg60Pro) and rs11764844 (Pro70Ser), present on haplotypes with the ss469415590- G allele. The role of these variants on *IFNL4* biological function and their impact on HCV clearance in different populations should be further explored.

Analysis of genomic sequences of 45 species available for *IFNL4* region in the UCSC genome browser showed that the unfavorable, *IFNL4*-generating ss469415590- G allele is an ancestral variant present in all the species. The existence of *IFNL4* protein could be predicted only in the genomes of macaques (marmoset and rhesus), orangutan, chimpanzee and humans (Supplementary Fig. 9). The beneficial insertion ss469415590-TT allele appears to be a recently derived variant, which became common in all human populations (93% in Asians, 68% in Europeans and 23% in Africans, based on HapMap samples), suggesting positive selection for this allele. Introduction of frame-shifts is considered to be an evolutionary mechanism for the rapid emergence of new proteins^{49,50}, but, in this case, an insertion allele that abrogates *IFNL4* seems to have been selected during evolution.

We found that the *IFNL4* protein of 179 aa induces STAT1 and STAT2 phosphorylation, activates the ISRE-Luc reporter and ISGs, and generates antiviral response in hepatoma cells. The mechanisms by which *IFNL4* induces these responses, but nevertheless impairs HCV clearance, is currently under investigation. *IFNL4* and *IFNL3* share similarity in the area that is known to interact with the primary receptor of *IFNL3* (*IFNLR1*), but differ in the region of *IFNL3* that interacts with the second chain of the *IFNL* receptor complex, *IL10R2*. Thus, it is possible that *IFNL4* activates JAK-STAT signaling through a unique receptor complex consisting of *IFNLR1* and a currently undefined second receptor chain or that *IFNL4* functions as a decoy cytokine competing with type-III IFNs for binding of *IFNLR1*. We also found that the *IFNL4*-caused pre-activation of interferon signaling prevents further activation by type-I and Type-III IFNs. We used an allele-specific mRNA expression assay (Supplementary Fig. 10) and explored endogenous *IFNL4* expression in PHH, where it was induced by PolyI:C, IFN- α (but not with *IFNL3*) and *in vitro* infection with HCV (Supplementary Fig. 11). However, no *IFNL4* mRNA expression was induced by PolyI:C, IFN- α or *IFNL3* in several transformed cell lines that carry the ss469415590- G allele (HepG2, HeLa, HEK293T, A549 and HH29). Experiments aimed at elucidating the triggers of *IFNL4* expression in diverse conditions and cell types and its receptor components are ongoing, and may provide greater insight regarding its mechanism of action.

Previous studies found that patients with chronic hepatitis C who carry rs12979860-T, which marks the ss469415590- G allele, have somewhat higher hepatic expression of ISGs before treatment, but poorer ISG response to pegIFN- α /RBV treatment^{19,41–44}. The rs12979860-T variant has also been associated with lower HCV RNA levels in the absence of treatment^{9,51}. Our *in vitro* experiments in HepG2 cells showed that *IFNL4* induced activation of ISGs, which was not further enhanced by exogenous treatment with IFN- α or *IFNL3*. Together, these data suggest that *IFNL4* induces weak expression of ISGs that provides some antiviral effect response which might lower the HCV load, but also reduces the responsiveness to type-I and type-III IFNs that is needed for efficient HCV clearance.

It has been reported that rs12979860 predicts early viral kinetics in HCV-infected patients receiving IFN- α -free treatment⁵². This genotype has also been associated with response to IFN- α based treatment of chronic hepatitis B virus (HBV) infection in some studies^{53,54}. Furthermore, IFN- α therapy is used for a number of other clinical conditions, including some forms of cancer⁵⁵. Thus, therapeutic inhibition of *IFNL4* might represent a novel biological target for the treatment of HCV and HBV infection and possibly other diseases, and *IFNL4* genotype could be used to select patients for this therapy.

ONLINE METHODS

Cells

Fresh primary human hepatocytes (PHH) from HCV un-infected liver donors were purchased from Lonza or Celsis. PHH received in suspension were cultured overnight in collagen-coated plates or chamber slides (BD Biosciences), unattached PHH were removed before treatment. Hepatoma HepG2 cells, cervical carcinoma HeLa and embryonic kidney 293T cells (all from ATCC) were cultured in DMEM with 10% FBS. Hepatoma Huh7-Lunet cells harboring a subgenomic, luciferase-expressing HCV JFH1 replicon were cultured as previously described⁴⁰. The PHH were treated with 50 µg/ml of PolyI:C (Imgenex), 100 ng/ml of IFN- β (PBL Interferon Source) or IFNL3 (custom); cell lines were treated with 10 ng/ml of IFN- α , IFNL3 or IFNL4 (custom).

Transfections

Transfections were performed using a Lipofectamine™ LTX Reagent and Opti-MEM medium, using standard protocols (Life Technologies).

HCV infection of PHH

PHH (0.35×10^5 /well) were infected with HCV (JFH1 strain)⁵⁶ for 0, 6 or 24 hours in collagen-coated 24-well plates or chamber slides at a multiplicity of infection (M.O.I.) of 2.

Antiviral assays

Huh7-Lunet cells were transfected with IFNL4, p131 or p107 constructs or an empty GFP vector (mock) in a 48-well plate and luciferase expression was measured 48 hours post-transfection.

Extraction of DNA, RNA and protein

DNA and RNA were prepared using a DNeasy or a RNeasy kit with DNase-I treatment (Qiagen) and evaluated with NanoDrop 8000 (Thermo Scientific) and BioAnalyzer 2100 (Agilent Technologies). Protein was prepared by lysing cells in RIPA buffer with protease inhibitors (Sigma Aldrich). Cell media was concentrated 10x and 100x using the 9K MWCO protein concentrator tubes (Thermo Scientific).

Western blotting

Proteins were resolved on 4–12% tris-glycine SDS-PAGE gels (Life Technologies). Detection was done using the custom anti-IFNL4 mouse and rabbit monoclonal antibodies, rabbit anti-Halo antibody (Promega), and secondary goat anti-rabbit (sc-2030) or goat anti-mouse (sc-2031) antibodies with IgG-HRP (Santa Cruz). The signals were detected with ECL Plus Western blotting detection system (GE Healthcare Life Sciences).

Analysis of STAT1/STAT2 phosphorylation

HepG2 cells in 6-well plates were untreated or transfected with expression constructs or empty Halo-tag vector, or were treated for 1 hour at 37°C with 50 ng/ml of recombinant IFNL3. Equal amounts (50 µg/lane) of whole-cell lysates prepared 48 hours post-transfection were used for analysis by Western blotting. Detection was performed as previously described⁵⁷ with rabbit anti-phospho-Tyr701-STAT1 (Cell Signaling Technology) and rabbit anti-phospho-Tyr689-STAT2 (Millipore) antibodies. The blots were stripped and re-probed with rabbit anti-STAT1 and anti-STAT2 antibodies (Santa Cruz Biotechnology) to measure the levels of total STAT1 and STAT2 proteins.

RNA-sequencing

Total RNA (1 ug) from PHH or HepG2 cells was used for library preparation with TruSeq PolyA kit (Illumina). Sequencing with Genome Analyzer (GAII) generated 47 million of 107 bp paired-end sequencing reads per sample. The TopHat v1.2.0 settings were changed to allow multiple read alignments (up to 10 regions, UCSC hg19) and 3 nucleotide mismatches per each 25-bp segment. Results were viewed with the UCSC genome browser <http://genome.ucsc.edu/> and the Integrative Genomics Viewer (IGV) software: broadinstitute.org/igv/.

Identification and cloning of novel splicing forms

Rapid amplification of cDNA ends (5' and 3' RACE) and cloning of full-length open reading frames were performed with SMARTer RACE cDNA kit (Clontech,) using a pool of DNase-I treated RNA samples from PolyI:C-treated PHHs from several liver donors (Supplementary Table 1 for primers). PCR reactions were performed with AmpliTaq Gold 360 Master Mix (Life Technologies) and 360 GC Enhancer (Life Technologies) using the touchdown PCR program: 10 minutes at 95 °C, 20 cycles of touchdown (30 seconds at 95 °C, 45 seconds from 70 to 60°C decreasing by 1 °C after each 2 cycles, 45 seconds at 72 °C); 25 additional cycles (30 seconds at 95 °C, 45 seconds at 60 °C and 45 seconds at 72 °C); and final extension time of 7 minutes at 72 °C. Gel-purified PCR fragments were cloned into a C-terminal pFC14A-Halo tag expression vector (Promega) and sequenced for validation. IFNL3-Halo expression construct was generated using the same approach. p179 was also cloned into a pcDNA3.1-FLAG-tagged expression vector.

Production of recombinant proteins

IFNL4 and IFNL3 bacmids were generated in pFastBac C-terminal His-tag vector (Life Technologies) and expressed in a sf9 baculoviral strain. Using the anti-His-tag antibody (Sigma), expression of IFNL3 was detected in cell media, which was used for protein purification. Expression of p179 was not detectable in cell media and protein was purified from the cell pellet after cultivation of cells for 3–5 days in 2 liters of SF-900 III medium (Life Technologies). Proteins were first purified on HisTrap 5-ml nickel column followed by size-exclusion chromatography preparative column TSK G3000pw of 21.5×600 mm (Tosoh). The purified protein fractions were concentrated and dialyzed into a buffer. High protein purity (>90%) was confirmed by Coomassie staining and Western blot analyses with anti-His antibody (#H1029, Sigma, 1:3000 dilution), anti-IFNL3 and custom mouse and rabbit monoclonal anti-p179 antibodies. The IFNL3 and p179 proteins were custom-produced by Protein One.

Development of anti-IFNL4 antibodies

A mouse monoclonal antibody was custom-developed for a synthetic peptide KALRDYEEEEALSWGQRNCSFRPRRDSRPS corresponding to amino acids 44–74 of p179 protein, by Precision Antibody. A rabbit monoclonal antibody was custom-developed for a synthetic peptide PGSSRKVPGAQKRRHKPRRADSPRC corresponding to amino acids 128–152 of p179 protein, by Epitomics.

Evaluation of biological activity of novel proteins

Luciferase Cignal 45-Pathway Finder Reporter Arrays were used in HepG2 cells according to instructions (Qiagen, full list of reporters tested is available at http://www.sabiosciences.com/reporter_assay_product/HTML/CCA-901L.html). Cells were transfected with expression constructs for p179, p170, p143, p131, p124 and p107 or treated for 24 h with purified recombinant proteins –10 ng/ml of IFN- or IFNL3 and/or IFNL4-p179. Validation was performed with an individual interferon-stimulated response element

(ISRE) luciferase Cignal reporter. All studies were performed using at least 8 biological replicates. A HepG2 cell line stably expressing the same ISRE-Luc reporter construct was generated by transduction of cells with a Luciferase Cignal Lenti ISRE reporter construct (Qiagen) and selection of positive clones by growth in DMEM + 10% FBS with 1x Antibiotic-Antimycotic (Life Technologies) and 2 ug/mL puromycin. The best HepG2-ISRE-stable clones were identified by testing with purified recombinant IFN- and IFNL3.

Global analysis of transcriptome and pathway analysis

HepG2 cells were mock-transfected with an empty Halo-tag vector or with IFNL4-Halo expression construct. High-quality RNA (RIN ~10) prepared from transfected cells (48 hours) was used for sequencing with HiSeq 2000 (Illumina), generating ~300M reads per sample. Standard analysis identified 535 transcripts with >2-fold difference in expression and an FDR<0.05. Ingenuity Pathway Analysis (IPA) performed on this set nominated a list of pathways and specific transcripts. mRNA expression of selected transcripts was evaluated in samples transfected with mock, IFNL4, p107, p131 constructs or/and treated with 10 ng/ml of IFN- or IFNL3, in 4 biological replicates. mRNA expression in all samples was evaluated with pathway-based RT² Profiler PCR arrays, according to instructions (Qiagen).

Confocal Imaging

PHH cultured on collagen-coated slides were treated with 50µg/ml PolyI:C for 0 h (untreated), 2, 4, 8 and 24 hrs. HepG2 cells were transiently transfected with IFNL4-Halo expression construct. Cells were fixed for 20 min with 4% formaldehyde (Sigma) in PBS, permeabilized with 0.5% TritonX 100 (Sigma) for 5 min, blocked with 4% BSA (Sigma) and then incubated overnight at 4°C with primary antibodies: mouse monoclonal anti-IFNL4 ab (custom), rabbit α -tubulin ab (ab-15246, Abcam), rabbit anti-Halo-tag ab (Promega), mouse α -tubulin ab (ab-7291, Abcam, all at 1:1000 dilution. Secondary antibodies were donkey anti-rabbit or anti-mouse Alexa Fluor 594 and donkey anti-rabbit and anti-mouse Alexa Fluor 488, all at 1:1000 dilutions (Life Technologies). Slides were covered with mounting media (Prolong Gold Antifade Reagent with DAPI). Immunofluorescent images were obtained with a confocal laser-scanning microscope (LSM 510 META, Carl Zeiss).

Analysis of *IFNL4* mRNA expression

All expression assays (Supplementary Table 1 and Supplementary Fig. 10) were purchased from Life Technologies. Expression analysis was performed with gene expression master mix (Life Technologies) on DNaseI-treated RNA samples on ABI SDS 7700 instrument. Expression was measured in Ct values (PCR cycle at detection threshold), which are log 2 values. Expression was normalized to *PPIA* (endogenous control) and analyzed according to relative quantification method, as $Ct = Ct_{PPIA} - Ct_{target}$. Fold difference between any two samples can be calculated as $fold = 2^{-(Ct_1 - Ct_2)}$.

Genotyping

Genotyping was performed with custom-designed TaqMan assays (Supplementary Table 1 and Supplementary Fig. 10), using Genotype Master Mix (Qiagen), on ABI SDS7700, with standard conditions. Testing was performed blinded to clinical phenotypes. Sanger sequencing of HapMap samples and subsets of clinical samples showed complete concordance with Taqman genotyping results.

Clinical and epidemiological studies

The studies had been approved by the institutional review boards of the participating institutions and all patients gave informed consent for genetic testing. Ancestral designation

was self-reported in all studies. Full details of the studies are provided in a Supplementary Note included in Supplementary Materials.

Statistical analysis of genetic association

All statistical comparisons of *IFNL4* ss469415590 and rs12979860 were limited to subjects successfully genotyped for both variants. The Kruskal-Wallis test was used to compare median HCV RNA levels between genotypes for each variant (e.g., ss469415590-TT/TT versus ss469415590- G/ G). The mean HCV RNA levels in each of the three ss469415590 genotype groups (i.e., G/ G, G/TT, TT/TT) were compared with the respective rs12979860 genotype groups (TT, CT, CC). The global null hypothesis assumed no difference in decreases of mean HCV RNA values in ss469415590 compared to corresponding rs12979860 genotype groups. Statistical significance of these three mean differences was based on a Wald statistic (3 df) for which the variance was computed using a bootstrap based on re-sampling subjects with replacement (1000 re-samplings). For dichotomous outcomes (e.g., SVR, spontaneous clearance) the odds ratios and accompanying p-values (Wald chi-square) were calculated using proc logistic (SAS 9.2 TS2M3). The differences in the area under the receiver operating characteristic curve (AUC)⁵⁸ values were evaluated with p-values based on a chi-square test (1 df) that used a bootstrap variance estimate computed by re-sampling subjects with replacement and then repeating the AUC computations for each bootstrap sample.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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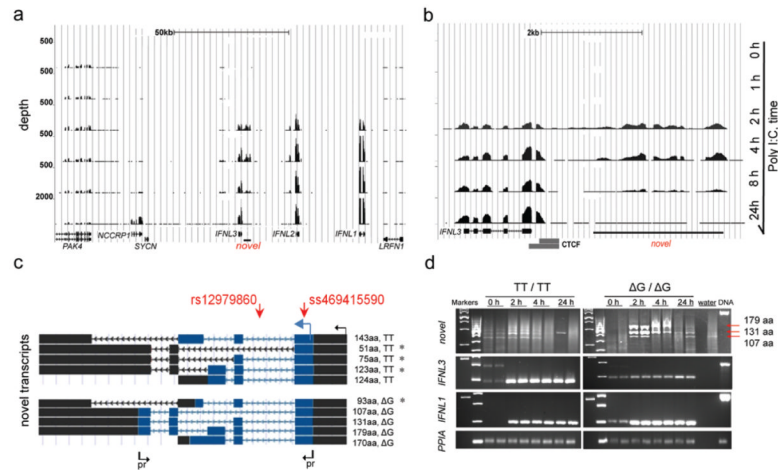


Figure 1. Identification of a novel transcribed region upstream of *IFNL3* gene

RNA-seq in primary human hepatocytes (PHH) treated with 50 ug/ml PolyI:C for 0, 1, 2, 4, 8 or 24 hours. RNA-seq plot of the 150-Kb region in USCS browser shows expression of *IFNL1*, *IFNL2* and *IFNL3*, and a novel transcribed region upstream of *IFNL3*. The number of reads (depth) corresponds to the level of mRNA expression.

a. Detailed view of the RNA-seq results for *IFNL3* and the novel transcribed region. A CTCF transcriptional insulator (ENCODE data²⁴) between these regions indicates their independence.

b. Splicing architecture of the ten novel transcripts (NCBI accession numbers are presented in Supplementary Table 2). The GWAS marker, rs12979860, is located within the first intron, while a novel marker, ss469415590-TT/ G, is located within the first exon, common for all transcripts. Transcription and translation start sites are marked by black and blue arrows; open reading frames are shaded in blue. * -transcripts which carry premature stop codons and are likely to be eliminated by nonsense-mediated decay. Arrows indicate location of primers (Supplementary Table 1) used to generate PCR-products presented on panel d.

c. PCR results in PHH cDNA using primers from panel c. No distinct PCR product is expected in the TT/TT sample; in the G/ G sample these primers capture transcripts producing proteins of p179, 131 and 107 aa, but not of 170 aa; a transcript producing a 93 aa protein fragment is expected to be degraded. *IFNL3*, *IFNL1* and *PPIA* (endogenous control) were measured in the same samples. Similar amounts of DNaseI-treated high quality RNA was used for all the reactions.

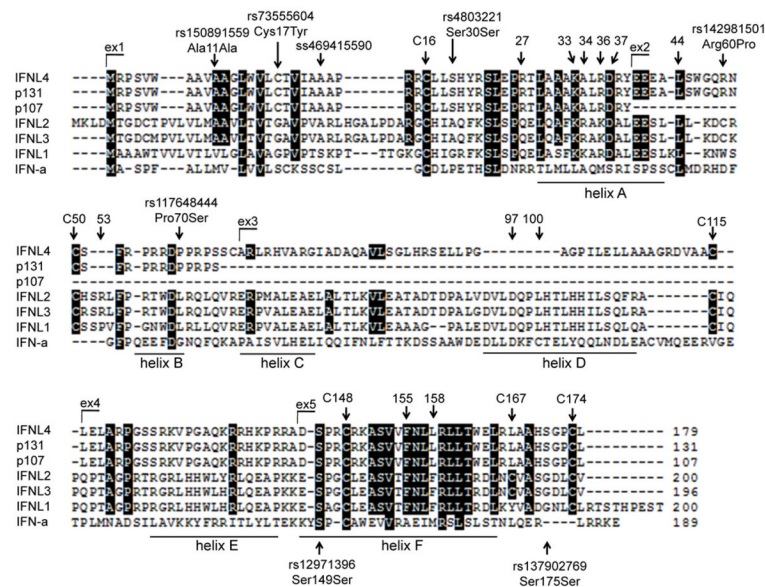


Figure 2. Protein sequence analysis

ClustalW protein sequence alignment for IFNL4 (p179), p131, p107, IFN- s (IFNL1, IFNL2 and IFNL3), and IFN- . Identical amino acids are shaded in black. Exon numbering and the location of ss469415590 and other variants identified by sequencing of 270 HapMap samples, are based on IFNL4 protein sequence. Annotations of protein helices, amino acid numbering and specific amino acids are based on the sequence of mature IFNL3 protein^{26,27} (without leader peptide). Indicated: cysteins conserved between IFNL4 and all other IFNL proteins (C16, C50, C115, C148 and C174), interaction sites of IFNLs with their first common receptor IFNLR1 (aa 27, 33, 34, 36, 37, 44, 53, 155, 158); and interaction sites with their second receptor, IL10R2 (aa 97, 100).

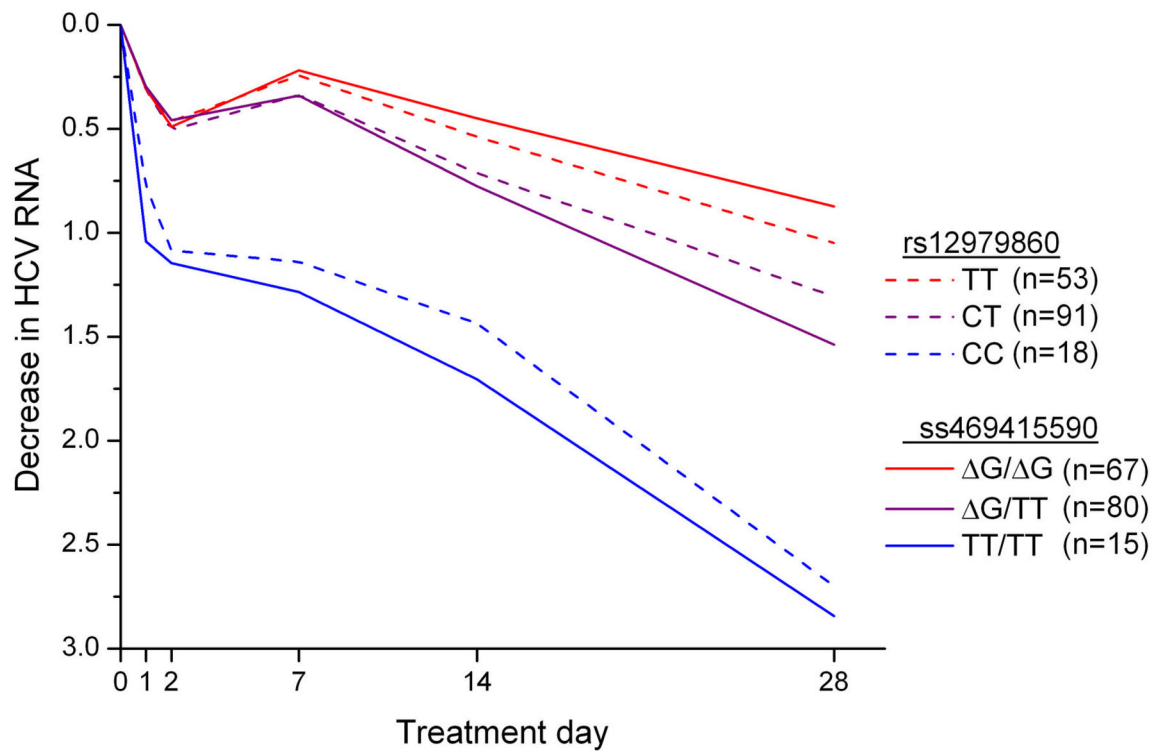


Figure 3. Median decrease in HCV RNA (log₁₀ IU/ml) in African-American participants in Virahep-C study during the first 28 days of treatment with pegIFN- α /RBV
 $P=0.015$ for comparison of mean differences in HCV RNA levels at day 28 for each of the three genotype groups for ss469415590 with the respective group for rs12979860.

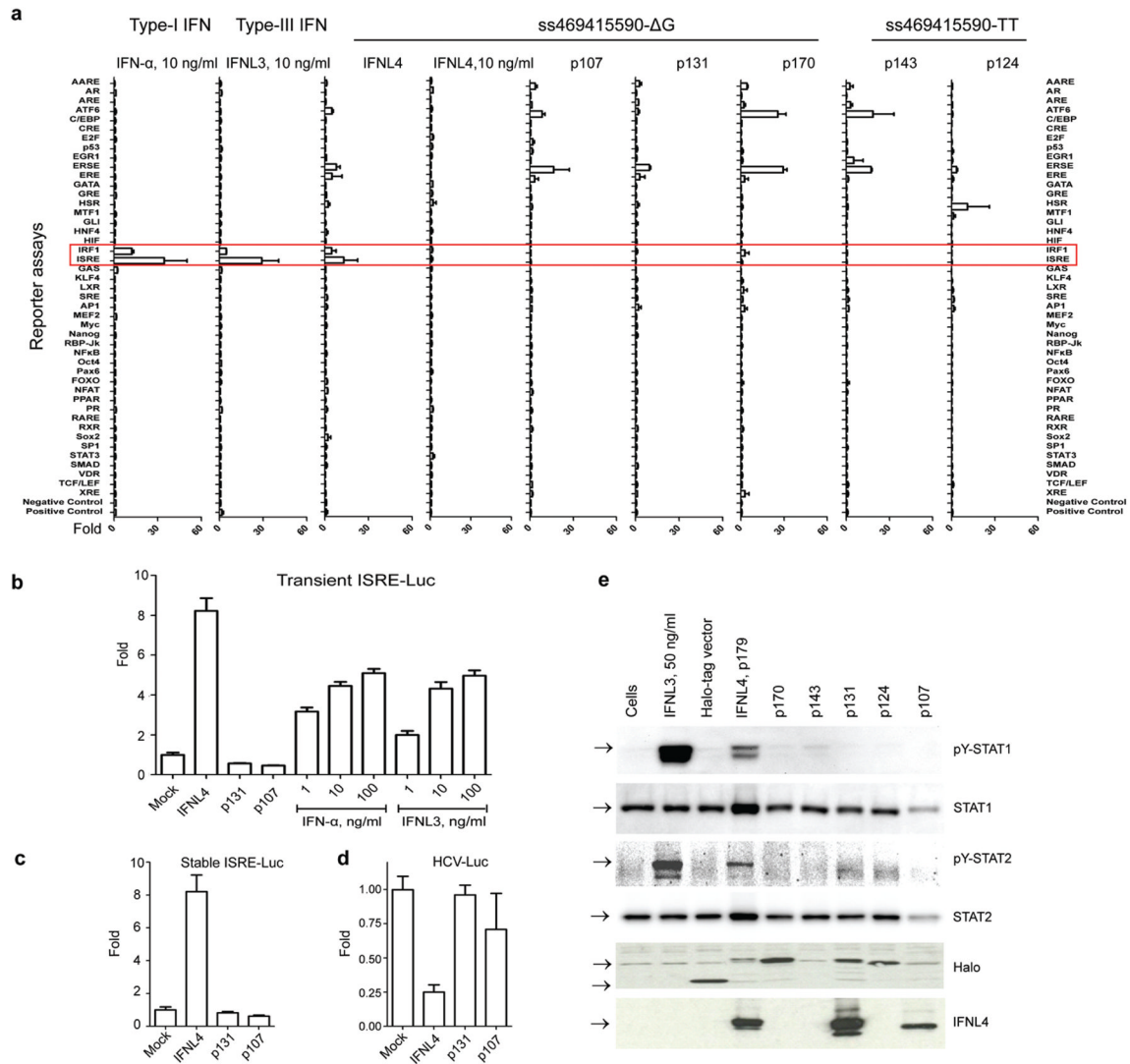


Figure 4. Analysis of biological activity of novel proteins

a. “Pathway finder” analysis using luciferase reporter constructs representing 45 human signaling pathways in HepG2 cells. The cells were transfected with expression constructs or an empty vector (mock), or treated with 10 ng/ml of recombinant purified IFN- α , IFNL3, IFNL4, or with PBS (mock). All results represent mean values of two independent biological transfection/treatment replicates, with standard deviations.

b. Results of transient transfection of the IFNL4, p131 and p107 expression constructs and treatment with recombinant purified IFN- α and IFNL3 proteins in HepG2 cell line transiently co-transfected with ISRE-Luc reporter. The results are normalized to transfection with an empty vector (mock) and represent mean values of 8 biological replicates, with standard errors.

c. Results of transient transfection of the IFNL4, p131 and p107 expression constructs in HepG2 cell line stably expressing the ISRE-Luc reporter. The results are normalized to transfection with an empty vector (mock) and represent mean values of 11 biological replicates, with standard errors.

d. Test for antiviral effects of the IFNL4, p131 and p107 expression constructs transiently transfected into Huh7-Lunet cells stably expressing a subgenomic, luciferase-expressing

HCV replicon (HCV-Luc), compared to an empty vector (mock). Results represent mean values of 4 biological replicates, with standard errors.

e. Western blot analysis of Y701-STAT1 and Y689-STAT2 phosphorylation in HepG2 cells transiently transfected with expression constructs for the six protein isoforms. All Halo-tag expression constructs produce proteins detectable with an antibody for the Halo-tag; a rabbit monoclonal anti-IFNL4 antibody recognizes IFNL4 (p179) as well as its nonfunctional isoforms p131 and p107.

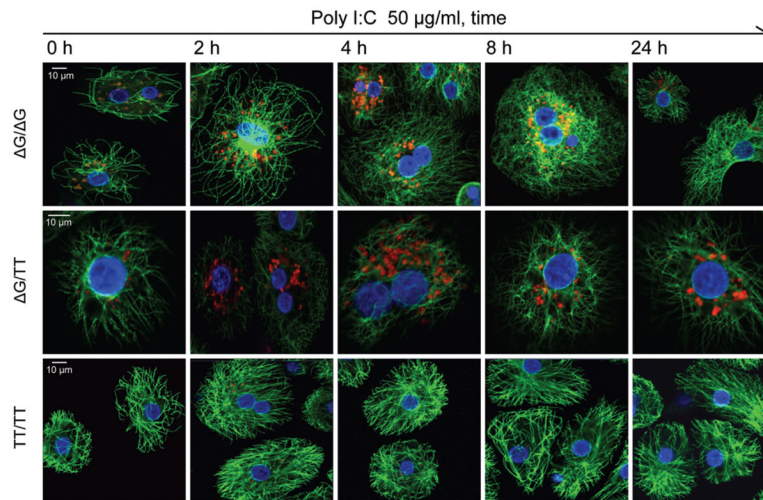


Figure 5. Confocal imaging of IFNL4 in primary human hepatocytes (PHH) from liver donors with different ss469415590 genotypes

Confocal imaging in PHH treated with 50 µg/ml of PolyI:C for 0, 2, 4, 8 or 24 hours. Red staining – IFNL4, green – cytoskeleton (-tubulin), blue – nuclei. Confocal imaging of endogenous IFNL4 expression in the same ss469415590- G/TT sample after *in-vitro* infection with JFH1-HCV strain is presented in Supplementary Fig. 6.

Table 1

Comparisons between p179 (IFNL4) and selected members of class-2 cytokine family

Protein	p179 (IFNL4)	IFNL3	IFNL1	IFNL2	IFN- 1	IL10	IL22	IFN- 1
Type	IFN-III	IFN-III	IFN-III	IFN-III	IFN-I	IL10-family	IL10-family	IFN-I
mRNA	JN806234	NM_172139	NM_172140	NM_172138	NM_002175	NM_000572	NM_020525	NM_002176
Protein ID	AFQ38559	A2BDEI	Q8IU54	Q45KQ8	P05014	Q6FGW4	Q9GZX6	Q5VWC9
Size, aa	179	196	200	200	189	178	179	187
Exons	5	5	5	6	1	5	5	1
Identity with p179, aa, n (%)	--	52 (29.1)	48 (26.8)	47 (26.3)	26 (14.5)	24 (13.4)	20 (11.1)	20 (11.1)
Similarity with p179, aa, n (%)	--	73 (40.8)	66 (36.8)	70 (39.1)	47 (26.2)	40 (22.3)	45 (25.1)	44 (24.5)

Table 2

Comparison of rs12979860 and ss469415590 genotypes among African-American participants of Virahep-C study and HALT-C Trial for associations with response to treatment with pegIFN- α /RBV

Variant	Genotype	N	Treatment Time Point								
			Week 20/24*			End-of-Treatment			SVR		
			Response Rate (%)	OR	P-value	Response Rate (%)	OR	P-value		Response Rate (%)	OR
Virahep-C (n = 169)											
rs12979860	TT	57	40.4	Ref.		36.8	Ref.		24.6	Ref.	
	CT	93	50.5	1.51	0.23	40.9	1.18	0.62	29.0	1.26	0.55
	CC	19	63.2	2.53	0.089	52.6	1.90	0.23	36.8	1.79	0.30
ss469415590	G/ G	71	35.2	Ref.		32.4	Ref.		21.1	Ref.	
	G/TT	82	56.1	2.35	0.010	45.1	1.72	0.11	31.7	1.73	0.14
	TT/TT	16	68.8	4.05	0.019	56.3	2.68	0.080	43.8	2.90	0.067
HALT-C Trial (n = 144)											
rs12979860	TT	61	9.8	Ref.		8.2	Ref.		3.3	Ref.	
	CT	72	16.7	1.83	0.26	12.5	1.60	0.42	6.9	2.20	0.36
	CC	11	45.5	7.64	6.2×10^{-3}	36.4	6.40	0.018	27.3	11.06	0.015
ss469415590	G/ G	68	8.8	Ref.		7.4	Ref.		2.9	Ref.	
	G/TT	68	19.1	2.44	0.090	14.7	2.17	0.18	8.8	3.19	0.16
	TT/TT	8	50.0	10.34	4.7×10^{-3}	37.5	7.56	0.019	25.0	11.0	0.027

* In Virahep-C³²-response is at 24 weeks after initiation of pegIFN- α /RBV treatment; in HALT-C³³-response is at 20 weeks after initiation of pegIFN- α /RBV treatment; SVR - sustained virological response; OR - odds ratio.

Table 3

Comparison of rs12979860 and ss469415590 genotypes among African-American participants of the Urban Health Study (UHS) and ALIVE for associations with spontaneous clearance of hepatitis C virus (HCV) infection

Variant	Genotype	Chronic	%*	Clear	%*	OR	P-value	AUC
Urban Health Study (n=459)								
rs12979860	TT	119	34.0	26	23.9	Ref.		0.58
	CT	183	52.3	54	49.5	1.35	0.26	
	CC	48	13.7	29	26.6	2.77	1.5×10^{-3}	
ss469415590	G/ G	137	39.1	26	23.9	Ref.		0.62
	G/TT	168	48	53	48.6	1.66	0.056	
	TT/TT	45	12.9	30	27.5	3.51	7.9×10^{-5}	
ALIVE (N=664)								
rs12979860	TT	228	38.9	15	19.2	Ref.		0.64
	CT	275	46.9	37	47.4	2.05	0.025	
	CC	83	14.2	26	33.3	4.76	7.6×10^{-6}	
ss469415590	G/ G	255	43.5	19	24.4	Ref.		0.64
	G/TT	265	45.2	36	46.2	1.82	0.043	
	TT/TT	66	11.3	23	29.5	4.68	5.5×10^{-6}	

* Percentage of subjects with indicated genotype; OR - odds ratio; AUC - area under the receiver operating characteristic curve; Urban Health Study³⁴ and ALIVE³⁵ are epidemiological studies of injection drug users who were evaluated for chronic HCV infection on the basis of testing for anti-HCV and HCV RNA.