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Multi-ancestry Fine Mapping of Interferon Lambda and the Outcome of Acute Hepatitis C Virus Infection

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Abstract

Clearance of acute infection with hepatitis C virus (HCV) is associated with the chr19q13.13 region containing the rs368234815 (TT/ G) polymorphism. We fine-mapped this region to detect possible causal variants that may contribute to HCV-clearance. First, we performed sequencing of *IFNL1-IFNL4* region in 64 individuals sampled according to rs368234815 genotype: TT/clearance (N=16) and G/persistent (N=15) (genotype-outcome concordant) or TT/persistent (N=19) and G/clearance (N=14) (discordant). 25 SNPs had a difference in counts of alternative allele > 5 between clearance and persistence individuals. Then, we evaluated those markers in an association analysis of HCV clearance conditioning on rs368234815 in two groups of European (692 clearance/1 025 persistence) and African ancestry (320 clearance/1 515 persistence) individuals. 10/25 variants were associated ($P < 0.05$) in the conditioned analysis led by rs4803221 ($P=4.9 \times 10^{-04}$) and rs8099917 ($P=5.5 \times 10^{-04}$). In the European ancestry group, individuals with the haplotype rs368234815 G/rs4803221C were 1.7x more likely to clear than those with the rs368234815 G/rs4803221G haplotype ($P=3.6 \times 10^{-05}$). For another nearby SNP, the haplotype of rs368234815 G/rs8099917T was associated with HCV-clearance compared to rs368234815 G/rs8099917G (OR: 1.6, $P=1.8 \times 10^{-04}$). We identified four possible causal variants: rs368234815, rs12982533, rs10612351 and rs4803221. Our results suggest a main signal of association represented by rs368234815, with contributions from rs4803221, and/or nearby SNPs including rs8099917.

Introduction

The outcome of the acute hepatitis C virus (HCV) infection is determined in part by host genetic factors. Previous genome-wide association studies (GWAS) and meta-analyses have identified significant associations of spontaneous clearance of HCV infection with several single nucleotide polymorphisms (SNPs) in the region harboring 4 interferon- λ genes (*IFNL1*, *IFNL2*, *IFNL3* and *IFNL4*) on chromosome 19q13.13 (1–3). Of particular importance is a dinucleotide variant in the first exon of *IFNL4*, rs368234815 (G/TT), which causes a shift in the open reading frame of the gene; the presence of the G allele at the variant position allows the expression of a fully functional IFN λ 4 protein of 179 amino-acids (4,5). This allele is implicated in reduced HCV clearance (4). On the contrary, the TT allele is predicted to induce nonsense-mediated mRNA decay and is associated with increased HCV clearance (4) (Figure 1, Top panel).

Despite the strong and replicated association, some HCV infected individuals carrying the favorable genotype (TT/TT) of rs368234815 do not clear the infection, while some patients

with the unfavorable genotypes spontaneously clear the infection (4,6–10). This discordant *IFNL* genotype with HCV infection outcomes are not explained by other determinants of spontaneous clearance such as polymorphisms in other known HCV related genes, sex, or HIV co-infection. Thus, we reasoned that other variants in the *IFNL* region may contribute to the observed spontaneous clearance.

The *IFNL1-IFNL4* region is under strong linkage disequilibrium (LD) which complicates the identification of causal alleles (11). Moreover, sequencing of the region is limited by the presence of genes with high homology that precludes the accurate assignment of reads to a specific location (12,13). In this study we sought to overcome these challenges and to identify variants that may contribute to clearance of HCV infection. We implemented two approaches to identify variants with an association independent of rs368234815 (Figure 2). First, we performed short-read sequencing analysis in a selected panel of individuals where the rs368234815 genotype was either concordant or discordant with the expected HCV outcome (clearance or persistence) using a sequencing strategy that allowed the precise assignment of the reads to specific coordinates in the locus and accurate calling of the variants. Second, we performed conditional analysis in a large independent set of individuals of European and African ancestry evaluated for display of HCV spontaneous clearance for whom we had genotypes imputed to the 1000 Genomes Project (14). To identify potential causal variants in the region we used well established statistical methods combining functional data from external sources with the association and LD patterns from our datasets (Figure 2). We also interrogated our dataset for association of two variants (rs1176648444 and rs4803217) that have been identified as functionally relevant in the region.

Materials and Methods

Genetic structure of the *IFNL* region:

The interferon lambda region spans 50Kb of human chromosome 19q (15,16), Figure 3. The 4 interferon- λ genes seem to originate from gene duplication events (4,17) with *IFNL2* and *IFNL3* more closely related to each other than *IFNL1* (4). *IFNL1* and *IFNL2* are transcribed from the positive strand with a coding region of 2,348 and 1,445 basepairs (bp), with 5 and 6 exons, respectively. *IFNL3* and *IFNL4* have 6 and 5 exons each, are transcribed from the negative strand and have a coding region of 1 336 and 2 543 bp, respectively (Figure 3) (16).

Short-read sequencing in panel of discordant and concordant individuals

Individuals for *IFNL* Sequencing: Individuals included in this approach are part of the HCV Extended Genetics Consortium (2,18). Each individual study obtained consent for genetic testing from their governing Institutional Review Board and the overall research was approved by the Johns Hopkins School of Medicine Institutional Review Board (3). For this analysis we selected 64 individuals based on the genotype of rs368234815 and HCV spontaneous clearance/persistence status in a similar approach presented by Rauch et al for rs8099917 (1). This included 45 individuals of African Ancestry (21 clearance/24 persistence) and 19 individuals of European Ancestry (9 clearance/10 persistence) (Table 1, Figure 1, Bottom panel). These individuals were either concordant between genotype and HCV outcome (i.e. favorable genotype of rs368234815 [TT/TT] and HCV spontaneous

clearance or unfavorable genotypes rs368234815 [G/ G] and HCV persistence) or were discordant (i.e. favorable genotype and HCV persistence or unfavorable genotype and HCV clearance) (Table 1, Figure 1, Bottom panel).

***IFNL* Sequencing:** Because the region containing the four *IFNL* genes has low sequence complexity, the alignment of short reads generated with standard high-throughput sequencing methods is challenging (12); thus, we designed a targeted sequencing approach where the entire 70.8 Kb region (chromosome 19:39721399–39792284, coordinates based on The Genome Reference Consortium Human build 37-GRCh37-) was amplified in eight segments with customized primers (Figure 3, Supplementary Table 1). This allowed alignment of reads specifically to the region of origin, resulting in more confident detection of individual variants across the whole region. Methods of DNA extraction and strategies for sequencing and alignment are described in detail in Supplementary Material.

Statistical Analysis of the sequenced panel: Counts of alternative (non-reference, non-ancestral) alleles at each position of the sequenced region were generated to compare differences in single-nucleotide variants (SNVs) between concordant and discordant individuals. We report all positions where the difference in alternative allele count is at least 5. Given sample size limitations, we did not perform formal statistical tests for differences between groups, but report all positions for validation in imputation data. Customized scripts in R (<https://www.r-project.org/>) were used to do the SNV analysis. Results of comparison of all variants included in the analysis of the region is available upon request.

Conditional Analysis of an independent imputed dataset.

Individuals of the independent imputed dataset: We analyzed the rest of the individuals of the HCV Extended Genetics Consortium (2,18), corresponding to an independent set of 1835 individuals of African Ancestry (320 clearance/1515 persistence) and 1717 individuals of European ancestry (692 clearance/1025 persistence). The rs368234815 G allele had a frequency of 0.63 in the African ancestry group and 0.31 in the European ancestry group (Table 1).

Genotyping and Imputation: Genotypes in this region were derived from a genome-wide association study previously described (2,3) and in Supplementary Material. For this analysis, 421 high quality imputed variants in the *IFNL* region were used in African ancestry individuals and 282 in European ancestry individuals.

Statistical Analysis of the independent imputed dataset: In each of the ancestry groups, we performed an association analysis of dosage of the variants in the region conditioned on the rs368234815 variant using an additive logistic regression model, adjusting for 3 principal components and HIV status using Mach2dat (19). Conditional analysis in the two ancestry groups were meta-analyzed using the fixed effects inverse variance method in METAL software (20). Given that this region has been highly replicated and to preserve power for detect secondary signals in the fine mapping, a value of $P < 0.05$ was considered as significant (21). Results from the imputation analysis were pulled to check for significance at any of the loci that were identified based on alternative allele

counts from the sequencing analysis. Candidate sites with difference in the allele count and significance in the imputed dataset were carried forward for the haplotype analysis.

Haplotype analysis: To further characterize the locus across populations, we conducted haplotype association analyses. We calculated LD and constructed haplotypes based on the candidate sites in the European ancestry and African ancestry populations. LD patterns in each population were calculated using the algorithm from Gabriel *et al* (22) in Haploview (23) in the imputed dataset. We performed haplotype analyses using the “haplo.stat” R package (24). We assumed an additive model in which the regression coefficient represented the expected change in the log odds of HCV clearance with each additional copy of the specific haplotype compared with the reference haplotype.

Identification of potential causal variants

To identify variants that may be causal or have a regulatory function we refined the region observed in a previous GWAS of HCV clearance (3). We used association summary statistics from GWAS for those markers in the *IFNL* region, leveraged functional data and LD information of the included markers and described a 99% credible set of variants using PAINTOR (25,26) as described in detail in Supplementary Materials. Aiming to optimize power for this analysis, we included the complete dataset of the HCV Extended Genetic consortium comprising 3608 people from two ancestry groups: 1869 individuals of African ancestry (340 clearance/1529 persistence) and 1736 of European ancestry (701 clearance/1,035 persistence). We considered PAINTOR predicted variants to be functional based on a posterior probability > 0.1, a threshold suggested previously (26). To investigate functional elements, the presence or absence of overlap was determined by the UCSC Table Browser intersecting the calculated credible set with the signal tracks described in Supplementary Materials.

Analysis of functionally relevant variants

Two markers (rs4803217 and rs117664844) has been described as modulators of the association given by rs368234815 (Supplementary Material). Given their potential functional role, we evaluated their allele count in the sequenced dataset and the association of each variant in the imputed dataset after conditioning on rs368234815. We also evaluated the residual association after conditioning on both rs368234815 and rs117664844 and the association of the rs368234815- rs4803217 and rs368234815- rs117664844 haplotypes in each population and using the methods described in haplotype analysis, we constructed and evaluated association of haplotypes based on the candidate sites common to European and African ancestry populations incorporating these functionally relevant variants.

Results

When analyzing all individuals of the sequencing group (concordants and discordants), we identified 25 positions (candidate SNVs) where the difference in the frequency of the alternative allele was >5 between the individuals with clearance and persistence (Table 2). The identified variants are located downstream of *IFNL3-IFNL4* and in the intergenic regions between *IFNL4-IFNL2* and *IFNL2-IFNL1* (Supplementary Figure 1).

Conditional Analysis in an independent imputed dataset.

From all the variants analyzed in the region in this dataset, we extracted the results of the 25 variants identified in the targeted sequencing panel. From those, 2 variants were not present in both ancestry groups and 10 candidate variants were significantly associated (P value < 0.05) in the meta-analysis (Supplementary Figure 1, Table 2). No other variants in the region was significantly associated in the conditional analysis.

The 10 candidate variants are located in an 11.3Kb region (chr19: 39732501–39743821) spanning 1.7 Kb downstream of *IFNL3* and 4.3Kb upstream of *IFNL4* (Figure 4, Panel A-B and Supplementary Figure 1). The association observed in this meta-analysis was driven mainly by the contribution of the European ancestry samples (Table 2). In this group, nine of ten associated variants have similar minor allele frequencies (~ 0.19) with the exception being rs4803222 (0.30). Rs4803221, a synonymous SNP in *IFNL4* (NM_001276254: S (TCG) --> S (TCC)), had the strongest association in the meta-analysis (P-value = 4.86×10^{-04}) and in the European ancestry group (P-value = 7.49×10^{-06}). In the African ancestry population, the direction of the effect is the same but no variants were significantly associated. The allele frequencies for seven of ten variants were similar across the ancestry groups. However, at rs8107030, rs8099917 and rs7248668 minor allele frequencies were lower in the African ancestry population (0.04–0.06) than in persons of European ancestry (0.19) (Table 2).

Haplotype analysis.

The markers included in the haplotype analysis were rs368234815 and the ten candidate variants (Figure 4, Panel C). Haplotype construction revealed that in the European ancestry individuals all 11 SNPs are within one unique haplotype block of 11kb with LD values consistently high ($r^2 > 0.89$), except for rs4803222 and rs368234815 with an $r^2 \sim 0.50$ with the other variants (Figure 4). Thus, the top SNP of the candidate variants (rs4803221) tags all associated variants in the block except for rs4803222 and rs368234815.

We estimated the frequency of the haplotypes based on the boundaries determined in the haplotype blocks for each population. In the European ancestry samples, the 11 markers formed 24 haplotypes of which four (denoted H1 to H4) had a frequency higher than 2 % so were included in the haplotype association analysis (Supplementary Table 2). H1 (containing the favorable TT allele of rs368234815) was the haplotype with highest prevalence overall and was more frequent in the clearance group (P-value = 4.4×10^{-22}). H2, H3 and H4 contained the unfavorable allele (G) of rs368234815. H3 and H4 and were significantly associated with persistence (P value < 0.05). H2 had a low prevalence (2%) and was not associated with HCV clearance (P value = 0.53).

In African ancestry individuals, there was unique haplotype block of 5Kb containing 9 out of the 11 variants with LD r^2 values ranging from 0.99 to 0.03 (Figure 4). In this population rs4803221 is able to capture information only from rs8105790, rs66531907, rs12983038, rs8109889 but not from rs8099917 or rs7248668. Similarly, rs8107030, rs368234815 and rs4803222 only capture information from themselves. Similar to the European ancestry population, rs368234815 had low LD r^2 values with the ten variants (Figure 4).

In African ancestry individuals, 21 haplotypes were present and five with the highest frequency (> 6%) were included in the analysis. Haplotypes H1-H4 are similar to those of the European ancestry populations for the shared markers. Similarly, H1 was more frequent in the clearance group (P value= 1.5×10^{-14}), however, this haplotype had a considerably lower prevalence in this sample compared to the European ancestry sample (37.5% vs. 68.1%), which can be explained by the differences in the allelic frequency of the G allele between those samples (Table 1).

In the African ancestry sample, H2 was the predominant haplotype conferring persistence and has a considerably higher prevalence in this African ancestry group (36% vs 2% in the European group). H3 and H4 were associated with persistence with comparable effect size but lower significance (P = 0.02). In summary, in both sample groups H1 was significantly associated with clearance. However, the predominant haplotypes conferring persistence were different in each sample group (H3 in European ancestry vs. H2 in African ancestry individuals), Supplementary Table 2. Similar results were observed in the haplotype analysis including common candidate variants and functionally relevant variants, except for the separation of H2 in African Ancestry individuals in H2a and H2b. H2b conserved similar direction and strength of effect than H2 (Supplementary Table 3).

Next, to determine whether an allele or haplotype could “overcome” the unfavorable allele (G) of rs368234815, we restricted our analysis to haplotypes containing this unfavorable allele in the European ancestry group. We found that the haplotypes with the C allele at rs4803221 were significantly associated with clearance compared to those containing the G allele (OR: 1.7, 95% CI: 1.3–2.29, P value = 3.6×10^{-05} , Table 3). This was not observed in African ancestry individuals (OR for haplotype with the C allele: 1.25; 95% CI: 0.81–1.9, P value = 0.29). Rs4803221 tags rs8099917 and rs7248668 in the European ancestry group but not in the African ancestry group. Similar to rs4803221, the haplotype containing the T allele of rs8099917 (and G allele of rs7248668) is significantly associated with clearance compared to the one containing the G allele of rs8099917 (and A allele of rs7248668: OR: 1.6, 95% CI: 1.3–2.16, P value: 1.76×10^{-04}) in the European ancestry individuals but not in African ancestry individuals (Table 3). These data are consistent with a main signal being shared across populations driven by one or more functional variants represented by rs368234815, with potential additional contributions from rs4803221, and/or proxies including rs8099917 and rs7248668 in the European ancestry population.

Identification of potential causal variants

Four SNPs were identified as likely functional (posterior probability > 0.1, Supplementary Table 4). The credible set obtained with PAINTOR, determined by 2 out of 4 variants of the credible set (rs368234815 and rs12982533), overlaps with the previously estimated credible set using a larger dataset (3), narrowing the signal to a 7251 bp region (19:39731904–39739155) located 2368bp downstream from *IFNL3* and extending until exon 1 of *IFNL4* (Supplementary Figure 2). The identified region includes rs368234815 which we confirmed as the main driver of the association signal. The variants identified in the fine-mapping credible set overlapped with regulatory regions in hepatocyte cell lines and liver tissue including CpG sites that are completely or partially methylated, target sites for transcription

factors, DNA methylation sites with 50–100% methylation in those cells, candidate weak enhancers, polycomb repressors and with transcription associated activity (Supplementary Figure 2). Two other variants (rs4803221 and rs10612351) also showed posterior probability values > 0.10 indicating that they might be considered causal even though rs10612351 is not included in calculated 99% credible set. We considered that these polymorphisms are plausible candidate variants based both on fine-mapping and regulatory overlap and these results support the findings of the haplotype analysis.

Analysis of functionally relevant variants

Rs4803217 and rs1176648444 had a difference of 1 and 0 respectively in the counts of the alternative allele between clearance and persistence in the sequenced panel. Rs4803217 showed no association in the imputed dataset after conditioned on rs368234815 (European ancestry conditioned P value= 0.15, African ancestry conditioned P value= 0.3, Meta-analysis conditioned P value= 0.08). Rs1176648444 was not associated in African Ancestry (P value= 0.38) but interestingly it showed a significant association in individuals of European Ancestry only in the conditioned analysis (Not conditioned P value= 0.07; conditioned P value=0.00003, conditioned meta-analysis P value = 0.06). In the double conditioned analysis with rs368234815 and rs1176648444, six out of ten variants associated in the single conditioned analysis showed residual association (Supplementary Table 5). Rs368234815TT- rs4803217C haplotype was significantly associated with clearance compared with the rs368234815 G-rs4803217A in both populations. In African ancestry population the haplotype rs368234815 G-rs4803217C was significantly associated with persistence (Supplementary Table 6). On the other hand, in the European ancestry population, the haplotype rs368234815 G- rs1176648444A (IFN λ 4-S70) was associated with clearance with an intermediate effect between rs368234815 G-rs1176648444G (IFN λ 4-P70) and rs368234815TT-rs1176648444G (no IFN λ 4), Supplementary Table 7.

Discussion

We performed a comprehensive, trans-ethnic analysis of genetic variation in the *IFNL* region and spontaneous recovery from HCV infection. We discovered variants with associations independent of the well-described rs368234815 variant that suggest additional genetic contributions to the outcome of this chronic infection.

We observed an rs368234815-independent signal led by rs4803221 (given mainly for the European Ancestry population) and ten other variants in LD including rs8099917 and rs7248668. In sensitivity analysis we confirmed that this signal was present even after conditioning on rs368234815 and rs1176648444 indicating a residual or modifying effect of the remaining variants. The LD structure of the region in the European ancestry group suggests that the rs4803221 association may be due to any one of a number of variants including rs8099917 and rs7248668. In fact, in the context of haplotypes conferring persistence in this group, the haplotype containing the C allele of rs4803221, the T allele of rs8099917 and the G allele of rs7248668 were significantly associated with HCV clearance. However, we do not observe a significant signal in individuals of African ancestry at rs4803221, even though its allele frequency and the sample size are similar to the European

ancestry group. It is possible that the association of rs4803221 observed in the European ancestry group is explained by linkage with rs8099917 and/or rs7248668, instead of being functional itself. Unfortunately, our power was limited to confirm this inference in the African ancestry group, where we detected an odds ratio of 0.79 with a MAF of 0.06 (power of only 0.38 at a significance level of 0.05, compared to 1 in the European ancestry group) (27).

Rs4803221 is a variant with multiple functions which has been previously linked to HCV spontaneous clearance in individuals with beta thalassemia (28). The SNP is located in exon one of *IFNL4*, 357 bp downstream from the transcription start site and 3522 bp upstream from the transcription start site of *IFNL3*; the G allele (MAF=0.2) abolishes a CpG site and induces a synonymous (Ser>Ser) change at position 30 of the *IFNL4* protein. Similar to our findings, Origa *et al*, found an association with rs4803221 that was independent of rs12979860 (which is itself in high LD with rs368234815) (28). Rs4803221 significantly improved the viral clearance prediction in patients carrying the un-favorable T allele of rs12979860 (in high LD with the un-favorable G allele of rs368234815). They hypothesized that the abolishment of methylation sites might increase expression of *IFNL3* and downregulate interferon sensitive genes, reducing net innate antiviral activity (28).

A potential 'causal' role has also been described for rs8099917 (1). In a GWAS including 1362 European ancestry individuals, G allele was associated with persistence of HCV infection (1). Several specific SNPs were identified as candidates for being causal, however rs368234815 was not described in this panel. In European HCV-infected individuals analyzed for response treatment, haplotypes tagged by the T allele of rs8099917 showed higher expression of *IFNL3* and *IFNL2* but no evaluation was reported on expression of *IFNL4* (29). Analogous results were found in a Japanese cohort where the expression *IFNL3* and *IFNL2* mRNA was lower in the carriers of the G allele (30). In our current study, T allele is associated with clearance in the context of the G allele of rs368234815, which corresponds with *IFNL4* transcription but HCV persistence (4). Rs8099917 is located 8.9 kb upstream from *IFNL3* and 16 kb upstream from *IFNL2*. If we assume the model that rs368234815 regulates the expression of *IFNL4* (Figure 1), it would be worthwhile to investigate if the statistically independent effect of rs8099917 observed in this study is perhaps caused by an increase in expression of *IFNL3* and *IFNL2*, a decrease in the production of *IFNL4* in those individuals with the G allele at rs368234815, or both.

SNP rs7248668 located in the 5' region of *IFNL4* is in high LD with rs8099917 in populations included in this analysis and in The 1000 Genomes Project independently of ancestry (14). In fine mapping analysis, the haplotype containing the G allele was associated with virologic response to pegylated interferon- α and ribavirin therapy for chronic hepatitis C in a Japanese population (30). Similarly, the patients with the GG genotype showed virologic response rates up to four times higher than those for patients with unfavorable genotypes in HIV/HCV co-infected patients of European ancestry (31). In our study the same G allele is associated with spontaneous clearance; even though the phenotypes are not completely comparable, in general the G allele favors the clearance of the virus in each context across studies. Due to their high LD the effect of rs7248668 is not separable from that of rs8099917.

Our fine mapping analysis using PAINITOR indicates that the potential causal variant in this locus is contained in the *IFNL3-IFNL4* gene region. This credible set informed by our analysis harbors the compound di-nucleotide exonic variant (rs368234815, G/TT) and the rs4803221 variant, but does not contain rs8099917 or rs7248668. It is possible that we did not find a high posterior probability for those 2 latter SNPs because they are in high LD with rs4803221 in European ancestry subjects, where the significant independent effect was observed. We consider that the expansion of the sample size of African ancestry individuals could allow disentanglement of the effects of rs4803221, rs8099917 and rs7248668. The coding nature of the rs368234815, the high significance and large effect-size, and the low LD between this variant and the others in the region (especially in the African ancestry population) contributed to determine this variant as functionally relevant.

The identification of rs12982533 as functionally relevant deserves further analysis. This variant has been included as part of haplotypes associated with response to treatment (13,32) but not with spontaneous HCV clearance; it is located 3.7kb 3' of *IFNL3* and its functional role is unknown. It is important to notice that we limited this analysis to only variants that were consistently present in both ancestry groups and it is possible that this set of variants fails to capture putatively important variation within or around the *IFNL* locus.

The results of the of rs368234815-rs1176648444 haplotype analysis in European ancestry agree with findings previously described by the Swiss Hepatitis Cohort Study Group (33) where they demonstrated that individuals with IFN λ 4-S70 have rates of HCV clearance that are intermediate to those with IFN λ 4-P70 and those with rs368234815TT/TT genotype, who do not produce the IFN λ 4 protein. Similarly, our findings on rs368234815-rs4803217 haplotype are in concordance with the association of rs368234815 G: rs4803217G with the poorest virologic response to peg- interferon alpha and ribavirin therapy in African Americans (34); even though it is not the same phenotype, it suggests an interaction of the two variants responsible for lower rate of resolution of the infection in general. The restriction of the haplotype effect to specific populations deserves further analysis including a larger sample capable of capturing all haplotype diversity.

One strength of this analysis is the sequencing strategy which allowed us to unambiguously map read pairs to specific segments of the *IFNL* region, and call the genetic variants with higher accuracy than using conventional methods of short-read sequencing. The “conditioned by design” composition of the panel with concordant and discordant individuals enabled the detection of variants conferring an effect on HCV clearance that is adjusted for the allele present at rs368234815. Even though the sample size of the sequencing panel is small, its particular configuration makes it suitable to detect variants with a large effect. The findings from this panel were supported by the results of the statistically conditioned analysis in a much larger sample size with similar characteristics adding reliability to the findings. One limitation of the study is that we established a rather high cut off for the selection of the variants with differences in the allele count since the size of the panel precluded the evaluation of rare variants using standard statistical tests and we excluded rare variants in the imputation panel since the imputation quality is usually low for those variants and any derived results would be considered uncertain.

In this study we fine-mapped the *IFNL* region and found results that support an independent genetic effect of several variants in this locus. Our results are applicable to the European ancestry population with our current sample sizes and are hypothesis-generating regarding additional factors contributing to the higher clearance in European ancestry and African ancestry individuals. Our findings are relevant and complementary to previous analyses aimed to understand the genetic basis of HCV clearance and the differences in the immune response to this infection across populations.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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2R01-AI148049, DA-04334, U19-AI088791, HHSN261200800001E, U01-AI35042, U01-AI35043, U01-AI35039, U01-AI35040, U01-AI35041, U01-AI35004, U01-AI31834, U01-AI34994, U01-AI34989, U01-AI34993, U01-AI42590, U01-HD32632, R01-HL076902, R01-HD-41224, R01-AI148049-21, R21AI139012, U19-AI082630, U01-AI1131314, R01-DA033541, U19-AI066345, DA12568, DA036297, R01-DA09532, R01-DA11860, N02CP91027, H79TI12103, R01-DA16159, R01-DA21550, UL1 RR024996.

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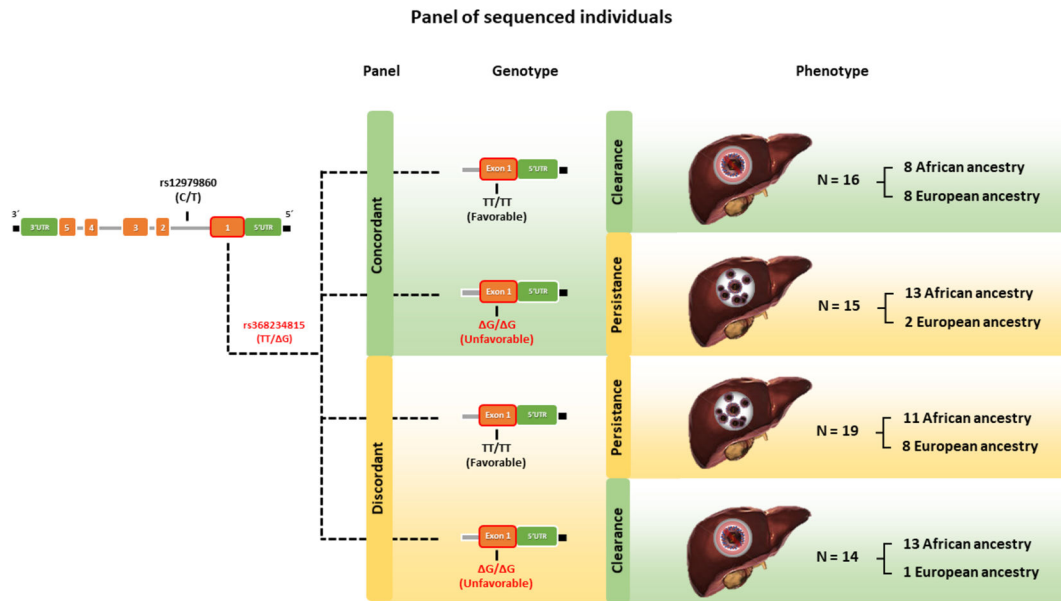
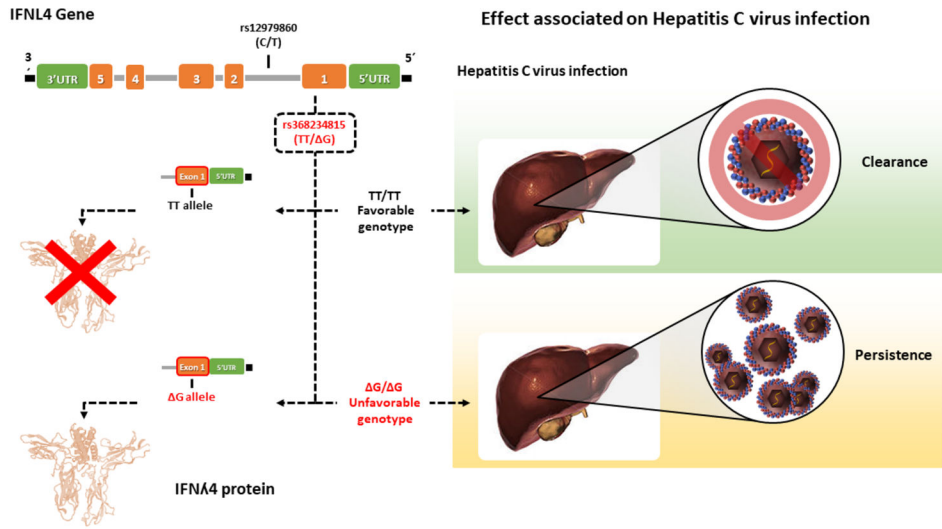


Figure 1. Top panel: Depiction of putative role of rs368234815 genotypes in HCV persistence or clearance. Bottom panel: Schematic representation of concordant and discordant panels of individuals used in the sequencing analysis.

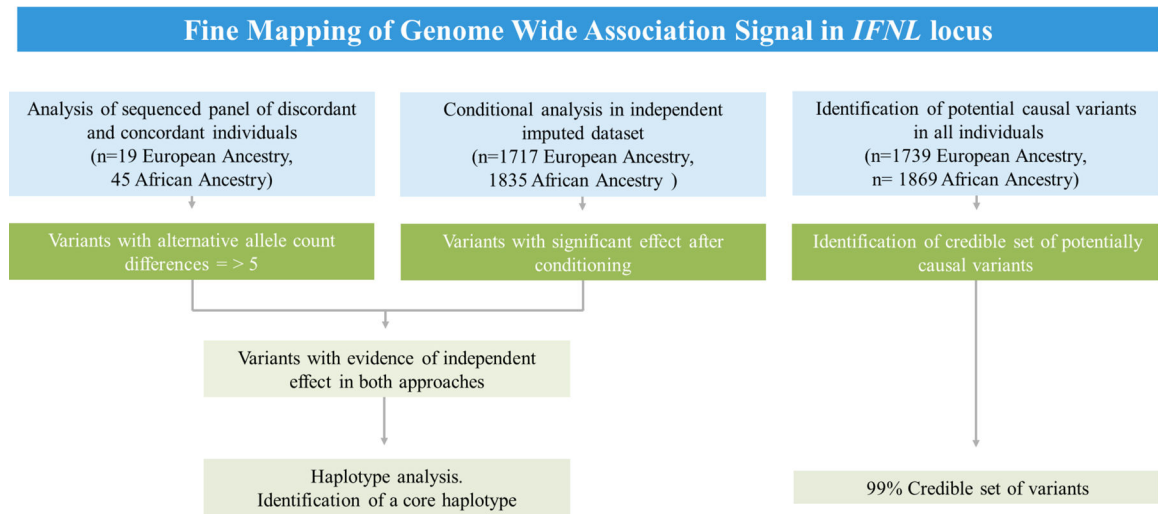


Figure 2. Schematic representation of the fine mapping analysis performed in this study.

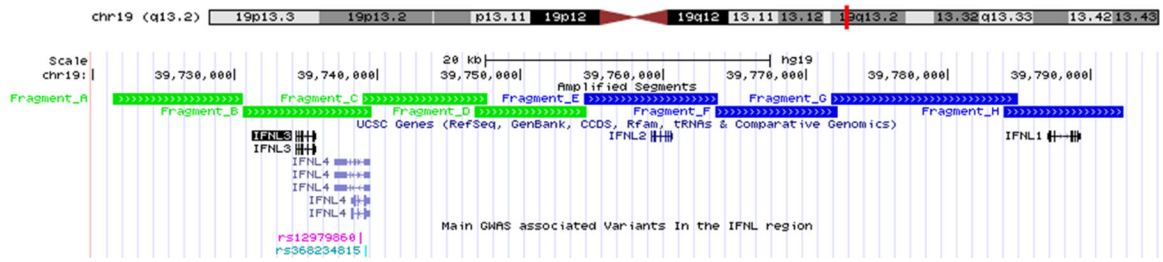


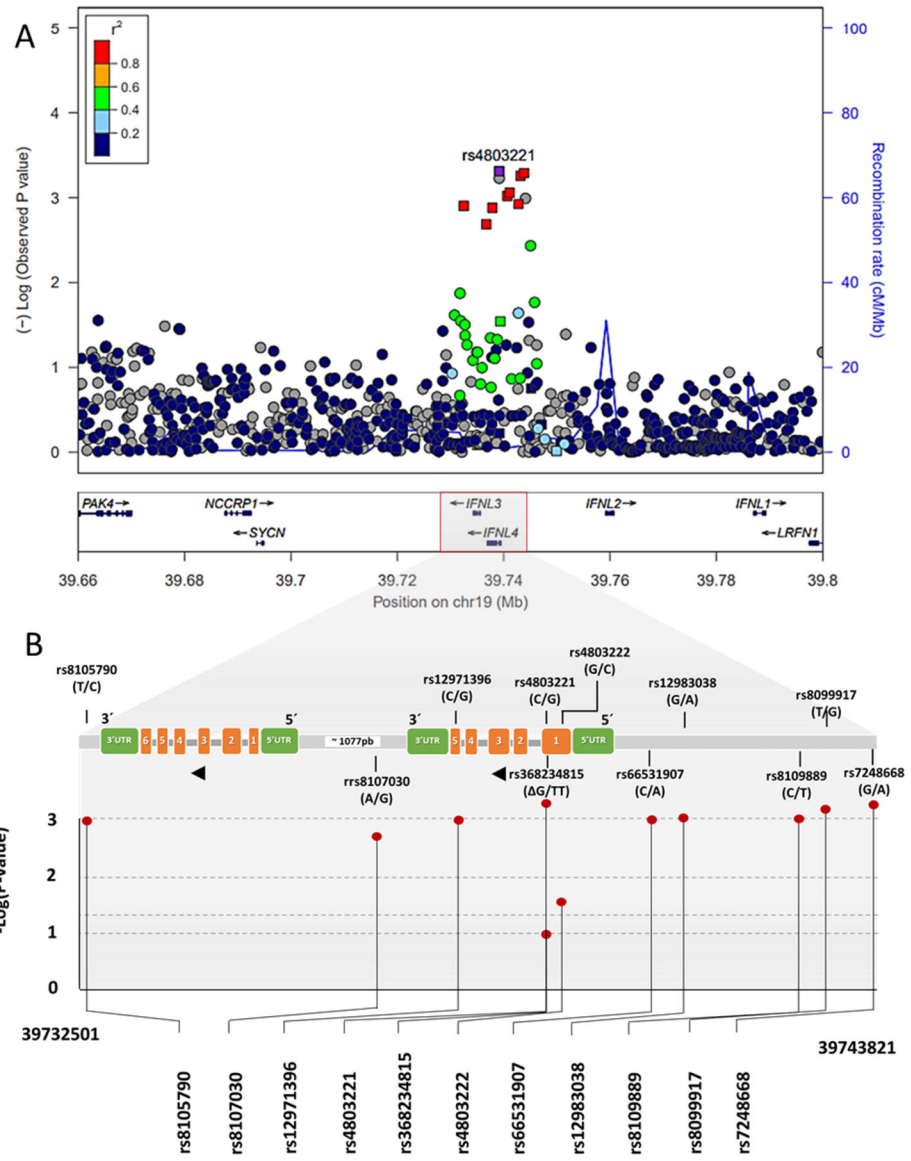
Figure 3. Genetic structure of the *IFNL* locus, amplified fragments used for targeted sequencing, and two main variants associated in prior GWAS studies with HCV clearance (rs12979860 and rs368234815). Genetic coordinates are based on The Genome Reference Consortium Human build 37 (GRCh37/hg19).

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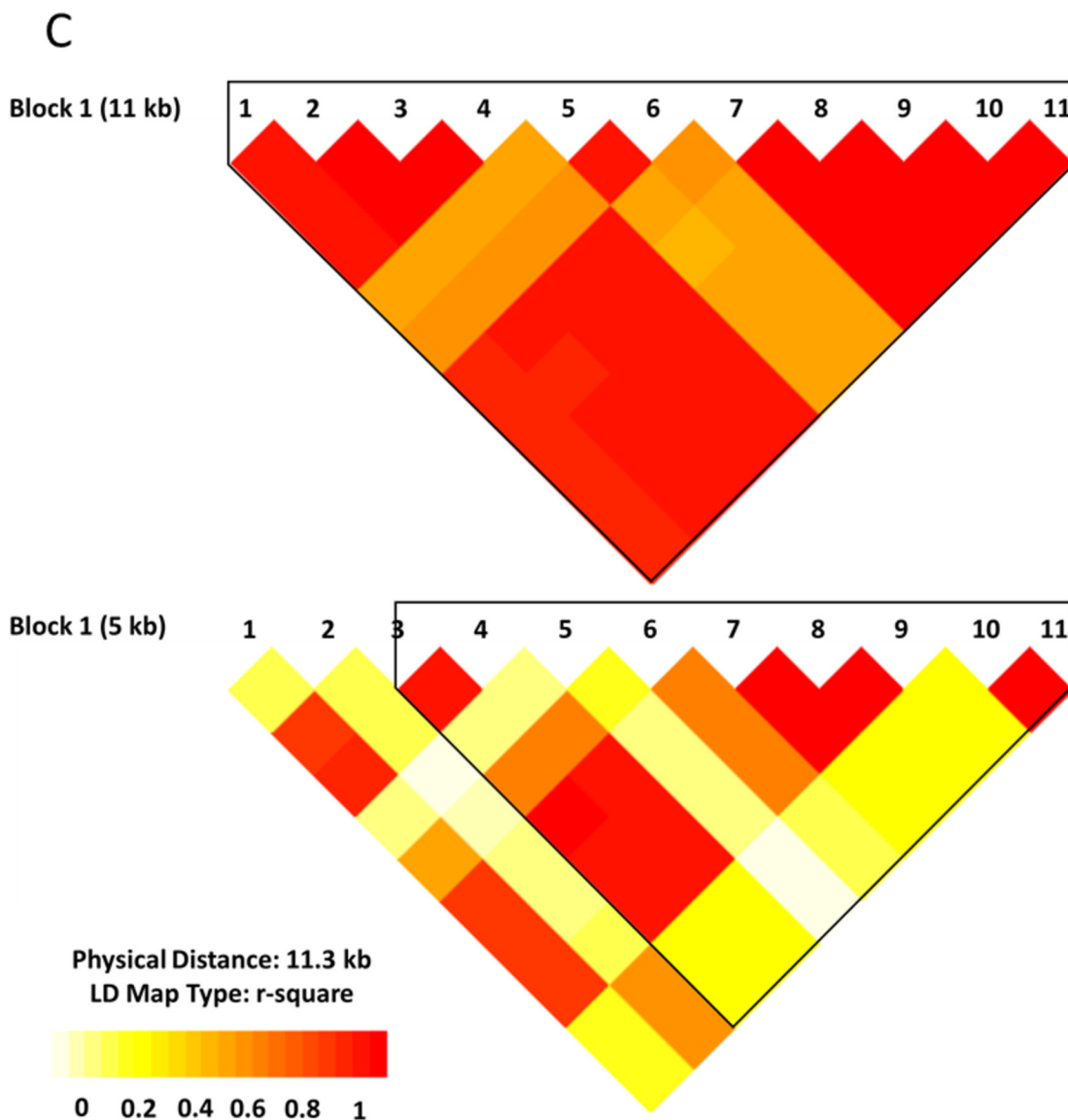


Figure 4. Results of the analysis conditioned on rs368234815 and LD patterns of the top associated variants from that analysis. A) Meta-analysis conditioned on rs368234815 genotype. Variants represented in squares in panel B are the 23 of 25 variants that showed a difference of at least 5 in counts between clearance and persistence groups in the sequencing analysis. Recombination in this region is plotted in the background in light blue. Pairwise LD between the top associated variant and other variants in the region were estimated using LD data in the European (EUR) population in the 1000 Genomes project (hg19/Nov 2014). The color from blue to red represents the r^2 values relative to the peak position after conditioning, rs4803221. B) P values of rs368234815 and the 10 SNPs with remaining significance in the conditional analysis and their location on the genes in the region. C) LD plot of those variants in individuals of European and African ancestry in the genotyped/imputed dataset. The value within each diamond of the LD plot represents the pairwise

correlation between tagging SNPs defined by sides of each the diamond. Shading represents the magnitude and significance of pairwise LD represented by the r^2 value, with a red-yellow gradient reflecting higher to lower LD values. Association plots were graphed with Locus Zoom, P value and LD plots were generated using the package `snp.plotter` implemented in R.

Genetic ancestry, HCV status and rs368234815 genotype distribution of the analyzed individuals.

Table 1.

| Ancestry group | HCV status | Sequencing analysis (N=64) | | | Imputation analysis (N=3552) | | | |
|-------------------|--------------|-----------------------------|-------|-------|------------------------------|-------|-------|-------|
| | | Genotype at rs368234815 (n) | | Total | Genotype at rs368234815 (n) | | | Total |
| | | G/ G | TT/TT | | G/ G | TT/ G | TT/TT | |
| African Ancestry | Clearance | 13 | 8 | 21 | 91 | 137 | 92 | 320 |
| | Persistence | 13 | 11 | 24 | 626 | 742 | 147 | 1515 |
| | Total | 26 | 19 | 45 | 717 | 879 | 239 | 1835 |
| European Ancestry | Clearance | 1 | 8 | 9 | 39 | 232 | 421 | 692 |
| | Persistence | 2 | 8 | 10 | 128 | 521 | 376 | 1025 |
| | Total | 3 | 16 | 19 | 167 | 753 | 797 | 1717 |

Table 2.

Variants with a difference 5 in alternative allele count in sequenced individuals and replication in the meta-analysis of the association test of imputed variants in the *IFNL* region conditioned on the rs36823481.5 genotype. Bold text indicates positions with meta-analysis $p < 0.05$ from imputed data.

| SNP | | | Analysis of individuals in sequencing panel (N=64) | | | | Analysis of imputed data conditioned on rs36823481.5 | | | | | | Meta-analysis (N=3,552) | |
|-------------------|-----------------|----------|--|----------|-----------|-----------|--|-------------|---------------------------------------|-------------|-------------|-------------|------------------------------|------------------------------|
| rsID | Position | Ref | Alt | Clear | Persist | Diff. | European Ancestry population (N=1,717) | | African Ancestry Population (N=1,835) | | | P Value | P Value | |
| | | | | | | | Freq. | OR | P Value | Freq. | OR | P Value | | |
| rs8107090 | 39721915 | T | A | 19 | 24 | -5 | 0.40 | 0.96 | 0.67 | 0.57 | 0.90 | 0.45 | 0.400 | 0.400 |
| rs35408086 | 39726810 | G | A | 11 | 19 | -8 | 0.39 | 0.98 | 0.80 | 0.21 | 0.95 | 0.66 | 0.621 | 0.621 |
| rs11883239 | 39727480 | G | A | 6 | 17 | -11 | 0.39 | 0.98 | 0.80 | 0.13 | 0.83 | 0.21 | 0.287 | 0.287 |
| rs11883201 | 39727490 | A | G | 19 | 24 | -5 | 0.40 | 0.97 | 0.69 | 0.59 | 0.93 | 0.59 | 0.507 | 0.507 |
| rs955155 | 39729479 | G | A | 2 | 8 | -6 | 0.26 | 0.98 | 0.84 | 0.07 | 0.86 | 0.41 | 0.459 | 0.459 |
| rs12609937 | 39731204 | A | G | 28 | 35 | -7 | 0.91 | 0.95 | 0.72 | 0.98 | 0.99 | 0.97 | 0.786 | 0.786 |
| rs115166799 | 39732212 | A | G | 12 | 6 | 6 | N/A | N/A | N/A | 0.19 | 0.98 | 0.88 | 0.882 | 0.882 |
| rs8105790 | 39732501 | T | C | 6 | 13 | -7 | 0.20 | 0.53 | 3.21×10⁻⁰⁵ | 0.19 | 0.94 | 0.64 | 0.001 | 0.001 |
| rs8102358 | 39735012 | G | A | 13 | 7 | 6 | NA | N/A | NA | 0.25 | 1.03 | 0.82 | 0.820 | 0.820 |
| rs8107030 | 39736719 | A | G | 0 | 7 | -7 | 0.19 | 0.54 | 4.84×10⁻⁰⁵ | 0.04 | 0.91 | 0.72 | 0.002 | 0.002 |
| rs12971396 | 39737866 | C | G | 7 | 13 | -6 | 0.20 | 0.53 | 2.79×10⁻⁰⁵ | 0.19 | 0.94 | 0.68 | 0.001 | 0.001 |
| rs4803221 | 39739129 | C | G | 7 | 13 | -6 | 0.20 | 0.51 | 7.49×10⁻⁰⁶ | 0.19 | 0.93 | 0.60 | 4.86×10⁻⁰⁴ | 4.86×10⁻⁰⁴ |
| rs73555604 | 39739170 | C | T | 12 | 6 | 6 | 0.01 | 1.31 | 0.47 | 0.22 | 1.01 | 0.97 | 0.597 | 0.597 |
| rs4803222 | 39739353 | G | C | 9 | 14 | -5 | 0.30 | 0.55 | 0.06 | 0.27 | 0.85 | 0.23 | 0.029 | 0.029 |
| rs66531907 | 39740675 | C | A | 6 | 12 | -6 | 0.19 | 0.55 | 5.90×10⁻⁰⁵ | 0.19 | 0.90 | 0.48 | 9.57×10⁻⁰⁴ | 9.57×10⁻⁰⁴ |
| rs12983038 | 39741124 | G | A | 6 | 11 | -5 | 0.19 | 0.54 | 3.22×10⁻⁰⁵ | 0.19 | 0.91 | 0.54 | 8.75×10⁻⁰⁴ | 8.75×10⁻⁰⁴ |
| rs8109889 | 39742770 | C | T | 6 | 12 | -6 | 0.19 | 0.57 | 1.01×10⁻⁰⁴ | 0.19 | 0.90 | 0.46 | 0.001 | 0.001 |
| rs8099917 | 39743165 | T | G | 0 | 5 | -5 | 0.19 | 0.57 | 1.22×10⁻⁰⁴ | 0.06 | 0.79 | 0.28 | 5.54×10⁻⁰⁴ | 5.54×10⁻⁰⁴ |
| rs7248668 | 39743821 | G | A | 0 | 5 | -5 | 0.19 | 0.57 | 9.41×10⁻⁰⁵ | 0.06 | 0.79 | 0.29 | 5.14×10⁻⁰⁴ | 5.14×10⁻⁰⁴ |
| rs10853728 | 39745146 | C | G | 26 | 34 | -8 | 0.65 | 0.94 | 0.58 | 0.74 | 0.85 | 0.18 | 0.177 | 0.177 |
| rs10775535 | 39745181 | C | T | 29 | 34 | -5 | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A |
| rs56116812 | 39747090 | G | A | 11 | 18 | -7 | 0.12 | 1.34 | 0.06 | 0.23 | 0.90 | 0.41 | 0.473 | 0.473 |

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| SNP | | | Analysis of individuals in sequencing panel (N=64) | | | | Analysis of imputed data conditioned on rs368234815 | | | | | | Meta-analysis (N=3,552) | |
|-------------|----------|-----|--|------------------------------|---------|-------|---|------|---------|---------------------------------------|------|---------|-------------------------|---------|
| rsID | Position | Ref | Alt | Counts of Alternative allele | | | European Ancestry population (N=1,717) | | | African Ancestry Population (N=1,835) | | | P Value | P value |
| | | | | Clear | Persist | Diff. | Freq. | OR | P Value | Freq. | OR | P Value | | |
| rs116236518 | 39749790 | C | T | 5 | 0 | 5 | N/A | N/A | N/A | 0.02 | 1.48 | 0.26 | 0.262 | |
| rs10424607 | 39749922 | A | C | 18 | 23 | -5 | 0.29 | 1.04 | 0.81 | 0.51 | 0.98 | 0.86 | 0.966 | |
| rs251908 | 39764449 | A | G | 30 | 35 | -5 | N/A | N/A | N/A | N/A | N/A | N/A | N/A | |

Abbreviations: Diff: Differences in the alternative allele count; Freq: Frequency of the alternative allele; OR: odds ratio; Clear: Clearance; Persist: Persistence.

Association analysis of the 2 variant haplotypes (rs4803221-rs368234815 and rs368234815-rs8099917) in individuals carrying the G allele of rs368234815.

Table 3.

| European Ancestry (Number of haplotypes= 1087) | | | | |
|---|---|---|--|--|
| Haplotype rs4803221- rs368234815 | | Frequency in Clearance (Number of haplotypes= 310) | Frequency in Persistence (Number of haplotypes= 777) | OR (95% CI, P value) |
| G- G Haplotype | G | 0.53 | 0.66 | 1 |
| C- G Haplotype | C | 0.47 | 0.34 | 1.7 (1.3-2.29, 3.6× 10 ⁻⁰⁵) |
| Haplotype rs368234815- rs8099917 | | | | |
| G-G Haplotype | G | 0.51 | 0.63 | 1 |
| G-T Haplotype | T | 0.49 | 0.37 | 1.6 (1.3-2.16, 1.76× 10 ⁻⁰⁴) |
| African Ancestry (Number of haplotypes= 2333) | | | | |
| Haplotype rs4803221- rs368234815 | | Frequency in Clearance (Number of haplotypes= 319) | Frequency in Persistence (Number of haplotypes= 1994) | OR (95% CI, P value) |
| G- G Haplotype | G | 0.29 | 0.30 | 1 |
| C- G Haplotype | C | 0.71 | 0.71 | 1.02 (0.78-1.32, 0.88) |
| Haplotype rs368234815- rs8099917 | | | | |
| G-G Haplotype | G | 0.08 | 0.10 | 1 |
| G-T Haplotype | T | 0.92 | 0.90 | 1.25 (0.81-1.9, 0.29) |