Figures and figure supplements

Adaptation of hepatitis C virus to interferon lambda polymorphism across multiple viral genotypes

Nimisha Chaturvedi et al
Figure 1. Per genotype integrated association analysis results. Manhattan plot for associations between human SNP rs12979860 and HCV amino acid variants. The dotted line shows the Bonferroni-corrected significance threshold.
DOI: https://doi.org/10.7554/eLife.42542.003
Figure 1—figure supplement 1. Per genotype integrated association analysis results corrected for HCV viral load. Manhattan plot for associations between human SNP rs12979860 and HCV amino acid variants, with (filled dots) and without HCV (filled triangles) viral load. The dotted line shows the Bonferroni-corrected significance threshold.

DOI: https://doi.org/10.7554/eLife.42542.004
Figure 1—figure supplement 2. Boxplot of transformed viral load stratified by rs12979860 genotypes (CC, CT, TT). The association p-values, together with r-squared and beta values, given in the brackets are for associations between rs12979860 and transformed HCV viral load.

DOI: https://doi.org/10.7554/eLife.42542.005
Figure 2. Per genotype viral load GWAS analysis results. Manhattan plot for associations between human Box-Cox transformed pre-treatment viral load and HCV amino acid variants. The dotted line shows the Bonferroni-corrected significance threshold.

DOI: https://doi.org/10.7554/eLife.42542.007
Figure 3. Associations between amino acid variables at position 2224 of NS5A, rs12979860 genotypes and HCV viral load in the group of patients infected with HCV genotype 1b. (A) Boxplot of transformed viral load stratified by amino acids present at position 2224 of NS5A. (B) Boxplot of transformed viral load stratified by rs12979860 genotypes (CC, CT, TT) and by presence or absence of leucine at position 2224 of NS5A.

DOI: https://doi.org/10.7554/eLife.42542.008
Figure 3—figure supplement 1. Boxplot of transformed viral load stratified by rs12979860 genotypes (CC, CT, TT) in samples infected with viral genotype 3a, whose virus carries Serine at position 2414.
DOI: https://doi.org/10.7554/eLife.42542.009
Genotype 1a

Genotype 1b

Genotype 2a

Genotype 2b

Genotype 3a

Genotype 4a

Figure 3—figure supplement 2. Per genotype viral load residual analysis results. Manhattan plot for associations between viral load residual and HCV amino acid variants. The dotted line shows the Bonferroni-corrected significance threshold.

DOI: https://doi.org/10.7554/eLife.42542.010
**Figure 3—figure supplement 3.** Per genotype integrated association analysis results in the European subgroup. Manhattan plot for associations between human SNP rs12979860 and HCV amino acid variants. The dotted line shows the Bonferroni-corrected significance threshold.

DOI: https://doi.org/10.7554/eLife.42542.011
Figure 3—figure supplement 4. European per genotype viral load GWAS analysis results. Manhattan plot for associations between human Box-Cox transformed pre-treatment viral load and HCV amino acid variants. The dotted line shows the Bonferroni-corrected significance threshold.

DOI: https://doi.org/10.7554/eLife.42542.012
Figure 3—figure supplement 5. European per genotype viral load residual GWAS analysis results. Manhattan plot for associations between viral load residual and HCV amino acid variants. The dotted line shows the Bonferroni-corrected significance threshold.

DOI: https://doi.org/10.7554/eLife.42542.013