Hepatitis C Virus (HCV) NS5A Drug Resistance by Sequencing
ARUP test code 2014139

NS5A Genotype

1a

INTERPRETIVE INFORMATION: HCV NS5A Drug Resistance by Sequencing

This assay detects resistance-associated variants in NS5A codons 20-101 for HCV genotypes 1a and 1b. Variants in viral sub-populations below 20 percent of total may not be detected. For further information, please refer to drug package inserts for the applicable direct acting antiviral drug and current HCV treatment guidelines (e.g. AASLD/IDSA guidelines or EASL HCV treatment recommendations).

Test developed and characteristics determined by ARUP Laboratories. See Compliance Statement B: aruplab.com/CS

NS5A Resistance

See Note

The following resistance-associated variants were identified:

   None

   Ledipasvir Resistance: Not Predicted
   Elbasvir Resistance: Not Predicted
   Ombitasvir Resistance: Not Predicted
   Daclatasvir Resistance: Not Predicted
   Velpatasvir Resistance: Not Predicted
   Pibrentasvir Resistance: Not Predicted

A result of Predicted resistance indicates that one or more resistance-associated variant (RAV) was detected. These RAVs have been known to confer varying levels of resistance to treatment regimens containing the NS5A inhibitors ledipasvir or elbasvir. Resistance and interpretation for these variants is reported based on current EASL HCV treatment guidelines (available: http://www.easl.eu/research/our-contributions/clinical-practice-guidelines).

A result of Possible resistance indicates that one or more resistance-associated variant (RAV) was detected. Current guidelines and in vitro and/or clinical studies have identified these variants as having a possible association with resistance but may require additional studies to confirm. Please refer to the individual Direct Acting Antiviral (DAA) package inserts for additional treatment implications and guidance.

A result of Not Predicted resistance indicates that no RAVs were detected and/or variants detected have uncertain or no impact on response to DAA-treatment. Additionally, variants in viral sub-populations below 20 percent of total may not be detected.

H=High, L=Low, *=Abnormal, C=Critical
## VERIFIED/REPORTED DATES

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