



<u>Procedure</u>	<u>Result</u>	<u>Units</u>	<u>Ref Interval</u>	<u>Accession</u>	<u>Collected</u>	<u>Received</u>	<u>Reported/Verified</u>
HCV Qnt by NAAT (IU/mL)	4100	IU/mL		18-161-900007	10-Jun-18 19:56:00	10-Jun-18 20:10:00	13-Jun-18 15:28:38
HCV Qnt by NAAT (log IU/mL)	3.61 f	log IU/mL		18-161-900007	10-Jun-18 19:56:00	10-Jun-18 20:10:00	13-Jun-18 15:28:38
HCV Genotype by Sequencing	1a			18-161-900007	10-Jun-18 19:56:00	10-Jun-18 20:10:00	13-Jun-18 15:30:16

10-Jun-18 19:56:00 HCV Qnt by NAAT (log IU/mL):

Hepatitis C Virus Genotype by Sequencing added.

10-Jun-18 19:56:00 HCV Qnt by NAAT (log IU/mL):
 INTERPRETIVE INFORMATION: HCV by Quantitative NAAT

Normal range for this assay is "Not Detected".
 The quantitative range of this assay is 10 - 100,000,000 IU/mL (1.0 - 8.0 log IU/mL).

Lower limit of quantitation (LLoQ):
 10 IU/mL (1.0 log IU/mL)
 LLoQ values do not apply to diluted specimens.

A result of "Not Detected" does not rule out the presence of inhibitors in the patient specimen or hepatitis C virus RNA concentrations below the level of detection of the test. Care should be taken when interpreting any single viral load determination.

This test should not be used for blood donor screening, associated re-entry protocols, or for screening Human Cell, Tissues and Cellular Tissue-Based Products (HCT/P).

10-Jun-18 19:56:00 HCV Genotype by Sequencing:
 INTERPRETIVE INFORMATION: Hepatitis C Genotyping

Hepatitis C Viral RNA is tested using reverse transcription polymerase chain reaction (RT-PCR) to amplify a specific portion of the 5' untranslated region (5' UTR) of the viral genome. The amplified nucleic acid is sequenced bi-directionally using dye-terminator chemistry (ABI). Sequencing data is compared to a database of characterized sequences.

Isolates of hepatitis C virus are grouped into six major genotypes (1-6). These genotypes are subtyped according to sequence characteristics. Due to high conservation of the 5' un-translated region of the HCV genome, this test has limitations in differentiating subtype 1a from 1b. Therefore, these subtypes will be reported as 1a or 1b. In rare instances, Type 6 virus may be misclassified as Type 1.

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

* Abnormal, # = Corrected, C = Critical, f = Footnote, H = High, L = Low, t = Interpretive Text, @ = Reference Lab