Hepatitis C Virus (HCV) GenoSure NS3 and NS4A

ARUP LABORATORIES

Patient: [redacted]
DOB: [redacted] Age: 61 Gender: M
Patient Identifiers: [redacted]
Visit Number (FIN): [redacted]

Client: [redacted]
Physician [redacted]

ARUP Test Code: 3001234

Collection Date: 06/07/2021
Received in lab: 06/09/2021
Completion Date: 06/25/2021

TEST INFORMATION

Test performed at Labcorp Monogram Biosciences, 345 Oyster Point Blvd., South San Francisco, CA 94080

PATIENT REPORT

Patient's results continue on following page(s).

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Jonathan R. Genzen, MD, PhD, Laboratory Director

Chart continues on following page(s)

HCV GenoSure® Drug Resistance Assay NS3/4A

Monogram BIOSCIENCES
LabCorp Specialty Testing Group

ARUP Interface Acct
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Salt Lake City, UT 84108
USA

Client: [redacted] Project: [redacted]
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Weidong Huang, MD, Medical Director
345 Oyster Point Blvd
South San Francisco, CA 94080 - Tel: (800) 777-0177

Patient Name	DOB	Patient ID/Medical Record #	Gender	Monogram Accession #
[redacted]	[redacted]		M	[redacted]
Date Collected	**Date Received**	**Date Reported**	**Mode**	**Report Status**
09-JUN-2021 00:01	10-JUN-2021 09:56 PT	22-JUN-2021 12:41 PT	F,L,W	**FINAL**
Referring Physician			Reference Lab ID/Order # 21-160-400248	
Comments				

Drug		HCV GenoSure® NS3/4A		Assessment		Comments
Generic Name	**Brand/ Regimen**	**Region**	**Drug Resistance Associated Variants* Detected**	**Drug**		
Glecaprevir	Mavyret	NS3	None	GLE	**None/Undetermined**	
Grazoprevir	Zepatier	NS3	None	GZR	**None/Undetermined**	
PI **Paritaprevir**	Viekira Pak	NS3	Q80K	PTV/r	**None/Undetermined**	
Simeprevir	Olysio	NS3	Q80K	SMV	**Resistance Possible**	
Voxilaprevir	Vosevi	NS3	None	VOX	**None/Undetermined**	

Important Definitions

- **Resistance Possible -** Resistance Associated Variants (RAVs) detected that (a) represent naturally-occurring polymorphisms or treatment-emergent variants associated with reductions in sustained virologic response (SVR) rates, (b) emerge during direct-acting antiviral (DAA)-treatment or relapse, and/or (c) may confer reductions in susceptibility based on *in vitro* data. Refer to prescribing information for specific details regarding the impact of these variants on treatment response in defined patient populations and when administered in combination with other antiviral agents.
- **None/Undetermined -** None; no RAVs detected. Undetermined; variants detected that have a subtle or uncertain impact on DAA-treatment responses.

Notes:
- All variants are reported relative to the HCV genotype/subtype specific reference H77
- Assessment is based on a rules-based algorithm (version 6)
- Naturally-occurring polymorphisms may impact the emergence of resistance, leading to failure of DAA combination therapy
- Naturally-occurring DAA resistance-associated polymorphisms identified at baseline may impact SVR if the treatment regimen, or adherence, is suboptimal. The impact of these polymorphisms may vary in treatment-naïve and treatment-experienced patients and with varying disease states (e.g. non-cirrhotic vs cirrhotic)
- Reduced susceptibility to any one component of a DAA-containing regimen may be overcome by the activity of the other components of the regimen and/or longer treatment duration
- Treatment emergent RAVs may persist for prolonged periods of time and may impact subsequent treatment regimens

Region		Genotype	Summary of All Variants Observed
NS3	Protease: aa 1-181 Helicase: aa 182-644	1a	Q80K, S91A, R119R/Q, L153I, N174S, V248I, I300V, S332P, F349F/Y, A379T, I386V, S410A, F418Y, C431S, T459T/A, F557L, I615V
NS4A	Protease cofactor: aa 1-54		I29V, Q46R

Comments: **Q80K DETECTED.** The Q80K polymorphism significantly impacts sustained virologic response in HCV GT 1a infected patients that (a) are treated with simeprevir in combination with pegylated interferon and ribavirin, or (b) have compensated cirrhosis and are treated with simeprevir plus sofosbuvir. In these clinical settings, a regimen that does not include simeprevir should be considered.

For more information on interpreting this report, please call Monogram Customer Service at 800-777-0177 between the hours of 6:30am to 5:00pm Pacific Time Monday through Friday.

This assay is performed using a next-generation sequencing platform that analyzes the specified non-structural coding regions of HCV. Variants are reported at a sensitivity that has been demonstrated to be equivalent to that of Sanger/population sequencing. Genotype assignment is determined from the sequence of the specified regions that are derived using subtype specific methodology, and should not be used to establish or confirm the HCV genotype. HCV genotype determination should only be done with an assay intended for that purpose. This assay was validated by testing samples with viral loads equal to or above 2000 IU/mL and should be interpreted only on such specimens. This assay meets the standards for performance characteristics and all other quality control and assurance requirements established by CLIA. The results should not be used as the sole criteria for patient management. This test was developed and its performance characteristics determined by Monogram Biosciences. It has not been cleared or approved by the FDA. This document contains private and confidential health information protected by state and federal law. If you have received this document in error, please call 800-777-0177.

Report Version: 28

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