

Client: Example Client ABC123
123 Test Drive
Salt Lake City, UT 84108
UNITED STATES

Physician: Doctor, Example

Patient: Patient, Example

DOB: 7/15/2022
Gender: Male
Patient Identifiers: 01234567890ABCD, 012345
Visit Number (FIN): 01234567890ABCD
Collection Date: 00/00/0000 00:00

Hereditary Hemolytic Anemia Panel Sequencing

ARUP test code 2012052

Her. Hemolytic Anemia Seq. Specimen whole Blood

Her. Hemolytic Anemia Sequencing Interp

Negative

RESULT

No pathogenic variants were detected in any of the genes tested by the hereditary hemolytic anemia panel.

INTERPRETATION

No pathogenic variants or variants of uncertain significance were identified in the targeted genes by massively parallel sequencing. This result decreases the likelihood of, but does not exclude, a heritable form of anemia. Please refer to the background information included in this report for a list of the genes analyzed and limitations of this test.

RECOMMENDATION

Hematologic and genetic consultation is indicated, including a discussion of medical screening and management.

COMMENTS

Likely benign and benign variants are not included in this report.
Variants in the following region(s) may not be detected by NGS with sufficient confidence in this sample due to technical limitations; reportable variants are confirmed by Sanger sequencing:
NONE

This result has been reviewed and approved by [REDACTED]

H=High, L=Low, *=Abnormal, C=Critical

BACKGROUND INFORMATION: Hereditary Hemolytic Anemia Panel, Sequencing

CHARACTERISTICS: Hereditary Hemolytic Anemia (HHA) comprises a diverse group of heterogeneous disorders characterized by premature red blood cell (RBC) destruction and anemia due to intrinsic RBC defects. Individuals with HHA have decreased hemoglobin concentration, hematocrit and RBC count. Additional characteristics include blood smear abnormalities, such as spherocytes, acanthocytes, schistocytes, bite cells, stomatocytes, polychromasia and target cells. Presentation may include hyperbilirubinemia or jaundice due to red cell hemolysis. Causes of HHA involve RBC membrane defects (eg, hereditary spherocytosis), RBC enzymopathies (eg, glucose-6-phosphate dehydrogenase or pyruvate kinase deficiencies) and hemoglobinopathies.

EPIDEMIOLOGY: Incidence is estimated at 1:500-1:1,100.

CAUSE: Pathogenic germline variants in genes associated with defects in the RBC membrane proteins, deficiencies of RBC enzymes, or hemoglobinopathies.

INHERITANCE: Varies by gene; autosomal dominant, autosomal recessive or X-linked recessive.

GENES TESTED: AK1, ALDOA, ANK1, CDAN1, CYB5R3, EPB41, EPB42, G6PD, GCLC, GPI, GSR, GSS, HK1, NT5C3A, PFKM, PGK1, PIEZO1, PKLR, SEC23B, SLC4A1, SLC01B1, SLC01B3, SPTA1, SPTB, TPI1, UGT1A1, UGT1A6, UGT1A7

METHODOLOGY: Targeted capture of all coding exons and exon-intron junctions of the targeted genes, followed by massively parallel sequencing. Sanger sequencing was performed as necessary to fill in regions of low coverage and confirm reported variants. Human genome build 19 (Hg 19) was used for data analysis.

ANALYTICAL SENSITIVITY: The analytical sensitivity of this test is approximately 99 percent for single nucleotide variants (SNVs) and greater than 93 percent for insertions/duplications/deletions from 1-10 base pairs in size. Variants greater than 10 base pairs may be detected, but the analytical sensitivity may be reduced.

LIMITATIONS: A negative result does not exclude a heritable form of hemolytic anemia. This test only detects variants within the coding regions and intron-exon boundaries of the targeted genes. The genes of the alpha- and beta-globin clusters are not analyzed. Regulatory region variants and deep intronic variants will not be identified. Deletions/duplications/insertions of any size may not be detected by massive parallel sequencing. Diagnostic errors can occur due to rare sequence variations. In some cases, variants may not be identified due to technical limitations in the presence of pseudogenes, repetitive, or homologous regions. This assay may not detect low-level somatic variants associated with disease. Interpretation of this test result may be impacted if this patient has had an allogeneic stem cell transplantation or recently received a blood transfusion. Non-coding transcripts were not analyzed.

This test was developed and its performance characteristics determined by ARUP Laboratories. It has not been cleared or approved by the US Food and Drug Administration. This test was performed in a CLIA certified laboratory and is intended for clinical purposes.

Counseling and informed consent are recommended for genetic testing. Consent forms are available online.

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| VERIFIED/REPORTED DATES | | | | |
|---|---------------|------------------|------------------|-------------------|
| Procedure | Accession | Collected | Received | Verified/Reported |
| Her. Hemolytic Anemia Seq. Specimen | 22-259-402849 | 00/00/0000 00:00 | 00/00/0000 00:00 | 00/00/0000 00:00 |
| Her. Hemolytic Anemia Sequencing Interp | 22-259-402849 | 00/00/0000 00:00 | 00/00/0000 00:00 | 00/00/0000 00:00 |

END OF CHART

H=High, L=Low, *=Abnormal, C=Critical