

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

Physician: Doctor, Example

**Patient: Patient, Example**

**DOB:** 12/31/1752  
**Gender:** Female  
**Patient Identifiers:** 01234567890ABCD, 012345  
**Visit Number (FIN):** 01234567890ABCD  
**Collection Date:** 01/01/2017 12:34

**Hereditary Paraganglioma-Pheochromocytoma (SDHB) Sequencing and Deletion/Duplication**

ARUP test code 2007108

HPGL-PCC (SDHB) Seq, DelDup Specimen      whole Blood

HPGL-PCC (SDHB) Seq, DelDup Interp      **Positive**      \*

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

Unless otherwise indicated, testing performed at:

TEST PERFORMED - 2007108  
TEST DESCRIPTION - Hereditary Paraganglioma-Pheochromocytoma (SDHB) Sequencing and Deletion/Duplication  
INDICATION FOR TEST - Confirm Diagnosis

RESULT  
One pathogenic variant detected in the SDHB gene.

DNA VARIANT  
Pathogenic  
Nucleic Acid Change: c.19\_41dup23; Heterozygous  
Amino Acid Alteration: Frameshift

INTERPRETATION  
One pathogenic variant, c.19\_41dup23, was detected in the SDHB gene by sequencing. This variant is listed in the dbSNP variant database (rs794728951) with no minor allele frequency reported in general population databases, and reported once as a pathogenic variant in ClinVar (see link). The c.19\_41dup23 variant causes a frameshift and is predicted to result in a truncated protein or an absent transcript; therefore, we consider this variant to be pathogenic. This result is consistent with a diagnosis of Hereditary Paraganglioma-Pheochromocytoma Syndrome; clinical manifestations are variable. Each of this individual's offspring have a 50 percent risk of inheriting the pathogenic variant.

No pathogenic variants were detected by deletion/duplication analysis.

RECOMMENDATIONS  
Genetic consultation is indicated, including a discussion of medical screening and management. At-risk family members should be offered targeted testing for the identified pathogenic variant (Familial Mutation, Targeted Sequencing, ARUP test code 2001961).

COMMENTS  
Reference Sequence: GenBank # NM\_003000.2 (SDHB)  
Nucleotide numbering begins at the "A" of the ATG initiation codon.  
Benign variants are not included on this report but are available upon request.

REFERENCES  
Link to Clinvar for c.19\_41dup23:  
<http://www.ncbi.nlm.nih.gov/clinvar/variation/201608/#summary-evidence>

This result has been reviewed and approved by [REDACTED]

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Unless otherwise indicated, testing performed at:

ARUP LABORATORIES | 800-522-2787 | aruplab.com  
500 Chipeta Way, Salt Lake City, UT 84108-1221  
Tracy I. George, MD, Laboratory Director

Patient: Patient, Example  
ARUP Accession: 17-017-110742  
Patient Identifiers: 01234567890ABCD, 012345  
Visit Number (FIN): 01234567890ABCD  
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**BACKGROUND INFORMATION:** Hereditary Paraganglioma-Pheochromocytoma (SDHB) Sequencing and Deletion/Duplication

**CHARACTERISTICS:** Hereditary paraganglioma-pheochromocytoma (PGL/PCC) syndromes are characterized by paragangliomas (neuroendocrine tumors of the autonomic nervous system) and pheochromocytomas (paragangliomas of the adrenal medulla). Pathogenic germline mutations in a number of genes, including SDHB, predispose to paraganglioma and pheochromocytoma with risk of malignant transformation.

**INCIDENCE:** About 1 in 300,000 per year.

**INHERITANCE:** Autosomal dominant.

**CAUSE:** Pathogenic succinate dehydrogenase, subunits B, C, and D (SDHB, SDHC, and SDHD) gene mutations. Mutations in other genes, including TMEM127, EGLN1, MAX, SDHA, and SDHAF2, may also be causative.

**CLINICAL SENSITIVITY:** 7-11 percent.

**METHODOLOGY:** Bidirectional sequencing of all coding regions and intron-exon boundaries of the SDHB gene; Multiplex Ligation-dependent Probe Amplification (MLPA) to detect large SDHB deletions /duplications.

**ANALYTICAL SENSITIVITY AND SPECIFICITY:** Sequencing: 99 percent. MLPA: 90 and 99 percent, respectively.

**LIMITATIONS:** Diagnostic errors can occur due to rare sequence variations. Regulatory region mutations and deep intronic mutations will not be detected. The breakpoints of large deletions/duplications will not be determined. Mutations in genes other than SDHB are not evaluated.

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

VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
HPGL-PCC (SDHB) Seq, DelDup Specimen	17-017-110742	1/17/2017 1:29:00 PM	1/17/2017 1:30 08 PM	3/8/2017 1:14:00 PM
HPGL-PCC (SDHB) Seq, DelDup Interp	17-017-110742	1/17/2017 1:29:00 PM	1/17/2017 1:30 08 PM	3/8/2017 1:14:00 PM

END OF CHART

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