Client: ARUP Example Report Only
500 Chipeta Way
Salt Lake City, UT 84108
UNITED STATES

Physician: arup, arup

Patient: PAH PANEL, POSITIVE EXAMPLE

DOB	
Sex:	Female
Patient Identifiers:	41722
Visit Number (FIN):	42047
Collection Date:	8/17/2022 09:41

Pulmonary Arterial Hypertension (PAH) Panel, Sequencing and Deletion/Duplication

ARUP test code 2009345

PAH Pan. Seq/DelDup, Specimen	Whole Blood
PAH Pan. Seq/DelDup, Interp	Positive

INDICATION FOR TESTING
Pulmonary hypertension

RESULT
One pathogenic variant was detected in the BMPR2 gene.

PATHOGENIC VARIANT
Gene: BMPR2 (NM_001204.7)
Nucleic Acid Change: c.631C>T; heterozygous
Amino Acid Alteration: p.Arg211Ter
Inheritance: Autosomal dominant

INTERPRETATION
One copy of a pathogenic variant, c.631C>T; p.Arg211Ter, was detected in the BMPR2 gene by massively parallel sequencing. Pathogenic variants in BMPR2 are inherited in an autosomal dominant manner with reduced penetrance and are associated with familial primary pulmonary hypertension, fenfluramine- or dexfenfluramine-associated primary pulmonary hypertension (MIM: 178600), and pulmonary venoocclusive disease 1 (MIM: 265450). Offspring of this individual have a 50 percent chance of inheriting the pathogenic variant; due to reduced penetrance, they would have a 20 percent risk for developing pulmonary arterial hypertension if the variant is present (Cogan, 2012).

No additional pathogenic variants were identified in the targeted genes by massively parallel sequencing or deletion/duplication analysis. Please refer to the background information included in this report for a list of the genes analyzed and limitations of this test.

Evidence for variant classification:
The BMPR2 c.631C>T; p.Arg211Ter variant (rs137852753) has been described in several individuals affected with familial and sporadic pulmonary hypertension (Humbert, 2002; Machado, 2001; Machado, 2006; Portillo, 2010; Sztrymf, 2008; Thomson, 2000). It has been reported as pathogenic by several laboratories in ClinVar (Variation ID: 8812) and is absent from general population databases (1000 Genomes Project, Exome Variant Server, and Genome Aggregation Database), indicating it is not a common polymorphism. This variant induces an early termination codon in exon 6 of 13 and is predicted to result in a truncated protein or mRNA subject to nonsense-mediated decay. Based on available information, this variant is considered pathogenic.

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

RECOMMENDATIONS
Genetic consultation is indicated, including a discussion of medical screening and management. At-risk family members should be offered testing for the identified pathogenic BMPR2 variant (Familial Mutation, Targeted Sequencing, ARUP test code 2001961).

COMMENTS
Likely benign and benign variants are not reported.
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

REFERENCES
Cogan J, et al. Role of BMPR2 alternative splicing in HPAH penetrance. Circulation. 2012;126(15):1907-16. PMID: 22923426.

Humbert M, et al. BMPR2 germline mutations in pulmonary hypertension associated with fenfluramine derivatives. Eur Respir J. 2002;20(3):518-23. PMID: 12358323.

Machado R, et al. BMPR2 haploinsufficiency as the inherited molecular mechanism for primary pulmonary hypertension. Am J Hum Genet. 2001;68(1):92-102. PMID: 11115378.

Machado R, et al. Mutations of the TGF-beta type II receptor BMPR2 in pulmonary arterial hypertension. Hum Mutat. 2006;27(2):121-32. PMID: 16429395.

Portillo K, et al. Study of the BMPR2 gene in patients with pulmonary arterial hypertension. Arch Bronconeumol. 2010;46(3):129-34. PMID: 20096498.

Sztrymf B et al. Clinical outcomes of pulmonary arterial hypertension in carriers of BMPR2 mutation. Am J Respir Crit Care Med. 2008;177(12):1377-83. PMID: 18356561.

Thomson J, et al. Sporadic primary pulmonary hypertension is associated with germline mutations of the gene encoding BMPR-II, a receptor member of the TGF-beta family. J Med Genet. 2000;37(10):741-5. PMID: 11015450.

This result has been reviewed and approved by [redacted]
BACKGROUND INFORMATION: Pulmonary Arterial Hypertension (PAH)Panel, Sequencing and Deletion/Duplication
CHARACTERISTICS: Pulmonary arterial hypertension (PAH) is caused by widespread occlusion or destruction of the smallest pulmonary arteries, leading to increased blood flow resistance, right ventricular hypertrophy, and heart failure. Approximately 80 percent of PAH is idiopathic and 20 percent is heritable.

EPIDEMIOLOGY: The incidence is 1-2 in 1,000,000.

INHERITANCE: Autosomal dominant (ACVRL1, BMPR2, CAV1, ENG, KCNA5, KCNK3, GDF2, and SMAD9); autosomal recessive (EIF2AK4, TBX4)

CLINICAL SENSITIVITY: 75-80 percent for familial cases, approximately 25 percent for simplex cases.

GENES TESTED: ACVRL1, BMPR2, CAV1, EIF2AK4, ENG,* KCNA5, KCNK3, GDF2, SMAD9, and TBX4

*One or more exons are not covered by deletion/duplication analysis; see limitations section below.

METHODOLOGY: Probe hybridization-based capture of all coding

exons and exon-intron junctions of the targeted genes (including the 5' UTR of ENG, and a region of ACVRL1 intron 9 encompassing the CT-rich variant hotspot region), followed by massively parallel sequencing. Sanger sequencing was performed as necessary to fill in regions of low coverage and to confirm reported variants that do not meet acceptable quality metrics. A proprietary bioinformatic algorithm was used to detect large (single exon-level or larger) deletions or duplications in the indicated genes. Large deletions/duplications confirmed using an orthogonal exon-level microarray. Human genome build 19 (Hg 19) was used for data analysis.

ANALYTICAL SENSITIVITY/SPECIFICITY: The analytical sensitivity is approximately 99 percent for single nucleotide variants (SNVs) and greater than 93 percent for insertions/duplications/deletions (indels) from 1-10 base pairs in size. Indels greater than 10 base pairs may be detected but the analytical sensitivity may be reduced. Deletions of 2 exons or larger are detected with sensitivity greater than 97 percent; single exon deletions are detected with 62 percent sensitivity. Duplications of 3 exons or larger are detected at greater than 83 percent sensitivity. Specificity is greater than 99.9 percent for all variant classes.
LIMITATIONS: A negative result does not exclude a heritable form of PAH. This test only detects variants within the coding regions and intron-exon boundaries of the targeted genes. Deletions/duplications/insertions of any size may not be detected by massively parallel sequencing. Regulatory region variants and deep intronic variants will not be identified. Precise breakpoints for large deletions or duplications are not determined in this assay and single exon deletions/duplications may not be detected based on the breakpoints of the rearrangement. The actual breakpoints for the deletion or duplication may extend beyond or be within the exon(s) reported. This test is not intended to detect duplications of 2 or fewer exons in size, though these may be identified. Single exon deletions are reported but called at a lower sensitivity. Diagnostic errors can occur due to rare sequence variations. In some cases, variants may not be identified due to technical limitations caused by the presence of pseudogenes, repetitive, or homologous regions. This test is not intended to detect low-level mosaic or somatic variants, gene conversion events, complex inversions, translocations, mitochondrial DNA (mtDNA) variants, or repeat expansions. Interpretation of this test result may be impacted if this patient has had an allogeneic stem cell transplantation. Noncoding transcripts were not analyzed.

Single exon deletions/duplications may not be called in the following exons: ENG (NM_001114753) 1

This test was developed and its performance characteristics determined by ARUP Laboratories. The U.S. Food and Drug Administration has not approved or cleared this test; however, FDA clearance or approval is not currently required for clinical use. The results are not intended to be used as the sole means for clinical diagnosis or patient management decisions.

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

VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
PAH Pan. Seq/DelDup, Specimen	22-229-102441	8/17/2022 9:41:00 AM	8/17/2022 9:41:54 AM	8/17/2022 9:44:00 AM

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

PAH Pan. Seq/DelDup, Interp	22-229-102441	8/17/2022 9:41:00 AM	8/17/2022 9:41:54 AM	8/17/2022 9:44:00 AM

END OF CHART

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