Pulmonary Arterial Hypertension (BMPR2) Sequencing and Deletion/Duplication
ARUP test code 2003405

BMPR2 FGA Specimen
Whole Blood

PAH (BMPR2) Interpretation

No pathogenic variants were detected in the BMPR2 gene.

INTERPRETATION
No pathogenic variants were detected in the BMPR2 gene by sequencing all coding regions and intron-exon boundaries or by deletion/duplication analysis. This result decreases the probability of, but does not exclude, a diagnosis of BMPR2-related pulmonary arterial hypertension. Please refer to the background information included in this report for the clinical sensitivity and limitations of this test.

RECOMMENDATIONS
Medical screening and management should rely on clinical findings and family history. Genetic consultation is recommended. If a genetic etiology for pulmonary arterial hypertension (PAH) is still suspected, consider testing to analyze other genes associated with PAH (Pulmonary Arterial Hypertension Panel, Sequencing and Deletion/Duplication, ARUP test code 2009345).

COMMENTS
Reference Sequence: GenBank # NM_001204.6 (BMPR2)
Nucleotide numbering begins at the "A" of the ATG initiation codon. Likely benign and benign variants are not included in this report.

This result has been reviewed and approved by Wei Shen, Ph.D.
BACKGROUND INFORMATION: Pulmonary Arterial Hypertension (BMPR2) Sequencing and Deletion/Duplication

CHARACTERISTICS: Primary pulmonary arterial hypertension (PAH) is caused by widespread occlusion/ destruction of the smallest pulmonary arteries that increases resistance to blood flow. INCIDENCE: 1 to 2 new cases per million individuals per year. INHERITANCE: Autosomal dominant. PENETRANCE: Approximately 20 percent. CAUSE: Pathogenic BMPR2 mutations. CLINICAL SENSITIVITY: Approximately 70 percent for familial PAH and 13 percent for idiopathic PAH. METHODOLOGY: Bidirectional sequencing of the entire BMPR2 coding region and intron-exon boundaries and Multiplex Ligation-dependent Probe Amplification (MLPA) to detect large BMPR2 coding region deletions and duplications. ANALYTICAL SENSITIVITY AND SPECIFICITY FOR SEQUENCING: 99 percent. ANALYTICAL SENSITIVITY AND SPECIFICITY FOR MLPA: 99 percent. LIMITATION: Diagnostic errors can occur due to rare sequence variations. Regulatory region mutations and deep intronic mutations will not be detected. Breakpoints of large deletions/duplications will not be determined. Mutations in genes other than BMPR2 are not evaluated.

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

<table>
<thead>
<tr>
<th>Procedure</th>
<th>Accession</th>
<th>Collected</th>
<th>Received</th>
<th>Verified/Reported</th>
</tr>
</thead>
<tbody>
<tr>
<td>BMPR2 FGA Specimen</td>
<td>19-203-400554</td>
<td>00/00/0000 00:00</td>
<td>00/00/0000 00:00</td>
<td>00/00/0000 00:00</td>
</tr>
<tr>
<td>PAH (BMPR2) Interpretation</td>
<td>19-203-400554</td>
<td>00/00/0000 00:00</td>
<td>00/00/0000 00:00</td>
<td>00/00/0000 00:00</td>
</tr>
</tbody>
</table>

END OF CHART

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