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

Physician: Doctor, Example

Patient: Patient, Example

DOB	Unknown
Gender:	Unknown
Patient Identifiers:	01234567890ABCD, 012345
Visit Number (FIN):	01234567890ABCD
Collection Date:	00/00/0000 00:00

Juvenile Polyposis (SMAD4) Sequencing and Deletion/Duplication

ARUP test code 2001971

SMAD4 FGA Specimen	Whole Blood

JPS (SMAD4) Seq and Del/Dup Interp: Negative

TEST PERFORMED - 2001971
TEST DESCRIPTION - Juvenile Polyposis (SMAD4) Sequencing and Deletion/Duplication
INDICATION FOR TEST - Confirm Diagnosis

RESULT
No pathogenic variants were detected in the SMAD4 gene.

INTERPRETATION
No pathogenic variants were detected in the SMAD4 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 juvenile polyposis syndrome (JPS). 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 clinically indicated, consideration may be given to BMPR1A full gene analysis, which detects additional variants causative for JPS (ARUP test code 2004992).

COMMENTS
Reference Sequence: GenBank # NM_005359.4 (SMAD4)
Nucleotide numbering begins at the "A" of the ATG initiation codon.
Likely benign and benign variants are not included in this report, but are available upon request.

This result has been reviewed and approved by Rong Mao, M.D.

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

BACKGROUND INFORMATION: Juvenile Polyposis (SMAD4)
Sequencing and Deletion/Duplication
CHARACTERISTICS OF JUVENILE POLYPOSIS SYNDROME (JPS): Gastrointestinal (GI) bleeding, multiple hamartomatous polyps in the GI tract, increased risk for GI carcinoma.
CHARACTERISTICS OF JP/HEREDITARY HEMORRHAGIC TELANGIECTASIA (HHT): Recurrent nosebleeds, telangiectases (mouth, face, hands, GI tract), arteriovenous malformations (lung, brain, liver, spine) and hamartomatous polyps in the GI tract.
INCIDENCE: 1 in 16,000 to 1 in 100,000 for JPS; unknown for JP/HHT.
INHERITANCE: Autosomal dominant; de novo mutations occur in 25 percent of JPS.
PENETRANCE: Suspected to be greater than 90 percent for JPS.
CAUSE FOR JPS: Mutations in SMAD4, BMPR1A, and other unknown genes.
CAUSE FOR JP/HHT: Mutations in SMAD4.
CLINICAL SENSITIVITY: Approximately 25 percent for JPS; unknown for JP/HHT.
METHODOLOGY: Bidirectional sequencing of the entire SMAD4 coding region and intron-exon boundaries. Multiplex ligation-dependent probe amplification (MLPA) to detect large SMAD4 coding region delections/duplictions.
ANALYTICAL SENSITIVITY AND SPECIFICITY: 99 percent.
LIMITATIONS: Diagnostic errors can occur due to rare sequence variations. Breakpoints for large deletions/duplications will not be determined. This assay is not designed to detect somatic variants associated with malignancy. Interpretation of this test result may be impacted if the patient has had an allogeneic stem cell transplantation.
Test developed and characteristics determined by ARUP Laboratories. See Compliance Statement C: aruplab.com/CS

VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
SMAD4 FGA Specimen	19-308-107373	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
JPS (SMAD4) Seq and Del/Dup Interp	19-308-107373	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