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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	[redacted]
Gender:	Male
Patient Identifiers:	01234567890ABCD, 012345
Visit Number (FIN):	01234567890ABCD
Collection Date:	00/00/0000 00:00

Multiple Endocrine Neoplasia Type 1 (MEN1) Sequencing

ARUP test code 2005359

MEN Type 1 (MEN1) Sequencing Specimen	Whole Blood	
MEN Type 1 (MEN1) Sequencing Interp	**Positive**	*

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

TEST PERFORMED - 2005359
TEST DESCRIPTION - MEN1-Multiple Endocrine Neoplasia Type 1 (MEN1) Sequencing
INDICATION FOR TEST - Not Provided

RESULT
One pathogenic variant was detected in the MEN1 gene.

DNA VARIANT
Classification: Pathogenic
Gene: MEN1
Nucleic Acid Change: c.682_685dupATGC; Heterozygous
Amino Acid Alteration: p.Arg229fs

INTERPRETATION
One copy of the pathogenic variant, c.682_685dupATGC; p.Arg229fs, was detected in the MEN1 gene by sequencing. This result is consistent with a diagnosis of multiple endocrine neoplasia type 1. Clinical manifestations are variable. Offspring of this individual have a 50 percent chance of inheriting the causative variant.

Evidence for variant classification: The MEN1 c.682_685dupATGC; p.Arg229fs variant (rs1114167519), to our knowledge, has not been published in the medical literature or in gene-specific databases. The variant is reported in the ClinVar database (Variation ID: 428061) and is absent from general population databases (Exome Variant Server, Genome Aggregation Database), indicating it is not a common polymorphism. This variant causes a frameshift by duplicating four nucleotides, so it is predicted to result in a truncated protein or mRNA subject to nonsense-mediated decay. Considering available information, this variant is classified as pathogenic.

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 variant (Familial Mutation, Targeted Sequencing; ARUP test code 2001961).

COMMENTS
Reference Sequence: GenBank # NM_130799.2 (MEN1)
Nucleotide numbering begins at the "A" of the ATG initiation codon.
Likely benign and benign variants are not reported.

This result has been reviewed and approved by Steven Steinberg, Ph.D.

BACKGROUND INFORMATION: Multiple Endocrine Neoplasia Type 1 (MEN1) Sequencing
CHARACTERISTICS: Multiple Endocrine Neoplasia Type 1 (MEN1) syndrome can include multiple endocrine and non-endocrine tumors. Common MEN1-related endocrine tumors include parathyroid (90-95 percent), pancreatic islets (30-80 percent), and pituitary (15-90 percent). Non-endocrine tumors include facial angiofibroma, collagenoma, lipoma, meningioma, ependymoma, and leiomyoma. Primary hyperparathyroidism is the most common and often the first manifestation of MEN1. High mortality rates occur in persons with gastrinoma and carcinoid tumors.
INCIDENCE: Approximately 1 in 30,000.
INHERITANCE: Autosomal dominant.
PENETRANCE: Approximately 50 percent by age 20 and 95 percent by age 40.
CAUSE: Pathogenic MEN1 gene mutations.
CLINICAL SENSITIVITY: Approaches 90 percent.
METHODOLOGY: Bidirectional sequencing of the entire coding region and intron-exon boundaries of the MEN1 gene.
ANALYTICAL SENSITIVITY AND SPECIFICITY: Approximately 98 percent.
LIMITATIONS: Diagnostic errors can occur due to rare sequence variations. Regulatory region mutations, deep intronic mutations, and large deletions/duplications will not be detected. Mutations in genes other than MEN1 are not evaluated. 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
MEN Type 1 (MEN1) Sequencing Specimen	19-343-131337	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
MEN Type 1 (MEN1) Sequencing Interp	19-343-131337	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