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

Physician: Doctor, Example

Patient: Patient, Example

DOB	11/13/2021
Sex:	Male
Patient Identifiers:	01234567890ABCD, 012345
Visit Number (FIN):	01234567890ABCD
Collection Date:	01/01/2017 12:34

Multiple Endocrine Neoplasia Type 1 (MEN1) Sequencing and Deletion/Duplication

ARUP test code 3004437

MEN1 Specimen	See Note
MEN1 Interp	Negative

RESULT
No pathogenic variants were detected in the MEN1 gene.

INTERPRETATION
No pathogenic variants were identified by massively parallel sequencing of the coding regions and exon-intron boundaries of the MEN1 gene. No large exonic deletions and duplications were identified in the MEN1 gene. This result decreases the likelihood of, but does not exclude, a diagnosis of multiple endocrine neoplasia type 1. 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. If suspicion remains for a hereditary cancer syndrome, consideration should be given to ordering the Hereditary Cancer Panel, Sequencing and Deletion/Duplication (ARUP test code 2012032). Genetic consultation is recommended.

COMMENTS
Likely benign and benign variants are not included in this report.

This result has been reviewed and approved by [redacted]

BACKGROUND INFORMATION: Multiple Endocrine Neoplasia Type 1 (MEN1) Sequencing and Deletion/Duplication

CHARACTERISTICS: Multiple endocrine neoplasia type 1 (MEN1) syndrome can include multiple endocrine and nonendocrine tumors. Common MEN1-related endocrine tumors include parathyroid, pancreatic islets, and pituitary. Nonendocrine 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 individuals with gastrinoma and carcinoid tumors.

EPIDEMIOLOGY: 1/10,000 to 1/100,000.

CAUSE: Pathogenic germline variants in the MEN1 gene.

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

INHERITANCE: Autosomal dominant.

PENETRANCE: Greater than 50 percent by age 20 and 95 percent by age 40.

CLINICAL SENSITIVITY: A pathogenic MEN1 variant is identified in 80 to 90 percent of individuals who meet clinical criteria for MEN1 syndrome and have a family history of related cancers.

GENE TESTED: MEN1 (NM_130799)

METHODOLOGY: Probe hybridization-based capture of all coding exons and exon-intron junctions of the targeted gene 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 two exons or larger are detected with sensitivity greater than 97 percent; single exon deletions are detected with 62 percent sensitivity. Duplications of three 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 diagnosis of MEN1. A negative result does not exclude all genetic diagnoses. This test only detects variants within the coding regions and intron-exon boundaries of the MEN1 gene. 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 two 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) mutations, 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.

VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
MEN1 Specimen	21-319-104599	11/15/2021 11:18:00 AM	11/15/2021 2:51:31 PM	11/15/2021 3:25:00 PM
MEN1 Interp	21-319-104599	11/15/2021 11:18:00 AM	11/15/2021 2:51:31 PM	11/15/2021 3:25:00 PM

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

END OF CHART

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