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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	9/25/1987
Gender:	Male
Patient Identifiers:	01234567890ABCD, 012345
Visit Number (FIN):	01234567890ABCD
Collection Date:	00/00/0000 00:00

Cystic Fibrosis (CFTR) Sequencing and Deletion/Duplication

ARUP test code 3004745

CFTR Specimen: Whole Blood

CFTR Interp: Negative

RESULT
No pathogenic variants were detected in the CFTR gene.

INTERPRETATION
No pathogenic variants were detected in the CFTR gene. This result decreases the likelihood of, but does not exclude, cystic fibrosis (CF) disease or carrier status. Please refer to the background information included in this report for the methodology and limitations of this test.

RECOMMENDATIONS
Medical screening and management should rely on clinical findings and family history. If this individual has a family history, determination of a causative familial variant in an affected family member is necessary for optimal interpretation of this negative result. Further testing may be warranted if there is a familial variant that is not detectable by this assay. Consideration may be given to additional analysis for the single exon 2 deletion via a different methodology, as this assay has reduced analytical sensitivity for this common variant, particularly if this individual is of Turkish ancestry. Genetic consultation is recommended.

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: None

This result has been reviewed and approved by [redacted]

BACKGROUND INFORMATION: Cystic Fibrosis (CFTR) Sequencing and Deletion/Duplication

CHARACTERISTICS: Cystic fibrosis (CF) and CFTR-related disorders are caused by biallelic pathogenic variants in the CFTR gene. Age of onset, manifestations, and symptom severity vary greatly. Symptoms of classic CF include chronic sinopulmonary disease, pancreatic insufficiency, hepatic disease, prolapsed rectum, meconium ileus, obstructive azoospermia, and salt loss syndromes. CFTR-related disorders are less severe and may be characterized by isolated pancreatitis, bilateral absence of the vas deferens, chronic bronchiectasis, and/or nasal polyposis.

EPIDEMIOLOGY: CF is more common in individuals of Ashkenazi

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

Jewish and Caucasian/White descent (approximately 1 in 2,300 and 1 in 2,500 individuals, respectively). CF is less common in individuals of Hispanic, African American/Black, and Asian American descent (approximately 1 in 13,500, 1 in 15,100, and 1 in 35,100, respectfully).

CAUSE: Biallelic pathogenic variants in the CFTR gene

INHERITANCE: Autosomal recessive

CLINICAL SENSITIVITY: 99 percent

GENE TESTED: CFTR (NM_000492)

METHODOLOGY: Probe hybridization-based capture of all coding exons and exon-intron junctions of the CFTR gene, followed by massively parallel sequencing. Sanger sequencing was performed as necessary to fill in regions of low coverage or known low quality, 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 CFTR gene. 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 CF. This test only detects variants within the coding regions and intron-exon boundaries of the CFTR 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.

This test was developed and its performance characteristics determined by ARUP Laboratories. It has not been cleared or approved by the U.S. Food and Drug Administration. This test was performed in a CLIA-certified laboratory and is intended for clinical purposes.

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

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VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
CFTR Specimen	24-320-118220	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CFTR Interp	24-320-118220	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