Date Collected: **mm/dd/yyyy** | Date Received: **mm/dd/yyyy** | Date Reported: **mm/dd/yyyy** | Date Entered: **mm/dd/yyyy**

Specimen Type: **Whole Blood**
Ethnicity: **Not Provided**
Indication: **Carrier Test / Screening**

Cystic Fibrosis (CF), 97 Variants

Summary: NEGATIVE

SAMPLE REPORT

Negative Results

Disorder *(Gene)*	Result	Interpretation
Cystic fibrosis *(CFTR)* NM_000492.3	NEGATIVE	This result reduces, but does not eliminate, the risk to be a carrier. **Risk:** At reduced risk for an affected pregnancy. For ethnic-specific risk revisions see Information Table.

Recommendations

Genetic counseling is recommended to discuss the potential clinical and/or reproductive implications of positive results, as well as recommendations for testing family members and, when applicable, this individual's partner. Genetic counseling services are available. To access Labcorp Genetic Counselors please visit https://womenshealth.labcorp.com/genetic-counseling or call (855) GC-CALLS (855-422-2557).

Additional Clinical Information

Cystic fibrosis (CF) is an autosomal recessive disorder with variable severity and age at onset. Signs and symptoms of classic CF may include elevated sweat chloride levels, progressive lung disease, pancreatic insufficiency, and male infertility. Symptoms of mild CF may include pancreatic sufficiency. Symptoms of *CFTR*-related disorders may include pancreatitis, bronchiectasis, and isolated male infertility due to congenital absence of the vas deferens (CBAVD). Treatment is dietary and supportive. Genotype-targeted therapies may be available for some individuals. In severely affected individuals, lung transplantation may be indicated. (Ong, PMID:20301428).

Comments

This interpretation is based on the clinical information provided and the current understanding of the molecular genetics of the disorder(s) tested. Information about the disorder(s) tested is available at https://womenshealth.labcorp.com.

Methods/Limitations

Next-generation Sequencing: Genomic regions of interest in the *CFTR* gene are selected using the Twist Biosciences® hybridization capture method and sequenced via the Illumina® next generation sequencing platform. Sequencing reads are aligned with the human genome reference GRCh37/hg19 build. Regions of interest include genomic regions encompassing targeted variants. Analytical sensitivity at 30X coverage is estimated to be >99% for single nucleotide variants, >99% for insertions/deletions less than six base pairs and >96% for insertions/deletions between six and forty-five base pairs. Variant detection is performed by QIAGEN CLC Genomics and in-house algorithms. Confirmatory testing is done by Sanger sequencing. Variants are specified using the numbering and nomenclature recommended by the Human Genome Variation Society (HGVS, http://www.hgvs.org/). Variant classification and confirmation are consistent with ACMG standards and guidelines (Richards, PMID:25741868; Rehm, PMID:23887774).

Analysis is restricted to 97 targeted CF variants, listed below.
c.54-5940_273+10250del21kb, c.178G>T (p.Glu60*), c.223C>T (p.Arg75*), c.254G>A (p.Gly85Glu), c.262_263delTT (p.Leu88Ilefs*22), c.273+1G>A, c.273+3A>C, c.274-1G>A, c.274G>T (p.Glu92*), c.313delA (p.Ile105Serfs*2), c.325_327delinsG (p.Tyr109Glyfs*4), c.349C>T (p.Arg117Cys), c.350G>A (p.Arg117His), c.366T>A (p.Tyr122*), c.442delA (p.Ile148Leufs*5), c.489+1G>T, c.531delT (p.Ile177Metfs*12), c.532G>A (p.Gly178Arg), c.579+1G>T, c.579+5G>A, c.580-1G>T, c.617T>G (p.Leu206Trp), c.803delA (p.Asn268Ilefs*17), c.805_806delAT (p.Ile269Profs*4), c.935_937delTCT (p.Phe312del), c.948delT (p.Phe316Leufs*12), c.988G>T (p.Gly330*), c.1000C>T (p.Arg334Trp), c.1013C>T (p.Thr338Ile), c.1040G>A (p.Arg347His), c.1040G>C (p.Arg347Pro), c.1055G>A (p.Arg352Gln), c.[1075C>A;1079C>A] (p.[Gln359Lys;Thr360Lys]), c.1155_1156dupTA (p.Asn386Ilefs*3), c.1364C>A (p.Ala455Glu), c.1438G>T (p.Gly480Cys), c.1477C>T (p.Gln493*), c.1519_1521delATC (p.Ile507del), c.1521_1523delCTT (p.Phe508del), c.1545_1546delTA (p.Tyr515*), c.1558G>T (p.Val520Phe), c.1572C>A (p.Cys524*), c.1585-1G>A, c.1624G>T (p.Gly542*), c.1646G>A (p.Ser549Asn), c.1647T>G (p.Ser549Arg), c.1652G>A (p.Gly551Asp), c.1654C>T (p.Gln552*), c.1657C>T (p.Arg553*), c.1675G>A (p.Ala559Thr), c.1679G>C (p.Arg560Thr), c.1680-1G>A, c.1721C>A (p.Pro574His), c.1766+1G>A, c.1766+5G>T, c.1820_1903del84 (p.Met607_Gln634del), c.1911delG (p.Gln637Hisfs*26), c.1923_1931delinsA (p.Ser641Argfs*5), c.1973_1985delinsAGAAA (p.Arg658Lysfs*4), c.1976delA (p.Asn659Ilefs*4), c.2012delT (p.Leu671*), c.2051_2052delinsG (p.Lys684Serfs*38), c.2052delA (p.Lys684Asnfs*38), c.2052dupA (p.Gln685Thrfs*4), c.2125C>T (p.Arg709*), c.2128A>T (p.Lys710*), c.2175dupA (p.Glu726Argfs*4), c.2290C>T (p.Arg764*), c.2657+5G>A, c.2668C>T (p.Gln890*), c.2737_2738insG (p.Tyr913*), c.2988G>A (p.Gln996=), c.2988+1G>A, c.3039delC (p.Tyr1014Thrfs*9), c.3067_3072delATAGTG (p.Ile1023_Val1024del), c.3196C>T (p.Arg1066Cys), c.3266G>A (p.Trp1089*), c.3276C>A (p.Tyr1092*), c.3276C>G (p.Tyr1092*), c.3302T>A (p.Met1101Lys), c.3454G>C (p.Asp1152His), c.3472C>T (p.Arg1158*), c.3484C>T (p.Arg1162*), c.3528delC (p.Lys1177Serfs*15), c.3536_3539delCCAA (p.Thr1179Asnfs*12), c.3587C>G (p.Ser1196*), c.3611G>A (p.Trp1204*), c.3659delC (p.Thr1220Lysfs*8), c.3712C>T (p.Gln1238*), c.3718-2477C>T, c.3744delA (p.Lys1250Argfs*9), c.3752G>A (p.Ser1251Asn), c.3764C>A (p.Ser1255*), c.3773dupT (p.Leu1258Phefs*7), c.3846G>A (p.Trp1282*), c.3889dupT (p.Ser1297Phefs*5), c.3909C>G (p.Asn1303Lys)

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Cystic Fibrosis (CF), 97 Variants

Methods/Limitations (Cont.)

Limitations: Technologies used do not detect germline mosaicism and do not rule out the presence of large chromosomal aberrations including rearrangements and gene fusions, or variants in regions or genes not included in this test, or possible inter/intragenic interactions between variants, or repeat expansions. Variant classification and/or interpretation may change over time if more information becomes available. False positive or false negative results may occur for reasons that include: rare genetic variants, sex chromosome abnormalities, pseudogene interference, blood transfusions, bone marrow transplantation, somatic or tissue-specific mosaicism, mislabeled samples, or erroneous representation of family relationships.

Information Table

Cystic fibrosis, 97 variants, risk reductions for individuals with no family history

Population	Detection rate	Pre-test carrier risk	Post-test carrier risk with negative result
African American	81%	1 in 61	1 in 316
Ashkenazi Jewish	97%	1 in 24	1 in 767
Asian American	55%	1 in 94	1 in 208
Caucasian	93%	1 in 25	1 in 343
Hispanic	78%	1 in 58	1 in 260
Mixed or other ethnic background	For counseling purposes, consider using the ethnic background with the most conservative risk estimates.		

References

Deignan JL, Astbury C, Cutting GR *et al*. CFTR variant testing: a technical standard of the American College of Medical Genetics and Genomics (ACMG). *Genet Med* 22, 1288 (2020). PMID: 32404922

Ong T, Marshall SG, Karczeski BA, *et al*. Cystic Fibrosis and Congenital Absence of the Vas Deferens. 2001 Mar26 [Updated 2017 Feb 2]. In: Adam MP, Ardinger HH, Pagon RA, et al., editors. GeneReviews® [Internet]. PMID: 20301428

Performing Labs

Component Type	Performed at	Laboratory Director
Technical component, processing	Laboratory Corporation of America, 1912 TW Alexander Drive, RTP, NC 27709-0150	Laboratory Director
Technical component, analysis	Laboratory Corporation of America, 1912 TW Alexander Drive, RTP, NC 27709-0150	Laboratory Director
Professional component	Laboratory Corporation of America, 1912 TW Alexander Drive, RTP, NC 27709-0150	Laboratory Director

For inquiries, the physician may contact the lab at 800-345-4363

This test was developed and its performance characteristics determined by Labcorp. It has not been cleared or approved by the Food and Drug Administration.

Patient Details
LASTNAME, FIRSTNAME

Phone:
Date of Birth: **mm/dd/yyyy**
Age: **00**
Sex: **Female**
Patient ID:
Alternate Patient ID:

Physician Details
CLIENT NAME
CLIENT ADDRESS

Phone: **00000000**
Account Number: **00000000**
Physician ID:
NPI:

Specimen Details
Specimen ID: **000-000-0000-0**
Control ID:
Alternate Control Number:
Date Collected: **mm/dd/yyyy 0000 Local**
Date Received: **mm/dd/yyyy 0823 ET**
Date Entered: **mm/dd/yyyy 1409 ET**
Date Reported: **mm/dd/yyyy 1052 ET**

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