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CLIA: 22D0957540

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Metroplex Pathology Associates
Lakewood Pathology Associates
Cohen Dermatopathology
Therapath Partners

Patient Information:
10916, Donor
DOB: [redacted]
Sex: M
MR#:
Patient#: FT-PT8770563

Partner Information:
Not Tested

Physician:
Kuan, James
ATTN: Kirk, Ashley
Phoenix Sperm Bank
4915 25th Avenue NE, Ste 204W
Seattle, WA 98105
Phone: (206) 588-1484

Laboratory:
Fulgent Therapeutics LLC
CAP#: 8042697
CLIA#: 05D2043189
Laboratory Director:
Lawrence M. Weiss, MD
Report Date: **Jul 10,2024**

Accession:
FT-7017368
Test#: FT-TS14877449
Specimen Type: Blood (EDTA)
Collected: Jun 25,2024

Accession:
N/A

FINAL RESULTS

No carrier mutations identified

TEST PERFORMED

Beacon Preconception Carrier Screening - 515 Genes (without X-linked Disorders)
(515 Gene Panel; gene sequencing with deletion and duplication analysis)

INTERPRETATION:

Notes and Recommendations:

- No carrier mutations were identified in the submitted specimen. A negative result does not rule out the possibility of a genetic predisposition nor does it rule out any pathogenic mutations in areas not assessed by this test or in regions that were covered at a level too low to reliably assess. Also, it does not rule out mutations that are of the sort not queried by this test; see Methods and Limitations for more information. A negative result reduces, but does not eliminate, the chance to be a carrier for any condition included in this screen. Please see the supplemental table for details.
- Testing for copy number changes in the SMN1 gene was performed to screen for the carrier status of Spinal Muscular Atrophy. The results for this individual are within the normal range for non-carriers. See Limitations section for more information.
- This carrier screening test does not screen for all possible genetic conditions, nor for all possible mutations in every gene tested. This report does not include variants of uncertain significance; only variants classified as pathogenic or likely pathogenic at the time of testing, and considered relevant for reproductive carrier screening, are reported. Please see the gene specific notes for details. Please note that the classification of variants can change over time.
- Patients may wish to discuss any carrier results with blood relatives, as there is an increased chance that they are also carriers. These results should be interpreted in the context of this individual's clinical findings, biochemical profile, and family history.
- X-linked genes are not routinely analyzed for male carrier screening tests. Gene specific notes and limitations may be present. See below.
- Genetic counseling is recommended. Available genetic counselors and additional resources can be found at the National Society of Genetic Counselors (NSGC; https://www.nsgc.org)

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GENES TESTED:

Beacon Preconception Carrier Screening - 515 Genes (without X-linked Disorders) - 515 Genes

This analysis was run using the Beacon Preconception Carrier Screening - 515 Genes (without X-linked Disorders) gene list. 515 genes were tested with 99.5% of targets sequenced at >20x coverage. For more gene-specific information and assistance with residual risk calculation, see the SUPPLEMENTAL TABLE.

AAAS, ABCA12, ABCA3, ABCA4, ABCB11, ABCB4, ABCC2, ABCC8, ACAD9, ACADM, ACADVL, ACAT1, ACOX1, ACSF3, ADA, ADAMTS2, ADAMTSL4, ADGRG1, ADGRV1, AGA, AGL, AGPS, AGXT, AHI1, AIPL1, AIRE, ALDH3A2, ALDH7A1, ALDOB, ALG1, ALG6, ALMS1, ALPL, AMN, AMT, ANO10, AP1S1, AQP2, ARG1, ARL6, ARSA, ARSB, ASL, ASNS, ASPA, ASS1, ATM, ATP6V1B1, ATP7B, ATP8B1, BBS1, BBS10, BBS12, BBS2, BBS4, BBS5, BBS7, BBS9, BCKDHA, BCKDHB, BCS1L, BLM, BLOC1S3, BLOC1S6, BMP1, BRIP1, BSND, CAD, CANT1, CAPN3, CASQ2, CBS, CC2D1A, CC2D2A, CCDC103, CCDC39, CCDC88C, CD3D, CD3E, CD40, CD59, CDH23, CEP152, CEP290, CERKL, CFTR, CHAT, CHRNE, CHRNG, CIITA, CLCN1, CLN3, CLN5, CLN6, CLN8, CLRN1, CNGB3, COL11A2, COL17A1, COL27A1, COL4A3, COL4A4, COL7A1, COX15, CPS1, CPT1A, CPT2, CRB1, CRTAP, CRYL1, CTNS, CTSA, CTSC, CTSD, CTSK, CYBA, CYP11A1, CYP11B1, CYP11B2, CYP17A1, CYP19A1, CYP1B1, CYP21A2, CYP27A1, CYP27B1, CYP7B1, DBT, DCAF17, DCLRE1C, DDX11, DGAT1, DGUOK, DHCR7, DHDDS, DLD, DLL3, DNAH11, DNAH5, DNAI1, DNAI2, DNMT3B, DOK7, DUOX2, DYNC2H1, DYSF, EIF2AK3, EIF2B1, EIF2B2, EIF2B3, EIF2B4, EIF2B5, ELP1, EPG5, ERCC2, ERCC6, ERCC8, ESCO2, ETFA, ETFB, ETFDH, ETHE1, EVC, EVC2, EXOSC3, EYS, FAH, FAM161A, FANCA, FANCC, FANCD2, FANCE, FANCG, FANCI, FANCL, FBP1, FBXO7, FH, FKBP10, FKRP, FKTN, FMO3, FOXN1, FOXRED1, FRAS1, FREM2, FUCA1, G6PC, G6PC3, GAA, GALC, GALE, GALK1, GALNS, GALNT3, GALT, GAMT, GATM, GBA, GBE1, GCDH, GCH1, GDF5, GFM1, GHR, GJB2, GJB6, GLB1, GLDC, GLE1, GNE, GNPAT, GNPTAB, GNPTG, GNS, GORAB, GRHPR, GRIP1, GSS, GUCY2D, GUSB, HADH, HADHA, HADHB, HAMP, HAX1, HBA1, HBA2, HBB, HEXA, HEXB, HGSNAT, HJV, HLCS, HMGCL, HMOX1, HOGA1, HPD, HPS1, HPS3, HPS4, HPS5, HPS6, HSD17B3, HSD17B4, HSD3B2, HYAL1, HYLS1, IDUA, IGHMBP2, IKBKB, IL7R, INVS, ITGA6, ITGB3, ITGB4, IVD, JAK3, KCNJ1, KCNJ11, LAMA2, LAMA3, LAMB3, LAMC2, LARGE1, LCA5, LDLR, LDLRAP1, LHX3, LIFR, LIG4, LIPA, LMBRD1, LOXHD1, LPL, LRAT, LRP2, LRPPRC, LYST, MAK, MAN2B1, MANBA, MCEE, MCOLN1, MCPH1, MECR, MED17, MESP2, MFSD8, MKKS, MKS1, MLC1, MLYCD, MMAA, MMAB, MMACHC, MMADHC, MOCS1, MOCS2, MPI, MPL, MPV17, MRE11, MTHFR, MTR, MTRR, MTTP, MUSK, MUT, MVK, MYO15A, MYO7A, NAGA, NAGLU, NAGS, NBN, NCF2, NDRG1, NDUFAF2, NDUFAF5, NDUFS4, NDUFS6, NDUFS7, NDUFV1, NEB, NEU1, NGLY1, NPC1, NPC2, NPHP1, NPHS1, NPHS2, NR2E3, NSMCE3, NTRK1, OAT, OCA2, OPA3, OSTM1, OTOA, OTOF, P3H1, PAH, PANK2, PC, PCBD1, PCCA, PCCB, PCDH15, PCNT, PDHB, PEPD, PET100, PEX1, PEX10, PEX12, PEX13, PEX16, PEX2, PEX26, PEX5, PEX6, PEX7, PFKM, PGM3, PHGDH, PHKB, PHKG2, PHYH, PIGN, PJVK, PKHD1, PLA2G6, PLEKHG5, PLOD1, PMM2, PNPO, POLG, POLH, POMGNT1, POMT1, POMT2, POR, POU1F1, PPT1, PRCD, PRDM5, PRF1, PROP1, PSAP, PTPRC, PTS, PUS1, PYGM, QDPR, RAB23, RAG1, RAG2, RAPSN, RARS2, RDH12, RLBP1, RMRP, RNASEH2A, RNASEH2B, RNASEH2C, RPE65, RPGRIP1L, RTEL1, RXYLT1, RYR1, SACS, SAMD9, SAMHD1, SCO2, SEC23B, SEPSECS, SGCA, SGCB, SGCD, SGCG, SGSH, SKIV2L, SLC12A1, SLC12A3, SLC12A6, SLC17A5, SLC19A2, SLC19A3, SLC1A4, SLC22A5, SLC25A13, SLC25A15, SLC25A20, SLC26A2, SLC26A3, SLC26A4, SLC27A4, SLC35A3, SLC37A4, SLC38A8, SLC39A4, SLC45A2, SLC4A11, SLC5A5, SLC7A7, SMARCAL1, SMN1, SMPD1, SNAP29, SPG11, SPR, SRD5A2, ST3GAL5, STAR, STX11, STXBP2, SUMF1, SUOX, SURF1, SYNE4, TANGO2, TAT, TBCD, TBCE, TCIRG1, TCN2, TECPR2, TERT, TF, TFR2, TG, TGM1, TH, TK2, TMC1, TMEM216, TMEM67, TMPRSS3, TPO, TPP1, TREX1, TRIM32, TRIM37, TRMU, TSEN54, TSFM, TSHB, TSHR, TTC37, TTPA, TULP1, TYMP, TYR, TYRP1, UBR1, UNC13D, USH1C, USH2A, VDR, VLDLR, VPS11, VPS13A, VPS13B, VPS45, VPS53, VRK1, VSX2, WISP3, WNT10A, WRN, XPA, XPC, ZBTB24, ZFYVE26, ZNF469

METHODS:

Genomic DNA was isolated from the submitted specimen indicated above (if cellular material was submitted). DNA was barcoded, and enriched for the coding exons of targeted genes using hybrid capture technology. Prepared DNA libraries were then sequenced using a Next Generation Sequencing technology. Following alignment to the human genome reference sequence (assembly GRCh37), variants were detected in regions of at least 10x coverage. For this specimen, 99.52% and 99.47% of coding regions and splicing junctions of genes listed had been sequenced with coverage of at least 10x and 20x, respectively, by NGS or by Sanger sequencing. The remaining regions did not have 10x coverage, and were not evaluated. Variants were interpreted manually using locus specific databases, literature searches, and other molecular biological principles. To minimize false positive results, any variants that do not meet internal quality standards are confirmed by Sanger sequencing. Variants classified as pathogenic, likely pathogenic, or risk allele which are located in the coding regions and nearby intronic regions (+/- 20bp) of the genes listed above are reported. Variants outside these intervals may be reported but are typically not guaranteed. When a single pathogenic or likely pathogenic variant is identified in a clinically relevant gene with autosomal recessive inheritance, the laboratory will attempt to ensure 100% coverage of coding sequences either through NGS or Sanger sequencing technologies ("fill-in"). All genes listed were evaluated for large deletions and/or duplications. However, single exon deletions or duplications will not be detected in this assay, nor will copy number alterations in regions of genes with significant pseudogenes. Putative deletions or duplications are analyzed using Fulgent Germline proprietary pipeline for this specimen. Bioinformatics: The Fulgent Germline v2019.2 pipeline was used to analyze this specimen.

LIMITATIONS:

General Limitations

These test results and variant interpretation are based on the proper identification of the submitted specimen, accuracy of any stated familial relationships, and use of the correct human reference sequences at the queried loci. In very rare instances, errors may result due to mix-up or co-mingling of specimens. Positive results do not imply that there are no other contributors, genetic or

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otherwise, to future pregnancies, and negative results do not rule out the genetic risk to a pregnancy. Official gene names change over time. Fulgent uses the most up to date gene names based on HUGO Gene Nomenclature Committee (https://www.genenames.org) recommendations. If the gene name on report does not match that of ordered gene, please contact the laboratory and details can be provided. Result interpretation is based on the available clinical and family history information for this individual, collected published information, and Alamut annotation available at the time of reporting. This assay is not designed or validated for the detection of low-level mosaicism or somatic mutations. This assay will not detect certain types of genomic aberrations such as translocations, inversions, or repeat expansions other than specified genes. DNA alterations in regulatory regions or deep intronic regions (greater than 20bp from an exon) may not be detected by this test. Unless otherwise indicated, no additional assays have been performed to evaluate genetic changes in this specimen. There are technical limitations on the ability of DNA sequencing to detect small insertions and deletions. Our laboratory uses a sensitive detection algorithm, however these types of alterations are not detected as reliably as single nucleotide variants. Rarely, due to systematic chemical, computational, or human error, DNA variants may be missed. Although next generation sequencing technologies and our bioinformatics analysis significantly reduce the confounding contribution of pseudogene sequences or other highly-homologous sequences, sometimes these may still interfere with the technical ability of the assay to identify pathogenic alterations in both sequencing and deletion/duplication analyses. Deletion/duplication analysis can identify alterations of genomic regions which include one whole gene (buccal swab specimens and whole blood specimens) and are two or more contiguous exons in size (whole blood specimens only); single exon deletions or duplications may occasionally be identified, but are not routinely detected by this test. When novel DNA duplications are identified, it is not possible to discern the genomic location or orientation of the duplicated segment, hence the effect of the duplication cannot be predicted. Where deletions are detected, it is not always possible to determine whether the predicted product will remain in-frame or not. Unless otherwise indicated, deletion/duplication analysis has not been performed in regions that have been sequenced by Sanger.

Gene Specific Notes and Limitations

ALG1: Due to the interference by highly homologous regions, our current testing method has less sensitivity to detect variants in exons 6-13 of the ALG1 gene (NM_019109.4). *CEP290:* Copy number analysis for exons 8-13 and exons 39-42 may have reduced sensitivity in the CEP290 gene. Confirmation of these exons are limited to individuals with a positive personal history of CEP290-related conditions and/or individuals carrying a pathogenic/likely pathogenic sequence variant. *CFTR:* Analysis of the intron 8 polymorphic region (e.g. IVS8-5T allele) is only performed if the p.Arg117His (R117H) mutation is detected. Single exon deletion/duplication analysis is limited to deletions of previously reported exons: 1, 2, 3, 11, 19, 20, 21. Analysis of the intron 8 polymorphic region (e.g. IVS8-5T allele) is only performed if the p.Arg117His (R117H) mutation is detected. Single exon deletion/duplication analysis is limited to deletions of previously reported exons: 1, 2, 3, 11, 19, 20, 21. CFTR variants primarily associated with CFTR-related isolated congenital bilateral absence of the vas deferens and CFTR-related pancreatitis are not included in this analysis. CFTR variants with insufficient evidence of being cystic fibrosis mutations will not be reported either. *CRYL1:* As mutations in the CRYL1 gene are not known to be associated with any clinical condition, sequence variants in this gene are not analyzed. However, to increase copy number detection sensitivity for large deletions including this gene and a neighboring on gene on the panel (GJB6, also known as connexin 30), this gene was evaluated for copy number variation. *CYP11B1:* The current testing method is not able to reliably detect certain pathogenic variants in this gene due to the interference by highly homologous regions. This analysis is not designed to detect or rule-out copy-neutral chimeric CYP11B1/CYP11B2 gene. *CYP11B2:* The current testing method is not able to reliably detect certain pathogenic variants in this gene due to the interference by highly homologous regions. This analysis is not designed to detect or rule-out copy-neutral chimeric CYP11B1/CYP11B2 gene. *CYP21A2:* Significant pseudogene interference and/or reciprocal exchanges between the CYP21A2 gene and its pseudogene, CYP21A1P, have been known to occur and may impact results. As such, the relevance of variants reported in this gene must be interpreted clinically in the context of the clinical findings, biochemical profile, and family history of each patient. LR-PCR is not routinely ordered for NM_000500.9:c.955C>T (p.Gln319Ter). Individuals with c.955C>T (p.Gln319Ter) will be reported as a Possible Carrier indicating that the precise nature of the variant has not been determined by LR-PCR and that the variant may occur in the CYP21A2 wild-type gene or in the CYP21A1P pseudogene. The confirmation test is recommended if the second reproductive partner is tested positive for variants associated with classic CAH. *DDX11:* Due to the interference by highly homologous regions, our current testing method has less sensitivity to detect variants in the DDX11 gene. *DUOX2:* The current testing method is not able to reliably detect variants in exons 6-8 of the DUOX2 gene (NM_014080.5) due to significant interference by the highly homologous gene, DUOX1. *FANCD2:* Due to pseudogene interference, copy-number-variants within exon 14-17 of the FANCD2 gene (NM _033084.4) are not evaluated and detection of single-nucleotide variants and small insertions/deletions in this region is not guaranteed. *GALT:* In general, the D2 "Duarte" allele is not reported if detected, but can be reported upon request. While this allele can cause positive newborn screening results, it is not known to cause clinical symptoms in any state. See GeneReviews for more information: https://www.ncbi.nlm.nih.gov/books/NBK1518/ *GBA:* Significant pseudogene interference and/or reciprocal exchanges between the GBA gene and its pseudogene, GBAP1, have been known to occur and may impact results. As such, the relevance of variants reported in this gene must be interpreted clinically in the context of this individual's clinical findings, biochemical profile, and family history. The current testing method cannot detect copy-neutral rearrangements between the pseudogene and the functional gene, which have been reported in very rare cases of Gaucher disease (PubMed: 21704274). *HBA1:* Significant interference

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from highly homologous regions in exons 1-2 of the HBA1 gene has been recognized to occur, potentially impeding the assay's technical capability to detect pathogenic alterations during sequencing analyses. *HBA2:* Significant interference from highly homologous regions in exons 1-2 of the HBA2 gene has been recognized to occur, potentially impeding the assay's technical capability to detect pathogenic alterations during sequencing analyses. *HSD17B4:* Copy number analysis for exons 4-6 may have reduced sensitivity in the HSD17B4 gene. Confirmation of these exons are limited to individuals with a positive personal history of D-bifunctional protein deficiency and Perrault syndrome and/or individuals carrying a pathogenic/likely pathogenic sequence variant. *LMBRD1:* Copy number analysis for exons 9-12 may have reduced sensitivity in the LMBRD1 gene. Confirmation of these exons are limited to individuals with a positive personal history of combined methylmalonic aciduria and homocystinuria and/or individuals carrying a pathogenic/likely pathogenic sequence variant. *MTHFR:* As recommended by ACMG, the two common polymorphisms in the MTHFR gene - c.1286A>C (p.Glu429Ala, also known as c.1298A>C) and c.665C>T (p.Ala222Val, also known as c.677C>T) - are not reported in this test due to lack of sufficient clinical utility to merit testing (PubMed: 23288205). *NEB:* This gene contains a 32-kb triplicate region (exons 82-105) which is not amenable to sequencing and deletion/duplication analysis. *NPHS2:* If detected, the variant NM_014625.3:c.686G>A (p.Arg229Gln) will not be reported as this variant is not significantly associated with disease when homozygous or in the compound heterozygous state with variants in exons 1-6 of NPHS2. *OTOA:* Due to pseudogene interference, our current testing method is not able to reliably detect variants in exons 20-28 (NM_144672.3) in the OTOA gene. *SMN1:* The current testing method detects sequencing variants in exon 7 and copy number variations in exons 7-8 of the SMN1 gene (NM_022874.2). Sequencing and deletion/duplication analysis are not performed on any other region in this gene. About 5%-8% of the population have two copies of SMN1 on a single chromosome and a deletion on the other chromosome, known as a [2+0] configuration (PubMed: 20301526). The current testing method cannot directly detect carriers with a [2+0] SMN1 configuration but can detect linkage between the silent carrier allele and certain population-specific single nucleotide changes. As a result, a negative result for carrier testing greatly reduces but does not eliminate the chance that a person is a carrier. Only abnormal results will be reported. *TERT:* The TERT promoter region is analyzed for both sequencing and copy number variants. *TYR:* Due to the interference by highly homologous regions, our current testing method has less sensitivity to detect variants in exons 4-5 of the TYR gene (NM_000372.5). *VPS45:* LoF is not a known disease mechanism *WRN:* Due to the interference by highly homologous regions within the WRN gene, our current testing method has less sensitivity to detect variants in exons 10-11 of WRN (NM_000553.6).

SIGNATURE:

Yan Meng, Ph.D., CGMB, FACMG on **7/10/2024**
Laboratory Director, Fulgent

DISCLAIMER:

This test was developed and its performance characteristics determined by Fulgent Therapeutics LLC CAP #8042697 CLIA #05D2043189; 4399 Santa Anita Ave., El Monte, CA, 91731. It has not been cleared or approved by the FDA. The laboratory is regulated under CLIA as qualified to perform high-complexity testing. This test is used for clinical purposes. It should not be regarded as investigational or for research. Since genetic variation, as well as systematic and technical factors, can affect the accuracy of testing, the results of testing should always be interpreted in the context of clinical and familial data. For assistance with interpretation of these results, healthcare professionals may contact us directly at **626-350-0537** or by email at **info@fulgentgenetics.com**. It is recommended that patients receive appropriate genetic counseling to explain the implications of the test result, including its residual risks, uncertainties and reproductive or medical options.

To view the supplemental table describing the carrier frequencies, detection rates, and residual risks associated with the genes on this test please visit the following link:
Beacon Expanded Carrier Screening Supplemental Table

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Patient Information:
10916, Donor
DOB: [redacted]
Sex: M
MR#:
Patient#: FT-PT8770563

Accession:
FT-7017368
Test#: FT-TS15588617
Order#: FT-OR15557914
Ext Test#: WP-TTS19660769
Ext Order#: WP-TOR19643757
Specimen Type: Blood (EDTA)
Collected: Jun 25,2024
Received Date: Jun 27,2024
Authorized Date: May 13,2026

Physician:
Kuan, James
ATTN: Kirk, Ashley
Phoenix Sperm Bank
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Ste 204
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Laboratory:
Fulgent Therapeutics LLC
CAP#: 8042697
CLIA#: 05D2043189
Laboratory Director:
Dr. Amar Jariwala
Report Date: **May 28,2026**

Final Report

TEST PERFORMED

CFTR Single Gene
(1 Gene Panel: *CFTR*; gene sequencing with deletion and duplication analysis)

RESULTS:

No diagnostic sequence or copy-number variants were identified. However, one variant of potential clinical relevance is reported.

Clinically Significant Variants

None

Additional Variants of Potential Clinical Relevance

Gene Info		Variant Info		
GENE	INHERITANCE	VARIANT	ZYGOSITY	CLASSIFICATION
CFTR NM_000492.4	Autosomal Dominant & Autosomal Recessive	c.1210-11T>G (p.?)	Heterozygous	**Risk Allele**

INTERPRETATION:

Notes and Recommendations:

- **Analysis of the intron 8 polymorphic region of CFTR was performed at the request of the ordering provider. The poly T and TG tract for this individual is 5T with 12TG and 7T with 12TG.**
- As requested, this report only includes variants classified as Pathogenic, Likely Pathogenic, or Risk Allele at the time of analysis. If detected, this report does not include variants classified as of uncertain significance.
- Gene specific notes and limitations may be present. See below.
- These results should be interpreted in the context of this individual's clinical findings, biochemical profile, and family history.
- Genetic counseling is recommended. Available genetic counselors and additional resources can be found at the National Society of Genetic Counselors (NSGC; https://www.nsgc.org)
- Guide to Interpreting Genomic Reports: A Genomics Toolkit (CSER Consortium; February 2017) (https://www.genome.gov/For-Health-Professionals/Provider-Genomics-Education-Resources#hep)

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About *CFTR*

Biallelic mutations in the CFTR gene have been associated with cystic fibrosis (CF) and CFTR-related disorders (CFTR-RD) such as congenital bilateral absence of vas deferens (CBAVD), while heterozygous mutations have been associated with idiopathic chronic pancreatitis (ICP) and bronchiectasis with or without elevated sweat chloride-1 (BESC1) (PubMed: 20301428; OMIM: 602421). The phenotype-genotype correlation between the CFTR gene and disease is highly complex and variable. Several alleles including the most common variants associated with CF have been reported with variable phenotypes (PubMed: 2233932, 21931512). Other variants show mild or no apparent phenotype when present in isolation, but are associated with CFTR-related phenotypes when found as complex alleles with other changes on the same chromosome (PubMed: 27738188). There is also some evidence for overlap of CFTR mutations and intestinal atresia (PubMed: 15495994, 23217263). Additionally, the presence of contributory variants in other genes has been reported to modify the pathogenicity of otherwise neutral variants in the CFTR gene (PubMed: 9654209, 12124743, 25053892). Given the complexity and variation in phenotype-genotype association, any CFTR variant reported here, including pathogenic variants, should be considered within the context of clinical and family history information. Additional genotype-phenotype correlation and CF/CFTR-RD specific considerations for the identification of pathogenic variants can be found in the literature (PubMed: 18456578, 23209179).

See OMIM gene entry for *CFTR* (OMIM: 602421) for further information.

CFTR NM_000492.4:c.1210-11T>G (p.?)

Classification: **Risk Allele**

Zygosity and Inheritance	• This heterozygous risk allele is consistent with an increased risk for a CFTR-related condition.
Variant Type	• Genomic change: Chr7(GRCh37):g.117188684T>G. • This variant is in the dbSNP database: rs73715573 • This variant is located in intron 9 of the *CFTR* gene, -11 nucleotides upstream of the splice acceptor site for exon 10. • The splice variant, NM_000492.3:c.1210-11T>G is also known as c.1210-7_1210-6del, IVS8-5T or simply 5T. **Note that 12 TG repeats were observed in cis with this variant.** Increased numbers of polyTG repeats in cis with 5T are typically associated with increased severity and penetrance of CF-related symptoms compared with individuals with 5T in cis with fewer poly TG repeats. (PubMed: 37310422).
Variant in Cases	• The 5T variant is a well-established pathogenic variant associated with CBAVD, although with incomplete penetrance. The 5T variant is thought to decrease the efficiency of intron 8 splicing resulting in exon 9 skipping. mRNA without exon 9 results in CFTR proteins that will not mature and will therefore not function as chloride channels in the apical membrane of epithelial cells. The 5T variant is the shortest of length variants of a polypyrimidine (polyT) tract within the splice acceptor site at the end of intron 8 of the CFTR gene. Two other polyT tract variants, 7T (reference allele) and 9T, are considered benign. By itself, 5T is not thought to act as a CF-causing variant. Instead, it typically acts as a modifier to make another variant in the same copy of CFTR (usually p.Arg117His) more severe. Therefore, Poly T testing is appropriate as a reflex test when an Arg117His variant is detected or an adult male is being evaluated for CBAVD. Occasionally, the 5T variant is present without p.Arg117His in the same copy of the CFTR gene. In this case, the 5T variant may act as a CF-causing variant if a certain form of the TG tract, in the same intron 8, is also present. The TG tract typically occurs in three forms: TG11, TG12, and TG13. A longer TG tract (12 or 13) in conjunction with a shorter poly T tract (5T) has the strongest adverse effect on proper intron 8 splicing (PubMed: 20301428). • This variant is classified as "Pathogenic" in literature (PubMed: 28152038, 29997923) • This variant is classified as a "Disease Mutation" (DM) in the Human Gene Mutation Database (HGMD). • This variant has one or more entries in ClinVar: RCV000507057.1, RCV000155471.1, RCV001329936.1, RCV000309488.4, RCV001095145.1, RCV000381834.3, RCV001010355.2

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Variant in Controls	• This variant has been observed at a frequency of 0.85% (2277/268042 alleles). • The highest allele frequency that this variant has been observed at in any sub-population with available data is 3.45% in the Ashkenazi Jewish population. • There are two homozygous control individuals for this variant. • The Broad Institute gnomAD database (>120,000 Individuals with no known severe, pediatric onset disease) was used for this analysis.
Other Variant Information	• No other information is available for this variant.

4399 Santa Anita Ave.
El Monte, CA, 91731
(p) 626-350-0537 (f) 626-454-1667
info@fulgentgenetics.com
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GENES TESTED:

CFTR Single Gene
1 genes tested (100.00% at >20x).

CFTR

Gene Specific Notes and Limitations

CFTR: For tests relevant to cystic fibrosis (CF) , analysis of the intron 8 polymorphic region (e.g. IVS8-5T allele) is only performed if the p.Arg117His (R117H) mutation is detected, or performed upon request.

METHODS:

Genomic DNA was isolated from the submitted specimen indicated above (if cellular material was submitted). DNA was barcoded, and enriched for the coding exons of targeted genes using hybrid capture technology. Prepared DNA libraries were then sequenced using a Next Generation Sequencing technology. Following alignment to the human genome reference sequence (assembly GRCh37), variants were detected in regions of at least 10x coverage. For this specimen, 100.00% and 100.00% of coding regions and splicing junctions of genes listed had been sequenced with coverage of at least 10x and 20x, respectively, by NGS or by Sanger sequencing. The remaining regions did not have 10x coverage, and were not evaluated. Variants were interpreted manually using locus specific databases, literature searches, and other molecular biological principles. To minimize false positive results, any variants that do not meet internal quality standards are confirmed by Sanger sequencing. Variants classified as pathogenic, likely pathogenic, or risk allele which are located in the coding regions and nearby intronic regions (+/- 20bp) of the genes listed above are reported. Variants outside these intervals may be reported but are typically not guaranteed. When a single pathogenic or likely pathogenic variant is identified in a clinically relevant gene with autosomal recessive inheritance, the laboratory will attempt to ensure 100% coverage of coding sequences either through NGS or Sanger sequencing technologies ("fill-in"). All genes listed were evaluated for large deletions and/or duplications. However, single exon deletions or duplications will not be detected in this assay, nor will copy number alterations in regions of genes with significant pseudogenes. Putative deletions or duplications identified by NGS are confirmed by an orthogonal method (qPCR or MLPA), unless exceeding an internally specified and validated quality score, beyond which deletions and duplications are considered real without further confirmation. Bioinformatics: The FPLMv2.0 pipeline was used to analyze this specimen.

LIMITATIONS:

These test results and variant interpretation are based on the proper identification of the submitted specimen, accuracy of any stated familial relationships, and use of the correct human reference sequences at the queried loci. In very rare instances, errors may result due to mix-up or co-mingling of specimens. Positive results do not imply that there are no other contributors, genetic or otherwise, to this individual's phenotype, and negative results do not rule out a genetic cause for the indication for testing. Official gene names change over time. Fulgent uses the most up to date gene names based on HUGO Gene Nomenclature Committee (https://www.genenames.org) recommendations. If the gene name on report does not match that of ordered gene, please contact the laboratory and details can be provided. Result interpretation is based on the available clinical and family history information for this individual, collected published information, and Alamut annotation available at the time of reporting. This assay is designed and validated for detection of germline variants only. It is not designed or validated for the detection of low-level mosaicism or somatic mutations. This assay will not detect certain types of genomic aberrations such as translocations, inversions, or repeat expansions (eg. trinucleotide or hexanucleotide repeat expansion). DNA alterations in regulatory regions or deep intronic regions (greater than 20bp from an exon) may not be detected by this test. Unless otherwise indicated, no additional assays have been performed to evaluate genetic changes in this specimen. There are technical limitations on the ability of DNA sequencing to detect small insertions and deletions. Our laboratory uses a sensitive detection algorithm for copy number variants, however these types of alterations are not detected as reliably as single nucleotide variants. Rarely, due to systematic chemical, computational, or human error, DNA variants may be missed. Although next generation sequencing technologies and our bioinformatics analysis significantly reduce the confounding contribution of pseudogene sequences or other highly-homologous sequences, sometimes these may still interfere with the technical ability of the assay to identify pathogenic alterations in both sequencing and deletion/duplication analyses. Deletion/duplication analysis can identify alterations of genomic regions which are two or more contiguous exons in size; single exon deletions or duplications may occasionally be identified, but are not routinely detected by this test. When novel DNA duplications are identified, it is not possible to discern the genomic location or orientation of the duplicated segment, hence the effect of the duplication cannot be predicted. Where deletions are detected, it is not always possible to determine whether the

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predicted product will remain in-frame or not. Unless otherwise indicated, deletion/duplication analysis has not been performed in regions that have been sequenced by Sanger.

SIGNATURE:

Volkan Okur, MD, FACMG, CGMBS on **05/28/2026**
Laboratory Director, Fulgent

DISCLAIMER:

This test was developed, performed, and its performance characteristics determined by **Fulgent Therapeutics LLC** (CAP# 8042697, CLIA# 05D2043189), 4399 Santa Anita Ave., El Monte, CA 91731. It has not been cleared or approved by the FDA. The laboratory is regulated under CLIA as qualified to perform high-complexity testing. This test is used for clinical purposes. It should not be regarded as investigational or for research. Since genetic variation, as well as systematic and technical factors, can affect the accuracy of testing, the results of testing should always be interpreted in the context of clinical and familial data. For assistance with interpretation of these results, healthcare professionals may contact us directly at **(626) 350-0537** or **info@fulgentgenetics.com**. It is recommended that patients receive appropriate genetic counseling to explain the implications of the test result, including its residual risks, uncertainties and reproductive or medical options.

Report Status FINAL
Route 2017 Ordered by:
Phoenix Sperm Bank
1492 S Mill Ave
Suite 306
Tempe, AZ 85281

James Kuan, MD

Sonora Quest Laboratories™
A Subsidiary of Laboratory Sciences of Arizona

Patient Information:
10916, DONOR

Order #: 181310000126 / NL102033240

Account: 18131
ID/MR#: 10916
Patient Lab ID:
667c2f52289e584a7e9e84f7

Collected: 06/25/2024 10:05 AM
Received: 06/26/2024 07:48 AM
Reported: 07/05/2024 02:59 PM

DOB: [redacted] Age: [redacted]
Sex: M
Patient Phone: 602-888-7255

[redacted] PL

GENETICS

Accession #:
CG240006900
Cell Type/Source:
Blood
Clinician Provided Information:
DONOR TESTING

Chromosome Analysis: Routine Blood

Analysis Details: PV
Metaphases/Cells Counted : 20
Metaphases/Cells Analyzed : 5
Metaphases Karyotyped : 3

Results: PV
NORMAL MALE KARYOTYPE

46,XY

Interpretation: PV
Normal

PV

Normal karyotype at the band level 550 or above as determined by the trypsin-Giemsa method. There was no evidence for a chromosome abnormality within the limits of the band level and technology utilized in this study.

PHA-stimulated lymphocyte chromosome analysis is an accurate technique to detect many constitutional chromosome abnormalities. More extensive investigation may be required to detect mosaicism or subtle structural rearrangement. It also should be noted that this type of testing does not rule out the possibility of mendelian, mitochondrial, multifactorial or environmental etiologies.

Cytogenetics Director: PV

Electronically signed by Liwen Lai R PhD, DABMGG, FACMG R
Verified 07/05/24

Tests Ordered: Chromosome Analysis: Routine Blood

Unless otherwise noted, testing performed by: Sonora Quest Laboratories, 424 S 56th St, Phoenix, AZ 85034 800.766.6721
Testing noted as PV performed by: Genetics/Genomics Div., Sonora Quest Laboratories, 424 S. 56th St, Phoenix, AZ 85034 602.685.5700

End of Report

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10916, Donor
Patient ID:
Specimen ID: **177-705-1989-0**

DOB: [redacted]
Age: [redacted]
Sex: **Male**

Patient Report

Account Number: **02003540**
Ordering Physician: **J KUAN**

labcorp

Date Collected: **06/25/2024** Date Received: **06/26/2024** Date Reported: **06/28/2024** Fasting: **Not Given**

Ordered Items: **LP+12AC+CBC/D/Plt+UA+Rh+ABO...**

Date Collected: **06/25/2024**

LP+12AC+CBC/D/Plt+UA+Rh+ABO...

Test	Current Result and Flag	Previous Result and Date	Units	Reference Interval
Glucose [01]	92		mg/dL	70-99
Uric Acid [01]	6.7		mg/dL	3.8-8.4
		Therapeutic target for gout patients: <6.0		
BUN [01]	15		mg/dL	6-20
Creatinine [01]	0.97		mg/dL	0.76-1.27
eGFR	115		mL/min/1.73	>59
Calcium [01]	9.3		mg/dL	8.7-10.2
Protein, Total [01]	7.5		g/dL	6.0-8.5
Albumin [01]	4.8		g/dL	4.3-5.2
Bilirubin, Total [01]	0.5		mg/dL	0.0-1.2
Alkaline Phosphatase [01]	105		IU/L	51-125
LDH [01]	188		IU/L	121-224
AST (SGOT) [01]	21		IU/L	0-40
ALT (SGPT) [01]	14		IU/L	0-44
Cholesterol, Total [01]	151		mg/dL	100-169
Triglycerides [01]	51		mg/dL	0-89
HDL Cholesterol [01]	57		mg/dL	>39
LDL Chol Calc (NIH)	83		mg/dL	0-109
LDL/HDL Ratio	1.5		ratio	0.0-3.6
Please Note: [01]				

LDL/HDL Ratio

	Men	Women
1/2 Avg.Risk	1.0	1.5
Avg.Risk	3.6	3.2
2X Avg.Risk	6.2	5.0
3X Avg.Risk	8.0	6.1

Hgb Fractionation by CE: [02]				
Hgb F [02]	0.0		%	0.0-2.0
Hgb A [02]	97.1		%	96.4-98.8
Hgb A2 [02]	2.9		%	1.8-3.2
Hgb S [02]	0.0		%	0.0
Interpretation: [02]				

Normal hemoglobin present; no hemoglobin variant or beta thalassemia identified.
Note: Alpha thalassemia may not be detected by the Hgb Fractionation Cascade panel. If alpha thalassemia is suspected, Labcorp offers Alpha-Thalassemia DNA Analysis (#511172).

ABO Grouping [01]	B			
Rh Factor [01]	Positive			

Please note: Prior records for this patient's ABO / Rh type are not available for additional verification.

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LP+12AC+CBC/D/Plt+UA+Rh+ABO... (Cont.)

.[01]			
CBC, Platelet Ct, and Diff[01]			
WBC[01]	5.8	x10E3/uL	3.4-10.8
RBC[01]	5.47	x10E6/uL	4.14-5.80
Hemoglobin[01]	15.8	g/dL	13.0-17.7
Hematocrit[01]	48.8	%	37.5-51.0
MCV[01]	89	fL	79-97
MCH[01]	28.9	pg	26.6-33.0
MCHC[01]	32.4	g/dL	31.5-35.7
RDW[01]	11.8	%	11.6-15.4
Platelets[01]	198	x10E3/uL	150-450
Neutrophils[01]	62	%	Not Estab.
Lymphs[01]	30	%	Not Estab.
Monocytes[01]	7	%	Not Estab.
Eos[01]	1	%	Not Estab.
Basos[01]	0	%	Not Estab.
Neutrophils (Absolute)[01]	3.6	x10E3/uL	1.4-7.0
Lymphs (Absolute)[01]	1.7	x10E3/uL	0.7-3.1
Monocytes(Absolute)[01]	0.4	x10E3/uL	0.1-0.9
Eos (Absolute)[01]	0.0	x10E3/uL	0.0-0.4
Baso (Absolute)[01]	0.0	x10E3/uL	0.0-0.2
Immature Granulocytes[01]	0	%	Not Estab.
Immature Grans (Abs)[01]	0.0	x10E3/uL	0.0-0.1
.[01]			
Urinalysis Gross Exam[01]			
Specific Gravity[01]	1.010		1.005-1.030
pH[01]	6.5		5.0-7.5
Urine-Color[01]	Yellow		Yellow
Appearance[01]	Clear		Clear
WBC Esterase[01]	Negative		Negative
Protein[01]	Negative		Negative/Trace
Glucose[01]	Negative		Negative
Ketones[01]	Negative		Negative
Occult Blood[01]	Negative		Negative
Bilirubin[01]	Negative		Negative
Urobilinogen,Semi-Qn[01]	0.2	mg/dL	0.2-1.0
Nitrite, Urine[01]	Negative		Negative
Microscopic Examination[01]	Microscopic not indicated and not performed.		

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Disclaimer
The Previous Result is listed for the most recent test performed by Labcorp in the past 5 years where there is sufficient patient demographic data to match the result to the patient. Results from certain tests are excluded from the Previous Result display.

Icon Legend
▲ Out of Reference Range ■ Critical or Alert

Performing Labs
01: PDLCA - Labcorp Phoenix, 5005 S 40th Street Ste 1200, Phoenix, AZ 85040-2969 Dir: Earle Collum, MD
02: BN - Labcorp Burlington, 1447 York Court, Burlington, NC 27215-3361 Dir: Sanjai Nagendra, MD
For Inquiries, the physician may contact Branch: 888-522-2677 Lab: 800-788-9743

Patient Details
10916, Donor

Phone:
Date of Birth: [redacted]
Age: [redacted]
Sex: **Male**
Patient ID:
Alternate Patient ID:

Physician Details
J KUAN
Phoenix Sperm Bank
1492 S Mill Ave Suite 306, Tempe, AZ, 85281

Phone: **602-888-7255**
Account Number: **02003540**
Physician ID:
NPI: **1891885745**

Specimen Details
Specimen ID: **177-705-1989-0**
Control ID: **L2404826385**
Alternate Control Number: **L2404826385**
Date Collected: **06/25/2024 1117 Local**
Date Received: **06/26/2024 0000 ET**
Date Entered: **06/25/2024 2309 ET**
Date Reported: **06/28/2024 0909 ET**

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