15 Crawford St., STE 100
Needham, MA 02494
(p) 626-350-0537
(f) 626-454-1667
Lab Director: Arash Radfar M.D.
CLIA: 22D0957540

fulgent | INFORM DIAGNOSTICS™ A FULGENT GENETICS COMPANY
Metroplex Pathology Associates
Lakewood Pathology Associates
Cohen Dermatopathology
Therapath Partners

Patient Information:
20061, Donor
DOB: [redacted]
Sex: M
MR#:
Patient#: FT-PT9063223

Partner Information:
Not Tested

Physician:
Kuan, JAMES
ATTN: Kuan, JAMES
Las Vegas Sperm Bank
2870 S Maryland Parkway
Ste 250
Lad Vegas, NV 89109
Phone: 2064664696

Laboratory:
Fulgent Therapeutics LLC
CAP#: 8042697
CLIA#: 05D2043189
Laboratory Director:
Dr. Amar Jariwala
Report Date: **May 10,2025**

Accession:
FT-7323362
Test#: FT-TS15174864
Specimen Type: Blood (EDTA)
Collected: Apr 21,2025

Accession:
N/A

FINAL RESULTS

4 Carrier for genetic conditions in **multiple** genes.

TEST PERFORMED

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

Condition and Gene	Inheritance	20061, Donor	Partner
Krabbe disease *GALC*	AR	⊕ Carrier c.1901T>C (p.Leu634Ser)	N/A
Limb-girdle muscular dystrophy, type 2D *SGCA*	AR	⊕ Carrier c.292C>T (p.Arg98Cys)	N/A
Spinal muscular atrophy silent carrier *SMN1*	AR	⊕ Possible Carrier c.*3+80T>G (p.?)	N/A
Limb-girdle muscular dystrophy type 2A *CAPN3*	AR	⊕ Carrier Deletion of Exons 8-10	N/A

INTERPRETATION:

Notes and Recommendations:

- **PLEASE NOTE: While some heterozygous variants in the CAPN3 gene have been associated with autosomal dominant limb-girdle muscular dystrophy or calpainopathy, the reported variant has not been associated with those findings.**
- Based on these results, this individual is positive for carrier mutations in 4 genes. Carrier screening for the reproductive partner is recommended to accurately assess the risk for any autosomal recessive conditions. 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.
- 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)

15 Crawford St., STE 100
Needham, MA 02494
(p) 626-350-0537
(f) 626-454-1667
Lab Director: Arash Radfar M.D.
CLIA: 22D0957540

fulgent | INFORM DIAGNOSTICS™ A FULGENT GENETICS COMPANY
Metroplex Pathology Associates
Lakewood Pathology Associates
Cohen Dermatopathology
Therapath Partners

KRABBE DISEASE

Patient	20061, Donor	Partner
Result	⊕ Carrier	N/A
Variant Details	***GALC*** (NM_000153.4) c.1901T>C (p.Leu634Ser)	N/A

What is Krabbe disease?

Krabbe disease (globoid cell leukodystrophy) is a degenerative disorder caused by a deficiency of the enzyme galactosylceramidase. This deficiency leads to the demyelination of nerve cells. Most individuals have infantile-onset Krabbe disease, presenting before 12 months of age with irritability, spasticity, developmental delay, feeding difficulties, vision loss, and seizures. Individuals with a later-onset form of Krabbe disease can be clinically normal until weakness, vision loss, and intellectual regression become apparent. The onset and progression of the later-onset forms can be quite variable, even among siblings.

What is my risk of having an affected child?

Krabbe disease is inherited in an autosomal recessive manner. If the patient and the partner are both carriers, the risk for an affected child is 1 in 4 (25%).

What kind of medical management is available?

Treatment of individuals with infantile-onset Krabbe disease who are diagnosed in a late stage is limited to supportive care to control irritability and spasticity. Hematopoietic stem cell transplantation (HSCT) may improve and preserve cognitive function in presymptomatic infants and older individuals with mild symptoms; however, many show progressive deterioration of the peripheral nervous system.

What mutation was detected?

The detected heterozygous variant was NM_000153.4:c.1901T>C (p.Leu634Ser). This variant, p.Leu634Ser (also reported as p.Leu618Ser), has been previously reported in both homozygous and compound heterozygous states in multiple individuals with Krabbe disease (PubMed: 24252386, 9272171, 27780934, 27679535, 24252386, 26865610, 33178108).While the allele frequency of this variant in the general population is relatively high, in vitro experimental studies have shown that this missense change impairs enzyme activity (PubMed: 27780934, 9272171, 27126738, 24252386, 27638593). Together these results suggest that this variant may exhibit reduced penetrance.This variant is classified as "Pathogenic" or "Likely Pathogenic" in ClinVar, with multiple submitters in agreement (ClinVar: 225368). The laboratory classifies this variant as pathogenic.

15 Crawford St., STE 100
Needham, MA 02494
(p) 626-350-0537
(f) 626-454-1667
Lab Director: Arash Radfar M.D.
CLIA: 22D0957540

fulgent | INFORM DIAGNOSTICS™ A FULGENT GENETICS COMPANY
Metroplex Pathology Associates
Lakewood Pathology Associates
Cohen Dermatopathology
Therapath Partners

LIMB-GIRDLE MUSCULAR DYSTROPHY, TYPE 2D

Patient	20061, Donor	Partner
Result	⊕ Carrier	N/A
Variant Details	***SGCA*** (NM_000023.4) c.292C>T (p.Arg98Cys)	N/A

What is Limb-girdle muscular dystrophy, type 2D?

Limb-girdle muscular dystrophy, type 2D is a neuromuscular disease that manifests as weakness and wasting of the muscles in the arms and legs, including the muscles of the shoulders, upper arms, pelvic area, and thighs as well. The severity, age of onset, and symptoms of limb-girdle muscle dystrophy vary among the subtypes of this condition and may be inconsistent within the same family. Signs and symptoms may first appear at any age and generally worsen with time, although in some cases they remain mild. In the early stages of limb-girdle muscular dystrophy, affected individuals may have an unusual gait, exercise intolerance, and may also have difficulty running. Affected individuals may need to use their arms to press themselves up from a squatting position because of their weak thigh muscles. As the condition progresses, people with limb-girdle muscular dystrophy, type 2D may eventually require wheelchair assistance. Muscle wasting may cause changes in posture with significant losses of strength and movement.

What is my risk of having an affected child?

Limb-girdle muscular dystrophy, type 2D is inherited in an autosomal recessive manner. If the patient and the partner are both carriers, the risk for an affected child is 1 in 4 (25%).

What kind of medical management is available?

The prognosis depends upon the severity of each condition. There is no cure for these conditions and management should be tailored to each individual's needs. Individuals should be treated and evaluated by a multidisciplinary team of specialists. Speech and physical therapies, use of respiratory aids and mobility devices (wheelchairs) may be required.

What mutation was detected?

The detected heterozygous variant was NM_000023.4:c.292C>T (p.Arg98Cys). This missense variant, p.Arg98Cys, has been reported in the compound heterozygous state in unrelated individuals with limb-girdle muscular dystrophy type 2D (PubMed: 7668821, 30107846).Another variants at the same residue, p.Arg98Gly and p.Arg98His, also have previously been reported in the compound heterozygous state in individuals with limb-girdle muscular dystrophy type 2D (PubMed: 7668821, 8069911, 9192266, 12746421, 22095924, 27120200). The laboratory classifies this variant as pathogenic.

15 Crawford St., STE 100
Needham, MA 02494
(p) 626-350-0537
(f) 626-454-1667
Lab Director: Arash Radfar M.D.
CLIA: 22D0957540

fulgent | INFORM DIAGNOSTICS™ A FULGENT GENETICS COMPANY
Metroplex Pathology Associates
Lakewood Pathology Associates
Cohen Dermatopathology
Therapath Partners

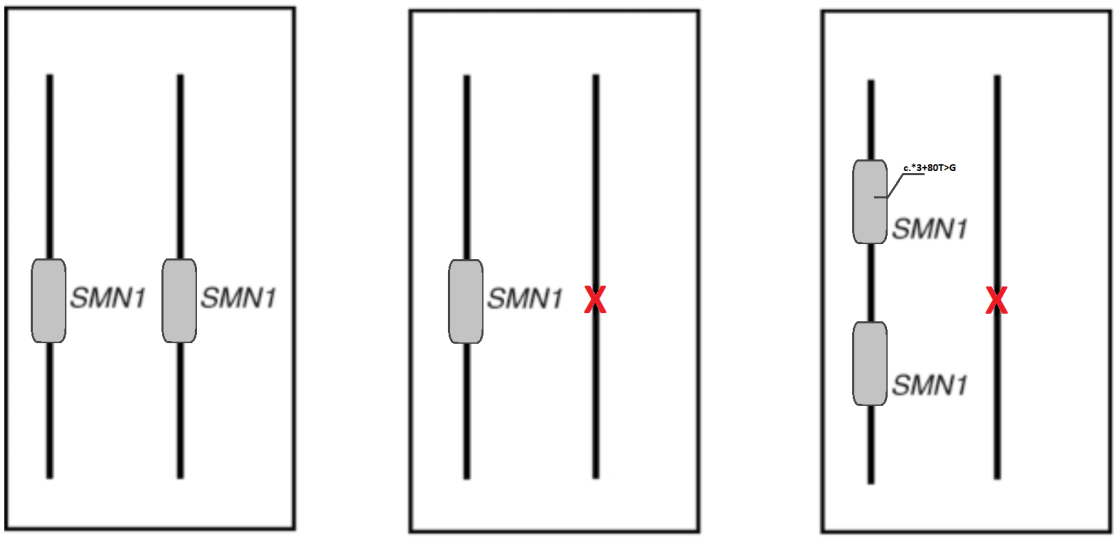
SPINAL MUSCULAR ATROPHY SILENT CARRIER

Patient	20061, Donor	Partner
Result	⊕ Possible Carrier	N/A
Variant Details	***SMN1*** (NM_000344.3) c.*3+80T>G (p.?)	N/A

What is Spinal muscular atrophy silent carrier?

Individuals typically have one copy of the *SMN1* gene on each chromosome, with carriers having a mutation in one copy that prevents normal function. A spinal muscular atrophy silent carrier is an individual who has two functional copies of the *SMN1* gene on one chromosome and zero copies of the *SMN1* gene on the other chromosome. This is a special scenario because the overall number of copies of *SMN1* may appear normal (i.e. two total copies of *SMN1*), however, that same person is considered a carrier for SMA since there are no functional copies of the *SMN1* gene on one chromosome. A person with this specific configuration of the *SMN1* genes is considered to be a "silent carrier".

Spinal muscular atrophy (SMA) affects nerve cells called motor neurons in the spinal cord and brainstem. The progressive degeneration of these nerve cells results in muscle weakness and atrophy (breakdown of muscle mass). Common symptoms include limited growth and poor weight gain, restrictive lung disease, and skeletal abnormalities, such as scoliosis or contractures of the joints. Severity and age of onset varies from severe and congenital (symptoms present at or before birth) (SMA type 0) to mild and adult-onset (SMA type 4). More than half of affected individuals have SMA type 1, in which symptoms usually start in the first 6 months of life and, without treatment, life expectancy is 2 years.



Wild type: 2 copies of *SMN1* (1+1) | Carrier: 1 copy of *SMN1* (1+0) | Silent carrier: 2 copies of *SMN1* (2+0)

For technical reasons, the chromosome with zero copies of SMN1 cannot always be directly observed in the DNA sequencing data (PubMed: 20301526, 32915251). Instead, silent carriers are observed based on the presence of two copies of the SMN1 gene and the specific variant c.*3+80T>G, which commonly occurs on the same chromosome with a duplication of the SMN1 gene. For individuals of Ashkenazi Jewish descent, c.*3+80T>G with two copies of SMN1 is considered as a positive finding for SMA carrier status (PubMed: 23788250, 36140824). While the positive predictive value of c.*3+80T>G with two copies of SMN1 can vary, nonetheless, for all other ethnic groups this variant is associated with an increased likelihood of being a carrier for SMA (PubMed: 36140824, 32066871, 36669496). Alternatively, in some individuals with c.*3+80T>G and two copies of SMN1 there is a possibility that these variants occur with a single copy of the SMN1 gene on each chromosome, and in that case the individual would not be considered a silent carrier for spinal muscular atrophy. In some cases, follow-up genetic testing of the parents of the SMN1 silent carrier may be helpful in further resolving the mutation status.

15 Crawford St., STE 100
Needham, MA 02494
(p) 626-350-0537
(f) 626-454-1667
Lab Director: Arash Radfar M.D.
CLIA: 22D0957540

What is my risk of having an affected child?

SMA is inherited in an autosomal recessive manner. This means that when both parents are carriers for the condition, there is a 25% (1 in 4) risk of having an affected child.

What kind of medical management is available?

Because it is important to provide proactive care and deliver timely intervention, the United States has recommended that SMA be added to state newborn screening panels, and most states, and some other countries, currently perform newborn screening for SMA. There is currently no cure for SMA, but management can include supportive, rehabilitative, and palliative care to manage symptoms and prevent complications. Treatments aim to address the effects of muscle weakness and may include dietary management and placement of a gastronomy tube (feeding tube), breathing exercises or machines to help with breathing problems, and surgical repair for scoliosis (spine curvature). Physical therapy can help with mobility, and assistive equipment such as wheelchairs or splints may also be necessary. There are FDA-approved drug and gene therapies to improve the symptoms and outcomes of SMA in some eligible individuals. Certain treatments must be given before symptoms begin in order to be effective. SMA type 3 (mild) and type 4 (adult-onset) typically do not affect life expectancy, but breathing issues are the largest cause of mortality in those with SMA types 0, 1, and 2, which occurs in infancy, childhood, or early adulthood depending on type of SMA and on treatment type and age of treatment initiation. Many drug therapies are still recent enough that their long-term effects on symptoms and life expectancy have not been studied completely, but they have been shown to greatly improve survival for those with SMA type 1. SMA treatment is an area of ongoing research; the most up-to-date information about clinical trials can be accessed from https://clinicaltrials.gov or from patient advocacy groups such as Cure SMA (https://www.curesma.org/) and the SMA Foundation (https://smafoundation.org/).

What mutation was detected?

The detected heterozygous variant was NM_000344.3:c.*3+80T>G (p.?). The detected variant NM_000344.3:c.*3+80T>G (p.?) is part of a SMN1 haplotype. In individuals with Ashkenazi Jewish heritage, the detection of this variant in concert with normal copy number of the SMN1 gene is considered positive for carrier status (PubMed: 23788250). For all other ethnic groups this variant is associated with an increased likelihood of being a carrier for SMA (PubMed: 36140824, 32066871, 36669496). This variant is located within the 3-prime untranslated region of the SMN1 gene, and has been linked with "silent carrier" status (or "[2+0]" configuration) where two copies of the SMN1 gene are present on the same chromosome and zero copies are present on the opposite chromosome. If an individual is detected as having two copies of SMN1 gene, these results would indicate that this individual may be a carrier for an SMN1 deletion on the other chromosome ("silent" carrier). The laboratory classifies this variant as pathogenic.

15 Crawford St., STE 100
Needham, MA 02494
(p) 626-350-0537
(f) 626-454-1667
Lab Director: Arash Radfar M.D.
CLIA: 22D0957540

fulgent | INFORM DIAGNOSTICS™ A FULGENT GENETICS COMPANY
Metroplex Pathology Associates
Lakewood Pathology Associates
Cohen Dermatopathology
Therapath Partners

LIMB-GIRDLE MUSCULAR DYSTROPHY TYPE 2A

Patient	20061, Donor	Partner
Result	⊕ Carrier	N/A
Variant Details	***CAPN3*** (NM_000070.3) Deletion of Exons 8-10	N/A

What is Limb-girdle muscular dystrophy type 2A?

Limb-girdle muscular dystrophy type 2A is a neuromuscular disease that manifests as weakness and wasting of the muscles in the arms and legs, including the muscles of the shoulders, upper arms, pelvic area, and thighs. The severity, age of onset, and features of limb-girdle muscular dystrophy vary among the many subtypes of this condition and may be inconsistent, even within the same family. Signs and symptoms may first appear at any age and generally worsen with time, although in some cases they remain mild. In the early stages of limb-girdle muscular dystrophy, affected individuals may have an unusual walking gait, exercise intolerance, and may have difficulty running. They may need to use their arms to press themselves up from a squatting position because of their weak thigh muscles. As the condition progresses, people with limb-girdle muscular dystrophy may eventually require wheelchair assistance. Muscle wasting may cause changes in posture or in the appearance of the shoulder, back, and arm. Some develop contractures and hypertrophy of the calf muscles occurs in some people with this form of limb-girdle muscular dystrophy. Patients with this particular form of LGMD do not develop cardiomyopathy or intellectual disability.

What is my risk of having an affected child?

Limb-girdle muscular dystrophy type 2A is inherited in an autosomal recessive manner. If the patient and the partner are both carriers, the risk for an affected child is 1 in 4 (25%).

What kind of medical management is available?

No cure exists for any form of LGMD. Treatment is aimed at the specific symptoms present in each individual. Specific treatment options may include physical and occupational therapy to improve muscle strength and prevent contractures, the use of various devices (e.g., canes, braces, walkers, wheelchairs) to assist with walking and mobility, surgery to correct skeletal abnormalities, such as scoliosis, and regular monitoring of the heart and the respiratory system for the development of such complications potentially associated with some forms of LGMD.

What mutation was detected?

The detected variant was a deletion of exons 8-10 in the CAPN3 gene (NM_000070.3). This exonic deletion is predicted to lead to an out-of-frame shift transcript and introduce a premature stop codon at least 50 nucleotides upstream of the canonical donor splice site of the penultimate exon, resulting in the loss of function of the protein product due to nonsense-mediated mRNA decay (PubMed: 25741868, 30192042, 27618451, 11532962, 18066079). There's sufficient evidence that loss of function in this gene is a known disease mechanism for limb girdle muscular dystrophy (PubMed: 10330340, 15689361, 28403181, 32528171, 31268554). This variant has not been reported as associated with a clinical condition in the Human Gene Mutation Database (HGMD). This copy number variant is absent from controls in the gnomAD structural variants database. The scope of the performed analysis is limited to the ordered genes and is not designed to determine the exact breakpoints or boundaries of copy number variants. The laboratory classifies this variant as likely pathogenic.

15 Crawford St., STE 100
Needham, MA 02494
(p) 626-350-0537
(f) 626-454-1667
Lab Director: Arash Radfar M.D.
CLIA: 22D0957540

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 99.7% 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, 99.78% and 99.74% 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 FPLMv2.0 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

15 Crawford St., STE 100
Needham, MA 02494
(p) 626-350-0537
(f) 626-454-1667
Lab Director: Arash Radfar M.D.
CLIA: 22D0957540

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. 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, 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 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.

15 Crawford St., STE 100
Needham, MA 02494
(p) 626-350-0537
(f) 626-454-1667
Lab Director: Arash Radfar M.D.
CLIA: 22D0957540

fulgent | INFORM DIAGNOSTICS™ A FULGENT GENETICS COMPANY
Metroplex Pathology Associates
Lakewood Pathology Associates
Cohen Dermatopathology
Therapath Partners

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 21-29 (NM_144672.4) 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). *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:

Geetu Mendiratta-Vij, PhD, FACMG, CGMBS on **5/10/2025**
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 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 tested on any Beacon panel, please visit the following link:
Beacon Expanded Carrier Screening Supplemental Table

Patient Information	Specimen Information	Client Information
20061, DONOR **DOB:** [redacted] **AGE:** [redacted] Gender: M Fasting: U Phone: 725.257.0900 Patient ID: 20061	Specimen: LV142328A Requisition: 0000052 Collected: 04/22/2025 / 13:05 PDT Received: 04/23/2025 / 02:35 PDT Reported: 04/29/2025 / 15:34 PDT	Client #: 88807473 MAIL500 FOORD, DYLAN R LAS VEGAS SPERM BANK 2870 S MARYLAND PKWY STE 250 LAS VEGAS, NV 89109-1548

COMMENTS: FASTING:UNKNOWN

Cytogenetic Report

CHROMOSOME ANALYSIS, BLOOD - 14596 Lab:EZ

CHROMOSOME ANALYSIS, BLOOD

Order ID: 25-215186
Specimen Type: Blood
Clinical Indication: GAMETE DONOR

RESULT:
NORMAL MALE KARYOTYPE

INTERPRETATION:
Chromosome analysis revealed normal G-band patterns within the limits of standard cytogenetic analysis.

Please expect the results of any other concurrent study in a separate report.

NOMENCLATURE:
46,XY

ASSAY INFORMATION:

Method: G-Band (Digital Analysis: MetaSyst
Cells Counted: 20
Band Level: 450
Cells Analyzed: 5
Cells Karyotyped: 5

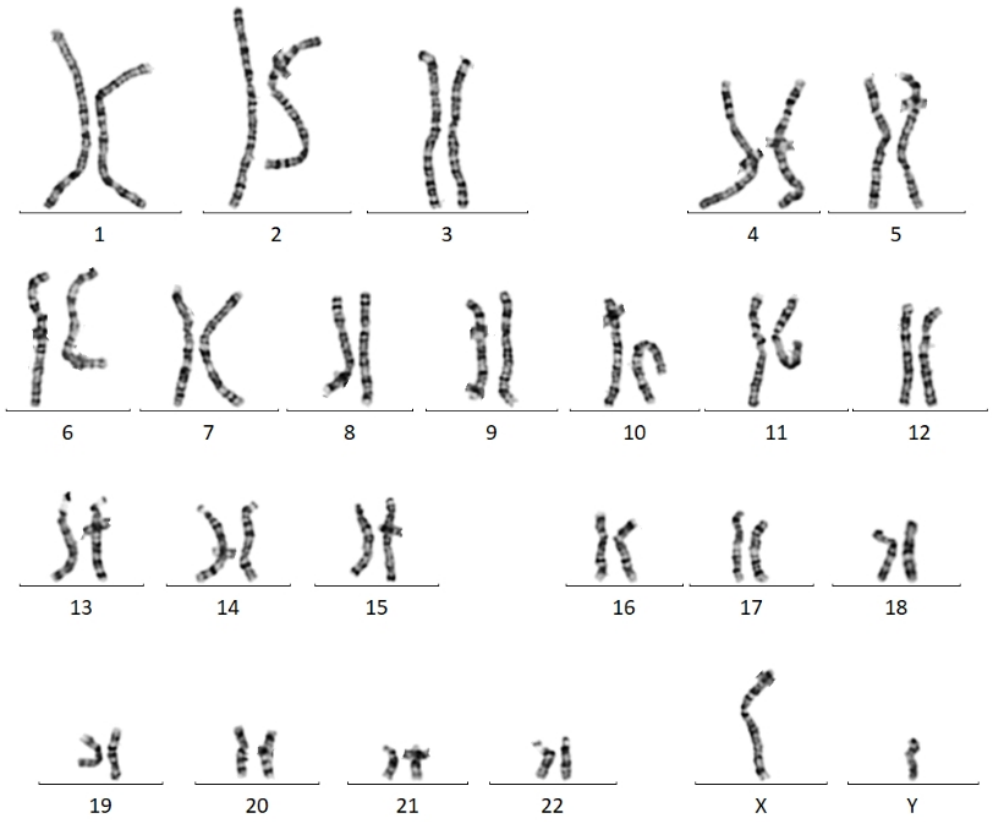
This test does not address genetic disorders that cannot be detected by standard cytogenetic methods or rare events such as low level mosaicism or subtle rearrangements.

Mark A. Micale, PhD, FACMG, [site SJC6]

Electronic Signature: 4/29/2025 5:47 PM

Quest, Quest Diagnostics, the associated logo and all associated Quest Diagnostics marks are the trademarks of Quest Diagnostics.

Patient Information	Specimen Information	Client Information
20061, DONOR **DOB:** [redacted] **AGE:** [redacted] Gender: M Fasting: U Patient ID: 20061	Specimen: LV142328A Collected: 04/22/2025 / 13:05 PDT Received: 04/23/2025 / 02:35 PDT Reported: 04/29/2025 / 15:34 PDT	Client #: 88807473 FOORD, DYLAN R



PERFORMING SITE:
EZ QUEST DIAGNOSTICS/NICHOLS SJC, 33608 ORTEGA HWY, SAN JUAN CAPISTRANO, CA 92675-2042 Laboratory Director: IRINA MARAMICA,MD,PHD,MBA, CLIA: 05D0643352

Quest, Quest Diagnostics, the associated logo and all associated Quest Diagnostics marks are the trademarks of Quest Diagnostics.