



Donor 6424

Genetic Testing Summary

Fairfax Cryobank recommends reviewing this genetic testing summary with your healthcare provider to determine suitability.

Last Updated: 06/18/24

Donor Reported Ancestry: Finish, Polish

Jewish Ancestry: No

| Genetic Test* | Result | Comments/Donor's Residual Risk** |
|--|---|---|
| Chromosome analysis (karyotype) | Normal male karyotype | 46, XY, Inv(9)(p12q13). Normal karyotype. Inv(9)(p12q13) is a well-known chromosome variant. with no clinical significance. |
| Hemoglobin evaluation | Normal hemoglobin fractionation and MCV/MCH results | Reduced risk to be a carrier for sickle cell anemia, beta thalassemia, alpha thalassemia trait (aa/-- and a-/a-) and other hemoglobinopathies |
| Cystic Fibrosis (CF) carrier screening | Negative by gene sequencing in the CFTR gene | 1/440 |
| Expanded Genetic Disease Carrier Screening Panel attached- 283 diseases by gene sequencing | <p>Carrier: Progressive Familial Intrahepatic Cholestasis, Type 2 (ABCB11)</p> <p>Carrier: Spinal Muscular Atrophy (SMN1)</p> <p>Negative for other genes sequenced</p> | Partner testing recommended before using this donor. |
| Special Testing | | |
| Genes: COL11A2, FMN2, TYR, SERPINA1 | Negative by gene sequencing | See attached for residual risks |

*No single test can screen for all genetic disorders. A negative screening result significantly reduces, but cannot eliminate, the risk for these conditions in a pregnancy.

**Donor residual risk is the chance the donor is still a carrier after testing negative.

Patient Information

Name: Donor 6424
 Date of Birth: [REDACTED]
 Sema4 ID: [REDACTED]
 Client: [REDACTED]
 Indication: Carrier Testing

Specimen Information

Specimen Type: Blood
 Date Collected: 04/12/2021
 Date Received: 04/13/2021
 Final Report: 05/04/2021

Referring Provider

[REDACTED]
 Fairfax Cryobank, Inc.
 [REDACTED]
 [REDACTED]
 [REDACTED]

Expanded Carrier Screen (283) Minus TSE

Number of genes tested: 283

SUMMARY OF RESULTS AND RECOMMENDATIONS

| ⊕ Positive | ⊖ Negative |
|--|---|
| <p>Carrier of Progressive Familial Intrahepatic Cholestasis, Type 2 (AR) Associated gene(s): <i>ABCB11</i> Variant(s) Detected: c.1445A>G, p.D482G, Pathogenic, Heterozygous (one copy)</p> <p>Carrier of Spinal Muscular Atrophy (AR) Associated gene(s): <i>SMN1</i> Variant(s) Detected: Loss of one copy of <i>SMN1</i></p> | <p>Negative for all other genes tested To view a full list of genes and diseases tested please see Table 1 in this report</p> |

AR=Autosomal recessive; XL=X-linked

Recommendations

- Testing the partner for the above positive disorder(s) and genetic counseling are recommended.
- Please note that for female carriers of X-linked diseases, follow-up testing of a male partner is not indicated.
- CGG repeat analysis of *FMR1* for fragile X syndrome is not performed on males as repeat expansion of premutation alleles is not expected in the male germline.
- Individuals of Asian, African, Hispanic and Mediterranean ancestry should also be screened for hemoglobinopathies by CBC and hemoglobin electrophoresis.
- Consideration of residual risk by ethnicity after a negative carrier screen is recommended for the other diseases on the panel, especially in the case of a positive family history for a specific disorder.

Interpretation of positive results

Progressive Familial Intrahepatic Cholestasis, Type 2 (AR)

Results and Interpretation

A heterozygous (one copy) pathogenic missense variant, c.1445A>G, p.D482G, was detected in the *ABCB11* gene (NM_003742.2). When this variant is present in trans with a pathogenic variant, it is considered to be causative for progressive familial intrahepatic cholestasis, type 2. Therefore, this individual is expected to be at least a carrier for progressive familial intrahepatic cholestasis, type 2. Heterozygous carriers are not expected to exhibit symptoms of this disease.

What is Progressive Familial Intrahepatic Cholestasis, Type 2?

Progressive familial intrahepatic cholestasis, type 2 is an autosomal recessive, pan-ethnic disorder caused by pathogenic variants in the gene *ABCB11*. Patients with this disease experience recurrent episodes of cholestasis, or a blockage of bile flow, in infancy. Excess bile salts are stored in the liver cells and leak into the bloodstream, resulting in severe itching, jaundice, and an enlarged liver. Damage of the liver cells frequently leads to liver failure and sometimes liver cancer. Many patients will require a liver transplant, usually before adulthood. Some patients with two pathogenic *ABCB11* variants will develop a disease known as benign recurrent intrahepatic cholestasis, type 2. These patients have recurrent cholestasis episodes but do not develop liver failure or cancer. Patients with null variants are more likely to develop progressive rather than benign disease, but it may not be possible to predict the severity of the disease in all patients. Life expectancy may be reduced in some patients with cancer, or those requiring liver transplants that experience complications.

Spinal Muscular Atrophy (AR)

Results and Interpretation

SMN1 copy number: 1

SMN2 copy number: >=3

c.'3+80T>G: Negative

Gene(s) analyzed: *SMN1* (NM_000344.3) and *SMN2* (NM_017411.3)

Inheritance: Autosomal Recessive

This patient is positive for loss of one copy of *SMN1* and is, therefore, a carrier for SMA. Complete loss of *SMN1* is causative in spinal muscular atrophy (SMA). One copy of *SMN1* was detected in this individual, which is consistent with being a carrier for SMA. This individual was found to be negative for c.'3+80T>G; however, given that this patient was found to be an SMA carrier by MLPA analysis, this finding does not modify residual risk.

What is spinal muscular atrophy?

Spinal muscular atrophy (SMA) is a pan-ethnic, autosomal recessive disease caused by loss of function of the *SMN1* gene. In over 95% of cases, patients are missing both copies of the *SMN1* gene. The disease is characterized by the degeneration of alpha motor neurons of the spinal cord anterior horn cells, leading to progressive symmetric weakness, atrophy of the proximal voluntary muscles and early death. Age of onset can be anywhere on a continuum from the prenatal period to adulthood.

- SMA 0 represents the most severe form. Infants are born with severe hypotonia and joint contractures; no motor milestones are achieved and patients die before 6 months of age.
- SMA I has an age of onset in the first six months of life. These cases are associated with death usually by age 2 and the lack of development of motor skills.
- SMA II has an age of onset between 3 and 15 months; patients may be able to sit independently. Intelligence is not affected. Life expectancy may vary from early childhood to early adulthood.
- SMA III has an age of onset after 18 months of age and as late as adolescence; patients may learn to stand and to walk short distances. These patients may have a normal lifespan.
- SMA IV is an adult-onset disorder of muscle weakness; life span is not shortened.

Most patients, regardless of the severity of disease, have a deletion of both *SMN1* copies. Patients with later-onset disease usually have three or more copies of *SMN2*, which encodes a small amount of residual protein and lessens the severity of the symptoms. However, other factors besides *SMN2* copy number may affect the phenotype, and therefore the severity of the disease may not be able to be accurately predicted in all patients based on genotype. New treatments may be available to infants and children to prevent development of symptoms and slow progression of the disease.



Test description

This patient was tested for a panel of diseases using a combination of sequencing, targeted genotyping and copy number analysis. Please note that negative results reduce but do not eliminate the possibility that this individual is a carrier for one or more of the disorders tested. Please see Table 1 for a list of genes and diseases tested, and [go.sema4.com/residualrisk](https://www.sema4.com/residualrisk) for specific detection rates and residual risk by ethnicity. With individuals of mixed ethnicity, it is recommended to use the highest residual risk estimate. Only variants determined to be pathogenic or likely pathogenic are reported in this carrier screening test.



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Laboratory Medical Consultant: George A. Diaz, M.D., Ph.D

Genes and diseases tested

For specific detection rates and residual risk by ethnicity, please visit go.sema4.com/residualrisk

Table 1: List of genes and diseases tested with detailed results

| Disease | Gene | Inheritance Pattern | Status | Detailed Summary |
|---|------------------|---------------------|--------------|--|
| ⊕ Positive | | | | |
| Progressive Familial Intrahepatic Cholestasis, Type 2 | <i>ABCB11</i> | AR | Carrier | c.1445A>G, p.D482G, Pathogenic, Heterozygous (one copy) |
| Spinal Muscular Atrophy | <i>SMN1</i> | AR | Carrier | <i>SMN1</i> copy number: 1 <i>SMN2</i> copy number: >=3 c.*3+80T>G: Negative |
| ⊖ Negative | | | | |
| 3-Beta-Hydroxysteroid Dehydrogenase Type II Deficiency | <i>HSD3B2</i> | AR | Reduced Risk | |
| 3-Methylcrotonyl-CoA Carboxylase Deficiency (MCCC1-Related) | <i>MCCC1</i> | AR | Reduced Risk | |
| 3-Methylcrotonyl-CoA Carboxylase Deficiency (MCCC2-Related) | <i>MCCC2</i> | AR | Reduced Risk | |
| 3-Methylglutaconic Aciduria, Type III | <i>OPA3</i> | AR | Reduced Risk | |
| 3-Phosphoglycerate Dehydrogenase Deficiency | <i>PHGDH</i> | AR | Reduced Risk | |
| 6-Pyruvoyl-Tetrahydropterin Synthase Deficiency | <i>PTS</i> | AR | Reduced Risk | |
| Abetalipoproteinemia | <i>MTTP</i> | AR | Reduced Risk | |
| Achromatopsia (CNGB3-related) | <i>CNGB3</i> | AR | Reduced Risk | |
| Acrodermatitis Enteropathica | <i>SLC39A4</i> | AR | Reduced Risk | |
| Acute Infantile Liver Failure | <i>TRMU</i> | AR | Reduced Risk | |
| Acyl-CoA Oxidase I Deficiency | <i>ACOX1</i> | AR | Reduced Risk | |
| Adenosine Deaminase Deficiency | <i>ADA</i> | AR | Reduced Risk | |
| Adrenoleukodystrophy, X-Linked | <i>ABCD1</i> | XL | Reduced Risk | |
| Aicardi-Goutieres Syndrome (SAMHD1-Related) | <i>SAMHD1</i> | AR | Reduced Risk | |
| Alpha-Mannosidosis | <i>MAN2B1</i> | AR | Reduced Risk | |
| Alpha-Thalassemia | <i>HBA1/HBA2</i> | AR | Reduced Risk | <i>HBA1</i> Copy Number: 2 <i>HBA2</i> Copy Number: 2 No pathogenic copy number variants detected <i>HBA1/HBA2</i> Sequencing: Negative |
| Alpha-Thalassemia Mental Retardation Syndrome | <i>ATRX</i> | XL | Reduced Risk | |
| Alport Syndrome (COL4A3-Related) | <i>COL4A3</i> | AR | Reduced Risk | |
| Alport Syndrome (COL4A4-Related) | <i>COL4A4</i> | AR | Reduced Risk | |
| Alport Syndrome (COL4A5-Related) | <i>COL4A5</i> | XL | Reduced Risk | |
| Alstrom Syndrome | <i>ALMS1</i> | AR | Reduced Risk | |

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|---|----------------|----|--------------|
| Andermann Syndrome | <i>SLC12A6</i> | AR | Reduced Risk |
| Argininosuccinic Aciduria | <i>ASL</i> | AR | Reduced Risk |
| Aromatase Deficiency | <i>CYP19A1</i> | AR | Reduced Risk |
| Arthrogryposis, Mental Retardation, and Seizures | <i>SLC35A3</i> | AR | Reduced Risk |
| Asparagine Synthetase Deficiency | <i>ASNS</i> | AR | Reduced Risk |
| Aspartylglycosaminuria | <i>AGA</i> | AR | Reduced Risk |
| Ataxia With Isolated Vitamin E Deficiency | <i>TTPA</i> | AR | Reduced Risk |
| Ataxia-Telangiectasia | <i>ATM</i> | AR | Reduced Risk |
| Autosomal Recessive Spastic Ataxia of Charlevoix-Saguenay | <i>SACS</i> | AR | Reduced Risk |
| Bardet-Biedl Syndrome (<i>BBS10</i> -Related) | <i>BBS10</i> | AR | Reduced Risk |
| Bardet-Biedl Syndrome (<i>BBS12</i> -Related) | <i>BBS12</i> | AR | Reduced Risk |
| Bardet-Biedl Syndrome (<i>BBS1</i> -Related) | <i>BBS1</i> | AR | Reduced Risk |
| Bardet-Biedl Syndrome (<i>BBS2</i> -Related) | <i>BBS2</i> | AR | Reduced Risk |
| Bare Lymphocyte Syndrome, Type II | <i>CIITA</i> | AR | Reduced Risk |
| Bartter Syndrome, Type 4A | <i>BSND</i> | AR | Reduced Risk |
| Bernard-Soulier Syndrome, Type A1 | <i>GP1BA</i> | AR | Reduced Risk |
| Bernard-Soulier Syndrome, Type C | <i>GP9</i> | AR | Reduced Risk |
| Beta-Globin-Related Hemoglobinopathies | <i>HBB</i> | AR | Reduced Risk |
| Beta-Ketothiolase Deficiency | <i>ACAT1</i> | AR | Reduced Risk |
| Bilateral Frontoparietal Polymicrogyria | <i>GPR56</i> | AR | Reduced Risk |
| Biotinidase Deficiency | <i>BTBD</i> | AR | Reduced Risk |
| Bloom Syndrome | <i>BLM</i> | AR | Reduced Risk |
| Canavan Disease | <i>ASPA</i> | AR | Reduced Risk |
| Carbamoylphosphate Synthetase I Deficiency | <i>CPS1</i> | AR | Reduced Risk |
| Carnitine Palmitoyltransferase IA Deficiency | <i>CPT1A</i> | AR | Reduced Risk |
| Carnitine Palmitoyltransferase II Deficiency | <i>CPT2</i> | AR | Reduced Risk |
| Carpenter Syndrome | <i>RAB23</i> | AR | Reduced Risk |
| Cartilage-Hair Hypoplasia | <i>RMRP</i> | AR | Reduced Risk |
| Cerebral Creatine Deficiency Syndrome 1 | <i>SLC6A8</i> | XL | Reduced Risk |
| Cerebral Creatine Deficiency Syndrome 2 | <i>GAMT</i> | AR | Reduced Risk |
| Cerebrotendinous Xanthomatosis | <i>CYP27A1</i> | AR | Reduced Risk |
| Charcot-Marie-Tooth Disease, Type 4D | <i>NDRG1</i> | AR | Reduced Risk |
| Charcot-Marie-Tooth Disease, Type 5 / Arts Syndrome | <i>PRPS1</i> | XL | Reduced Risk |
| Charcot-Marie-Tooth Disease, X-Linked | <i>GJB1</i> | XL | Reduced Risk |
| Choreoacanthocytosis | <i>VPS13A</i> | AR | Reduced Risk |
| Choroideremia | <i>CHM</i> | XL | Reduced Risk |
| Chronic Granulomatous Disease (<i>CYBA</i> -Related) | <i>CYBA</i> | AR | Reduced Risk |

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|---|----------|----|--|
| Chronic Granulomatous Disease (CYBB-Related) | CYBB | XL | Reduced Risk |
| Citrin Deficiency | SLC25A13 | AR | Reduced Risk |
| Citrullinemia, Type 1 | ASS1 | AR | Reduced Risk |
| Cohen Syndrome | VPS13B | AR | Reduced Risk |
| Combined Malonic and Methylmalonic Aciduria | ACSF3 | AR | Reduced Risk |
| Combined Oxidative Phosphorylation Deficiency 1 | GFM1 | AR | Reduced Risk |
| Combined Oxidative Phosphorylation Deficiency 3 | TSFM | AR | Reduced Risk |
| Combined Pituitary Hormone Deficiency 2 | PROP1 | AR | Reduced Risk |
| Combined Pituitary Hormone Deficiency 3 | LHX3 | AR | Reduced Risk |
| Combined SAP Deficiency | PSAP | AR | Reduced Risk |
| Congenital Adrenal Hyperplasia due to 17-Alpha-Hydroxylase Deficiency | CYP17A1 | AR | Reduced Risk |
| Congenital Adrenal Hyperplasia due to 21-Hydroxylase Deficiency | CYP21A2 | AR | Reduced Risk CYP21A2 copy number: 2 CYP21A2 sequencing: Negative |
| Congenital Amegakaryocytic Thrombocytopenia | MPL | AR | Reduced Risk |
| Congenital Disorder of Glycosylation, Type Ia | PMM2 | AR | Reduced Risk |
| Congenital Disorder of Glycosylation, Type Ib | MPI | AR | Reduced Risk |
| Congenital Disorder of Glycosylation, Type Ic | ALG6 | AR | Reduced Risk |
| Congenital Insensitivity to Pain with Anhidrosis | NTRK1 | AR | Reduced Risk |
| Congenital Myasthenic Syndrome (CHRNE-Related) | CHRNE | AR | Reduced Risk |
| Congenital Myasthenic Syndrome (RAPSN-Related) | RAPSN | AR | Reduced Risk |
| Congenital Neutropenia (HAX1-Related) | HAX1 | AR | Reduced Risk |
| Congenital Neutropenia (VPS45-Related) | VPS45 | AR | Reduced Risk |
| Corneal Dystrophy and Perceptive Deafness | SLC4A11 | AR | Reduced Risk |
| Corticosterone Methyloxidase Deficiency | CYP11B2 | AR | Reduced Risk |
| Cystic Fibrosis | CFTR | AR | Reduced Risk |
| Cystinosis | CTNS | AR | Reduced Risk |
| D-Bifunctional Protein Deficiency | HSD17B4 | AR | Reduced Risk |
| Deafness, Autosomal Recessive 77 | LOXHD1 | AR | Reduced Risk |
| Duchenne Muscular Dystrophy / Becker Muscular Dystrophy | DMD | XL | Reduced Risk |
| Dyskeratosis Congenita (RTEL1-Related) | RTEL1 | AR | Reduced Risk |
| Dystrophic Epidermolysis Bullosa | COL7A1 | AR | Reduced Risk |
| Ehlers-Danlos Syndrome, Type VIIC | ADAMTS2 | AR | Reduced Risk |
| Ellis-van Creveld Syndrome (EVC-Related) | EVC | AR | Reduced Risk |
| Emery-Dreifuss Myopathy 1 | EMD | XL | Reduced Risk |
| Enhanced S-Cone Syndrome | NR2E3 | AR | Reduced Risk |
| Ethylmalonic Encephalopathy | ETHE1 | AR | Reduced Risk |
| Fabry Disease | GLA | XL | Reduced Risk |

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|---|----------------|----|--------------|--|
| Factor IX Deficiency | <i>F9</i> | XL | Reduced Risk | |
| Factor XI Deficiency | <i>F11</i> | AR | Reduced Risk | |
| Familial Autosomal Recessive Hypercholesterolemia | <i>LDLRAP1</i> | AR | Reduced Risk | |
| Familial Dysautonomia | <i>IKBKAP</i> | AR | Reduced Risk | |
| Familial Hypercholesterolemia | <i>LDLR</i> | AR | Reduced Risk | |
| Familial Hyperinsulinism (<i>ABCC8</i> -Related) | <i>ABCC8</i> | AR | Reduced Risk | |
| Familial Hyperinsulinism (<i>KCNJ11</i> -Related) | <i>KCNJ11</i> | AR | Reduced Risk | |
| Familial Mediterranean Fever | <i>MEFV</i> | AR | Reduced Risk | |
| Fanconi Anemia, Group A | <i>FANCA</i> | AR | Reduced Risk | |
| Fanconi Anemia, Group C | <i>FANCC</i> | AR | Reduced Risk | |
| Fanconi Anemia, Group G | <i>FANCG</i> | AR | Reduced Risk | |
| Fragile X Syndrome | <i>FMR1</i> | XL | Reduced Risk | <i>FMR1</i> CGG repeat sizes: Not Performed <i>FMR1</i> Sequencing: Negative Fragile X CGG triplet repeat expansion testing was not performed at this time, as the patient has either been previously tested or is a male. |
| Fumarase Deficiency | <i>FH</i> | AR | Reduced Risk | |
| GRACILE Syndrome and Other <i>BCS1L</i> -Related Disorders | <i>BCS1L</i> | AR | Reduced Risk | |
| Galactokinase Deficiency | <i>GALK1</i> | AR | Reduced Risk | |
| Galactosemia | <i>GALT</i> | AR | Reduced Risk | |
| Gaucher Disease | <i>GBA</i> | AR | Reduced Risk | |
| Gitelman Syndrome | <i>SLC12A3</i> | AR | Reduced Risk | |
| Glutaric Acidemia, Type I | <i>GCDH</i> | AR | Reduced Risk | |
| Glutaric Acidemia, Type IIa | <i>ETFA</i> | AR | Reduced Risk | |
| Glutaric Acidemia, Type IIc | <i>ETFDH</i> | AR | Reduced Risk | |
| Glycine Encephalopathy (<i>AMT</i> -Related) | <i>AMT</i> | AR | Reduced Risk | |
| Glycine Encephalopathy (<i>GLDC</i> -Related) | <i>GLDC</i> | AR | Reduced Risk | |
| Glycogen Storage Disease, Type II | <i>GAA</i> | AR | Reduced Risk | |
| Glycogen Storage Disease, Type III | <i>AGL</i> | AR | Reduced Risk | |
| Glycogen Storage Disease, Type IV / Adult Polyglucosan Body Disease | <i>GBE1</i> | AR | Reduced Risk | |
| Glycogen Storage Disease, Type Ia | <i>G6PC</i> | AR | Reduced Risk | |
| Glycogen Storage Disease, Type Ib | <i>SLC37A4</i> | AR | Reduced Risk | |
| Glycogen Storage Disease, Type V | <i>PYGM</i> | AR | Reduced Risk | |
| Glycogen Storage Disease, Type VII | <i>PFKM</i> | AR | Reduced Risk | |
| HMG-CoA Lyase Deficiency | <i>HMGCL</i> | AR | Reduced Risk | |
| Hemochromatosis, Type 2A | <i>HFE2</i> | AR | Reduced Risk | |
| Hemochromatosis, Type 3 | <i>TFR2</i> | AR | Reduced Risk | |
| Hereditary Fructose Intolerance | <i>ALDOB</i> | AR | Reduced Risk | |

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|---|-----------------|----|--------------|
| Hereditary Spastic Paraparesis 49 | <i>TECP2</i> | AR | Reduced Risk |
| Hermansky-Pudlak Syndrome, Type 1 | <i>HPS1</i> | AR | Reduced Risk |
| Hermansky-Pudlak Syndrome, Type 3 | <i>HPS3</i> | AR | Reduced Risk |
| Holocarboxylase Synthetase Deficiency | <i>HLCS</i> | AR | Reduced Risk |
| Homocystinuria (CBS-Related) | <i>CBS</i> | AR | Reduced Risk |
| Homocystinuria due to <i>MTHFR</i> Deficiency | <i>MTHFR</i> | AR | Reduced Risk |
| Homocystinuria, cblE Type | <i>MTRR</i> | AR | Reduced Risk |
| Hydrolethalus Syndrome | <i>HYLS1</i> | AR | Reduced Risk |
| Hyperornithinemia-Hyperammonemia-Homocitrullinuria Syndrome | <i>SLC25A15</i> | AR | Reduced Risk |
| Hypohidrotic Ectodermal Dysplasia 1 | <i>EDA</i> | XL | Reduced Risk |
| Hypophosphatasia | <i>ALPL</i> | AR | Reduced Risk |
| Inclusion Body Myopathy 2 | <i>GNE</i> | AR | Reduced Risk |
| Infantile Cerebral and Cerebellar Atrophy | <i>MED17</i> | AR | Reduced Risk |
| Isovaleric Acidemia | <i>IVD</i> | AR | Reduced Risk |
| Joubert Syndrome 2 | <i>TMEM216</i> | AR | Reduced Risk |
| Joubert Syndrome 7 / Meckel Syndrome 5 / COACH Syndrome | <i>RPGRIP1L</i> | AR | Reduced Risk |
| Junctional Epidermolysis Bullosa (<i>LAMA3</i> -Related) | <i>LAMA3</i> | AR | Reduced Risk |
| Junctional Epidermolysis Bullosa (<i>LAMB3</i> -Related) | <i>LAMB3</i> | AR | Reduced Risk |
| Junctional Epidermolysis Bullosa (<i>LAMC2</i> -Related) | <i>LAMC2</i> | AR | Reduced Risk |
| Krabbe Disease | <i>GALC</i> | AR | Reduced Risk |
| Lamellar Ichthyosis, Type 1 | <i>TGM1</i> | AR | Reduced Risk |
| Leber Congenital Amaurosis 10 and Other CEP290-Related Ciliopathies | <i>CEP290</i> | AR | Reduced Risk |
| Leber Congenital Amaurosis 13 | <i>RDH12</i> | AR | Reduced Risk |
| Leber Congenital Amaurosis 2 / Retinitis Pigmentosa 20 | <i>RPE65</i> | AR | Reduced Risk |
| Leber Congenital Amaurosis 5 | <i>LCA5</i> | AR | Reduced Risk |
| Leber Congenital Amaurosis 8 / Retinitis Pigmentosa 12 / Pigmented Paravenous Chorioretinal Atrophy | <i>CRB1</i> | AR | Reduced Risk |
| Leigh Syndrome, French-Canadian Type | <i>LRPPRC</i> | AR | Reduced Risk |
| Lethal Congenital Contracture Syndrome 1 / Lethal Arthrogryposis with Anterior Horn Cell Disease | <i>GLE1</i> | AR | Reduced Risk |
| Leukoencephalopathy with Vanishing White Matter | <i>EIF2B5</i> | AR | Reduced Risk |
| Limb-Girdle Muscular Dystrophy, Type 2A | <i>CAPN3</i> | AR | Reduced Risk |
| Limb-Girdle Muscular Dystrophy, Type 2B | <i>DYSF</i> | AR | Reduced Risk |
| Limb-Girdle Muscular Dystrophy, Type 2C | <i>SGCG</i> | AR | Reduced Risk |
| Limb-Girdle Muscular Dystrophy, Type 2D | <i>SGCA</i> | AR | Reduced Risk |
| Limb-Girdle Muscular Dystrophy, Type 2E | <i>SGCB</i> | AR | Reduced Risk |
| Limb-Girdle Muscular Dystrophy, Type 2I | <i>FKRP</i> | AR | Reduced Risk |

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| Lipoamide Dehydrogenase Deficiency | <i>DLD</i> | AR | Reduced Risk |
| Lipoid Adrenal Hyperplasia | <i>STAR</i> | AR | Reduced Risk |
| Lipoprotein Lipase Deficiency | <i>LPL</i> | AR | Reduced Risk |
| Long-Chain 3-Hydroxyacyl-CoA Dehydrogenase Deficiency | <i>HADHA</i> | AR | Reduced Risk |
| Lysinuric Protein Intolerance | <i>SLC7A7</i> | AR | Reduced Risk |
| Maple Syrup Urine Disease, Type 1a | <i>BCKDHA</i> | AR | Reduced Risk |
| Maple Syrup Urine Disease, Type 1b | <i>BCKDHB</i> | AR | Reduced Risk |
| Meckel Syndrome 1 / Bardet-Biedl Syndrome 13 | <i>MKS1</i> | AR | Reduced Risk |
| Medium Chain Acyl-CoA Dehydrogenase Deficiency | <i>ACADM</i> | AR | Reduced Risk |
| Megalencephalic Leukoencephalopathy with Subcortical Cysts | <i>MLC1</i> | AR | Reduced Risk |
| Menkes Disease | <i>ATP7A</i> | XL | Reduced Risk |
| Metachromatic Leukodystrophy | <i>ARSA</i> | AR | Reduced Risk |
| Methylmalonic Acidemia (MMAA-Related) | <i>MMAA</i> | AR | Reduced Risk |
| Methylmalonic Acidemia (MMAB-Related) | <i>MMAB</i> | AR | Reduced Risk |
| Methylmalonic Acidemia (MUT-Related) | <i>MUT</i> | AR | Reduced Risk |
| Methylmalonic Aciduria and Homocystinuria, Cobalamin C Type | <i>MMACHC</i> | AR | Reduced Risk |
| Methylmalonic Aciduria and Homocystinuria, Cobalamin D Type | <i>MMADHC</i> | AR | Reduced Risk |
| Microphthalmia / Anophthalmia | <i>VSX2</i> | AR | Reduced Risk |
| Mitochondrial Complex I Deficiency (ACAD9-Related) | <i>ACAD9</i> | AR | Reduced Risk |
| Mitochondrial Complex I Deficiency (NDUFAF5-Related) | <i>NDUFAF5</i> | AR | Reduced Risk |
| Mitochondrial Complex I Deficiency (NDUFS6-Related) | <i>NDUFS6</i> | AR | Reduced Risk |
| Mitochondrial DNA Depletion Syndrome 6 / Navajo Neurohepatopathy | <i>MPV17</i> | AR | Reduced Risk |
| Mitochondrial Myopathy and Sideroblastic Anemia 1 | <i>PUS1</i> | AR | Reduced Risk |
| Mucopolipidosis II / IIIA | <i>GNPTAB</i> | AR | Reduced Risk |
| Mucopolipidosis III Gamma | <i>GNPTG</i> | AR | Reduced Risk |
| Mucopolipidosis IV | <i>MCOLN1</i> | AR | Reduced Risk |
| Mucopolysaccharidosis Type I | <i>IDUA</i> | AR | Reduced Risk |
| Mucopolysaccharidosis Type II | <i>IDS</i> | XL | Reduced Risk |
| Mucopolysaccharidosis Type IIIA | <i>SGSH</i> | AR | Reduced Risk |
| Mucopolysaccharidosis Type IIIB | <i>NAGLU</i> | AR | Reduced Risk |
| Mucopolysaccharidosis Type IIIC | <i>HGSNAT</i> | AR | Reduced Risk |
| Mucopolysaccharidosis Type IIID | <i>GNS</i> | AR | Reduced Risk |
| Mucopolysaccharidosis Type IVb / GM1 Gangliosidosis | <i>GLB1</i> | AR | Reduced Risk |
| Mucopolysaccharidosis type IX | <i>HYAL1</i> | AR | Reduced Risk |

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|---|----------------|----|--------------|
| Mucopolysaccharidosis type VI | <i>ARSB</i> | AR | Reduced Risk |
| Multiple Sulfatase Deficiency | <i>SUMF1</i> | AR | Reduced Risk |
| Muscle-Eye-Brain Disease and Other <i>POMGNT1</i> -Related Congenital Muscular Dystrophy-Dystroglycanopathies | <i>POMGNT1</i> | AR | Reduced Risk |
| Myoneurogastrointestinal Encephalopathy | <i>TYMP</i> | AR | Reduced Risk |
| Myotubular Myopathy 1 | <i>MTM1</i> | XL | Reduced Risk |
| N-Acetylglutamate Synthase Deficiency | <i>NAGS</i> | AR | Reduced Risk |
| Nemaline Myopathy 2 | <i>NEB</i> | AR | Reduced Risk |
| Nephrogenic Diabetes Insipidus, Type II | <i>AQP2</i> | AR | Reduced Risk |
| Nephrotic Syndrome (<i>NPHS1</i> -Related) / Congenital Finnish Nephrosis | <i>NPHS1</i> | AR | Reduced Risk |
| Nephrotic Syndrome (<i>NPHS2</i> -Related) / Steroid-Resistant Nephrotic Syndrome | <i>NPHS2</i> | AR | Reduced Risk |
| Neuronal Ceroid-Lipofuscinosis (<i>CLN3</i> -Related) | <i>CLN3</i> | AR | Reduced Risk |
| Neuronal Ceroid-Lipofuscinosis (<i>CLN5</i> -Related) | <i>CLN5</i> | AR | Reduced Risk |
| Neuronal Ceroid-Lipofuscinosis (<i>CLN6</i> -Related) | <i>CLN6</i> | AR | Reduced Risk |
| Neuronal Ceroid-Lipofuscinosis (<i>CLN8</i> -Related) | <i>CLN8</i> | AR | Reduced Risk |
| Neuronal Ceroid-Lipofuscinosis (<i>MFSD8</i> -Related) | <i>MFSD8</i> | AR | Reduced Risk |
| Neuronal Ceroid-Lipofuscinosis (<i>PPT1</i> -Related) | <i>PPT1</i> | AR | Reduced Risk |
| Neuronal Ceroid-Lipofuscinosis (<i>TPP1</i> -Related) | <i>TPP1</i> | AR | Reduced Risk |
| Niemann-Pick Disease (<i>SMPD1</i> -Related) | <i>SMPD1</i> | AR | Reduced Risk |
| Niemann-Pick Disease, Type C (<i>NPC1</i> -Related) | <i>NPC1</i> | AR | Reduced Risk |
| Niemann-Pick Disease, Type C (<i>NPC2</i> -Related) | <i>NPC2</i> | AR | Reduced Risk |
| Nijmegen Breakage Syndrome | <i>NBN</i> | AR | Reduced Risk |
| Non-Syndromic Hearing Loss (<i>GJB2</i> -Related) | <i>GJB2</i> | AR | Reduced Risk |
| Odonto-Onycho-Dermal Dysplasia / Schopf-Schulz-Passarge Syndrome | <i>WNT10A</i> | AR | Reduced Risk |
| Omenn Syndrome (<i>RAG2</i> -Related) | <i>RAG2</i> | AR | Reduced Risk |
| Omenn Syndrome / Severe Combined Immunodeficiency, Athabaskan-Type | <i>DCLRE1C</i> | AR | Reduced Risk |
| Ornithine Aminotransferase Deficiency | <i>OAT</i> | AR | Reduced Risk |
| Ornithine Transcarbamylase Deficiency | <i>OTC</i> | XL | Reduced Risk |
| Osteopetrosis 1 | <i>TCIRG1</i> | AR | Reduced Risk |
| Pendred Syndrome | <i>SLC26A4</i> | AR | Reduced Risk |
| Phenylalanine Hydroxylase Deficiency | <i>PAH</i> | AR | Reduced Risk |
| Polycystic Kidney Disease, Autosomal Recessive | <i>PKHD1</i> | AR | Reduced Risk |
| Polyglandular Autoimmune Syndrome, Type 1 | <i>AIRE</i> | AR | Reduced Risk |
| Pontocerebellar Hypoplasia, Type 1A | <i>VRK1</i> | AR | Reduced Risk |
| Pontocerebellar Hypoplasia, Type 6 | <i>RARS2</i> | AR | Reduced Risk |
| Primary Carnitine Deficiency | <i>SLC22A5</i> | AR | Reduced Risk |

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|---|-----------------|----|--------------|
| Primary Ciliary Dyskinesia (<i>DNAH5</i> -Related) | <i>DNAH5</i> | AR | Reduced Risk |
| Primary Ciliary Dyskinesia (<i>DNAI1</i> -Related) | <i>DNAI1</i> | AR | Reduced Risk |
| Primary Ciliary Dyskinesia (<i>DNAI2</i> -Related) | <i>DNAI2</i> | AR | Reduced Risk |
| Primary Hyperoxaluria, Type 1 | <i>AGXT</i> | AR | Reduced Risk |
| Primary Hyperoxaluria, Type 2 | <i>GRHPR</i> | AR | Reduced Risk |
| Primary Hyperoxaluria, Type 3 | <i>HOGA1</i> | AR | Reduced Risk |
| Progressive Cerebello-Cerebral Atrophy | <i>SEPSECS</i> | AR | Reduced Risk |
| Propionic Acidemia (<i>PCCA</i> -Related) | <i>PCCA</i> | AR | Reduced Risk |
| Propionic Acidemia (<i>PCCB</i> -Related) | <i>PCCB</i> | AR | Reduced Risk |
| Pycnodysostosis | <i>CTSK</i> | AR | Reduced Risk |
| Pyruvate Dehydrogenase E1-Alpha Deficiency | <i>PDHA1</i> | XL | Reduced Risk |
| Pyruvate Dehydrogenase E1-Beta Deficiency | <i>PDHB</i> | AR | Reduced Risk |
| Renal Tubular Acidosis and Deafness | <i>ATP6V1B1</i> | AR | Reduced Risk |
| Retinitis Pigmentosa 25 | <i>EYS</i> | AR | Reduced Risk |
| Retinitis Pigmentosa 26 | <i>CERKL</i> | AR | Reduced Risk |
| Retinitis Pigmentosa 28 | <i>FAM161A</i> | AR | Reduced Risk |
| Retinitis Pigmentosa 59 | <i>DHDDS</i> | AR | Reduced Risk |
| Rhizomelic Chondrodysplasia Punctata, Type 1 | <i>PEX7</i> | AR | Reduced Risk |
| Rhizomelic Chondrodysplasia Punctata, Type 3 | <i>AGPS</i> | AR | Reduced Risk |
| Roberts Syndrome | <i>ESCO2</i> | AR | Reduced Risk |
| Salla Disease | <i>SLC17A5</i> | AR | Reduced Risk |
| Sandhoff Disease | <i>HEXB</i> | AR | Reduced Risk |
| Schimke Immunoosseous Dysplasia | <i>SMARCAL1</i> | AR | Reduced Risk |
| Segawa Syndrome | <i>TH</i> | AR | Reduced Risk |
| Sjogren-Larsson Syndrome | <i>ALDH3A2</i> | AR | Reduced Risk |
| Smith-Lemli-Opitz Syndrome | <i>DHCR7</i> | AR | Reduced Risk |
| Spondylothoracic Dysostosis | <i>MESP2</i> | AR | Reduced Risk |
| Steel Syndrome | <i>COL27A1</i> | AR | Reduced Risk |
| Stuve-Wiedemann Syndrome | <i>LIFR</i> | AR | Reduced Risk |
| Sulfate Transporter-Related Osteochondrodysplasia | <i>SLC26A2</i> | AR | Reduced Risk |
| Tay-Sachs Disease | <i>HEXA</i> | AR | Reduced Risk |
| Tyrosinemia, Type I | <i>FAH</i> | AR | Reduced Risk |
| Usher Syndrome, Type IB | <i>MYO7A</i> | AR | Reduced Risk |
| Usher Syndrome, Type IC | <i>USH1C</i> | AR | Reduced Risk |
| Usher Syndrome, Type ID | <i>CDH23</i> | AR | Reduced Risk |
| Usher Syndrome, Type IF | <i>PCDH15</i> | AR | Reduced Risk |
| Usher Syndrome, Type IIA | <i>USH2A</i> | AR | Reduced Risk |
| Usher Syndrome, Type III | <i>CLRN1</i> | AR | Reduced Risk |

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|--|---------------|----|--------------|
| Very Long Chain Acyl-CoA Dehydrogenase Deficiency | <i>ACADVL</i> | AR | Reduced Risk |
| Walker-Warburg Syndrome and Other <i>FKTN</i> -Related Dystrophies | <i>FKTN</i> | AR | Reduced Risk |
| Wilson Disease | <i>ATP7B</i> | AR | Reduced Risk |
| Wolman Disease / Cholesteryl Ester Storage Disease | <i>LIPA</i> | AR | Reduced Risk |
| X-Linked Juvenile Retinoschisis | <i>RS1</i> | XL | Reduced Risk |
| X-Linked Severe Combined Immunodeficiency | <i>IL2RG</i> | XL | Reduced Risk |
| Zellweger Syndrome Spectrum (<i>PEX10</i> -Related) | <i>PEX10</i> | AR | Reduced Risk |
| Zellweger Syndrome Spectrum (<i>PEX1</i> -Related) | <i>PEX1</i> | AR | Reduced Risk |
| Zellweger Syndrome Spectrum (<i>PEX2</i> -Related) | <i>PEX2</i> | AR | Reduced Risk |
| Zellweger Syndrome Spectrum (<i>PEX6</i> -Related) | <i>PEX6</i> | AR | Reduced Risk |

AR=Autosomal recessive; XL=X-linked

Test methods and comments

Genomic DNA isolated from this patient was analyzed by one or more of the following methodologies, as applicable:

Fragile X CGG Repeat Analysis (Analytical Detection Rate >99%)

PCR amplification using Asuragen, Inc. AmpliDeX[®]*FMR1* PCR reagents followed by capillary electrophoresis for allele sizing was performed. Samples positive for *FMR1* CGG repeats in the premutation and full mutation size range were further analyzed by Southern blot analysis to assess the size and methylation status of the *FMR1* CGG repeat.

Genotyping (Analytical Detection Rate >99%)

Multiplex PCR amplification and allele specific primer extension analyses using the MassARRAY[®] System were used to identify certain recurrent variants that are complex in nature or are present in low copy repeats. Rare sequence variants may interfere with assay performance.

Multiplex Ligation-Dependent Probe Amplification (MLPA) (Analytical Detection Rate >99%)

MLPA[®] probe sets and reagents from MRC-Holland were used for copy number analysis of specific targets versus known control samples. False positive or negative results may occur due to rare sequence variants in target regions detected by MLPA probes. Analytical sensitivity and specificity of the MLPA method are both 99%.

For alpha thalassemia, the copy numbers of the *HBA1* and *HBA2* genes were analyzed. Alpha-globin gene deletions, triplications, and the Constant Spring (CS) mutation are assessed. This test is expected to detect approximately 90% of all alpha-thalassemia mutations, varying by ethnicity. Carriers of alpha-thalassemia with three or more *HBA* copies on one chromosome, and one or no copies on the other chromosome, may not be detected. With the exception of triplications, other benign alpha-globin gene polymorphisms will not be reported. Analyses of *HBA1* and *HBA2* are performed in association with long-range PCR of the coding regions followed by short-read sequencing.

For Duchenne muscular dystrophy, the copy numbers of all *DMD* exons were analyzed. Potentially pathogenic single exon deletions and duplications are confirmed by a second method. Analysis of *DMD* is performed in association with sequencing of the coding regions.

For congenital adrenal hyperplasia, the copy number of the *CYP21A2* gene was analyzed. This analysis can detect large deletions typically due to unequal meiotic crossing-over between *CYP21A2* and the pseudogene *CYP21A1P*. Classic 30-kb deletions make up approximately 20% of *CYP21A2* pathogenic alleles. This test may also identify certain point mutations in *CYP21A2* caused by gene conversion events between *CYP21A2* and *CYP21A1P*. Some carriers may not be identified by dosage sensitive methods as this testing cannot detect individuals with two copies (duplication) of the *CYP21A2* gene on one

chromosome and loss of *CYP21A2* (deletion) on the other chromosome. Analysis of *CYP21A2* is performed in association with long-range PCR of the coding regions followed by short-read sequencing.

For spinal muscular atrophy (SMA), the copy numbers of the *SMN1* and *SMN2* genes were analyzed. The individual dosage of exons 7 and 8 as well as the combined dosage of exons 1, 4, 6 and 8 of *SMN1* and *SMN2* were assessed. Copy number gains and losses can be detected with this assay. Depending on ethnicity, 6 - 29 % of carriers will not be identified by dosage sensitive methods as this testing cannot detect individuals with two copies (duplication) of the *SMN1* gene on one chromosome and loss of *SMN1* (deletion) on the other chromosome (silent 2+0 carrier) or individuals that carry an intragenic mutation in *SMN1*. Please also note that 2% of individuals diagnosed with SMA have a causative *SMN1* variant that occurred *de novo*, and therefore cannot be picked up by carrier screening in the parents. Analysis of *SMN1* is performed in association with short-read sequencing of exons 2a-7, followed by confirmation using long-range PCR (described below).

The presence of the c.*3+80T>G (chr5:70,247,901T>G) variant allele in an individual with Ashkenazi Jewish or Asian ancestry is typically indicative of a duplication of *SMN1*. When present in an Ashkenazi Jewish or Asian individual with two copies of *SMN1*, c.*3+80T>G is likely indicative of a silent (2+0) carrier. In individuals with two copies of *SMN1* with African American, Hispanic or Caucasian ancestry, the presence or absence of c.*3+80T>G significantly increases or decreases, respectively, the likelihood of being a silent 2+0 carrier.

MLPA for Gaucher disease (*GBA*), cystic fibrosis (*CFTR*), and non-syndromic hearing loss (*GJB2/GJB6*) will only be performed if indicated for confirmation of detected CNVs. If *GBA* analysis was performed, the copy numbers of exons 1, 3, 4, and 6 - 10 of the *GBA* gene (of 11 exons total) were analyzed. If *CFTR* analysis was performed, the copy numbers of all 27 *CFTR* exons were analyzed. If *GJB2/GJB6* analysis was performed, the copy number of the two *GJB2* exons were analyzed, as well as the presence or absence of the two upstream deletions of the *GJB2* regulatory region, del(*GJB6*-D13S1830) and del(*GJB6*-D13S1854).

Next Generation Sequencing (NGS) (Analytical Detection Rate >95%)

NGS was performed on a panel of genes for the purpose of identifying pathogenic or likely pathogenic variants.

Agilent SureSelect™XT Low Input technology was used with a custom capture library to target the exonic regions and intron/exon splice junctions of the relevant genes, as well as a number of UTR, intronic or promoter regions that contain previously reported mutations. Libraries were pooled and sequenced on the Illumina NovaSeq 9000 platform, using paired-end 100 bp reads. The sequencing data was analyzed using a custom bioinformatics algorithm designed and validated in house.

The coding exons and splice junctions of the known protein-coding RefSeq genes were assessed for the average depth of coverage (minimum of 20X) and data quality threshold values. Most exons not meeting a minimum of >20X read depth across the exon are further analyzed by Sanger sequencing. Please note that several genomic regions present difficulties in mapping or obtaining read depth >20X. These regions, which are described below, will not be reflexed to Sanger sequencing if the mapping quality or coverage is poor. Any variants identified during testing in these regions are confirmed by a second method and reported if determined to be pathogenic or likely pathogenic. However, as there is a possibility of false negative results within these regions, detection rates and residual risks for these genes have been calculated with the presumption that variants in these exons will not be detected, unless included in the MassARRAY® genotyping platform.

Exceptions: *ABCD1* (NM_000033.3) exons 8 and 9; *ADA* (NM_000022.2) exon 1; *ADAMTS2* (NM_014244.4) exon 1; *AGPS* (NM_003659.3) chr2:178,257,512 - 178,257,649 (partial exon 1); *ALMS1* (NM_015120.4) chr2:73,612,990 - 73,613,041 (partial exon 1); *CEP290* (NM_025114.3) exon 5, exon 7, chr12:88,519,017 - 88,519,039 (partial exon 13), chr12:88,514,049 - 88,514,058 (partial exon 15), chr12:88,502,837 - 88,502,841 (partial exon 23), chr12:88,481,551 - 88,481,589 (partial exon 32), chr12:88,471,605 - 88,471,700 (partial exon 40); *CFTR* (NM_000492.3) exon 10; *COL4A4* (NM_000092.4) chr2:227,942,604 - 227,942,619 (partial exon 25); *CYP11B2* (NM_000498.3) exons 3 - 7; *DNAI2* (NM_023036.4) chr17:72,308,136 - 72,308,147 (partial exon 12); *EVC* (NM_153717.2) exon 1; *FH* (NM_000143.3) exon 1; *GAMT* (NM_000156.5) exon 1; *GLDC* (NM_000170.2) exon 1; *GNPTAB* (NM_024312.4) chr17:4,837,000 - 4,837,400 (partial exon 2); *GNPTG* (NM_032520.4) exon 1; *HGSNAT* (NM_152419.2) exon 1; *IDS* (NM_000202.6) exon 3; *LIFR* (NM_002310.5) exon 19; *NEB* (NM_001271208.1) exons 82 - 105; *NPC1* (NM_000271.4) chr18:21,123,519 - 21,123,538 (partial exon 14); *PUS1* (NM_025215.5) ; chr12:132,414,446 - 132,414,532 (partial exon 2); *RPGRIP1L* (NM_015272.2) exon 23; *SGSH* (NM_000199.3) chr17:78,194,022 - 78,194,072 (partial exon 1); *SLC6A8* (NM_005629.3) exons 3 and 4.

This test will detect variants within the exons and the intron-exon boundaries of the target regions. Variants outside these regions may not be detected, including, but not limited to, UTRs, promoters, and deep intronic areas, or regions that fall into the Exceptions mentioned above. This technology may not detect all small insertion/deletions and is not diagnostic for repeat expansions and structural genomic variation. In addition, a mutation(s) in a gene not included on the panel could be present in this patient.

Variation interpretation and classification was performed based on the American College of Medical Genetics Standards and Guidelines for the Interpretation of Sequence Variants (Richards et al. 2015). All potentially pathogenic variants may be confirmed by either a specific genotyping assay or Sanger sequencing, if indicated. Any benign variants, likely benign variants or variants of uncertain significance identified during this analysis will not be reported.

Next Generation Sequencing for SMN1

Exonic regions and intron/exon splice junctions of *SMN1* and *SMN2* were captured, sequenced, and analyzed as described above. Any variants located within exons 2a-7 and classified as pathogenic or likely pathogenic were confirmed to be in either *SMN1* or *SMN2* using gene-specific long-range PCR analysis followed by Sanger sequencing. Variants located in exon 1 cannot be accurately assigned to either *SMN1* or *SMN2* using our current methodology, and so these variants are considered to be of uncertain significance and are not reported.

Copy Number Variant Analysis (Analytical Detection Rate >95%)

Large duplications and deletions were called from the relative read depths on an exon-by-exon basis using a custom exome hidden Markov model (XHMM) algorithm. Deletions or duplications determined to be pathogenic or likely pathogenic were confirmed by either a custom arrayCGH platform, quantitative PCR, or MLPA (depending on CNV size and gene content). While this algorithm is designed to pick up deletions and duplications of 2 or more exons in length, potentially pathogenic single-exon CNVs will be confirmed and reported, if detected.

Exon Array (Confirmation method) (Accuracy >99%)

The customized oligonucleotide microarray (Oxford Gene Technology) is a highly-targeted exon-focused array capable of detecting medically relevant microdeletions and microduplications at a much higher resolution than traditional aCGH methods. Each array matrix has approximately 180,000 60-mer oligonucleotide probes that cover the entire genome. This platform is designed based on human genome NCBI Build 37 (hg19) and the CGH probes are enriched to target the exonic regions of the genes in this panel.

Quantitative PCR (Confirmation method) (Accuracy >99%)

The relative quantification PCR is utilized on a Roche Universal Library Probe (UPL) system, which relates the PCR signal of the target region in one group to another. To test for genomic imbalances, both sample DNA and reference DNA is amplified with primer/probe sets that specific to the target region and a control region with known genomic copy number. Relative genomic copy numbers are calculated based on the standard $\Delta\Delta C_t$ formula.

Long-Range PCR (Analytical Detection Rate >99%)

Long-range PCR was performed to generate locus-specific amplicons for *CYP21A2*, *HBA1* and *HBA2* and *GBA*. The PCR products were then prepared for short-read NGS sequencing and sequenced. Sequenced reads were mapped back to the original genomic locus and run through the bioinformatics pipeline. If indicated, copy number from MLPA was correlated with the sequencing output to analyze the results. For *CYP21A2*, a certain percentage of healthy individuals carry a duplication of the *CYP21A2* gene, which has no clinical consequences. In cases where two copies of a gene are located on the same chromosome in tandem, only the second copy will be amplified and assessed for potentially pathogenic variants, due to size limitations of the PCR reaction. However, because these alleles contain at least two copies of the *CYP21A2* gene in tandem, it is expected that this patient has at least one functional gene in the tandem allele and this patient is therefore less likely to be a carrier. When an individual carries both a duplication allele and a pathogenic variant, or multiple pathogenic variants, the current analysis may not be able to determine the phase (cis/trans configuration) of the *CYP21A2* alleles identified. Family studies may be required in certain scenarios where phasing is required to determine the carrier status.

Residual Risk Calculations

Carrier frequencies and detection rates for each ethnicity were calculated through the combination of internal curations of >30,000 variants and genomic frequency data from >138,000 individuals across seven ethnic groups in the gnomAD database. Additional variants in HGMD and novel deleterious variants were also incorporated into the calculation. Residual risk values are calculated using a Bayesian analysis combining the *a priori* risk of being a pathogenic mutation carrier (carrier frequency) and the detection rate. They are provided only as a guide for assessing approximate risk given a negative result, and values will vary based on the exact ethnic background of an individual. This report does not represent medical advice but should be interpreted by a genetic counselor, medical geneticist or physician skilled in genetic result interpretation and the relevant medical literature.

Personalized Residual Risk Calculations

Agilent SureSelect™XT Low-Input technology was utilized in order to create whole-genome libraries for each patient sample. Libraries were then pooled and sequenced on the Illumina NovaSeq platform. Each sequencing lane was multiplexed to achieve 0.4-2x genome coverage, using paired-end 100 bp reads. The sequencing data underwent ancestral analysis using a customized, licensed bioinformatics algorithm that was validated in house. Identified sub-ethnic groupings were binned into one of 7 continental-level groups (African, East Asian, South Asian, Non-Finnish European, Finnish, Native American, and Ashkenazi Jewish) or, for those ethnicities that matched poorly to the continental-level groups, an 8th "unassigned" group, which were then used to select residual risk values for each gene. For individuals belonging to multiple high-level ethnic groupings, a weighting strategy was used to select the most appropriate residual risk. For genes that had insufficient data to calculate ethnic-specific residual risk values, or for sub-ethnic groupings that fell into the "unassigned" group, a "worldwide" residual risk was used. This "worldwide" residual risk was calculated using data from all available continental-level groups.

Sanger Sequencing (Confirmation method) (Accuracy >99%)

Sanger sequencing, as indicated, was performed using BigDye Terminator chemistry with the ABI 3730 DNA analyzer with target specific amplicons. It also may be used to supplement specific guaranteed target regions that fail NGS sequencing due to poor quality or low depth of coverage (<20 reads) or as a confirmatory method for NGS positive results. False negative results may occur if rare variants interfere with amplification or annealing.

Please note these tests were developed and their performance characteristics were determined by Mount Sinai Genomics, Inc. They have not been cleared or approved by the FDA. These analyses generally provide highly accurate information regarding the patient's carrier or affected status. Despite this high level of accuracy, it should be kept in mind that there are many potential sources of diagnostic error, including misidentification of samples, polymorphisms, or other rare genetic variants that interfere with analysis. Families should understand that rare diagnostic errors may occur for these reasons.

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Carrier Screening

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Luo M et al. An Ashkenazi Jewish SMN1 haplotype specific to duplication alleles improves pan-ethnic carrier screening for spinal muscular atrophy. *Genet Med.* 2014 16:149-56.

Ashkenazi Jewish Disorders:

Scott SA et al. Experience with carrier screening and prenatal diagnosis for sixteen Ashkenazi Jewish Genetic Diseases. *Hum. Mutat.* 2010 31:1-11.

Duchenne Muscular Dystrophy:

Flanigan KM et al. Mutational spectrum of DMD mutations in dystrophinopathy patients: application of modern diagnostic techniques to a large cohort. *Hum Mutat.* 2009 30:1657-66.

Variant Classification:

Richards S et al. Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. *Genet Med.* 2015 May;17(5):405-24

Additional disease-specific references available upon request.

Patient Information

Name: Donor 6424
 Date of Birth: [REDACTED]
 Sema4 ID: [REDACTED]
 Client ID: [REDACTED]
 Indication: Carrier Screening

Specimen Information

Specimen Type: Purified DNA
 Date Collected: 11/09/2022
 Date Received: 11/09/2022
 Final Report: 11/30/2022

Referring Provider

[REDACTED]
 Fairfax Cryobank, Inc.
 [REDACTED]
 [REDACTED]

Custom Carrier Screen (1 gene)
 with Personalized Residual Risk

SUMMARY OF RESULTS AND RECOMMENDATIONS

⊖ Negative

Negative for all genes tested: *COL11A2*
 To view a full list of genes and diseases tested
 please see Table 1 in this report

AR=Autosomal recessive; XL=X-linked

Recommendations

- Consideration of residual risk by ethnicity after a negative carrier screen is recommended for the other diseases on the panel, especially in the case of a positive family history for a specific disorder. Please note that residual risks for X-linked diseases (including full repeat expansions for Fragile X syndrome) may not be accurate for males and the actual residual risk is likely to be lower.
- As genetic technologies may improve and variant classifications may change over time, it is recommended to obtain a new carrier screening test or reanalysis when a new pregnancy is being considered.

Test description

This patient was tested for the genes listed above using one or more of the following methodologies: target capture and short-read sequencing, long-range PCR followed by short-read sequencing, targeted genotyping, and/or copy number analysis. Please note that negative results reduce but do not eliminate the possibility that this individual is a carrier for one or more of the disorders tested. Please see Table 1 for a list of genes and diseases tested with the patient's personalized residual risk. If personalized residual risk is not provided, please see the complete residual risk table at go.sema4.com/residualrisk. Only known pathogenic or likely pathogenic variants are reported. This carrier screening test does not report likely benign variants and variants of uncertain significance (VUS). If reporting of likely benign variants and VUS are desired in this patient, please contact the laboratory at 800-298-6470, option 2 to request an amended report.



Anastasia Larmore, Ph.D., Associate Laboratory Director

Genes and diseases tested

The personalized residual risks listed below are specific to this individual. The complete residual risk table is available at go.sema4.com/residualrisk

Table 1: List of genes and diseases tested with detailed results

| Disease | Gene | Inheritance Pattern | Status | Detailed Summary |
|---|---------|---------------------|--------------|--|
| ⊖ Negative | | | | |
| Otospondylomegapiphyseal Dysplasia / Deafness / Fibrochondrogenesis 2 | COL11A2 | AR | Reduced Risk | Personalized Residual Risk: 1 in 2,700 |

AR=Autosomal recessive; XL=X-linked

Test methods and comments

Genomic DNA isolated from this patient was analyzed by one or more of the following methodologies, as applicable:

Fragile X CGG Repeat Analysis (Analytical Detection Rate >99%)

PCR amplification using Asuragen, Inc. AmpliDeX[®] *FMR1* PCR reagents followed by capillary electrophoresis for allele sizing was performed. Samples positive for *FMR1* premutations and full mutations greater than 90 CGG repeats in length were further analyzed by Southern blot analysis or methylation PCR to assess the size and methylation status of the *FMR1* CGG repeat. Additional testing to determine the status of AGG interruptions within the *FMR1* CGG repeat will be automatically performed for premutation alleles ranging from 55 to 90 repeats. These results, which may modify risk for expansion, will follow in a separate report.

Genotyping (Analytical Detection Rate >99%)

Multiplex PCR amplification and single-base pair probe extension analyses using the Agena Bioscience iPLEX Pro chemistry on a MassARRAY[®] System were used to identify certain recurrent variants that are complex in nature or are present in low copy repeats. Rare sequence variants may interfere with assay performance.

Multiplex Ligation-Dependent Probe Amplification (MLPA) (Analytical Detection Rate >99%)

Conventional MLPA and/or digitalMLPA[®] probe sets and reagents from MRC-Holland were used for copy number variations (CNVs) analysis of specific targets versus known control samples. digitalMLPA[®] is a semi-quantitative technique, based on the well-established conventional MLPA method, followed by Illumina based sequencing to determine read number for amplicon quantification. False positive or negative results may occur due to rare sequence variants in target regions detected by conventional MLPA or digitalMLPA[®] probes. Analytical sensitivity and specificity of both the conventional MLPA method and the digitalMLPA[®] method are greater than 99%.

For alpha thalassemia, the copy numbers of the *HBA1* and *HBA2* genes were analyzed. Alpha-globin gene deletions, duplications, and the Constant Spring (CS) mutation are assessed. This test is expected to detect approximately 90% of all alpha-thalassemia mutations, varying by ethnicity. Carriers of alpha-thalassemia with three or more *HBA* copies on one chromosome, and one or no copies on the other chromosome, may not be precisely specified without phase analysis. With the exception of duplications, other benign alpha-globin gene polymorphisms will not be reported. Analyses of *HBA1* and *HBA2* are performed in association with long-range PCR of the coding regions followed by short-read sequencing.

For Duchenne muscular dystrophy, the copy numbers of all *DMD* exons were analyzed. Potentially pathogenic single exon deletions and duplications are confirmed by a second method. Analysis of *DMD* is performed in association with sequencing of the coding regions.

For congenital adrenal hyperplasia, the copy number of the *CYP21A2* gene was analyzed. This analysis can detect large deletions typically due to unequal meiotic crossing-over between *CYP21A2* and the pseudogene *CYP21A1P*. Classic 30-kb deletions make up approximately 20% of *CYP21A2* pathogenic alleles. This test may also identify certain point mutations in *CYP21A2* caused by gene conversion events between *CYP21A2* and *CYP21A1P*. Some carriers may not be identified by dosage sensitive methods as this testing cannot detect individuals with two copies (duplication) of the *CYP21A2* gene on one chromosome and loss of *CYP21A2* (deletion) on the other chromosome. Analysis of *CYP21A2* is performed in association with long-range PCR of the coding regions followed by short-read sequencing.

For spinal muscular atrophy (SMA), the copy numbers of the *SMN1* and *SMN2* genes were analyzed. The individual dosage of exons 7 and 8 as well as the combined dosage of exons 1, 4, 6 and 8 of *SMN1* and *SMN2* were assessed. Copy number gains and losses can be detected. Depending on ethnicity, 6 - 29 % of carriers will not be identified by dosage sensitive methods as this testing cannot distinguish individuals with two copies (duplication) of the *SMN1* gene on one chromosome and loss of *SMN1* (deletion) on the other chromosome (silent 2+0 carrier) or identify intragenic mutation in *SMN1*. Please also note that 2% of individuals diagnosed with SMA have a causative *SMN1* variant that occurred de novo, therefore cannot be picked up by carrier screening in the parents. Analysis of *SMN1* is performed in association with short-read sequencing of exons 2a-7, followed by confirmation using long-range PCR (described below).

In individuals with two copies of *SMN1* with Ashkenazi Jewish, East Asian, African American, Native American or Caucasian ancestry, the presence or absence of c.3+80T>G significantly increases or decreases, respectively, the likelihood of being a silent 2+0 silent carrier.

MLPA for Gaucher disease (*GBA*), cystic fibrosis (*CFTR*), and non-syndromic hearing loss (*GJB2/GJB6*) will only be performed if indicated for confirmation of detected CNVs. If *GBA* analysis was performed, the copy numbers of exons 1, 3, 4, and 6 - 10 of the *GBA* gene (of 11 exons total) were analyzed. If *CFTR* analysis was performed, the copy numbers of all 27 *CFTR* exons were analyzed. If *GJB2/GJB6* analysis was performed, the copy number of the two *GJB2* exons were analyzed, as well as the presence or absence of the two upstream deletions of the *GJB2* regulatory region, del(*GJB6*-D13S1830) and del(*GJB6*-D13S1854).

Next Generation Sequencing (NGS) (Analytical Detection Rate >95%)

NGS was performed on a panel of genes for the purpose of identifying pathogenic or likely pathogenic variants.

Agilent SureSelect™XT Low Input technology was used with a custom capture library to target the exonic regions and intron/exon splice junctions of the relevant genes, as well as a number of UTR, intronic or promoter regions that contain previously reported mutations. Libraries were pooled and sequenced on the Illumina NovaSeq 6000 platform, using paired-end 100 bp reads. The sequencing data was analyzed using a custom bioinformatics algorithm designed and validated in house.

The coding exons and splice junctions of the known protein-coding RefSeq genes were assessed for the average depth of coverage (minimum of 20X) and data quality threshold values. Most exons not meeting a minimum of >20X read depth across the exon are further analyzed by Sanger sequencing. Please note that several genomic regions present difficulties in mapping or obtaining read depth >20X. These regions, which are described below, will not be reflexed to Sanger sequencing if the mapping quality or coverage is poor. Any variants identified during testing in these regions are confirmed by a second method and reported if determined to be pathogenic or likely pathogenic. However, as there is a possibility of false negative results within these regions, detection rates and residual risks for these genes have been calculated with the presumption that variants in these exons will not be detected, unless included in the MassARRAY® genotyping platform.

Exceptions: *ABCD1* (NM_000033.3) exons 8 and 9; *ACADSB* (NM_001609.3) chr10:124,810,695-124,810,707 (partial exon 9); *ADA* (NM_000022.2) exon 1; *ADAMTS2* (NM_014244.4) exon 1; *AGPS* (NM_003659.3) chr2:178,257,512-178,257,649 (partial exon 1); *ALDH7A1* (NM_001182.4) chr5:125,911,150-125,911,163 (partial exon 7) and chr5:125,896,807-125,896,821 (partial exon 10); *ALMS1* (NM_015120.4) chr2:73,612,990-73,613,041 (partial exon 1); *APOPT1* (NM_032374.4) chr14:104,040,437-104,040,455 (partial exon 3); *CDAN1* (NM_138477.2) exon 2; *CEP152* (NM_014985.3) chr15:49,061,146-49,061,165 (partial exon 14) and exon 22; *CEP290* (NM_025114.3) exon 5, exon 7, chr12:88,519,017-88,519,039 (partial exon 13), chr12:88,514,049-88,514,058 (partial exon 15), chr12:88,502,837-88,502,841 (partial exon 23), chr12:88,481,551-88,481,589 (partial exon 32), chr12:88,471,605-88,471,700 (partial exon 40); *CFTR* (NM_000492.3) exon 10; *COL4A4* (NM_000092.4) chr2:227,942,604-227,942,619 (partial exon 25); *COX10* (NM_001303.3) exon 6; *CYP11B1* (NM_000497.3) exons 3-7; *CYP11B2* (NM_000498.3) exons 3-7; *DNAI2* (NM_023036.4) chr17:72,308,136-72,308,147 (partial exon 12); *DOK7* (NM_173660.4) chr4:3,465,131-3,465,161 (partial exon 1) and exon 2; *DUOX2* (NM_014080.4) exons 6-8; *EIF2AK3* (NM_004836.5) exon 8; *EVC* (NM_153717.2) exon 1; *F5* (NM_000130.4) chr1:169,551,662-169,551,679 (partial exon 2); *FH* (NM_000143.3) exon 1; *GAMT* (NM_000156.5) exon 1; *GLDC* (NM_000170.2) exon 1; *GNPTAB* (NM_024312.4) chr17:4,837,000-4,837,400 (partial exon 2); *GNPTG* (NM_032520.4) exon 1; *GHR* (NM_000163.4) exon 3; *GYS2* (NM_021957.3) chr12:21,699,370-21,699,409 (partial exon 12); *HGSNAT* (NM_152419.2) exon 1; *IDS* (NM_000202.6) exon 3; *ITGB4* (NM_000213.4) chr17:73,749,976-73,750,060 (partial exon 33); *JAK3* (NM_000215.3) chr19:17,950,462-17,950,483 (partial exon 10); *LIFR* (NM_002310.5) exon 19; *LMBRD1* (NM_018368.3) chr6:70,459,226-70,459,257 (partial exon 5), chr6:70,447,828-70,447,836 (partial exon 7) and exon 12; *LYST* (NM_000081.3) chr1:235,944,158-235,944,176 (partial exon 16) and chr1:235,875,350-235,875,362 (partial exon 43); *MLYCD* (NM_012213.2) chr16:83,933,242-83,933,282 (partial exon 1); *MTR* (NM_000254.2) chr1:237,024,418-237,024,439 (partial exon 20) and chr1:237,038,019-237,038,029 (partial exon 24); *NBEAL2* (NM_015175.2) chr3:47,021,385-47,021,407 (partial exon 1); *NEB* (NM_001271208.1) exons 82-105; *NPC1* (NM_000271.4) chr18:21,123,519-21,123,538 (partial exon 14); *NPHP1* (NM_000272.3) chr2:110,937,251-110,937,263 (partial exon 3); *OCRL* (NM_000276.3) chrX:128,674,450-128,674,460 (partial exon 1); *PHKB* (NM_000293.2) exon 1 and chr16:47,732,498-47,732,504 (partial exon 30); *PIGN* (NM_176787.4) chr18:59,815,547-59,815,576 (partial exon 8); *PIP5K1C* (NM_012398.2) exon 1 and chr19:3637602-3637616 (partial exon 17); *POU1F1* (NM_000306.3) exon 5; *PTPRC* (NM_002838.4) exons 11 and 23; *PUS1* (NM_025215.5) chr12:132,414,446-132,414,532 (partial exon 2); *RPGRIP1L* (NM_015272.2) exon 23; *SGSH* (NM_000199.3) chr17:78,194,022-78,194,072 (partial exon 1); *SLC6A8* (NM_005629.3) exons 3 and 4; *ST3GAL5* (NM_003896.3) exon 1; *SURF1* (NM_003172.3) chr9:136,223,269-136,223,307 (partial exon 1); *TRPM6* (NM_017662.4) chr9:77,362,800-77,362,811 (partial exon 31); *TSEN54*

(NM_207346.2) exon 1; *TYR* (NM_000372.4) exon 5; *VWF* (NM_000552.3) exons 24-26, chr12:6,125,675-6,125,684 (partial exon 30), chr12:6,121,244-6,121,265 (partial exon 33), and exon 34.

This test will detect variants within the exons and the intron-exon boundaries of the target regions. Variants outside these regions may not be detected, including, but not limited to, UTRs, promoters, and deep intronic areas, or regions that fall into the Exceptions mentioned above. This technology may not detect all small insertion/deletions and is not diagnostic for repeat expansions and structural genomic variation. In addition, a mutation(s) in a gene not included on the panel could be present in this patient.

Variant interpretation and classification was performed based on the American College of Medical Genetics Standards and Guidelines for the Interpretation of Sequence Variants (Richards et al, 2015). All potentially pathogenic variants may be confirmed by either a specific genotyping assay or Sanger sequencing, if indicated. Any benign variants, likely benign variants or variants of uncertain significance identified during this analysis will not be reported.

Next Generation Sequencing for *SMN1*

Exonic regions and intron/exon splice junctions of *SMN1* and *SMN2* were captured, sequenced, and analyzed as described above. Any variants located within exons 2a-7 and classified as pathogenic or likely pathogenic were confirmed to be in either *SMN1* or *SMN2* using gene-specific long-range PCR analysis followed by Sanger sequencing. Variants located in exon 1 cannot be accurately assigned to either *SMN1* or *SMN2* using our current methodology, and so these variants are not reported.

Copy Number Variant (CNV) Analysis (Analytical Detection Rate >98% for CNVs of 3 exons and larger, >90% for CNVs of 2 exons)

Large duplications and deletions were called from the relative read depths on an exon-by-exon basis using a custom exome hidden Markov model (XHMM) algorithm. Deletions or duplications determined to be pathogenic or likely pathogenic were confirmed by either a custom arrayCGH platform, quantitative PCR, or MLPA (depending on CNV size and gene content). While this algorithm is designed to pick up deletions and duplications of 2 or more exons in length, potentially pathogenic single-exon CNVs will be confirmed and reported, if detected. Deletions and duplications near the lower limit of detection may not be detected due to run variability. Genomic regions with high homology or highly repetitive sequences are excluded from this analysis.

Exon Array Comparative Genomic Hybridization (aCGH) (Confirmation method) (Accuracy >99%)

The customized oligonucleotide microarray (Oxford Gene Technology) is a highly-targeted exon-focused array capable of detecting medically relevant microdeletions and microduplications at a much higher resolution than traditional aCGH methods. Each array matrix has approximately 1,000,000 60-mer oligonucleotide probes that cover the entire genome. This platform is designed based on human genome NCBI Build 37 (hg19) and the CGH probes are enriched to target the exonic regions of the genes in this panel.

Quantitative PCR (Confirmation method) (Accuracy >99%)

The relative quantification PCR is utilized on a Roche SYBR Green reagents on a LightCycler[®] 480 System, which relates the PCR signal of the target region in one group to another. To test for genomic imbalances, both sample DNA and reference DNA is amplified with primer/probe sets that specific to the target region and a control region with known genomic copy number. Relative genomic copy numbers are calculated based on the standard $\Delta\Delta C_t$ formula.

Long-Range PCR (Analytical Detection Rate >99%)

Long-range PCR was performed to generate locus-specific amplicons for *CYP21A2*, *HBA1* and *HBA2* and *GBA*. The PCR products were then prepared for short-read NGS sequencing and sequenced. Sequenced reads were mapped back to the original genomic locus and run through the bioinformatics pipeline. If indicated, copy number from MLPA was correlated with the sequencing output to analyze the results. Please note that in rare cases, allele drop-out may occur, which has the potential to lead to false negative results. For *CYP21A2*, a certain percentage of healthy individuals carry a duplication of the *CYP21A2* gene, which has no clinical consequences. In cases where multiple copies of *CYP21A2* are located on the same chromosome in tandem, only the last copy will be amplified and assessed for potentially pathogenic variants, due to size limitations of the PCR reaction. However, because these alleles contain at least two copies of the *CYP21A2* gene in tandem, it is expected that this patient has at least one functional gene in the tandem allele and this patient is therefore less likely to be a carrier. A *CYP21A1P/CYP21A2* hybrid gene detected only by MLPA but not by long-range PCR will not be reported when the long-range PCR indicates the presence of two full *CYP21A2* gene copies (one on each chromosome), as the additional hybrid gene is nonfunctional. Classic 30-kb deletions are identified by MLPA and are also identified by the presence of multiple common pathogenic *CYP21A2* variants by long-range PCR. Since multiple pseudogene-derived variants are detected in all cases with the classic 30kb deletion, we cannot rule out the possibility that some variant(s) detected could be present in trans with the chimeric *CYP21A1P/CYP21A2* gene created by the 30kb deletion. When an individual carries both a duplication allele and a pathogenic variant, or multiple pathogenic variants, the current analysis may not be able to determine the phase (cis/trans configuration) of the *CYP21A2* alleles identified. Family studies may be required in certain scenarios where phasing is required to determine the carrier status.

Residual Risk Calculations

Carrier frequencies and detection rates for each ethnicity were calculated through the combination of internal curations of >30,000 variants and genomic frequency data from >138,000 individuals across seven ethnic groups in the gnomAD database. Additional variants in HGMD and novel deleterious variants were also incorporated into the calculation. Residual risk values are calculated using a Bayesian analysis combining the a priori risk of being a pathogenic mutation carrier (carrier frequency) and the detection rate. They are provided only as a guide for assessing approximate risk given a negative result, and values will vary based on the exact ethnic background of an individual. This report does not represent medical advice but should be interpreted by a genetic counselor, medical geneticist or physician skilled in genetic result interpretation and the relevant medical literature.

Personalized Residual Risk Calculations

Agilent SureSelect™XT Low-Input technology was utilized in order to create whole-genome libraries for each patient sample. Libraries were then pooled and sequenced on the Illumina NovaSeq platform. Each sequencing lane was multiplexed to achieve 0.4-2x genome coverage, using paired-end 100 bp reads. The sequencing data underwent ancestral analysis using a customized, licensed bioinformatics algorithm that was validated in house. Identified sub-ethnic groupings were binned into one of 7 continental-level groups (African, East Asian, South Asian, Non-Finnish European, Finnish, Native American, and Ashkenazi Jewish) or, for those ethnicities that matched poorly to the continental-level groups, an 8th "unassigned" group, which were then used to select residual risk values for each gene. For individuals belonging to multiple high-level ethnic groupings, a weighting strategy was used to select the most appropriate residual risk. For genes that had insufficient data to calculate ethnic-specific residual risk values, or for sub-ethnic groupings that fell into the "unassigned" group, a "worldwide" residual risk was used. This "worldwide" residual risk was calculated using data from all available continental-level groups.

Several genes have multiple residual risks associated to reflect the likelihood of the tested individual being a carrier for different diseases that are attributed to non-overlapping pathogenic variants in that gene. When calculating the couples' combined reproductive risk, the highest residual risk for each patient was selected.

Sanger Sequencing (Confirmation method) (Accuracy >99%)

Sanger sequencing, as indicated, was performed using BigDye Terminator chemistry with the ABI 3730 DNA analyzer with target specific amplicons. It also may be used to supplement specific guaranteed target regions that fail NGS sequencing due to poor quality or low depth of coverage (<20 reads) or as a confirmatory method for NGS positive results. False negative results may occur if rare variants interfere with amplification or annealing.

Tay-Sachs Disease (TSD) Enzyme Analysis (Analytical Detection Rate ≥98%)

Hexosaminidase activity and Hex A% activity were measured by a standard heat-inactivation, fluorometric method using artificial 4-MU-β-N-acetyl glucosaminide (4-MUG) substrate. This assay is highly sensitive and accurate in detecting Tay-Sachs carriers and individuals affected with TSD. Normal ranges of Hex A% activity are 55.0-72.0 for white blood cells and 58.0-72.0 for plasma. It is estimated that less than 0.5% of Tay-Sachs carriers have non-carrier levels of percent Hex A activity, and therefore may not be identified by this assay. In addition, this assay may detect individuals that are carriers of or are affected with Sandhoff disease. False positive results may occur if benign variants, such as pseudodeficiency alleles, interfere with the enzymatic assay. False negative results may occur if both *HEXA* and *HEXB* pathogenic or pseudodeficiency variants are present in the same individual.

Please note that it is not possible to perform Tay-Sachs disease enzyme analysis on saliva samples, buccal swabs, tissue samples, semen samples, or on samples received as extracted DNA.

This test was developed, and its performance characteristics determined by Sema4 Opco, Inc. It has not been cleared or approved by the US Food and Drug Administration. FDA does not require this test to go through premarket FDA review. This test is used for clinical purposes. It should not be regarded as investigational or for research. This laboratory is certified under the Clinical Laboratory Improvement Amendments (CLIA) as qualified to perform high complexity clinical laboratory testing. These analyses generally provide highly accurate information regarding the patient's carrier or affected status. Despite this high level of accuracy, it should be kept in mind that there are many potential sources of diagnostic error, including misidentification of samples, polymorphisms, or other rare genetic variants that interfere with analysis. Families should understand that rare diagnostic errors may occur for these reasons.

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Additional disease-specific references available upon request.



Patient Information:

6424, Donor

DOB: [REDACTED]

Sex: M

MR#: 6424

Patient#: [REDACTED]

Accession:

[REDACTED]

Test#: [REDACTED]

Order#: [REDACTED]

Ext Test#: [REDACTED]

Ext Order#: [REDACTED]

Specimen Type: DNA

Collected: Not provided

Received Date: Jul 28,2023

Authorized Date: Aug 07,2023

Physician:

Seitz, Suzanne

ATTN: Seitz, Suzanne

Fairfax Cryobank

3015 Williams Drive

Fairfax, VA 22031

Phone:

Fax:

Laboratory:

Fulgent Genetics

CAP#: 8042697

CLIA#: 05D2043189

Laboratory Director:

Dr. Hanlin (Harry) Gao

Report Date: **Aug 27,2023**

Final Report

TEST PERFORMED

FMN2 Single Gene

(1 Gene Panel: *FMN2*; gene sequencing with deletion and duplication analysis)

RESULTS:

No clinically significant sequence or copy-number variants 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 of the sort not queried by this test or in areas not reliably assessed by this test.

INTERPRETATION:

Notes and Recommendations:

- 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>)

GENES TESTED:

FMN2 Single Gene

1 genes tested (99.75% at >20x).

FMN2

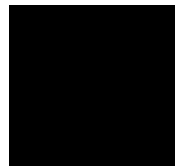
Gene Specific Notes and Limitations

No gene specific limitations apply to the genes on the tested panel.

METHODS:

Patient: 6424, Donor; Sex: M;
DOB: [REDACTED] MR#: 6424

Accession#: [REDACTED]; FD Patient# [REDACTED];



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, 99.75% and 99.75% 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. New York patients: diagnostic findings are confirmed by Sanger, MLPA, or qPCR; exception SNV variants in genes for which confirmation of NGS results has been performed ≥ 10 times may not be confirmed if identified with high quality by NGS. Bioinformatics: The Fulgent Germline v2019.2 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, 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 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:

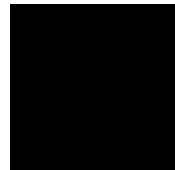


Yan Meng, Ph.D., CGMB, FACMG on 8/27/2023 03:05 PM PDT
Electronically signed



DISCLAIMER:

This test was developed and its performance characteristics determined by **Fulgent Genetics**. 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.



Patient Information:

6424, Donor

DOB: [REDACTED]

Sex: M

MR#: 6424

Patient#: [REDACTED]

Accession:

[REDACTED]

Test#: [REDACTED]

Order#: [REDACTED]

Ext Test#: [REDACTED]

Ext Order#: [REDACTED]

Specimen Type: DNA

Collected: Not provided

Received Date: Jul 28,2023

Authorized Date: Aug 04,2023

Physician:

Seitz, Suzanne

ATTN: Seitz, Suzanne

Fairfax Cryobank

3015 Williams Drive

Fairfax, VA 22031

Phone:

Fax:

Laboratory:

Fulgent Genetics

CAP#: 8042697

CLIA#: 05D2043189

Laboratory Director:

Dr. Hanlin (Harry) Gao

Report Date: **Aug 27,2023**

Final Report

TEST PERFORMED

TYR Single Gene

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

RESULTS:

No clinically significant sequence or copy-number variants 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 of the sort not queried by this test or in areas not reliably assessed by this test.

INTERPRETATION:

Notes and Recommendations:

- 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#hpep>)

GENES TESTED:

TYR Single Gene

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

TYR

Gene Specific Notes and Limitations

No gene specific limitations apply to the genes on the tested panel.

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. New York patients: diagnostic findings are confirmed by Sanger, MLPA, or qPCR; exception SNV variants in genes for which confirmation of NGS results has been performed ≥ 10 times may not be confirmed if identified with high quality by NGS. Bioinformatics: The Fulgent Germline v2019.2 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, 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 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:



A handwritten signature in black ink, appearing to read 'Yan Meng'.

Yan Meng, Ph.D., CGMB, FACMG on 8/27/2023 03:06 PM PDT
Electronically signed



DISCLAIMER:

This test was developed and its performance characteristics determined by **Fulgent Genetics**. 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.



Patient Information:

6424, Donor

DOB: [REDACTED]

Sex: M

MR#: 6424

Patient#: [REDACTED]

Partner Information:

Not Tested

Physician:

Seitz, Suzanne

ATTN: Seitz, Suzanne

Fairfax Cryobank

3015 Williams Drive

Fairfax, VA 22031

Laboratory:

Fulgent Therapeutics LLC

CAP#: 8042697

CLIA#: 05D2043189

Laboratory Director:

Lawrence M. Weiss, MD

Report Date: Jun 12, 2024

Accession:

[REDACTED]

Test# [REDACTED]

Specimen Type: DNA

Collected: Not Provided

Accession:

N/A

FINAL RESULTS



No carrier mutations identified

TEST PERFORMED

Single Gene Carrier Screening: SERPINA1

(1 Gene Panel: *SERPINA1*; 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.
- 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.
- 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>)



GENES TESTED:

Custom Beacon Carrier Screening Panel - Gene

This analysis was run using the Custom Beacon Carrier Screening Panel gene list. 1 genes were tested with 100.0% of targets sequenced at >20x coverage. For more gene-specific information and assistance with residual risk calculation, see the SUPPLEMENTAL TABLE.

SERPINA1

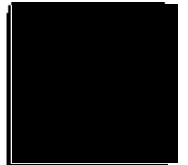
METHODS:

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 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 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

SERPINA1: If detected the variant NM_000295.5:c.863A>T (p.Glu288Val) will not be reported as this variant is associated with low disease penetrance and is not associated with severe early onset disease.

SIGNATURE:



A handwritten signature in black ink that reads "Harry Gao".

Dr. Harry Gao, DABMG, FACMG on 6/12/2024
Laboratory Director, Fulgent

DISCLAIMER:

This test was developed and its performance characteristics determined by **Fulgent Therapeutics LLC**. 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.

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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](#)



Patient: 6424, Donor; Sex: M;
DOB: [REDACTED] MR#: 6424

Accession#: [REDACTED] FD Patient#: [REDACTED]
DocID: [REDACTED] PAGE 4 of 4