



## Donor 6747

### Genetic Testing Summary

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

Last Updated: 12/12/24

Donor Reported Ancestry: English, Scottish, Irish

Jewish Ancestry: No

Genetic Test*	Result	Comments/Donor's Residual Risk**
Chromosome analysis (karyotype)	Normal male karyotype	No evidence of clinically significant chromosome abnormalities
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
Spinal Muscular Atrophy (SMA) carrier screening	Negative for deletions of exon 7 and gene sequencing in the SMN1 gene	1/1107
Expanded Genetic Disease Carrier Screening Panel attached- 283 diseases by gene sequencing	Carrier: Primary Hyperoxaluria, Type 3 (HOGA1)  Negative for other genes sequenced	Partner testing recommended before using this donor.
<b>Special Testing</b>		
Genes: POLG, AMN, MRE11, CC2D2A, NAGA, SERPINA1, GALNT3, MYO15A, AP4E1, MARS2, TSEN2, TNXB, BBS9	Negative by gene sequencing	See attached reports

\*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 6747  
 Date of Birth: [REDACTED]  
 Sema4 ID: [REDACTED]  
 Client ID: [REDACTED]  
 Indication: Carrier Screening

**Specimen Information**

Specimen Type: Blood  
 Date Collected: 11/05/2021  
 Date Received: 11/06/2021  
 Final Report: 11/22/2021

**Referring Provider**

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

Expanded Carrier Screen Minus TSE (283 genes)  
 with Personalized Residual Risk

**SUMMARY OF RESULTS AND RECOMMENDATIONS**

⊕ Positive	⊖ Negative
<p><b>Carrier of Primary Hyperoxaluria, Type 3 (AR)</b>            Associated gene(s): <i>HOGA1</i>            Variant(s) Detected: c.208C&gt;T, p.R70X, Pathogenic,            Heterozygous (one copy)</p>	<p><b>Negative for all other genes tested</b>            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

**Primary Hyperoxaluria, Type 3 (AR)**

**Results and Interpretation**

A heterozygous (one copy) pathogenic premature stop codon, c.208C>T, p.R70X, was detected in the *HOGA1* gene (NM\_138413.3). When this variant is present in trans with a pathogenic variant, it is considered to be causative for primary hyperoxaluria, type 3. Therefore, this individual is expected to be at least a carrier for primary hyperoxaluria, type 3. Heterozygous carriers are not expected to exhibit symptoms of this disease.

**What is Primary Hyperoxaluria, Type 3?**

Primary hyperoxaluria, type 3 is an autosomal recessive disease caused by pathogenic variants in the *HOGA1* gene. While it has been diagnosed in patients of various ethnicities, it may be more prevalent in individuals of Ashkenazi Jewish descent due to the presence of a founder mutation. Age of onset is typically in childhood, and the disease is characterized by the accumulation of calcium oxalate in the kidney and urinary tract, leading to kidney stone formation. Some patients have a milder phenotype where they do not develop kidney stones. Life expectancy is not thought to be affected, and no genotype-phenotype correlation has been reported.



## 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 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](https://go.sema4.com/residualrisk). Only variants determined to be pathogenic or likely pathogenic are reported in this carrier screening test.

**Alice Tanner, Ph.D., M.S., CGC, FACMG, Laboratory Director**

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

## 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](https://go.sema4.com/residualrisk)

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

Disease	Gene	Inheritance Pattern	Status	Detailed Summary
<b>Positive</b>				
Primary Hyperoxaluria, Type 3	HOGA1	AR	Carrier	c.208C>T, p.R70X, Pathogenic, Heterozygous (one copy)
<b>Negative</b>				
3-Beta-Hydroxysteroid Dehydrogenase Type II Deficiency	HSD3B2	AR	Reduced Risk	Personalized Residual Risk: 1 in 3,300
3-Methylcrotonyl-CoA Carboxylase Deficiency (MCCC1-Related)	MCCC1	AR	Reduced Risk	Personalized Residual Risk: 1 in 3,400
3-Methylcrotonyl-CoA Carboxylase Deficiency (MCCC2-Related)	MCCC2	AR	Reduced Risk	Personalized Residual Risk: 1 in 1,200
3-Methylglutaconic Aciduria, Type III	OPA3	AR	Reduced Risk	Personalized Residual Risk: 1 in 50,000
3-Phosphoglycerate Dehydrogenase Deficiency	PHGDH	AR	Reduced Risk	Personalized Residual Risk: 1 in 63,000
6-Pyruvoyl-Tetrahydropterin Synthase Deficiency	PTS	AR	Reduced Risk	Personalized Residual Risk: 1 in 1,800
Abetalipoproteinemia	MTTP	AR	Reduced Risk	Personalized Residual Risk: 1 in 3,200
Achromatopsia (CNGB3-related)	CNGB3	AR	Reduced Risk	Personalized Residual Risk: 1 in 8,600
Acrodermatitis Enteropathica	SLC39A4	AR	Reduced Risk	Personalized Residual Risk: 1 in 12,000
Acute Infantile Liver Failure	TRMU	AR	Reduced Risk	Personalized Residual Risk: 1 in 9,400
Acyl-CoA Oxidase I Deficiency	ACOX1	AR	Reduced Risk	Personalized Residual Risk: 1 in 39,000
Adenosine Deaminase Deficiency	ADA	AR	Reduced Risk	Personalized Residual Risk: 1 in 5,100
Adrenoleukodystrophy, X-Linked	ABCD1	XL	Reduced Risk	Personalized Residual Risk: 1 in 19,000
Aicardi-Goutieres Syndrome (SAMHD1-Related)	SAMHD1	AR	Reduced Risk	Personalized Residual Risk: 1 in 10,000
Alpha-Mannosidosis	MAN2B1	AR	Reduced Risk	Personalized Residual Risk: 1 in 6,200
Alpha-Thalassemia	HBA1/HBA2	AR	Reduced Risk	HBA1 Copy Number: 2 HBA2 Copy Number: 2 No pathogenic copy number variants detected HBA1/HBA2 Sequencing: Negative Personalized Residual Risk: 1 in 10,000
Alpha-Thalassemia Intellectual Disability Syndrome	ATRX	XL	Reduced Risk	Personalized Residual Risk: 1 in 48,000
Alport Syndrome (COL4A3-Related)	COL4A3	AR	Reduced Risk	Personalized Residual Risk: 1 in 1,800
Alport Syndrome (COL4A4-Related)	COL4A4	AR	Reduced Risk	Personalized Residual Risk: 1 in 1,800
Alport Syndrome (COL4A5-Related)	COL4A5	XL	Reduced Risk	Personalized Residual Risk: 1 in 150,000
Alstrom Syndrome	ALMS1	AR	Reduced Risk	Personalized Residual Risk: 1 in 3,800
Andermann Syndrome	SLC12A6	AR	Reduced Risk	Personalized Residual Risk: 1 in 151,000
Argininosuccinic Aciduria	ASL	AR	Reduced Risk	Personalized Residual Risk: 1 in 1,200
Aromatase Deficiency	CYP19A1	AR	Reduced Risk	Personalized Residual Risk: 1 in 5,400
Arthrogryposis, Mental Retardation, and Seizures	SLC35A3	AR	Reduced Risk	Personalized Residual Risk: 1 in 454,000
Asparagine Synthetase Deficiency	ASNS	AR	Reduced Risk	Personalized Residual Risk: 1 in 202,000
Aspartylglycosaminuria	AGA	AR	Reduced Risk	Personalized Residual Risk: 1 in 13,000
Ataxia With Isolated Vitamin E Deficiency	TTPA	AR	Reduced Risk	Personalized Residual Risk: 1 in 61,000
Ataxia-Telangiectasia	ATM	AR	Reduced Risk	Personalized Residual Risk: 1 in 1,300

Autosomal Recessive Spastic Ataxia of Charlevoix-Saguenay	<i>SACS</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 2,600
Bardet-Biedl Syndrome ( <i>BBS10</i> -Related)	<i>BBS10</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 2,700
Bardet-Biedl Syndrome ( <i>BBS12</i> -Related)	<i>BBS12</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 9,900
Bardet-Biedl Syndrome ( <i>BBS1</i> -Related)	<i>BBS1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 6,400
Bardet-Biedl Syndrome ( <i>BBS2</i> -Related)	<i>BBS2</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,200
Bare Lymphocyte Syndrome, Type II	<i>CIITA</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 35,000
Bartter Syndrome, Type 4A	<i>BSND</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 91,000
Bernard-Soulier Syndrome, Type A1	<i>GP1BA</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 42,000
Bernard-Soulier Syndrome, Type C	<i>GP9</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 3,300
Beta-Globin-Related Hemoglobinopathies	<i>HBB</i>	AR	Reduced Risk	<b>Personalized Residual Risk (Beta-Globin-Related Hemoglobinopathies):</b> 1 in 2,000 <b>Personalized Residual Risk (Beta-Globin-Related Hemoglobinopathies: HbS Variant):</b> 1 in 790,000 <b>Personalized Residual Risk (Beta-Globin-Related Hemoglobinopathies: HbC Variant):</b> 1 in 2,107,000
Beta-Ketothiolase Deficiency	<i>ACAT1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 5,400
Bilateral Frontoparietal Polymicrogyria	<i>GPR56</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 203,000
Biotinidase Deficiency	<i>BTBD</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 500
Bloom Syndrome	<i>BLM</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 7,400
Canavan Disease	<i>ASPA</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 4,000
Carbamoylphosphate Synthetase I Deficiency	<i>CPS1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,100
Carnitine Palmitoyltransferase IA Deficiency	<i>CPT1A</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 24,000
Carnitine Palmitoyltransferase II Deficiency	<i>CPT2</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 670
Carpenter Syndrome	<i>RAB23</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 21,000
Cartilage-Hair Hypoplasia	<i>RMRP</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 960
Cerebral Creatine Deficiency Syndrome 1	<i>SLC6A8</i>	XL	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 208,000
Cerebral Creatine Deficiency Syndrome 2	<i>GAMT</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 2,100
Cerebrotendinous Xanthomatosis	<i>CYP27A1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 3,900
Charcot-Marie-Tooth Disease, Type 4D	<i>NDRG1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 730,000
Charcot-Marie-Tooth Disease, Type 5 / Arts Syndrome	<i>PRPS1</i>	XL	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 114,000
Charcot-Marie-Tooth Disease, X-Linked	<i>GJB1</i>	XL	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 11,000
Choreoacanthocytosis	<i>VPS13A</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 13,000
Choroideremia	<i>CHM</i>	XL	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 125,000
Chronic Granulomatous Disease ( <i>CYBA</i> -Related)	<i>CYBA</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 5,000
Chronic Granulomatous Disease ( <i>CYBB</i> -Related)	<i>CYBB</i>	XL	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 294,000
Citrin Deficiency	<i>SLC25A13</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 12,000
Citrullinemia, Type 1	<i>ASS1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 2,500
Cohen Syndrome	<i>VPS13B</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 6,400
Combined Malonic and Methylmalonic Aciduria	<i>ACSF3</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 2,400
Combined Oxidative Phosphorylation Deficiency 1	<i>GFM1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 13,000
Combined Oxidative Phosphorylation Deficiency 3	<i>TSM</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 27,000
Combined Pituitary Hormone Deficiency 2	<i>PROP1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 2,800
Combined Pituitary Hormone Deficiency 3	<i>LHX3</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 140,000
Combined SAP Deficiency	<i>PSAP</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 44,000
Congenital Adrenal Hyperplasia due to 17-Alpha-Hydroxylase Deficiency	<i>CYP17A1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,800

<b>Congenital Adrenal Hyperplasia due to 21-Hydroxylase Deficiency</b>	<i>CYP21A2</i>	AR	Reduced Risk	CYP21A2 copy number: 2 CYP21A2 sequencing: Negative <b>Personalized Residual Risk (Congenital Adrenal Hyperplasia due to 21-Hydroxylase Deficiency (Non-Classic)):</b> 1 in 200 <b>Personalized Residual Risk (Congenital Adrenal Hyperplasia due to 21-Hydroxylase Deficiency (Classic)):</b> 1 in 1,300
<b>Congenital Amegakaryocytic Thrombocytopenia</b>	<i>MPL</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 3,100
<b>Congenital Disorder of Glycosylation, Type Ia</b>	<i>PMM2</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 540
<b>Congenital Disorder of Glycosylation, Type Ib</b>	<i>MPI</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 5,600
<b>Congenital Disorder of Glycosylation, Type Ic</b>	<i>ALG6</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 4,100
<b>Congenital Insensitivity to Pain with Anhidrosis</b>	<i>NTRK1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 5,700
<b>Congenital Myasthenic Syndrome (CHRNA3-Related)</b>	<i>CHRNA3</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 4,100
<b>Congenital Myasthenic Syndrome (RAPSN-Related)</b>	<i>RAPSN</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 2,900
<b>Congenital Neutropenia (HAX1-Related)</b>	<i>HAX1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 82,000
<b>Congenital Neutropenia (VPS45-Related)</b>	<i>VPS45</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 163,000
<b>Corneal Dystrophy and Perceptive Deafness</b>	<i>SLC4A11</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 4,600
<b>Corticosterone Methyltransferase Deficiency</b>	<i>CYP11B2</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,500
<b>Cystic Fibrosis</b>	<i>CFTR</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 440
<b>Cystinosis</b>	<i>CTNS</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 7,700
<b>D-Bifunctional Protein Deficiency</b>	<i>HSD17B4</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 5,000
<b>Deafness, Autosomal Recessive 77</b>	<i>LOXHD1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 6,700
<b>Duchenne Muscular Dystrophy / Becker Muscular Dystrophy</b>	<i>DMD</i>	XL	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 10,000
<b>Dyskeratosis Congenita (RTEL1-Related)</b>	<i>RTEL1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 9,800
<b>Dystrophic Epidermolysis Bullosa</b>	<i>COL7A1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 900
<b>Ehlers-Danlos Syndrome, Type VIIC</b>	<i>ADAMTS2</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 243,000
<b>Ellis-van Creveld Syndrome (EVC-Related)</b>	<i>EVC</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 4,200
<b>Emery-Dreifuss Myopathy 1</b>	<i>EMD</i>	XL	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 833,000
<b>Enhanced S-Cone Syndrome</b>	<i>NR2E3</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,600
<b>Ethylmalonic Encephalopathy</b>	<i>ETHE1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 3,400
<b>Fabry Disease</b>	<i>GLA</i>	XL	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 7,700
<b>Factor IX Deficiency</b>	<i>F9</i>	XL	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 5,100
<b>Factor XI Deficiency</b>	<i>F11</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,500
<b>Familial Autosomal Recessive Hypercholesterolemia</b>	<i>LDLRAP1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 136,000
<b>Familial Dysautonomia</b>	<i>IKBKAP</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 51,000
<b>Familial Hypercholesterolemia</b>	<i>LDLR</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 280
<b>Familial Hyperinsulinism (ABCC8-Related)</b>	<i>ABCC8</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 450
<b>Familial Hyperinsulinism (KCNJ11-Related)</b>	<i>KCNJ11</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 5,300
<b>Familial Mediterranean Fever</b>	<i>MEFV</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,200
<b>Fanconi Anemia, Group A</b>	<i>FANCA</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,100
<b>Fanconi Anemia, Group C</b>	<i>FANCC</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 12,000
<b>Fanconi Anemia, Group G</b>	<i>FANCG</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 28,000
<b>Fragile X Syndrome</b>	<i>FMR1</i>	XL	Reduced Risk	FMR1 CGG repeat sizes: Not Performed FMR1 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. <b>Personalized Residual Risk:</b> 1 in 19,000
<b>Fumarate Deficiency</b>	<i>FH</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 2,500
<b>GRACILE Syndrome and Other BCS1L-Related Disorders</b>	<i>BCS1L</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 3,900

Galactokinase Deficiency	<i>GALK1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 2,700
Galactosemia	<i>GALT</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 3,200
Gaucher Disease	<i>GBA</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,300
Gitelman Syndrome	<i>SLC12A3</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 290
Glutaric Acidemia, Type I	<i>GCDH</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 2,700
Glutaric Acidemia, Type IIa	<i>ETFA</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 4,700
Glutaric Acidemia, Type IIc	<i>ETFDH</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,700
Glycine Encephalopathy (AMT-Related)	<i>AMT</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 5,700
Glycine Encephalopathy (GLDC-Related)	<i>GLDC</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 760
Glycogen Storage Disease, Type II	<i>GAA</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 520
Glycogen Storage Disease, Type III	<i>AGL</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 5,600
Glycogen Storage Disease, Type IV / Adult Polyglucosan Body Disease	<i>GBE1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 2,400
Glycogen Storage Disease, Type Ia	<i>G6PC</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 5,300
Glycogen Storage Disease, Type Ib	<i>SLC37A4</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 7,300
Glycogen Storage Disease, Type V	<i>PYGM</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,200
Glycogen Storage Disease, Type VII	<i>PFKM</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 4,300
HMG-CoA Lyase Deficiency	<i>HMGCL</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 2,700
Hemochromatosis, Type 2A	<i>HFE2</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 12,000
Hemochromatosis, Type 3	<i>TFR2</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 11,000
Hereditary Fructose Intolerance	<i>ALDOB</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,900
Hereditary Spastic Paraparesis 49	<i>TECPR2</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 116,000
Hermansky-Pudlak Syndrome, Type 1	<i>HPS1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 3,500
Hermansky-Pudlak Syndrome, Type 3	<i>HPS3</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 49,000
Holocarboxylase Synthetase Deficiency	<i>HLCS</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 5,500
Homocystinuria (CBS-Related)	<i>CBS</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,400
Homocystinuria due to MTHFR Deficiency	<i>MTHFR</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,300
Homocystinuria, cblE Type	<i>MTRR</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 9,600
Hydrolethalus Syndrome	<i>HYLS1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 52,000
Hyperornithinemia-Hyperammonemia-Homocitrullinuria Syndrome	<i>SLC25A15</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 5,700
Hypohidrotic Ectodermal Dysplasia 1	<i>EDA</i>	XL	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 22,000
Hypophosphatasia	<i>ALPL</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 790
Inclusion Body Myopathy 2	<i>GNE</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 2,000
Infantile Cerebral and Cerebellar Atrophy	<i>MED17</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 129,000
Isovaleric Acidemia	<i>IVD</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 2,000
Joubert Syndrome 2	<i>TMEM216</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 152,000
Joubert Syndrome 7 / Meckel Syndrome 5 / COACH Syndrome	<i>RPGRIP1L</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 32,000
Junctional Epidermolysis Bullosa (LAMA3-Related)	<i>LAMA3</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 21,000
Junctional Epidermolysis Bullosa (LAMB3-Related)	<i>LAMB3</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,900
Junctional Epidermolysis Bullosa (LAMC2-Related)	<i>LAMC2</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 77,000
Krabbe Disease	<i>GALC</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 860
Lamellar Ichthyosis, Type 1	<i>TGM1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,500
Leber Congenital Amaurosis 10 and Other CEP290-Related Ciliopathies	<i>CEP290</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,100
Leber Congenital Amaurosis 13	<i>RDH12</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 5,500
Leber Congenital Amaurosis 2 / Retinitis Pigmentosa 20	<i>RPE65</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 2,500
Leber Congenital Amaurosis 5	<i>LCA5</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 14,000

<b>Leber Congenital Amaurosis 8 / Retinitis Pigmentosa 12 / Pigmented Paravenous Chorioretinal Atrophy</b>	<i>CRB1</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 990</b>
<b>Leigh Syndrome, French-Canadian Type</b>	<i>LRPPRC</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 32,000</b>
<b>Lethal Congenital Contracture Syndrome 1 / Lethal Arthrogyrosis with Anterior Horn Cell Disease</b>	<i>GLE1</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 10,000</b>
<b>Leukoencephalopathy with Vanishing White Matter</b>	<i>EIF2B5</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 2,300</b>
<b>Limb-Girdle Muscular Dystrophy, Type 2A</b>	<i>CAPN3</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 960</b>
<b>Limb-Girdle Muscular Dystrophy, Type 2B</b>	<i>DYSF</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 1,100</b>
<b>Limb-Girdle Muscular Dystrophy, Type 2C</b>	<i>SGCG</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 4,900</b>
<b>Limb-Girdle Muscular Dystrophy, Type 2D</b>	<i>SGCA</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 3,500</b>
<b>Limb-Girdle Muscular Dystrophy, Type 2E</b>	<i>SGCB</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 31,000</b>
<b>Limb-Girdle Muscular Dystrophy, Type 2I</b>	<i>FKRP</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 1,400</b>
<b>Lipoamide Dehydrogenase Deficiency</b>	<i>DLG</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 14,000</b>
<b>Lipoid Adrenal Hyperplasia</b>	<i>STAR</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 3,600</b>
<b>Lipoprotein Lipase Deficiency</b>	<i>LPL</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 2,400</b>
<b>Long-Chain 3-Hydroxyacyl-CoA Dehydrogenase Deficiency</b>	<i>HADHA</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 5,900</b>
<b>Lysinuric Protein Intolerance</b>	<i>SLC7A7</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 3,000</b>
<b>Maple Syrup Urine Disease, Type 1a</b>	<i>BCKDHA</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 5,100</b>
<b>Maple Syrup Urine Disease, Type 1b</b>	<i>BCKDHB</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 1,100</b>
<b>Meckel Syndrome 1 / Bardet-Biedl Syndrome 13</b>	<i>MKS1</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 1,700</b>
<b>Medium Chain Acyl-CoA Dehydrogenase Deficiency</b>	<i>ACADM</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 1,800</b>
<b>Megalencephalic Leukoencephalopathy with Subcortical Cysts</b>	<i>MLC1</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 4,300</b>
<b>Menkes Disease</b>	<i>ATP7A</i>	XL	Reduced Risk	<b>Personalized Residual Risk: 1 in 172,000</b>
<b>Metachromatic Leukodystrophy</b>	<i>ARSA</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 1,000</b>
<b>Methylmalonic Acidemia (MMAA-Related)</b>	<i>MMAA</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 15,000</b>
<b>Methylmalonic Acidemia (MMAB-Related)</b>	<i>MMAB</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 12,000</b>
<b>Methylmalonic Acidemia (MUT-Related)</b>	<i>MUT</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 1,300</b>
<b>Methylmalonic Aciduria and Homocystinuria, Cobalamin C Type</b>	<i>MMACHC</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 6,800</b>
<b>Methylmalonic Aciduria and Homocystinuria, Cobalamin D Type</b>	<i>MMADHC</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 219,000</b>
<b>Microphthalmia / Anophthalmia</b>	<i>VSX2</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 40,000</b>
<b>Mitochondrial Complex I Deficiency (ACAD9-Related)</b>	<i>ACAD9</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 1,800</b>
<b>Mitochondrial Complex I Deficiency (NDUFAF5-Related)</b>	<i>NDUFAF5</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 98,000</b>
<b>Mitochondrial Complex I Deficiency (NDUFS6-Related)</b>	<i>NDUFS6</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 353,000</b>
<b>Mitochondrial DNA Depletion Syndrome 6 / Navajo Neurohepatopathy</b>	<i>MPV17</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 4,400</b>
<b>Mitochondrial Myopathy and Sideroblastic Anemia 1</b>	<i>PUS1</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 449,000</b>
<b>Mucopolidosis II / IIIA</b>	<i>GNPTAB</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 2,100</b>
<b>Mucopolidosis III Gamma</b>	<i>GNPTG</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 68,000</b>
<b>Mucopolidosis IV</b>	<i>MCOLN1</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 9,400</b>
<b>Mucopolysaccharidosis Type I</b>	<i>IDUA</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 3,300</b>
<b>Mucopolysaccharidosis Type II</b>	<i>IDS</i>	XL	Reduced Risk	<b>Personalized Residual Risk: 1 in 76,000</b>
<b>Mucopolysaccharidosis Type IIIA</b>	<i>SGSH</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 2,700</b>
<b>Mucopolysaccharidosis Type IIIB</b>	<i>NAGLU</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 950</b>
<b>Mucopolysaccharidosis Type IIIC</b>	<i>HGSNAT</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 3,200</b>
<b>Mucopolysaccharidosis Type IIID</b>	<i>GNS</i>	AR	Reduced Risk	<b>Personalized Residual Risk: 1 in 137,000</b>



Mucopolysaccharidosis Type IVb / GM1 Gangliosidosis	<i>GLB1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,700
Mucopolysaccharidosis type IX	<i>HYAL1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 149,000
Mucopolysaccharidosis type VI	<i>ARSB</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,300
Multiple Sulfatase Deficiency	<i>SUMF1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 69,000
Muscle-Eye-Brain Disease and Other <i>POMGNT1</i> -Related Congenital Muscular Dystrophy-Dystroglycanopathies	<i>POMGNT1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 4,200
Myoneurogastrointestinal Encephalopathy	<i>TYMP</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 2,100
Myotubular Myopathy 1	<i>MTM1</i>	XL	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 192,000
N-Acetylglutamate Synthase Deficiency	<i>NAGS</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 3,200
Nemaline Myopathy 2	<i>NEB</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 2,400
Nephrogenic Diabetes Insipidus, Type II	<i>AQP2</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 3,400
Nephrotic Syndrome ( <i>NPHS1</i> -Related) / Congenital Finnish Nephrosis	<i>NPHS1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 920
Nephrotic Syndrome ( <i>NPHS2</i> -Related) / Steroid-Resistant Nephrotic Syndrome	<i>NPHS2</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 780
Neuronal Ceroid-Lipofuscinosis ( <i>CLN3</i> -Related)	<i>CLN3</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 9,200
Neuronal Ceroid-Lipofuscinosis ( <i>CLN5</i> -Related)	<i>CLN5</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 4,300
Neuronal Ceroid-Lipofuscinosis ( <i>CLN6</i> -Related)	<i>CLN6</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 8,600
Neuronal Ceroid-Lipofuscinosis ( <i>CLN8</i> -Related)	<i>CLN8</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 3,100
Neuronal Ceroid-Lipofuscinosis ( <i>MFSD8</i> -Related)	<i>MFSD8</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 6,200
Neuronal Ceroid-Lipofuscinosis ( <i>PPT1</i> -Related)	<i>PPT1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 7,500
Neuronal Ceroid-Lipofuscinosis ( <i>TPP1</i> -Related)	<i>TPP1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 6,300
Niemann-Pick Disease ( <i>SMPD1</i> -Related)	<i>SMPD1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,800
Niemann-Pick Disease, Type C ( <i>NPC1</i> -Related)	<i>NPC1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 690
Niemann-Pick Disease, Type C ( <i>NPC2</i> -Related)	<i>NPC2</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 6,600
Nijmegen Breakage Syndrome	<i>NBN</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 14,000
Non-Syndromic Hearing Loss ( <i>GJB2</i> -Related)	<i>GJB2</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 600
Odonto-Onycho-Dermal Dysplasia / Schopf-Schulz-Passarge Syndrome	<i>WNT10A</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,900
Omenn Syndrome ( <i>RAG2</i> -Related)	<i>RAG2</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 17,000
Omenn Syndrome / Severe Combined Immunodeficiency, Athabaskan-Type	<i>DCLRE1C</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 5,500
Ornithine Aminotransferase Deficiency	<i>OAT</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 6,400
Ornithine Transcarbamylase Deficiency	<i>OTC</i>	XL	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 103,000
Osteopetrosis 1	<i>TCIRG1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 4,700
Pendred Syndrome	<i>SLC26A4</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 390
Phenylalanine Hydroxylase Deficiency	<i>PAH</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 340
Polycystic Kidney Disease, Autosomal Recessive	<i>PKHD1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 450
Polyglandular Autoimmune Syndrome, Type 1	<i>AIRE</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 5,300
Pontocerebellar Hypoplasia, Type 1A	<i>VRK1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 25,000
Pontocerebellar Hypoplasia, Type 6	<i>RARS2</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 8,600
Primary Carnitine Deficiency	<i>SLC22A5</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,500
Primary Ciliary Dyskinesia ( <i>DNAH5</i> -Related)	<i>DNAH5</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,500
Primary Ciliary Dyskinesia ( <i>DNAI1</i> -Related)	<i>DNAI1</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 5,000
Primary Ciliary Dyskinesia ( <i>DNAI2</i> -Related)	<i>DNAI2</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 76,000
Primary Hyperoxaluria, Type 1	<i>AGXT</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 1,900
Primary Hyperoxaluria, Type 2	<i>GRHPR</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 11,000
Progressive Cerebello-Cerebral Atrophy	<i>SEPSECS</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 6,400
Progressive Familial Intrahepatic Cholestasis, Type 2	<i>ABCB11</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 950

Propionic Acidemia (PCCA-Related)	PCCA	AR	Reduced Risk	Personalized Residual Risk: 1 in 2,600
Propionic Acidemia (PCCB-Related)	PCCB	AR	Reduced Risk	Personalized Residual Risk: 1 in 12,000
Pycnodysostosis	CTSK	AR	Reduced Risk	Personalized Residual Risk: 1 in 5,100
Pyruvate Dehydrogenase E1-Alpha Deficiency	PDHA1	XL	Reduced Risk	Personalized Residual Risk: 1 in 139,000
Pyruvate Dehydrogenase E1-Beta Deficiency	PDHB	AR	Reduced Risk	Personalized Residual Risk: 1 in 15,000
Renal Tubular Acidosis and Deafness	ATP6V1B1	AR	Reduced Risk	Personalized Residual Risk: 1 in 6,600
Retinitis Pigmentosa 25	EYS	AR	Reduced Risk	Personalized Residual Risk: 1 in 1,800
Retinitis Pigmentosa 26	CERKL	AR	Reduced Risk	Personalized Residual Risk: 1 in 13,000
Retinitis Pigmentosa 28	FAM161A	AR	Reduced Risk	Personalized Residual Risk: 1 in 34,000
Retinitis Pigmentosa 59	DHDDS	AR	Reduced Risk	Personalized Residual Risk: 1 in 601,000
Rhizomelic Chondrodysplasia Punctata, Type 1	PEX7	AR	Reduced Risk	Personalized Residual Risk: 1 in 10,000
Rhizomelic Chondrodysplasia Punctata, Type 3	AGPS	AR	Reduced Risk	Personalized Residual Risk: 1 in 620,000
Roberts Syndrome	ESCO2	AR	Reduced Risk	Personalized Residual Risk: 1 in 139,000
Salla Disease	SLC17A5	AR	Reduced Risk	Personalized Residual Risk: 1 in 8,400
Sandhoff Disease	HEXB	AR	Reduced Risk	Personalized Residual Risk: 1 in 1,800
Schimke Immunoosseous Dysplasia	SMARCAL1	AR	Reduced Risk	Personalized Residual Risk: 1 in 3,800
Segawa Syndrome	TH	AR	Reduced Risk	Personalized Residual Risk: 1 in 6,100
Sjogren-Larsson Syndrome	ALDH3A2	AR	Reduced Risk	Personalized Residual Risk: 1 in 5,500
Smith-Lemli-Opitz Syndrome	DHCR7	AR	Reduced Risk	Personalized Residual Risk: 1 in 750
Spinal Muscular Atrophy	SMN1	AR	Reduced Risk	SMN1 copy number: 2 SMN2 copy number: 2 c.:3+80T>G: Negative SMN1 Sequencing: Negative Personalized Residual Risk: 1 in 1,107
Spondylothoracic Dysostosis	MESP2	AR	Reduced Risk	Personalized Residual Risk: 1 in 382,000
Steel Syndrome	COL27A1	AR	Reduced Risk	Personalized Residual Risk: 1 in 93,000
Stuve-Wiedemann Syndrome	LIFR	AR	Reduced Risk	Personalized Residual Risk: 1 in 6,000
Sulfate Transporter-Related Osteochondrodysplasia	SLC26A2	AR	Reduced Risk	Personalized Residual Risk: 1 in 1,800
Tay-Sachs Disease	HEXA	AR	Reduced Risk	Personalized Residual Risk: 1 in 1,400
Tyrosinemia, Type I	FAH	AR	Reduced Risk	Personalized Residual Risk: 1 in 1,900
Usher Syndrome, Type IB	MYO7A	AR	Reduced Risk	Personalized Residual Risk: 1 in 1,000
Usher Syndrome, Type IC	USH1C	AR	Reduced Risk	Personalized Residual Risk: 1 in 1,600
Usher Syndrome, Type ID	CDH23	AR	Reduced Risk	Personalized Residual Risk: 1 in 1,400
Usher Syndrome, Type IF	PCDH15	AR	Reduced Risk	Personalized Residual Risk: 1 in 3,800
Usher Syndrome, Type IIA	USH2A	AR	Reduced Risk	Personalized Residual Risk: 1 in 290
Usher Syndrome, Type III	CLRN1	AR	Reduced Risk	Personalized Residual Risk: 1 in 1,300
Very Long Chain Acyl-CoA Dehydrogenase Deficiency	ACADVL	AR	Reduced Risk	Personalized Residual Risk: 1 in 920
Walker-Warburg Syndrome and Other FKTN-Related Dystrophies	FKTN	AR	Reduced Risk	Personalized Residual Risk: 1 in 4,200
Wilson Disease	ATP7B	AR	Reduced Risk	Personalized Residual Risk: 1 in 350
Wolman Disease / Cholesteryl Ester Storage Disease	LIPA	AR	Reduced Risk	Personalized Residual Risk: 1 in 3,200
X-Linked Juvenile Retinoschisis	RS1	XL	Reduced Risk	Personalized Residual Risk: 1 in 40,000
X-Linked Severe Combined Immunodeficiency	IL2RG	XL	Reduced Risk	Personalized Residual Risk: 1 in 250,000
Zellweger Syndrome Spectrum (PEX10-Related)	PEX10	AR	Reduced Risk	Personalized Residual Risk: 1 in 6,300
Zellweger Syndrome Spectrum (PEX1-Related)	PEX1	AR	Reduced Risk	Personalized Residual Risk: 1 in 2,000
Zellweger Syndrome Spectrum (PEX2-Related)	PEX2	AR	Reduced Risk	Personalized Residual Risk: 1 in 77,000
Zellweger Syndrome Spectrum (PEX6-Related)	PEX6	AR	Reduced Risk	Personalized Residual Risk: 1 in 1,600

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<sup>®</sup> *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<sup>®</sup> 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<sup>®</sup> 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 20 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.\*380T>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.\*380T>G is likely indicative of a silent (20) carrier. In individuals with two copies of *SMN1* with African American, Hispanic or Caucasian ancestry, the presence or absence of c.\*380T>G significantly increases or decreases, respectively, the likelihood of being a silent 20 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<sup>TM</sup>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<sup>®</sup> genotyping platform.

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 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<sup>TM</sup>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 8<sup>th</sup> "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.

**Exceptions:**

Gene	Transcript	Exceptions
ABC D1	NM_000333	Exons 8 and 9
ADA	NM_000222	Exon 1
ADA MTS 2	NM_014244.4	Exon 1
AGP S	NM_003659.3	chr2:178,257,512 - 178,257,649 (partial exon 1)
ALM S1	NM_015120.4	chr2:73,612,990 - 73,613,041 (partial exon 1)
CEP 290	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)
CFT R	NM_000492.3	Exon 10
COL 4A4	NM_000924	chr2:227,942,604 - 227,942,619 (partial exon 25)
CYP 11B2	NM_000498.3	Exons 3 - 7
DNA I2	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
GA MT	NM_000156.5	Exon 1
GLD C	NM_000170.2	Exon 1
GNP TAB	NM_024312.4	chr17:4,837,000 - 4,837,400 (partial exon 2)
GNP TG	NM_032520.4	Exon 1
HGS NAT	NM_152419.2	Exon 1
IDS	NM_000202.6	Exon 3
LIFR	NM_002310.5	Exon 19
NEB	NM_001271208.1	Exons 82 - 105

<i>NPC1</i>	NM_000271.4	chr18:21,123,519 - 21,123,538 (partial exon 14)
<i>PUS1</i>	NM_005215.5	chr12:132,414,446 - 132,414,532 (partial exon 2)
<i>RPG1</i> <i>RIP1L</i>	NM_005272.2	Exon 23
<i>SGSH</i>	NM_000199.3	chr17:78,194,022 - 78,194,072 (partial exon 1)
<i>SLC6A8</i>	NM_005629.3	<p>Exons 3 and 4</p> <p><b>SELECTED REFERENCES</b></p> <p><b>Carrier Screening</b> Grody W et al. ACMG position statement on prenatal/preconception expanded carrier screening. <i>Genet Med.</i> 2013 15:482-3.</p> <p><b>Fragile X syndrome:</b> Chen L et al. An information-rich CGG repeat primed PCR that detects the full range of Fragile X expanded alleles and minimizes the need for Southern blot analysis. <i>J Mol Diag</i> 2010 12:589-600.</p> <p><b>Spinal Muscular Atrophy:</b> Luo M et al. An Ashkenazi Jewish SMN1 haplotype specific to duplication alleles improves pan-ethnic carrier screening for spinal muscular atrophy. <i>Genet Med.</i> 2014 16:149-56.</p> <p><b>Ashkenazi Jewish Disorders:</b> Scott SA et al. Experience with carrier screening and prenatal diagnosis for sixteen Ashkenazi Jewish Genetic Diseases. <i>Hum. Mutat.</i> 2010 31:1-11.</p> <p><b>Duchenne Muscular Dystrophy:</b> Flanigan KM et al. Mutational spectrum of DMD mutations in dystrophinopathy patients: application of modern diagnostic techniques to a large cohort. <i>Hum Mutat.</i> 2009 30:1657-66.</p> <p><b>Variant Classification:</b> 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. <i>Genet Med.</i> 2015 May;17(5):405-24</p> <p>Additional disease-specific references available upon request.</p>



Patient Information	Specimen Information	Client Information
<b>6747, DONOR</b>  <b>DOB:</b> [REDACTED] <b>AGE:</b> [REDACTED] Gender: M Phone: NG Patient ID: [REDACTED]	Specimen: [REDACTED] Requisition: [REDACTED] Lab Ref #: [REDACTED]  Collected: 11/05/2021 Received: 11/06/2021 / 23:06 EST Reported: 11/16/2021 / 23:16 EST	Client #: 48041578     NYNJMAIL GENOMICS, SEMA4 SEMA4 62 SOUTHFIELD AVE STAMFORD, CT 06902-7229

Ward:     FFAXCB
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**Cytogenetic Report**

**CHROMOSOME ANALYSIS, BLOOD - 14596** **Lab:EZ**

**CHROMOSOME ANALYSIS, BLOOD**

Order ID:                     21-344705  
 Specimen Type:             Blood  
 Clinical Indication:        RULE OUT CHROMOSOME ABNORMALITY

**RESULT:**  
 NORMAL MALE KARYOTYPE

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

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

**NOMENCLATURE:**  
 46,XY

**ASSAY INFORMATION:**

Method:                     G-Band (Digital Analysis: MetaSyst)  
 Cells Counted:             20  
 Band Level:                450  
 Cells Analyzed:            5  
 Cells Karyotyped:         4

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

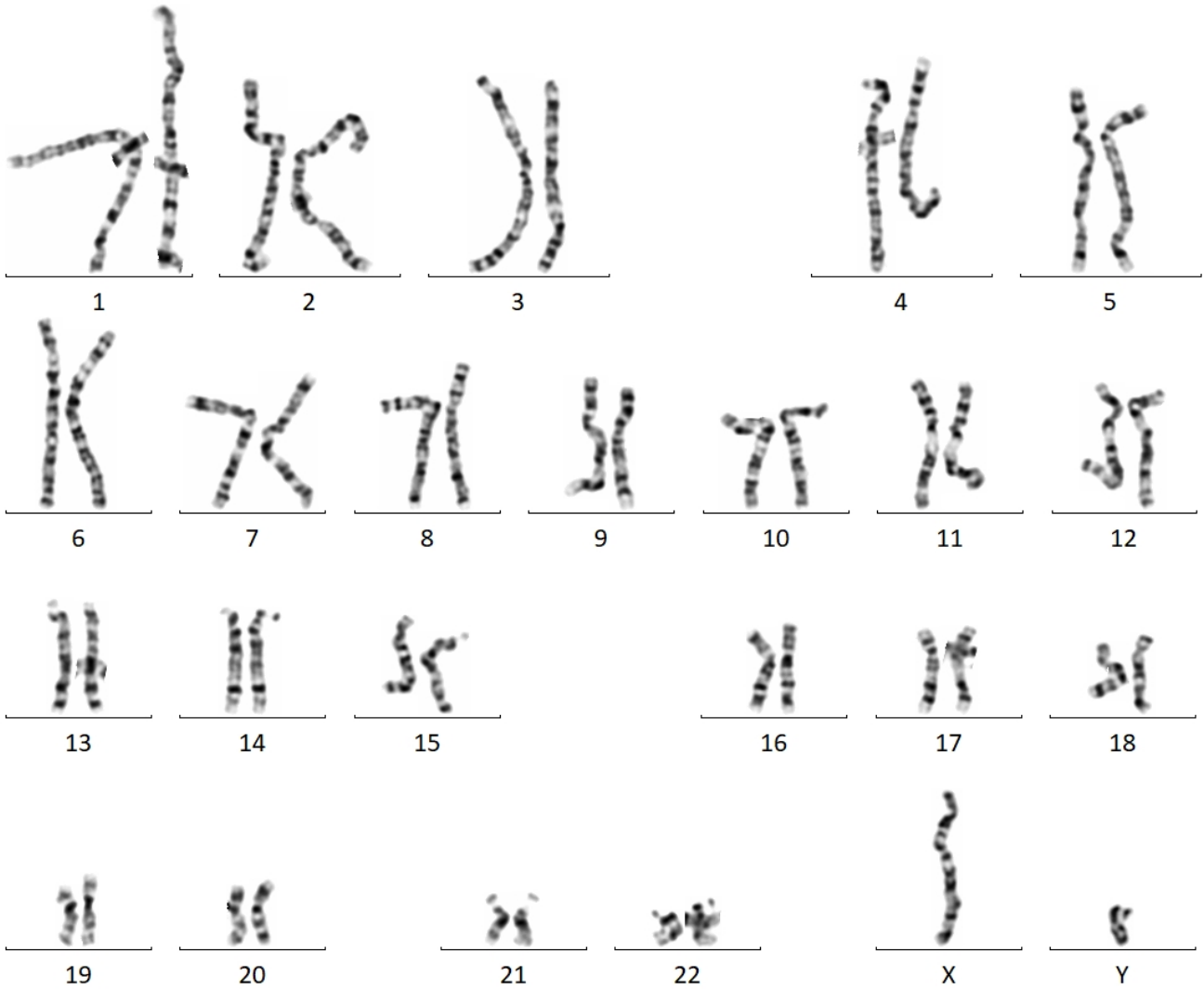
Lakshmi J. Nemana, Ph.D., FACMG

Electronic Signature:        11/16/2021 10:18 PM





Patient Information	Specimen Information	Client Information
<b>6747, DONOR</b>  <b>DOB:</b> [REDACTED] <b>AGE:</b> [REDACTED] Gender: M Patient ID: [REDACTED]	Specimen: [REDACTED] Collected: 11/05/2021 Received: 11/06/2021 / 23:06 EST Reported: 11/16/2021 / 23:16 EST	Client #: 48041578 GENOMICS, SEMA4



**PERFORMING SITE:**

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



Patient Information	Specimen Information	Client Information
<b>6747, DONOR</b>  <b>DOB:</b> [REDACTED] <b>AGE:</b> [REDACTED] Gender: M Phone: NG Patient ID: [REDACTED]	Specimen: [REDACTED] Requisition: [REDACTED] Lab Ref #: [REDACTED]  Collected: 11/05/2021 Received: 11/06/2021 / 22:24 EST Reported: 11/09/2021 / 12:57 EST	Client #: 48041578     NYNJMAIL GENOMICS, SEMA4 SEMA4 62 SOUTHFIELD AVE STAMFORD, CT 06902-7229

Ward:     FFXCB

Test Name	In Range	Out Of Range	Reference Range	Lab
HEMOGLOBINOPATHY EVALUATION				
RED BLOOD CELL COUNT	5.44		4.20-5.80 Million/uL	Z99
HEMOGLOBIN	15.9		13.2-17.1 g/dL	
HEMATOCRIT	46.6		38.5-50.0 %	
MCV	85.7		80.0-100.0 fL	
MCH	29.2		27.0-33.0 pg	
RDW	12.9		11.0-15.0 %	
HEMOGLOBIN A	97.4		>96.0 %	Z99
HEMOGLOBIN F	<1.0		<2.0 %	
HEMOGLOBIN A2 (QUANT)	2.6		2.2-3.2 %	
INTERPRETATION	*			
Normal phenotype.				

**PERFORMING SITE:**

Z99    QUEST DIAGNOSTICS CLIFTON, 1 INSIGHTS DRIVE, CLIFTON, NJ 07012-2355 Laboratory Director: SHELLA K MONGIA,MD, CLIA: 31D0696246



Patient Information:

6747, Donor

DOB: [REDACTED]

Sex: M

MR#: 6747

Patient#: [REDACTED]

Accession:

[REDACTED]

Test#: [REDACTED]

Order#: [REDACTED]

Ext Test#: [REDACTED]

Ext Order#: [REDACTED]

Specimen Type: DNA

Collected: Apr 06,2023

Received Date: Apr 18,2023

Authorized Date: Apr 20,2023

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: **Apr 26,2023**

Final Report

TEST PERFORMED

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**POLG Single Gene**

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

RESULTS:

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**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:

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**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#hlep>)

GENES TESTED:

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**POLG Single Gene**

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

*POLG*

**Gene Specific Notes and Limitations**

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

METHODS:

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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  $\geq 10$  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:

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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:

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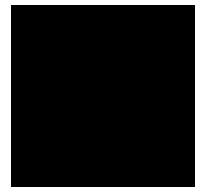
**Zhenbin Chen, Ph.D., CGMS, FACMG** on 4/26/2023 04:34 PM PDT  
Electronically signed



**DISCLAIMER:**

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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](mailto: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:

6747, Donor

DOB: [REDACTED]

Sex: M

MR#: 6747

Patient#: [REDACTED]

Partner Information:

Not Tested

Physician:

Seitz, Suzanne

ATTN: Seitz, Suzanne

Fairfax Cryobank

3015 Williams Drive

Fairfax, VA 22031

Laboratory:

Fulgent Genetics

CAP#: 8042697

CLIA#: 05D2043189

Laboratory Director:

Dr. Hanlin (Harry) Gao

Report Date: Dec 24, 2023

Accession:

[REDACTED]

Test# [REDACTED]

Specimen Type: DNA

Collected: Apr 06, 2023

Accession:

N/A

## FINAL RESULTS



No carrier mutations identified

## TEST PERFORMED

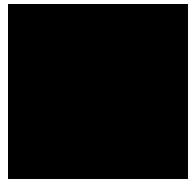
### Custom Beacon Carrier Screening Panel

(2 Gene Panel: *AMN* and *MRE11*;  
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.
- This carrier screening test does not screen for all possible genetic conditions, nor for all possible mutations in every gene tested. Individuals with negative test results may still have up to a 3-4% risk to have a child with a birth defect due to genetic and/or environmental factors.
- Patients may wish to discuss any carrier results with blood relatives, as there is an increased chance that they are also carriers. These results should be interpreted in the context of this individual's clinical findings, biochemical profile, and family history.
- X-linked genes are not routinely analyzed for male carrier screening tests. Gene specific notes and limitations may be present. See below.
- This report does not include variants of uncertain significance.
- 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:

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### Custom Beacon Carrier Screening Panel - 2 Genes

This analysis was run using the Custom Beacon Carrier Screening Panel gene list. 2 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.

AMN, MRE11

## METHODS:

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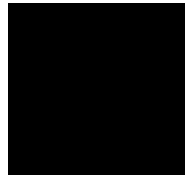
Genomic DNA was isolated from the submitted specimen indicated above (if cellular material was submitted). DNA was barcoded, and enriched for the coding exons of targeted genes using hybrid capture technology. Prepared DNA libraries were then sequenced using a Next Generation Sequencing technology. Following 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

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

### SIGNATURE:

---

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

**Dr. Harry Gao, DABMG, FACMG** on 12/24/2023 3:58 PM PST  
Electronically signed

### DISCLAIMER:

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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](mailto: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.





Supplemental Table

Gene	Condition	Inheritance	Ethnicity	Carrier Rate	Detection Rate	Post-test Carrier Probability*	Residual Risk*
<i>AMN</i>	Megaloblastic anemia 1	AR	General Population	<1 in 500	99%	1 in 49,901	<1 in 10 million
<i>MRE11</i>	Ataxia-Telangiectasia-Like Disorder 1	AR	General Population	<1 in 500	99%	1 in 49,901	<1 in 10 million

\* For genes that have tested negative

Abbreviations: AR, autosomal recessive; XL, X-linked



Patient Information:

6747, Donor

DOB: [REDACTED]

Sex: M

MR#: 6747

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:

Dr. Hanlin (Harry) Gao

Report Date: Feb 29, 2024

Accession:

[REDACTED]

Test#: [REDACTED]

Specimen Type: DNA

Collected: Apr 06, 2023

Accession:

N/A

## FINAL RESULTS



No carrier mutations identified

## TEST PERFORMED

### Custom Beacon Carrier

### Screening Panel

(3 Gene Panel: *CC2D2A*, *NAGA*, and *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.
- X-linked genes are not routinely analyzed for male carrier screening tests. Gene specific notes and limitations may be present. See below.
- Genetic counseling is recommended. Available genetic counselors and additional resources can be found at the National Society of Genetic Counselors (NSGC; <https://www.nsgc.org>)



## GENES TESTED:

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### Custom Beacon Carrier Screening Panel - 3 Genes

This analysis was run using the Custom Beacon Carrier Screening Panel gene list. 3 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.

*CC2D2A, NAGA, SERPINA1*

## METHODS:

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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:

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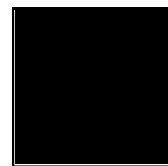


Yan Meng, Ph.D., CGMB, FACMG on 2/29/2024  
Laboratory Director, Fulgent

### 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](mailto: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.



Supplemental Table

Gene	Condition	Inheritance	Ethnicity	Carrier Rate	Detection Rate	Post-test Carrier Probability*	Residual Risk*
<i>CC2D2A</i>	Joubert syndrome 9	AR	General Population	1 in 201	99%	1 in 20,001	1 in 16,080,804
<i>NAGA</i>	Schindler disease types 1 and 3	AR	General Population	1 in 94	99%	1 in 9,301	1 in 3,497,176
<i>SERPINA1</i>	Alpha-1 antitrypsin deficiency	AR	General Population	1 in 33	95%	1 in 641	1 in 84,612
			Caucasian / European Population	1 in 19	95%	1 in 361	1 in 27,436

\* For genes that have tested negative

Abbreviations: AR, autosomal recessive; XL, X-linked



Patient Information:

6747, Donor

DOB: [REDACTED]

Sex: M

MR#: 6747

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:

Dr. Hanlin (Harry) Gao

Report Date: Mar 31, 2024

Accession:

[REDACTED]

Test#: [REDACTED]

Specimen Type: DNA

Collected: Apr 06, 2023

Accession:

N/A

## FINAL RESULTS



No carrier mutations identified

## TEST PERFORMED

### Custom Beacon Carrier Screening Panel

(2 Gene Panel: *GALNT3* and *MYO15A*; 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.
- X-linked genes are not routinely analyzed for male carrier screening tests. Gene specific notes and limitations may be present. See below.
- Genetic counseling is recommended. Available genetic counselors and additional resources can be found at the National Society of Genetic Counselors (NSGC; <https://www.nsgc.org>)



## GENES TESTED:

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### Custom Beacon Carrier Screening Panel - 2 Genes

This analysis was run using the Custom Beacon Carrier Screening Panel gene list. 2 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.

*GALNT3, MYO15A*

## METHODS:

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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:

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### 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

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

### SIGNATURE:

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

**Dr. Harry Gao, DABMG, FACMG on 3/31/2024**  
Laboratory Director, Fulgent

### DISCLAIMER:

---

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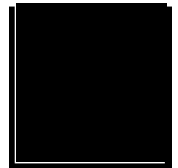


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El Monte, CA, 91731  
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[info@fulgentgenetics.com](mailto:info@fulgentgenetics.com)  
[www.fulgentgenetics.com](http://www.fulgentgenetics.com)



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 Information:

6747, Donor

DOB: [REDACTED]

Sex: M

MR#: 6747

Patient#: [REDACTED]

Accession:

[REDACTED]

Test#: [REDACTED]

Order#: [REDACTED]

Ext Test#: [REDACTED]

Ext Order#: [REDACTED]

Specimen Type: DNA

Collected: Apr 06,2023

Received Date: Apr 18,2023

Authorized Date: Aug 15,2024

Physician:

Seitz, Suzanne

ATTN: Seitz, Suzanne

Fairfax Cryobank

3015 Williams Drive

Fairfax, VA 22031

Phone:

Fax:

Laboratory:

Fulgent Therapeutics LLC

CAP#: 8042697

CLIA#: 05D2043189

Laboratory Director:

Lawrence M. Weiss, MD

Report Date: Aug 24,2024

Final Report

TEST PERFORMED

**Custom NGS Panel - 3 Genes**

(3 Gene Panel: *AP4E1*, *MARS2*, and *TSEN2*; 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:

**Custom NGS Panel - 3 Genes**

3 genes tested (99.97% at >20x).

*AP4E1*, *MARS2*, *TSEN2*

**Gene Specific Notes and Limitations**

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



## METHODS:

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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 99.97% 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  $\geq 10$  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:

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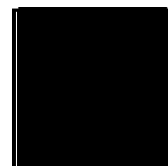
These test results and variant interpretation are based on the proper identification of the submitted specimen, accuracy of any stated familial relationships, and use of the correct human reference sequences at the queried loci. In very rare instances, errors may result due to mix-up or co-mingling of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

---



**Dr. Harry Gao, DABMG, FACMG on 8/24/2024**  
Laboratory Director, Fulgent



**DISCLAIMER:**

---

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Patient Information:

6747, Donor

DOB: [REDACTED]

Sex: M

MR#: 6747

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: Oct 10, 2024

Accession:

[REDACTED]

Test#: [REDACTED]

Specimen Type: DNA

Collected: Apr 06, 2023

Accession:

N/A

## FINAL RESULTS



No carrier mutations identified

## TEST PERFORMED

### Single Gene Carrier Screening: TNXB

(1 Gene Panel: *TNXB*; 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:

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### 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.

TNXB

## METHODS:

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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:

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### General Limitations

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### Gene Specific Notes and Limitations

TNXB: This gene is susceptible to significant pseudogene interference, particularly for exons 32-44 (NM\_019105.6). Among these exons, copy number analysis is available for only exon 35. SNV analysis is available for only exons 35 and 40.

### SIGNATURE:

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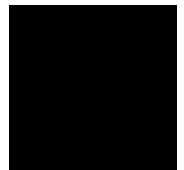
**Dr. Harry Gao, DABMG, FACMG** on 10/10/2024  
Laboratory Director, Fulgent

### DISCLAIMER:

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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 Information:

6747, Donor

DOB: [REDACTED]

Sex: M

MR#: 6747

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: Nov 26, 2024

Accession:

[REDACTED]

Specimen Type: DNA

Collected: Apr 06, 2023

Accession:

N/A

## FINAL RESULTS



No carrier mutations identified

## TEST PERFORMED

### Single Gene Carrier Screening: BBS9

(1 Gene Panel: *BBS9*; 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:

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### 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.

BBS9

## METHODS:

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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:

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### General Limitations

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### Gene Specific Notes and Limitations

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

### SIGNATURE:

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A handwritten signature in black ink that reads "Geetu" with a horizontal line underneath.

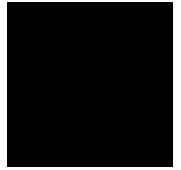
**Geetu Mendiratta-Vij, PhD, FACMG, CGMBS** on 11/26/2024  
Laboratory Director, Fulgent

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