



Donor 6419

Genetic Testing Summary

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

Last Updated: 12/12/22

Donor Reported Ancestry: Columbian, English, Welsh, Norwegian, 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
Expanded Genetic Disease Carrier Screening Panel attached- 283 diseases by gene sequencing	<p>Increased Carrier Risk: Spinal Muscular Atrophy (SMN1). Carrier risk is 1/23</p> <p>Carrier: Zellweger Syndrome Spectrum (PEX1-Related)</p> <p>Negative for other genes sequenced</p>	Partner testing recommended before using this donor.
Special Testing		
Genes: EVC2, POLG	Negative by gene sequencing	See attached for residual risks

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

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

Patient Information

Name: Donor 6419
 Date of Birth: [REDACTED]
 Sema4 ID: [REDACTED]
 Client ID: [REDACTED]
 Indication: Carrier Testing

Specimen Information

Specimen Type: Blood
 Date Collected: 03/05/2021
 Date Received: 03/06/2021
 Final Report: 03/27/2021

Referring Provider

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

Expanded Carrier Screen (283)

Number of genes tested: 283

SUMMARY OF RESULTS AND RECOMMENDATIONS

⊕ Positive	⊖ Negative
<p>Increased Risk of being a Silent (2+0) Carrier of Spinal Muscular Atrophy (AR) Associated gene(s): <i>SMN1</i> Variant(s) Detected: c.*3+80T>G positive with 2 copies of <i>SMN1</i></p> <p>Carrier of Zellweger Syndrome Spectrum (PEX1-Related) (AR) Associated gene(s): <i>PEX1</i> Variant(s) Detected: c.2097dupT, p.I700YfsX42, Pathogenic, Heterozygous (one copy)</p>	<p>Negative for all other genes tested To view a full list of genes and diseases tested please see Table 1 in this report</p>

AR=Autosomal recessive; XL=X-linked

Recommendations

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

Interpretation of positive results

Spinal Muscular Atrophy (AR)

Results and Interpretation

SMN1 copy number: 2

SMN2 copy number: 2

c.*3+80T>G: Detected

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

Inheritance: Autosomal Recessive

This patient is negative for loss of *SMN1* copy number. Complete loss of *SMN1* is causative in spinal muscular atrophy (SMA). Two copies of *SMN2* were detected in this individual, which is considered a negative copy number result. However, parallel testing to assess the presence of an *SMN1* duplication allele was also performed to detect a single nucleotide polymorphism (SNP), c.*3+80T>G, in intron 7 of the *SMN1* gene. This individual was found to be positive for this change and is therefore, at an increased risk of being a silent (2+0) carrier. See *SMA Table* for residual risk estimates based on ethnicity.

SMA Table: Carrier detection and residual risk estimates before and after testing for c.*3+80T>G

Ethnicity	Carrier Frequency	Detection rate	Residual risk after negative result*	Detection rate with <i>SMN1</i> c.*3+80T>G	Residual risk c.*3+80T>G negative	Residual risk c.*3+80T>G positive
African American	1 in 85	71%	1 in 160	91%	1 in 455	1 in 49
Ashkenazi Jewish	1 in 76	90%	1 in 672	93%	1 in 978	1 in 10
East Asian	1 in 53	94%	1 in 864	95%	1 in 901	1 in 12
European (Non-Finnish)	1 in 48	95%	1 in 803	95%	1 in 894	1 in 23
Native American	1 in 63	91%	1 in 609	94%	1 in 930	1 in 47
South Asian	1 in 103	87%	1 in 637	87%	1 in 637	1 in 608
Sephardic Jewish	1 in 34	96%	1 in 696	97%	1 in 884	1 in 12

*Residual risk with two copies *SMN1* detected using dosage sensitive methods. The presence of three or more copies of *SMN1* reduces the risk of being an *SMN1* carrier between 5 - 10 fold, depending on ethnicity.

FOR INDIVIDUALS WITH MIXED ETHNICITY, USE HIGHEST RESIDUAL RISK ESTIMATE

^ Parental follow-up will be requested for confirmation

What is spinal muscular atrophy?

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

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

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

Zellweger Syndrome Spectrum (*PEX1*-Related) (AR)

Results and Interpretation

A heterozygous (one copy) pathogenic frameshift variant, c.2097dupT, p.L700YfsX42, was detected in the *PEX1* gene (NM_000466.2). When this variant is present in trans with a pathogenic variant, it is considered to be causative for Zellweger syndrome spectrum (*PEX1*-related). Therefore, this individual is expected to be at least a carrier for Zellweger syndrome spectrum (*PEX1*-related). Heterozygous carriers are not expected to exhibit symptoms of this disease.

What is Zellweger Syndrome Spectrum (*PEX1*-Related)?

Zellweger syndrome spectrum (*PEX1*-related) is an autosomal recessive, pan-ethnic disease of peroxisome biogenesis. It is comprised of three diseases that make up a continuum of severity, from the most severe, known as Zellweger syndrome, to neonatal adrenoleukodystrophy, to infantile Refsum disease, which is the mildest.

- Zellweger syndrome is characterized by demyelination of structures in the brain leading to leukodystrophy, resulting in seizures and vision loss. Clinical features also include dysmorphic features, hypotonia, cardiac problems, and dysfunction of the liver and kidneys. Death typically occurs in the first year of life.
- Neonatal adrenoleukodystrophy and infantile Refsum disease share many overlapping features. Onset of symptoms may be in infancy, or may be noticed later in childhood. Features include developmental delay and loss of vision and hearing; some children present with bleeding in the brain. The severity and course of the disease can vary between individuals; some may learn to walk and talk, and rarely, patients may survive until adulthood; others never walk or talk. Many patients do not survive childhood. Symptoms tend to progress in severity over the course of the patient's life.

Specific *PEX1* variants have been reported to be associated with a more severe or milder phenotype; additionally, frameshift variants have been to be associated with more severe disease presentations.

Test description

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

R. Zimmerman

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Genes and diseases tested

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

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

Disease	Gene	Inheritance Pattern	Status	Detailed Summary
⊕ Positive				
Spinal Muscular Atrophy	SMN1	AR	Increased Risk	SMN1 copy number: 2 SMN2 copy number: 2 c.*3+80T>G: Detected
Zellweger Syndrome Spectrum (PEX1-Related)	PEX1	AR	Carrier	c.2097dupT, p.L700YfsX42, Pathogenic, Heterozygous (one copy)
⊖ Negative				
3-Beta-Hydroxysteroid Dehydrogenase Type II Deficiency	HSD3B2	AR	Reduced Risk	
3-Methylcrotonyl-CoA Carboxylase Deficiency (MCCC1-Related)	MCCC1	AR	Reduced Risk	
3-Methylcrotonyl-CoA Carboxylase Deficiency (MCCC2-Related)	MCCC2	AR	Reduced Risk	
3-Methylglutaconic Aciduria, Type III	OPA3	AR	Reduced Risk	
3-Phosphoglycerate Dehydrogenase Deficiency	PHGDH	AR	Reduced Risk	
6-Pyruvoyl-Tetrahydropterin Synthase Deficiency	PTS	AR	Reduced Risk	
Abetalipoproteinemia	MTTP	AR	Reduced Risk	
Achromatopsia (CNGB3-related)	CNGB3	AR	Reduced Risk	
Acrodermatitis Enteropathica	SLC39A4	AR	Reduced Risk	
Acute Infantile Liver Failure	TRMU	AR	Reduced Risk	
Acyl-CoA Oxidase I Deficiency	ACOX1	AR	Reduced Risk	
Adenosine Deaminase Deficiency	ADA	AR	Reduced Risk	
Adrenoleukodystrophy, X-Linked	ABCD1	XL	Reduced Risk	
Aicardi-Goutieres Syndrome (SAMHD1-Related)	SAMHD1	AR	Reduced Risk	
Alpha-Mannosidosis	MAN2B1	AR	Reduced Risk	
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
Alpha-Thalassemia Mental Retardation Syndrome	ATRX	XL	Reduced Risk	
Alport Syndrome (COL4A3-Related)	COL4A3	AR	Reduced Risk	
Alport Syndrome (COL4A4-Related)	COL4A4	AR	Reduced Risk	
Alport Syndrome (COL4A5-Related)	COL4A5	XL	Reduced Risk	
Alstrom Syndrome	ALMS1	AR	Reduced Risk	
Andermann Syndrome	SLC12A6	AR	Reduced Risk	
Argininosuccinic Aciduria	ASL	AR	Reduced Risk	
Aromatase Deficiency	CYP19A1	AR	Reduced Risk	
Arthrogryposis, Mental Retardation, and Seizures	SLC35A3	AR	Reduced Risk	
Asparagine Synthetase Deficiency	ASNS	AR	Reduced Risk	
Aspartylglycosaminuria	AGA	AR	Reduced Risk	

Ataxia With Isolated Vitamin E Deficiency	TTPA	AR	Reduced Risk	
Ataxia-Telangiectasia	ATM	AR	Reduced Risk	
Autosomal Recessive Spastic Ataxia of Charlevoix-Saguenay	SACS	AR	Reduced Risk	
Bardet-Biedl Syndrome (BBS10-Related)	BBS10	AR	Reduced Risk	
Bardet-Biedl Syndrome (BBS12-Related)	BBS12	AR	Reduced Risk	
Bardet-Biedl Syndrome (BBS1-Related)	BBS1	AR	Reduced Risk	
Bardet-Biedl Syndrome (BBS2-Related)	BBS2	AR	Reduced Risk	
Bare Lymphocyte Syndrome, Type II	CIITA	AR	Reduced Risk	
Bartter Syndrome, Type 4A	BSND	AR	Reduced Risk	
Bernard-Soulier Syndrome, Type A1	GP1BA	AR	Reduced Risk	
Bernard-Soulier Syndrome, Type C	GP9	AR	Reduced Risk	
Beta-Globin-Related Hemoglobinopathies	HBB	AR	Reduced Risk	
Beta-Ketothiolase Deficiency	ACAT1	AR	Reduced Risk	
Bilateral Frontoparietal Polymicrogyria	GPR56	AR	Reduced Risk	
Biotinidase Deficiency	BTD	AR	Reduced Risk	
Bloom Syndrome	BLM	AR	Reduced Risk	
Canavan Disease	ASPA	AR	Reduced Risk	
Carbamoylphosphate Synthetase I Deficiency	CPS1	AR	Reduced Risk	
Camitine Palmitoyltransferase IA Deficiency	CPT1A	AR	Reduced Risk	
Camitine Palmitoyltransferase II Deficiency	CPT2	AR	Reduced Risk	
Carpenter Syndrome	RAB23	AR	Reduced Risk	
Cartilage-Hair Hypoplasia	RMRP	AR	Reduced Risk	
Cerebral Creatine Deficiency Syndrome 1	SLC6A8	XL	Reduced Risk	
Cerebral Creatine Deficiency Syndrome 2	GAMT	AR	Reduced Risk	
Cerebrotendinous Xanthomatosis	CYP27A1	AR	Reduced Risk	
Charcot-Marie-Tooth Disease, Type 4D	NDRG1	AR	Reduced Risk	
Charcot-Marie-Tooth Disease, Type 5 / Arts Syndrome	PRPS1	XL	Reduced Risk	
Charcot-Marie-Tooth Disease, X-Linked	GJB1	XL	Reduced Risk	
Choreoacanthocytosis	VPS13A	AR	Reduced Risk	
Choroideremia	CHM	XL	Reduced Risk	
Chronic Granulomatous Disease (CYBA-Related)	CYBA	AR	Reduced Risk	
Chronic Granulomatous Disease (CYBB-Related)	CYBB	XL	Reduced Risk	
Citrin Deficiency	SLC25A13	AR	Reduced Risk	
CitruUlinemia, Type 1	ASS1	AR	Reduced Risk	
Cohen Syndrome	VPS13B	AR	Reduced Risk	
Combined Malonic and Methylmalonic Aciduria	ACSF3	AR	Reduced Risk	
Combined Oxidative Phosphorylation Deficiency 1	GFM1	AR	Reduced Risk	
Combined Oxidative Phosphorylation Deficiency 3	TSFM	AR	Reduced Risk	
Combined Pituitary Hormone Deficiency 2	PROP1	AR	Reduced Risk	
Combined Pituitary Hormone Deficiency 3	LHX3	AR	Reduced Risk	
Combined SAP Deficiency	PSAP	AR	Reduced Risk	
Congenital Adrenal Hyperplasia due to 17-Alpha-Hydroxylase Deficiency	CYP17A1	AR	Reduced Risk	
Congenital Adrenal Hyperplasia due to 21-Hydroxylase Deficiency	CYP21A2	AR	Reduced Risk	CYP21A2 copy number: 2 CYP21A2 sequencing: Negative
Congenital Amegakaryocytic Thrombocytopenia	MPL	AR	Reduced Risk	
Congenital Disorder of Glycosylation, Type Ia	PMM2	AR	Reduced Risk	
Congenital Disorder of Glycosylation, Type Ib	MPI	AR	Reduced Risk	
Congenital Disorder of Glycosylation, Type Ic	ALG6	AR	Reduced Risk	
Congenital Insensitivity to Pain with Anhidrosis	NTRK1	AR	Reduced Risk	
Congenital Myasthenic Syndrome (CHRNE-Related)	CHRNE	AR	Reduced Risk	
Congenital Myasthenic Syndrome (RAPSN-Related)	RAPSN	AR	Reduced Risk	
Congenital Neutropenia (HAX1-Related)	HAX1	AR	Reduced Risk	
Congenital Neutropenia (VPS45-Related)	VPS45	AR	Reduced Risk	
Corneal Dystrophy and Perceptive Deafness	SLC4A11	AR	Reduced Risk	
Corticosterone Methyloxidase Deficiency	CYP11B2	AR	Reduced Risk	
Cystic Fibrosis	CFTR	AR	Reduced Risk	
Cystinosis	CTNS	AR	Reduced Risk	
D-Bifunctional Protein Deficiency	HSD17B4	AR	Reduced Risk	

Deafness, Autosomal Recessive 77	<i>LOXHD1</i>	AR	Reduced Risk	
Duchenne Muscular Dystrophy / Becker Muscular Dystrophy	<i>DMD</i>	XL	Reduced Risk	
Dyskeratosis Congenita (<i>RTEL1</i> -Related)	<i>RTEL1</i>	AR	Reduced Risk	
Dystrophic Epidermolysis Bullosa	<i>COL7A1</i>	AR	Reduced Risk	
Ehlers-Danlos Syndrome, Type VIIC	<i>ADAMTS2</i>	AR	Reduced Risk	
Ellis-van Creveld Syndrome (<i>EVC</i> -Related)	<i>EVC</i>	AR	Reduced Risk	
Emery-Dreifuss Myopathy 1	<i>EMD</i>	XL	Reduced Risk	
Enhanced S-Cone Syndrome	<i>NR2E3</i>	AR	Reduced Risk	
Ethylmalonic Encephalopathy	<i>ETHE1</i>	AR	Reduced Risk	
Fabry Disease	<i>GLA</i>	XL	Reduced Risk	
Factor IX Deficiency	<i>F9</i>	XL	Reduced Risk	
Factor XI Deficiency	<i>F11</i>	AR	Reduced Risk	
Familial Autosomal Recessive Hypercholesterolemia	<i>LDLRAP1</i>	AR	Reduced Risk	
Familial Dysautonomia	<i>IKBKAP</i>	AR	Reduced Risk	
Familial Hypercholesterolemia	<i>LDLR</i>	AR	Reduced Risk	
Familial Hyperinsulinism (<i>ABCC8</i> -Related)	<i>ABCC8</i>	AR	Reduced Risk	
Familial Hyperinsulinism (<i>KCNJ11</i> -Related)	<i>KCNJ11</i>	AR	Reduced Risk	
Familial Mediterranean Fever	<i>MEFV</i>	AR	Reduced Risk	
Fanconi Anemia, Group A	<i>FANCA</i>	AR	Reduced Risk	
Fanconi Anemia, Group C	<i>FANCC</i>	AR	Reduced Risk	
Fanconi Anemia, Group G	<i>FANCG</i>	AR	Reduced Risk	
Fragile X Syndrome	<i>FMR1</i>	XL	Reduced Risk	<i>FMR1</i> CGG repeat sizes: Not Performed <i>FMR1</i> Sequencing: Negative Fragile X CGG triplet repeat expansion testing was not performed at this time, as the patient has either been previously tested or is a male.
Fumarase Deficiency	<i>FH</i>	AR	Reduced Risk	
GRACILE Syndrome and Other <i>BCS1L</i> -Related Disorders	<i>BCS1L</i>	AR	Reduced Risk	
Galactokinase Deficiency	<i>GALK1</i>	AR	Reduced Risk	
Galactosemia	<i>GALT</i>	AR	Reduced Risk	
Gaucher Disease	<i>GBA</i>	AR	Reduced Risk	
Gitelman Syndrome	<i>SLC12A3</i>	AR	Reduced Risk	
Glutaric Acidemia, Type I	<i>GCDH</i>	AR	Reduced Risk	
Glutaric Acidemia, Type IIa	<i>ETFA</i>	AR	Reduced Risk	
Glutaric Acidemia, Type IIc	<i>ETFDH</i>	AR	Reduced Risk	
Glycine Encephalopathy (<i>AMT</i> -Related)	<i>AMT</i>	AR	Reduced Risk	
Glycine Encephalopathy (<i>GLDC</i> -Related)	<i>GLDC</i>	AR	Reduced Risk	
Glycogen Storage Disease, Type II	<i>GAA</i>	AR	Reduced Risk	
Glycogen Storage Disease, Type III	<i>AGL</i>	AR	Reduced Risk	
Glycogen Storage Disease, Type IV / Adult Polyglucosan Body Disease	<i>GBE1</i>	AR	Reduced Risk	
Glycogen Storage Disease, Type Ia	<i>G6PC</i>	AR	Reduced Risk	
Glycogen Storage Disease, Type Ib	<i>SLC37A4</i>	AR	Reduced Risk	
Glycogen Storage Disease, Type V	<i>PYGM</i>	AR	Reduced Risk	
Glycogen Storage Disease, Type VII	<i>PFKM</i>	AR	Reduced Risk	
HMG-CoA Lyase Deficiency	<i>HMGCL</i>	AR	Reduced Risk	
Hemochromatosis, Type 2A	<i>HFE2</i>	AR	Reduced Risk	
Hemochromatosis, Type 3	<i>TFR2</i>	AR	Reduced Risk	
Hereditary Fructose Intolerance	<i>ALDOB</i>	AR	Reduced Risk	
Hereditary Spastic Paraparesis 49	<i>TECPR2</i>	AR	Reduced Risk	
Hermansky-Pudlak Syndrome, Type 1	<i>HPS1</i>	AR	Reduced Risk	
Hermansky-Pudlak Syndrome, Type 3	<i>HPS3</i>	AR	Reduced Risk	
Holocarboxylase Synthetase Deficiency	<i>HLCS</i>	AR	Reduced Risk	
Homocystinuria (<i>CBS</i> -Related)	<i>CBS</i>	AR	Reduced Risk	
Homocystinuria due to <i>MTHFR</i> Deficiency	<i>MTHFR</i>	AR	Reduced Risk	
Homocystinuria, cb1E Type	<i>MTRR</i>	AR	Reduced Risk	
Hydrolethalus Syndrome	<i>HYLS1</i>	AR	Reduced Risk	
Hyperomithinemia-Hyperammonemia-Homocitrullinuria Syndrome	<i>SLC25A15</i>	AR	Reduced Risk	

Hypohidrotic Ectodermal Dysplasia 1	EDA	XL	Reduced Risk
Hypophosphatasia	ALPL	AR	Reduced Risk
Inclusion Body Myopathy 2	GNE	AR	Reduced Risk
Infantile Cerebral and Cerebellar Atrophy	MED17	AR	Reduced Risk
Isovaleric Acidemia	IVD	AR	Reduced Risk
Joubert Syndrome 2	TMEM216	AR	Reduced Risk
Joubert Syndrome 7 / Meckel Syndrome 5 / COACH Syndrome	RPGRIP1L	AR	Reduced Risk
Junctional Epidermolysis Bullosa (LAMA3-Related)	LAMA3	AR	Reduced Risk
Junctional Epidermolysis Bullosa (LAMB3-Related)	LAMB3	AR	Reduced Risk
Junctional Epidermolysis Bullosa (LAMC2-Related)	LAMC2	AR	Reduced Risk
Krabbe Disease	GALC	AR	Reduced Risk
Lamellar Ichthyosis, Type 1	TGM1	AR	Reduced Risk
Leber Congenital Amaurosis 10 and Other CEP290-Related Ciliopathies	CEP290	AR	Reduced Risk
Leber Congenital Amaurosis 13	RDH12	AR	Reduced Risk
Leber Congenital Amaurosis 2 / Retinitis Pigmentosa 20	RPE65	AR	Reduced Risk
Leber Congenital Amaurosis 5	LCA5	AR	Reduced Risk
Leber Congenital Amaurosis 8 / Retinitis Pigmentosa 12 / Pigmented Paravenous Chorioretinal Atrophy	CRB1	AR	Reduced Risk
Leigh Syndrome, French-Canadian Type	LRPPRC	AR	Reduced Risk
Lethal Congenital Contracture Syndrome 1 / Lethal Arthrogryposis with Anterior Horn Cell Disease	GLE1	AR	Reduced Risk
Leukoencephalopathy with Vanishing White Matter	EIF2B5	AR	Reduced Risk
Limb-Girdle Muscular Dystrophy, Type 2A	CAPN3	AR	Reduced Risk
Limb-Girdle Muscular Dystrophy, Type 2B	DYSF	AR	Reduced Risk
Limb-Girdle Muscular Dystrophy, Type 2C	SGCG	AR	Reduced Risk
Limb-Girdle Muscular Dystrophy, Type 2D	SGCA	AR	Reduced Risk
Limb-Girdle Muscular Dystrophy, Type 2E	SGCB	AR	Reduced Risk
Limb-Girdle Muscular Dystrophy, Type 2I	FKRP	AR	Reduced Risk
Lipoamide Dehydrogenase Deficiency	DLD	AR	Reduced Risk
Lipoid Adrenal Hyperplasia	STAR	AR	Reduced Risk
Lipoprotein Lipase Deficiency	LPL	AR	Reduced Risk
Long-Chain 3-Hydroxyacyl-CoA Dehydrogenase Deficiency	HADHA	AR	Reduced Risk
Lysinuric Protein Intolerance	SLC7A7	AR	Reduced Risk
Maple Syrup Urine Disease, Type 1a	BCKDHA	AR	Reduced Risk
Maple Syrup Urine Disease, Type 1b	BCKDHB	AR	Reduced Risk
Meckel 1 / Bardet-Biedl Syndrome 13	MKS1	AR	Reduced Risk
Medium Chain Acyl-CoA Dehydrogenase Deficiency	ACADM	AR	Reduced Risk
Megalencephalic Leukoencephalopathy with Subcortical Cysts	MLC1	AR	Reduced Risk
Menkes Disease	ATP7A	XL	Reduced Risk
Metachromatic Leukodystrophy	ARSA	AR	Reduced Risk
Methylmalonic Acidemia (MMAA-Related)	MMAA	AR	Reduced Risk
Methylmalonic Acidemia (MMAB-Related)	MMAB	AR	Reduced Risk
Methylmalonic Acidemia (MUT-Related)	MUT	AR	Reduced Risk
Methylmalonic Aciduria and Homocystinuria, Cobalamin C Type	MMACHC	AR	Reduced Risk
Methylmalonic Aciduria and Homocystinuria, Cobalamin D Type	MMADHC	AR	Reduced Risk
Microphthalmia / Anophthalmia	VSX2	AR	Reduced Risk
Mitochondrial Complex I Deficiency (ACAD9-Related)	ACAD9	AR	Reduced Risk
Mitochondrial Complex I Deficiency (NDUFA5-Related)	NDUFA5	AR	Reduced Risk
Mitochondrial Complex I Deficiency (NDUFS6-Related)	NDUFS6	AR	Reduced Risk
Mitochondrial DNA Depletion Syndrome 6 / Navajo Neurohepatopathy	MPV17	AR	Reduced Risk
Mitochondrial Myopathy and Sideroblastic Anemia 1	PUS1	AR	Reduced Risk

Mucopolipidosis II / IIIA	<i>GNPTAB</i>	AR	Reduced Risk
Mucopolipidosis III Gamma	<i>GNPTG</i>	AR	Reduced Risk
Mucopolipidosis IV	<i>MCOLN1</i>	AR	Reduced Risk
Mucopolysaccharidosis Type I	<i>IDUA</i>	AR	Reduced Risk
Mucopolysaccharidosis Type II	<i>IDS</i>	XL	Reduced Risk
Mucopolysaccharidosis Type IIIA	<i>SGSH</i>	AR	Reduced Risk
Mucopolysaccharidosis Type IIIB	<i>NAGLU</i>	AR	Reduced Risk
Mucopolysaccharidosis Type IIIC	<i>HGSNAT</i>	AR	Reduced Risk
Mucopolysaccharidosis Type IIID	<i>GNS</i>	AR	Reduced Risk
Mucopolysaccharidosis Type IVb / GM1 Gangliosidosis	<i>GLB1</i>	AR	Reduced Risk
Mucopolysaccharidosis type IX	<i>HYAL1</i>	AR	Reduced Risk
Mucopolysaccharidosis type VI	<i>ARSB</i>	AR	Reduced Risk
Multiple Sulfatase Deficiency	<i>SUMF1</i>	AR	Reduced Risk
Muscle-Eye-Brain Disease and Other <i>POMGNT1</i> -Related Congenital Muscular Dystrophy-Dystroglycanopathies	<i>POMGNT1</i>	AR	Reduced Risk
Myoneurogastrointestinal Encephalopathy	<i>TYMP</i>	AR	Reduced Risk
Myotubular Myopathy 1	<i>MTM1</i>	XL	Reduced Risk
N-Acetylglutamate Synthase Deficiency	<i>NAGS</i>	AR	Reduced Risk
Nemaline Myopathy 2	<i>NEB</i>	AR	Reduced Risk
Nephrogenic Diabetes Insipidus, Type II	<i>AQP2</i>	AR	Reduced Risk
Nephrotic Syndrome (<i>NPHS1</i> -Related) / Congenital Finnish Nephrosis	<i>NPHS1</i>	AR	Reduced Risk
Nephrotic Syndrome (<i>NPHS2</i> -Related) / Steroid-Resistant Nephrotic Syndrome	<i>NPHS2</i>	AR	Reduced Risk
Neuronal Ceroid-Lipofuscinosis (<i>CLN3</i> -Related)	<i>CLN3</i>	AR	Reduced Risk
Neuronal Ceroid-Lipofuscinosis (<i>CLN5</i> -Related)	<i>CLN5</i>	AR	Reduced Risk
Neuronal Ceroid-Lipofuscinosis (<i>CLN6</i> -Related)	<i>CLN6</i>	AR	Reduced Risk
Neuronal Ceroid-Lipofuscinosis (<i>CLN8</i> -Related)	<i>CLN8</i>	AR	Reduced Risk
Neuronal Ceroid-Lipofuscinosis (<i>MFSD8</i> -Related)	<i>MFSD8</i>	AR	Reduced Risk
Neuronal Ceroid-Lipofuscinosis (<i>PPT1</i> -Related)	<i>PPT1</i>	AR	Reduced Risk
Neuronal Ceroid-Lipofuscinosis (<i>TPP1</i> -Related)	<i>TPP1</i>	AR	Reduced Risk
Niemann-Pick Disease (<i>SMPD1</i> -Related)	<i>SMPD1</i>	AR	Reduced Risk
Niemann-Pick Disease, Type C (<i>NPC1</i> -Related)	<i>NPC1</i>	AR	Reduced Risk
Niemann-Pick Disease, Type C (<i>NPC2</i> -Related)	<i>NPC2</i>	AR	Reduced Risk
Nijmegen Breakage Syndrome	<i>NBN</i>	AR	Reduced Risk
Non-Syndromic Hearing Loss (<i>GJB2</i> -Related)	<i>GJB2</i>	AR	Reduced Risk
Odonto-Onycho-Dermal Dysplasia / Schopf-Schulz-Passarge Syndrome	<i>WNT10A</i>	AR	Reduced Risk
Omenn Syndrome (<i>RAG2</i> -Related)	<i>RAG2</i>	AR	Reduced Risk
Omenn Syndrome / Severe Combined Immunodeficiency, Athabaskan-Type	<i>DCLRE1C</i>	AR	Reduced Risk
Ornithine Aminotransferase Deficiency	<i>OAT</i>	AR	Reduced Risk
Ornithine Transcarbamylase Deficiency	<i>OTC</i>	XL	Reduced Risk
Osteopetrosis 1	<i>TCIRG1</i>	AR	Reduced Risk
Pendred Syndrome	<i>SLC26A4</i>	AR	Reduced Risk
Phenylalanine Hydroxylase Deficiency	<i>PAH</i>	AR	Reduced Risk
Polycystic Kidney Disease, Autosomal Recessive	<i>PKHD1</i>	AR	Reduced Risk
Polyglandular Autoimmune Syndrome, Type 1	<i>AIRE</i>	AR	Reduced Risk
Pontocerebellar Hypoplasia, Type 1A	<i>VRK1</i>	AR	Reduced Risk
Pontocerebellar Hypoplasia, Type 6	<i>RARS2</i>	AR	Reduced Risk
Primary Carnitine Deficiency	<i>SLC22A5</i>	AR	Reduced Risk
Primary Ciliary Dyskinesia (<i>DNAH5</i> -Related)	<i>DNAH5</i>	AR	Reduced Risk
Primary Ciliary Dyskinesia (<i>DNAI1</i> -Related)	<i>DNAI1</i>	AR	Reduced Risk
Primary Ciliary Dyskinesia (<i>DNAI2</i> -Related)	<i>DNAI2</i>	AR	Reduced Risk
Primary Hyperoxaluria, Type 1	<i>AGXT</i>	AR	Reduced Risk
Primary Hyperoxaluria, Type 2	<i>GRHPR</i>	AR	Reduced Risk
Primary Hyperoxaluria, Type 3	<i>HOGA1</i>	AR	Reduced Risk
Progressive Cerebello-Cerebral Atrophy	<i>SEPSECS</i>	AR	Reduced Risk

Progressive Familial Intrahepatic Cholestasis, Type 2	<i>ABCB11</i>	AR	Reduced Risk
Propionic Acidemia (<i>PCCA</i> -Related)	<i>PCCA</i>	AR	Reduced Risk
Propionic Acidemia (<i>PCCB</i> -Related)	<i>PCCB</i>	AR	Reduced Risk
Pycnodysostosis	<i>CTSK</i>	AR	Reduced Risk
Pyruvate Dehydrogenase E1-Alpha Deficiency	<i>PDHA1</i>	XL	Reduced Risk
Pyruvate Dehydrogenase E1-Beta Deficiency	<i>PDHB</i>	AR	Reduced Risk
Renal Tubular Acidosis and Deafness	<i>ATP6V1B1</i>	AR	Reduced Risk
Retinitis Pigmentosa 25	<i>EYS</i>	AR	Reduced Risk
Retinitis Pigmentosa 26	<i>CERKL</i>	AR	Reduced Risk
Retinitis Pigmentosa 28	<i>FAM161A</i>	AR	Reduced Risk
Retinitis Pigmentosa 59	<i>DHDDS</i>	AR	Reduced Risk
Rhizomelic Chondrodysplasia Punctata, Type 1	<i>PEX7</i>	AR	Reduced Risk
Rhizomelic Chondrodysplasia Punctata, Type 3	<i>AGPS</i>	AR	Reduced Risk
Roberts Syndrome	<i>ESCO2</i>	AR	Reduced Risk
Salla Disease	<i>SLC17A5</i>	AR	Reduced Risk
Sandhoff Disease	<i>HEXB</i>	AR	Reduced Risk
Schimke Immunoosseous Dysplasia	<i>SMARCA1</i>	AR	Reduced Risk
Segawa Syndrome	<i>TH</i>	AR	Reduced Risk
Sjogren-Larsson Syndrome	<i>ALDH3A2</i>	AR	Reduced Risk
Smith-Lemli-Opitz Syndrome	<i>DHCR7</i>	AR	Reduced Risk
Spondylothoracic Dysostosis	<i>MESP2</i>	AR	Reduced Risk
Steel Syndrome	<i>COL27A1</i>	AR	Reduced Risk
Stuve-Wiedemann Syndrome	<i>LIFR</i>	AR	Reduced Risk
Sulfate Transporter-Related Osteochondrodysplasia	<i>SLC26A2</i>	AR	Reduced Risk
Tay-Sachs Disease	<i>HEXA</i>	AR	Reduced Risk
Tyrosinemia, Type I	<i>FAH</i>	AR	Reduced Risk
Usher Syndrome, Type IB	<i>MYO7A</i>	AR	Reduced Risk
Usher Syndrome, Type IC	<i>USH1C</i>	AR	Reduced Risk
Usher Syndrome, Type ID	<i>CDH23</i>	AR	Reduced Risk
Usher Syndrome, Type IF	<i>PCDH15</i>	AR	Reduced Risk
Usher Syndrome, Type IIA	<i>USH2A</i>	AR	Reduced Risk
Usher Syndrome, Type III	<i>CLRN1</i>	AR	Reduced Risk
Very Long Chain Acyl-CoA Dehydrogenase Deficiency	<i>ACADVL</i>	AR	Reduced Risk
Walker-Warburg Syndrome and Other <i>FKTN</i> -Related Dystrophies	<i>FKTN</i>	AR	Reduced Risk
Wilson Disease	<i>ATP7B</i>	AR	Reduced Risk
Wolman Disease / Cholesteryl Ester Storage Disease	<i>LIPA</i>	AR	Reduced Risk
X-Linked Juvenile Retinoschisis	<i>RS1</i>	XL	Reduced Risk
X-Linked Severe Combined Immunodeficiency	<i>IL2RG</i>	XL	Reduced Risk
Zellweger Syndrome Spectrum (<i>PEX10</i> -Related)	<i>PEX10</i>	AR	Reduced Risk
Zellweger Syndrome Spectrum (<i>PEX2</i> -Related)	<i>PEX2</i>	AR	Reduced Risk
Zellweger Syndrome Spectrum (<i>PEX6</i> -Related)	<i>PEX6</i>	AR	Reduced Risk

AR=Autosomal recessive; XL=X-linked

Test methods and comments

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

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

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

Genotyping (Analytical Detection Rate >99%)

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

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

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

and specificity of the MLPA method are both 99%.

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

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

For congenital adrenal hyperplasia, the copy number of the *CYP21A2* gene was analyzed. This analysis can detect large deletions due to unequal meiotic crossing-over between *CYP21A2* and the pseudogene *CYP21A1P*. These 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 with SMA have an *SMN1* mutation that occurred *de novo*. Typically in these cases, only one parent is an SMA carrier.

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.

Pathogenic or likely pathogenic sequence variants in exon 7 may be detected during testing for the c.*380T>G variant allele; these will be reported if confirmed to be located in *SMN1* using locus-specific Sanger primers

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™ QXT 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. Samples were pooled and sequenced on the Illumina HiSeq 2500 platform in the Rapid Run mode or the Illumina NovaSeq platform in the Xp workflow, using 100 bp paired-end 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. The exons contained within these regions are noted within Table 1 (as "Exceptions") and will not be reflexed to Sanger sequencing if the mapping quality or coverage is poor. Any variants identified during testing in these regions are confirmed by a second method and reported if determined to be pathogenic or likely pathogenic. However, as there is a possibility of false negative results within these regions, detection rates and residual risks for these genes have been calculated with the presumption that variants in these exons will not be detected, unless included in the MassARRAY® genotyping platform.

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.

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 array CGH 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 >28,000 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.

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

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

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

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

Please note 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.

SELECTED REFERENCES

Carrier Screening

Grody W et al. ACMG position statement on prenatal/preconception expanded carrier screening. *Genet Med*. 2013 15:482-3.

Fragile X syndrome:

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. *J Mol Diag* 2010 12:589-600.

Spinal Muscular Atrophy:

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

Ashkenazi Jewish Disorders:

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

Duchenne Muscular Dystrophy:

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

Variant Classification:

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

Additional disease-specific references available upon request.

Patient Information

Name: Donor 6419
 Date of Birth: [REDACTED]
 Sema4 ID: [REDACTED]
 Client ID: [REDACTED]
 Indication: Carrier Screening

Specimen Information

Specimen Type: Purified DNA
 Date Collected: 10/14/2022
 Date Received: 10/25/2022
 Final Report: 11/08/2022

Referring Provider

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

Custom Carrier Screen (2 genes)
 with Personalized Residual Risk

SUMMARY OF RESULTS AND RECOMMENDATIONS

⊖ Negative

Negative for all genes tested: *POLG, and EVC2*
 To view a full list of genes and diseases tested
 please see Table 1 in this report

AR=Autosomal recessive; XL=X-linked

Recommendations

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

Test description

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



Ruth Kornreich, Ph.D., FACMG, Laboratory Director

Genes and diseases tested

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

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

Disease	Gene	Inheritance Pattern	Status	Detailed Summary
⊖ Negative				
Ellis-Van Creveld Syndrome (EVC2-Related)	EVC2	AR	Reduced Risk	Personalized Residual Risk: 1 in 6,300
Mitochondrial DNA Depletion Syndrome 4A and 4B and other POLG-Related Disorders	POLG	AR	Reduced Risk	Personalized Residual Risk: 1 in 320

AR=Autosomal recessive; XL=X-linked

Test methods and comments

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

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

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

Genotyping (Analytical Detection Rate >99%)

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

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

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

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

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

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

For spinal muscular atrophy (SMA), the copy numbers of the *SMN1* and *SMN2* genes were analyzed. The individual dosage of exons 7 and 8 as well as the combined dosage of exons 1, 4, 6 and 8 of *SMN1* and *SMN2* were assessed. Copy number gains and losses can be detected with this assay. Depending on ethnicity, 6 - 29 % of carriers will not be identified by dosage sensitive methods as this testing cannot detect individuals with two copies (duplication) of the *SMN1* gene on one chromosome and loss of *SMN1* (deletion) on the other chromosome (silent

2+0 carrier) or individuals that carry an intragenic mutation in *SMN1*. Please also note that 2% of individuals diagnosed with SMA have a causative *SMN1* variant that occurred de novo, and therefore cannot be picked up by carrier screening in the parents. Analysis of *SMN1* is performed in association with short-read sequencing of exons 2a-7, followed by confirmation using long-range PCR (described below).

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

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

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

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

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

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

Exceptions: *ABCD1* (NM_000033.3) exons 8 and 9; *ACADSB* (NM_001609.3) chr10:124,810,695-124,810,707 (partial exon 9); *ADA* (NM_000022.2) exon 1; *ADAMTS2* (NM_014244.4) exon 1; *AGPS* (NM_003659.3) chr2:178,257,512-178,257,649 (partial exon 1); *ALDH7A1* (NM_001182.4) chr5:125,911,150-125,911,163 (partial exon 7) and chr5:125,896,807-125,896,821 (partial exon 10); *ALMS1* (NM_015120.4) chr2:73,612,990-73,613,041 (partial exon 1); *APOPT1* (NM_032374.4) chr14:104,040,437-104,040,455 (partial exon 3); *CDAN1* (NM_138477.2) exon 2; *CEP152* (NM_014985.3) chr15:49,061,146-49,061,165 (partial exon 14) and exon 22; *CEP290* (NM_025114.3) exon 5, exon 7, chr12:88,519,017-88,519,039 (partial exon 13), chr12:88,514,049-88,514,058 (partial exon 15), chr12:88,502,837-88,502,841 (partial exon 23), chr12:88,481,551-88,481,589 (partial exon 32), chr12:88,471,605-88,471,700 (partial exon 40); *CFTR* (NM_000492.3) exon 10; *COL4A4* (NM_000092.4) chr2:227,942,604-227,942,619 (partial exon 25); *COX10* (NM_001303.3) exon 6; *CYP11B1* (NM_000497.3) exons 3-7; *CYP11B2* (NM_000498.3) exons 3-7; *DNAI2* (NM_023036.4) chr17:72,308,136-72,308,147 (partial exon 12); *DOK7* (NM_173660.4) chr4:3,465,131-3,465,161 (partial exon 1) and exon 2; *DUOX2* (NM_014080.4) exons 6-8; *EIF2AK3* (NM_004836.5) exon 8; *EVC* (NM_153717.2) exon 1; *F5* (NM_000130.4) chr1:169,551,662-169,551,679 (partial exon 2); *FH* (NM_000143.3) exon 1; *GAMT* (NM_000156.5) exon 1; *GLDC* (NM_000170.2) exon 1; *GNPTAB* (NM_024312.4) chr17:4,837,000-4,837,400 (partial exon 2); *GNPTG* (NM_032520.4) exon 1; *GHR* (NM_000163.4) exon 3; *GYS2* (NM_021957.3) chr12:21,699,370-21,699,409 (partial exon 12); *HGSNAT* (NM_152419.2) exon 1; *IDS* (NM_000202.6) exon 3; *ITGB4* (NM_000213.4) chr17:73,749,976-73,750,060 (partial exon 33); *JAK3* (NM_000215.3) chr19:17,950,462-17,950,483 (partial exon 10); *LIFR* (NM_002310.5) exon 19; *LMBRD1* (NM_018368.3) chr6:70,459,226-70,459,257 (partial exon 5), chr6:70,447,828-70,447,836 (partial exon 7) and exon 12; *LYST* (NM_000081.3) chr1:235,944,158-235,944,176 (partial exon 16) and chr1:235,875,350-235,875,362 (partial exon 43); *MLYCD* (NM_012213.2) chr16:83,933,242-83,933,282 (partial exon 1); *MTR* (NM_000254.2) chr1:237,024,418-237,024,439 (partial exon 20) and chr1:237,038,019-237,038,029 (partial exon 24); *NBEAL2* (NM_015175.2) chr3:47,021,385-47,021,407 (partial exon 1); *NEB* (NM_001271208.1) exons 82-105; *NPC1* (NM_000271.4) chr18:21,123,519-21,123,538 (partial exon 14); *NPHP1* (NM_000272.3) chr2:110,937,251-110,937,263 (partial exon 3); *OCRL* (NM_000276.3) chrX:128,674,450-128,674,460 (partial exon 1); *PHKB* (NM_000293.2) exon 1 and chr16:47,732,498-47,732,504 (partial exon 30); *PIGN* (NM_176787.4) chr18:59,815,547-59,815,576 (partial exon 8); *PIP5K1C* (NM_012398.2) exon 1 and chr19:3637602-3637616 (partial exon 17); *POU1F1* (NM_000306.3) exon 5; *PTPRC* (NM_002838.4) exons 11 and 23; *PUS1* (NM_025215.5) chr12:132,414,446-132,414,532 (partial exon 2); *RPGRIP1L* (NM_015272.2) exon 23; *SGSH* (NM_000199.3) chr17:78,194,022-78,194,072 (partial exon 1); *SLC6A8* (NM_005629.3) exons 3 and 4; *ST3GAL5* (NM_003896.3) exon 1; *SURF1* (NM_003172.3) chr9:136,223,269-136,223,307 (partial exon 1); *TRPM6* (NM_017662.4) chr9:77,362,800-77,362,811 (partial exon 31); *TSEN54* (NM_207346.2) exon 1; *TYR* (NM_000372.4) exon 5; *VWF* (NM_000552.3) exons 24-26, chr12:6,125,675-6,125,684 (partial exon 30), chr12:6,121,244-6,121,265 (partial exon 33), and exon 34.

This test will detect variants within the exons and the intron-exon boundaries of the target regions. Variants outside these regions may not be detected, including, but not limited to, UTRs, promoters, and deep intronic areas, or regions that fall into the Exceptions mentioned above. This

technology may not detect all small insertion/deletions and is not diagnostic for repeat expansions and structural genomic variation. In addition, a mutation(s) in a gene not included on the panel could be present in this patient.

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

Next Generation Sequencing for *SMN1*

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

Copy Number Variant 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. Deletions and duplications near the lower limit of detection may not be detected due to run variability.

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

Residual Risk Calculations

Carrier frequencies and detection rates for each ethnicity were calculated through the combination of internal curations of >30,000 variants and genomic frequency data from >138,000 individuals across seven ethnic groups in the gnomAD database. Additional variants in HGMD and novel deleterious variants were also incorporated into the calculation. Residual risk values are calculated using a Bayesian analysis combining the a priori risk of being a pathogenic mutation carrier (carrier frequency) and the detection rate. They are provided only as a guide for assessing approximate risk given a negative result, and values will vary based on the exact ethnic background of an individual. This report does

not represent medical advice but should be interpreted by a genetic counselor, medical geneticist or physician skilled in genetic result interpretation and the relevant medical literature.

Personalized Residual Risk Calculations

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

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

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

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

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

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

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

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

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Additional disease-specific references available upon request.