

Donor 6248

Genetic Testing Summary

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

Last Updated: 01/31/2025

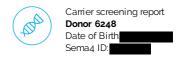
Donor Reported Ancestry: Polish, Swedish English Jewish Ancestry: No

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 in the SMN1 gene	1/894
Expanded Genetic Disease Carrier Screening Panel attached- 283 diseases by gene sequencing	Carrier: Alpha Thalassemia (HBA1/HBA2) Duplication aaa/aa Carrier: Muscle-Eye-Brain Disease and Other POMGNT1 -Related Congenital Muscular Dystrophy- Dystroglycanopathies (POMGNT1)	Partner screening for <u>Beta</u> Thalassemia is indicated (see report attached) Partner testing is indicted before using this donor.
Special Testing		
Tay Sachs Enzyme Analysis	Non carrier by Hex A analysis	
GHRHR	Neg via gene sequencing with deletion and duplication analysis	

^{*}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 6248

Date of Birth:

Sema4 ID:

Client ID
Indication: Carrier Testing

Specimen Information

Specimen Type: Blood

Date Collected: 11/21/2019
Date Received: 11/22/2019

Final Report: 12/06/2019

Referring Provider

Fairfax Cryobank, Inc.

Expanded Carrier Screen (283) Minus TSE

Number of genes tested: 283

SUMMARY OF RESULTS AND RECOMMENDATIONS

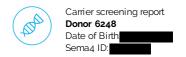
① Positive	○ Negative
Variant Detected for Alpha-Thalassemia (AR) Associated gene(s): HBA1/HBA2 Variant(s) Detected: One copy of the alpha 3.7 duplication Carrier of Muscle-Eye-Brain Disease and Other POMGNT1-Related Congenital Muscular Dystrophy-Dystroglycanopathies (AR) Associated gene(s): POMGNT1 Variant(s) Detected: c.1895+1G>T, Pathogenic, Heterozygous (one copy)	Negative for all other genes tested To view a full list of genes and diseases tested please see Table 1 in this report

AR=Autosomal recessive; XL=X-linked

Recommendations

- · Testing the partner for the above positive disorder(s) and genetic counseling are recommended.
- An alpha-thalassemia duplication allele is generally considered to be a benign polymorphism. Testing the partner for beta-thalassemia is recommended in order to rule out the possibility of being a thalassemia intermedia carrier couple.
- 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

Alpha-Thalassemia (AR)

Results and Interpretation

HBA1 Copy Number: 2 *HBA2* Copy Number: 3

One copy of the alpha 3.7 duplication detected

HBA1/HBA2 Sequencing: Negative

Gene(s) analyzed: HBA1 (NM_000558.4) and HBA2 (NM_000517.4)

Inheritance: Autosomal Recessive

This patient carries an alpha 3.7 duplication allele, resulting in a total of five copies of the alpha-globin gene (aaa/aa). This duplication allele is considered to be a benign polymorphism and therefore the chance that this patient is an alpha-thalassemia carrier is decreased. However, testing the partner for beta-thalassemia is recommended in order to rule out the possibility of being a thalassemia intermedia carrier couple. The literature indicates that co-inheritance of a *beta*-thalassemia pathogenic variant with additional copies of the *HBA* genes (more than 4) can lead to a thalassaemia intermedia phenotype with a variable clinical presentation. No pathogenic or likely pathogenic variants were identified by sequence analysis.

Typically, individuals have four functional alpha-globin genes: 2 copies of *HBA1* and 2 copies of *HBA2*, whose expression is regulated by a cis-acting regulatory element HS-40. Alpha-thalassemia carriers have three (silent carrier) or two (carrier of the alpha-thalassemia trait) functional alpha-globin genes with or without a mild phenotype. Individuals with only one functional alpha-globin gene have HbH disease with microcytic, hypochromic hemolytic anemia and hepatosplenomegaly. Loss of all four alpha-globin genes results in Hb Barts syndrome with the accumulation of Hb Barts in red blood cells and hydrops fetalis, which is fatal in utero or shortly after birth.

Muscle-Eye-Brain Disease and Other POMGNT1-Related Congenital Muscular Dystrophy-Dystroglycanopathies (AR)

Results and Interpretation

A heterozygous (one copy) pathogenic splice site variant, c.1895+1G>T, was detected in the *POMGNT1* gene (NM_017739.3). When this variant is present in trans with a pathogenic variant, it is considered to be causative for a *POMGNT1* -related congenital muscular dystrophydystroglycanopathy. Therefore, this individual is expected to be at least a carrier for a *POMGNT1* -related congenital muscular dystrophydystroglycanopathy. Heterozygous carriers are not expected to exhibit symptoms of this disease.

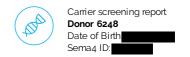
What is Muscle-Eye-Brain Disease and Other POMGNT1-Related Congenital Muscular Dystrophy-Dystroglycanopathies?

POMGNT1 -related congenital muscular dystrophy-dystroglycanopathies are a group of autosomal recessive neuromuscular diseases caused by pathogenic variants in the gene *POMGNT1*. While they are found in individuals of different ethnicities, they are more prevalent in individuals of Finnish descent due to the presence of a founder mutation. The *POMGNT1* -related congenital muscular dystrophydystroglycanopathies vary in severity.

- Type A3 (also known as muscle-eye-brain disease), which is both the most common and the most severe, has an onset at birth or sometimes in the prenatal period. It is characterized by severe brain malformations and intellectual disability, seizures, vision problems, and hypotonia. Death usually occurs in the first year of life.
- Type B3 is characterized by brain malformations, intellectual disability, delayed motor development and visual problems. It is extremely
- Type C₃ is the mildest form and is also very rare. Onset is in early childhood and is characterized by a progressive muscle wasting, weakness and fatigue. Joint contractures and spinal deformities are present.

To date, very few patients have been reported with type B3 and type C3 disease. Therefore, it may not be possible to predict the severity of the disease based on the genotype.





Test description

Wagn

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** 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.

Wanqiong Qiao Ph.D. Assistant Lab Director

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

Genes and diseases tested

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

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

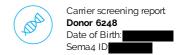
	Disease	Gene	Inheritance Pattern	Status	Detailed Summary
⊕	Positive				
	Alpha-Thalassemia	HBA1/HBA2	AR	Reduced Risk (Duplication Detected)	HBA1 Copy Number: 2 HBA2 Copy Number: 3 One copy of the alpha 3.7 duplication detected HBA1/HBA2 Sequencing: Negative
	Muscle-Eye-Brain Disease and Other <i>POMGNT1</i> -Related Congenital Muscular Dystrophy-Dystroglycanopathies	POMGNT1	AR	Carrier	c.1895+1G>T, Pathogenic, Heterozygous (one copy)
Θ	Negative				
	3-Beta-Hydroxysteroid Dehydrogenase Type II Deficiency	HSD3B2	AR	Reduced Risk	
	3-Methylcrotonyl-CoA Carboxylase Deficiency (<i>MCCC1</i> -Related)	MCCC1	AR	Reduced Risk	
	3-Methylcrotonyl-CoA Carboxylase Deficiency (<i>MCCC2</i> -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 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





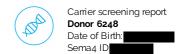
Carnitine Palmitoyltransferase IA Deficiency	CPT1A	AR	Reduced Risk	
Carnitine Palmitoyltransferase II Deficiency	СРТ2	AR	Reduced Risk	
Carpenter Syndrome	RAB23	AR	Reduced Risk	
Cartilage-Hair Hypoplasia	RMRP	AR	Reduced Risk	
Cerebral Creatine Deficiency Syndrome 1	SLC6A8	XL	Reduced Risk	
Cerebral Creatine 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	СНМ	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	
Citrullinemia, Type 1	ASS1	AR	Reduced Risk	
Cohen Syndrome	VPS13B	AR	Reduced Risk	
Combined Malonic and Methylmalonic Aciduria	ACSF3	AR	Reduced Risk	
Combined Oxidative Phosphorylation Deficiency 1	GFM1	AR	Reduced Risk	
Combined Oxidative Phosphorylation Deficiency 3	TSFM	AR	Reduced Risk	
Combined Pituitary Hormone Deficiency 2	PROP1	AR	Reduced Risk	
Combined Pituitary Hormone Deficiency 3	LHX3	AR	Reduced Risk	
Combined SAP Deficiency	PSAP	AR	Reduced Risk	
Congenital Adrenal Hyperplasia due to 17-Alpha- Hydroxylase Deficiency	CYP17A1	AR	Reduced Risk	
Congenital Adrenal Hyperplasia due to 21-Hydroxylase Deficiency	CYP21A2	AR	Reduced Risk	CYP21A2 copy number: 2 CYP21A2 sequencing: Negative
Congenital Amegakaryocytic Thrombocytopenia	MPL	AR	Reduced Risk	
Congenital Disorder of Glycosylation, Type la	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 (<i>HAX1</i> -Related)	HAX1	AR	Reduced Risk	
Congenital Neutropenia (<i>VPS45</i> -Related)	VPS45	AR	Reduced Risk	
Corneal Dystrophy and Perceptive Deafness	SLC4A11	AR	Reduced Risk	





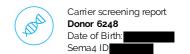
Corticosterone Methyloxidase Deficiency	CYP11B2	AR	Reduced Risk	
Cystic Fibrosis	CFTR	AR	Reduced Risk	
Cystinosis	CTNS	AR	Reduced Risk	
D-Bifunctional Protein Deficiency	HSD17B4	AR	Reduced Risk	
Deafness, Autosomal Recessive 77	LOXHD1	AR	Reduced Risk	
Duchenne Muscular Dystrophy / Becker Muscular Dystrophy	DMD	XL	Reduced Risk	
Dyskeratosis Congenita (RTEL1-Related)	RTEL1	AR	Reduced Risk	
Dystrophic Epidermolysis Bullosa	COL7A1	AR	Reduced Risk	
Ehlers-Danlos Syndrome, Type VIIC	ADAMTS2	AR	Reduced Risk	
Ellis-van Creveld Syndrome (EVC-Related)	EVC	AR	Reduced Risk	
Emery-Dreifuss Myopathy 1	EMD	XL	Reduced Risk	
Enhanced S-Cone Syndrome	NR2E3	AR	Reduced Risk	
Ethylmalonic Encephalopathy	ETHE1	AR	Reduced Risk	
Fabry Disease	GLA	XL	Reduced Risk	
Factor IX Deficiency	F9	XL	Reduced Risk	
Factor XI Deficiency	F11	AR	Reduced Risk	
Familial Autosomal Recessive Hypercholesterolemia	LDLRAP1	AR	Reduced Risk	
Familial Dysautonomia	IKBKAP	AR	Reduced Risk	
Familial Hypercholesterolemia	LDLR	AR	Reduced Risk	
Familial Hyperinsulinism (ABCC8-Related)	ABCC8	AR	Reduced Risk	
Familial Hyperinsulinism (KCNJ11-Related)	KCNJ11	AR	Reduced Risk	
Familial Mediterranean Fever	MEFV	AR	Reduced Risk	
Fanconi Anemia, Group A	FANCA	AR	Reduced Risk	
Fanconi Anemia, Group C	FANCC	AR	Reduced Risk	
Fanconi Anemia, Group G	FANCG	AR	Reduced Risk	
Fragile X Syndrome	FMR1	XL	Reduced Risk	FMR1 CGG repeat sizes: Not Performed FMR1 Sequencing: Negative Fragile X CGG triplet repeat expansion testing wanot performed at this time, as the patient has eithbeen previously tested or is a male.
Fumarase Deficiency	FH	AR	Reduced Risk	
GRACILE Syndrome and Other BCS1L-Related Disorders	BCS1L	AR	Reduced Risk	
Galactokinase Deficiency	GALK1	AR	Reduced Risk	
Galactosemia	GALT	AR	Reduced Risk	
Gaucher Disease	GBA	AR	Reduced Risk	
Gitelman Syndrome	SLC12A3	AR	Reduced Risk	
Glutaric Acidemia, Type I	GCDH	AR	Reduced Risk	





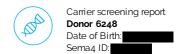
Glutaric Acidemia, Type Ila	ETFA	AR	Reduced Risk
Glutaric Acidemia, Type IIc	ETFDH	AR	Reduced Risk
Glycine Encephalopathy (AMT-Related)	AMT	AR	Reduced Risk
Glycine Encephalopathy (GLDC-Related)	GLDC	AR	Reduced Risk
Glycogen Storage Disease, Type II	GAA	AR	Reduced Risk
Glycogen Storage Disease, Type III	AGL	AR	Reduced Risk
Glycogen Storage Disease, Type IV / Adult Polyglucosan Body Disease	GBE1	AR	Reduced Risk
Glycogen Storage Disease, Type la	G6PC	AR	Reduced Risk
Glycogen Storage Disease, Type Ib	SLC37A4	AR	Reduced Risk
Glycogen Storage Disease, Type V	PYGM	AR	Reduced Risk
Glycogen Storage Disease, Type VII	PFKM	AR	Reduced Risk
HMG-CoA Lyase Deficiency	HMGCL	AR	Reduced Risk
Hemochromatosis, Type 2A	HFE2	AR	Reduced Risk
Hemochromatosis, Type 3	TFR2	AR	Reduced Risk
Hereditary Fructose Intolerance	ALDOB	AR	Reduced Risk
Hereditary Spastic Paraparesis 49	TECPR2	AR	Reduced Risk
Hermansky-Pudlak Syndrome, Type 1	HPS1	AR	Reduced Risk
Hermansky-Pudlak Syndrome, Type 3	HPS3	AR	Reduced Risk
Holocarboxylase Synthetase Deficiency	HLCS	AR	Reduced Risk
Homocystinuria (CBS-Related)	CBS	AR	Reduced Risk
Homocystinuria due to MTHFR Deficiency	MTHFR	AR	Reduced Risk
Homocystinuria, cblE Type	MTRR	AR	Reduced Risk
Hydrolethalus Syndrome	HYLS1	AR	Reduced Risk
Hyperomithinemia-Hyperammonemia-Homocitrullinuria Syndrome	SLC25A15	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 (<i>LAMA3</i> -Related)	LAMA3	AR	Reduced Risk
Junctional Epidermolysis Bullosa (<i>LAMB3</i> -Related)	LAMB3	AR	Reduced Risk
Junctional Epidermolysis Bullosa (<i>LAMC2</i> -Related)	LAMC2	AR	Reduced Risk





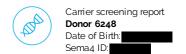
Krabbe Disease	GALC	AR	Reduced Risk
Lamellar Ichthyosis, Type 1	TGM1	AR	Reduced Risk
Leber Congenital Amaurosis 10 and Other CEP290- Related Ciliopathies	CEP290	AR	Reduced Risk
Leber Congenital Amaurosis 13	RDH12	AR	Reduced Risk
Leber Congenital Amaurosis 2 / Retinitis Pigmentosa 20	RPE65	AR	Reduced 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 21	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 (<i>MMAA</i> -Related)	MMAA	AR	Reduced Risk
Methylmalonic Acidemia (<i>MMAB</i> -Related)	MMAB	AR	Reduced Risk
Methylmalonic Acidemia (<i>MUT</i> -Related)	MUT	AR	Reduced Risk
Methylmalonic Aciduria and Homocystinuria, Cobalamin C Type	ММАСНС	AR	Reduced Risk





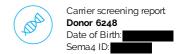
Methylmalonic Aciduria and Homocystinuria, Cobalamin D Type	MMADHC	AR	Reduced Risk
Microphthalmia / Anophthalmia	VSX2	AR	Reduced Risk
Mitochondrial Complex I Deficiency (ACAD9-Related)	ACAD9	AR	Reduced Risk
Mitochondrial Complex Deficiency (NDUFAF5-Related)	NDUFAF5	AR	Reduced Risk
Mitochondrial Complex 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
Mucolipidosis II / IIIA	GNPTAB	AR	Reduced Risk
Mucolipidosis III Gamma	GNPTG	AR	Reduced Risk
Mucolipidosis IV	MCOLN1	AR	Reduced Risk
Mucopolysaccharidosis Type I	IDUA	AR	Reduced Risk
Mucopolysaccharidosis Type II	IDS	XL	Reduced Risk
Mucopolysaccharidosis Type IIIA	SGSH	AR	Reduced Risk
Mucopolysaccharidosis Type IIIB	NAGLU	AR	Reduced Risk
Mucopolysaccharidosis Type IIIC	HGSNAT	AR	Reduced Risk
Mucopolysaccharidosis Type IIID	GNS	AR	Reduced Risk
Mucopolysaccharidosis Type IVb / GM1 Gangliosidosis	GLB1	AR	Reduced Risk
Mucopolysaccharidosis type IX	HYAL1	AR	Reduced Risk
Mucopolysaccharidosis type VI	ARSB	AR	Reduced Risk
Multiple Sulfatase Deficiency	SUMF1	AR	Reduced Risk
Myoneurogastrointestinal Encephalopathy	TYMP	AR	Reduced Risk
Myotubular Myopathy 1	MTM1	XL	Reduced Risk
N-Acetylglutamate Synthase Deficiency	NAGS	AR	Reduced Risk
Nemaline Myopathy 2	NEB	AR	Reduced Risk
Nephrogenic Diabetes Insipidus, Type II	AQP2	AR	Reduced Risk
Nephrotic Syndrome (<i>NPHS1</i> -Related) / Congenital Finnish Nephrosis	NPHS1	AR	Reduced Risk
Nephrotic Syndrome (<i>NPHS2</i> -Related) / Steroid- Resistant Nephrotic Syndrome	NPHS2	AR	Reduced Risk
Neuronal Ceroid-Lipofuscinosis (CLN3-Related)	CLN3	AR	Reduced Risk
Neuronal Ceroid-Lipofuscinosis (CLN5-Related)	CLN5	AR	Reduced Risk
Neuronal Ceroid-Lipofuscinosis (CLN6-Related)	CLN6	AR	Reduced Risk
Neuronal Ceroid-Lipofuscinosis (CLN8-Related)	CLN8	AR	Reduced Risk
Neuronal Ceroid-Lipofuscinosis (MFSD8-Related)	MFSD8	AR	Reduced Risk
Neuronal Ceroid-Lipofuscinosis (PPT1-Related)	PPT1	AR	Reduced Risk





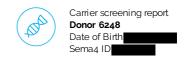
Neuronal Ceroid-Lipofuscinosis (TPP1-Related)	TPP1	AR	Reduced Risk
Niemann-Pick Disease (SMPD1-Related)	SMPD1	AR	Reduced Risk
Niemann-Pick Disease, Type C (NPC1-Related)	NPC1	AR	Reduced Risk
Niemann-Pick Disease, Type C (NPC2-Related)	NPC2	AR	Reduced Risk
Nijmegen Breakage Syndrome	NBN	AR	Reduced Risk
Non-Syndromic Hearing Loss (<i>GJB2</i> -Related)	GJB2	AR	Reduced Risk
Odonto-Onycho-Dermal Dysplasia / Schopf-Schulz- Passarge Syndrome	WNT10A	AR	Reduced Risk
Omenn Syndrome (<i>RAG2</i> -Related)	RAG2	AR	Reduced Risk
Omenn Syndrome / Severe Combined Immunodeficiency, Athabaskan-Type	DCLRE1C	AR	Reduced Risk
Ornithine Aminotransferase Deficiency	OAT	AR	Reduced Risk
Ornithine Transcarbomylase Deficiency	ОТС	XL	Reduced Risk
Osteopetrosis 1	TCIRG1	AR	Reduced Risk
Pendred Syndrome	SLC26A4	AR	Reduced Risk
Phenylalanine Hydroxylase Deficiency	PAH	AR	Reduced Risk
Polycystic Kidney Disease, Autosomal Recessive	PKHD1	AR	Reduced Risk
Polyglandular Autoimmune Syndrome, Type 1	AIRE	AR	Reduced Risk
Pontocerebellar Hypoplasia, Type 1A	VRK1	AR	Reduced Risk
Pontocerebellar Hypoplasia, Type 6	RARS2	AR	Reduced Risk
Primary Carnitine Deficiency	SLC22A5	AR	Reduced Risk
Primary Ciliary Dyskinesia (<i>DNAH5</i> -Related)	DNAH5	AR	Reduced Risk
Primary Ciliary Dyskinesia (<i>DNAl1</i> -Related)	DNAl1	AR	Reduced Risk
Primary Ciliary Dyskinesia (<i>DNAl2</i> -Related)	DNAI2	AR	Reduced Risk
Primary Hyperoxaluria, Type 1	AGXT	AR	Reduced Risk
Primary Hyperoxaluria, Type 2	GRHPR	AR	Reduced Risk
Primary Hyperoxaluria, Type 3	HOGA1	AR	Reduced Risk
Progressive Cerebello-Cerebral Atrophy	SEPSECS	AR	Reduced Risk
Progressive Familial Intrahepatic Cholestasis, Type 2	ABCB11	AR	Reduced Risk
Propionic Acidemia (PCCA-Related)	PCCA	AR	Reduced Risk
Propionic Acidemia (<i>PCCB</i> -Related)	PCCB	AR	Reduced Risk
Pycnodysostosis	CTSK	AR	Reduced Risk
Pyruvate Dehydrogenase E1-Alpha Deficiency	PDHA1	XL	Reduced Risk
Pyruvate Dehydrogenase E1-Beta Deficiency	PDHB	AR	Reduced Risk
Renal Tubular Acidosis and Deafness	ATP6V1B1	AR	Reduced Risk
Retinitis Pigmentosa 25	EYS	AR	Reduced Risk
Retinitis Pigmentosa 26	CERKL	AR	Reduced Risk





Retinitis Pigmentosa 28	FAM161A	AR	Reduced Risk	
Retinitis Pigmentosa 59	DHDDS	AR	Reduced Risk	
Rhizomelic Chondrodysplasia Punctata, Type 1	PEX7	AR	Reduced Risk	
Rhizomelic Chondrodysplasia Punctata, Type 3	AGPS	AR	Reduced Risk	
Roberts Syndrome	ESCO2	AR	Reduced Risk	
Salla Disease	SLC17A5	AR	Reduced Risk	
Sandhoff Disease	HEXB	AR	Reduced Risk	
Schimke Immunoosseous Dysplasia	SMARCAL1	AR	Reduced Risk	
Segawa Syndrome	TH	AR	Reduced Risk	
Sjogren-Larsson Syndrome	ALDH3A2	AR	Reduced Risk	
Smith-Lemli-Opitz Syndrome	DHCR7	AR	Reduced Risk	
Spinal Muscular Atrophy	SMN1	AR	Reduced Risk	SMN1 copy number: 2 SMN2 copy number: 0 c.*3+80T>G: Negative
Spondylothoracic Dysostosis	MESP2	AR	Reduced Risk	
Steel Syndrome	COL27A1	AR	Reduced Risk	
Stuve-Wiedemann Syndrome	LIFR	AR	Reduced Risk	
Sulfate Transporter-Related Osteochondrodysplasia	SLC26A2	AR	Reduced Risk	
Tay-Sachs Disease	HEXA	AR	Reduced Risk	
Tyrosinemia, Type I	FAH	AR	Reduced Risk	
Usher Syndrome, Type IB	MYO7A	AR	Reduced Risk	
Usher Syndrome, Type IC	USH1C	AR	Reduced Risk	
Usher Syndrome, Type ID	CDH23	AR	Reduced Risk	
Usher Syndrome, Type IF	PCDH15	AR	Reduced Risk	
Usher Syndrome, Type IIA	USH2A	AR	Reduced Risk	
Usher Syndrome, Type III	CLRN1	AR	Reduced Risk	
Very Long Chain Acyl-CoA Dehydrogenase Deficiency	ACADVL	AR	Reduced Risk	
Walker-Warburg Syndrome and Other FKTN-Related Dystrophies	FKTN	AR	Reduced Risk	
Wilson Disease	ATP7B	AR	Reduced Risk	
Wolman Disease / Cholesteryl Ester Storage Disease	LIPA	AR	Reduced Risk	
X-Linked Juvenile Retinoschisis	RS1	XL	Reduced Risk	
X-Linked Severe Combined Immunodeficiency	IL2RG	XL	Reduced Risk	
Zellweger Syndrome Spectrum (PEX10-Related)	PEX10	AR	Reduced Risk	
Zellweger Syndrome Spectrum (PEX1-Related)	PEX1	AR	Reduced Risk	
Zellweger Syndrome Spectrum (PEX2-Related)	PEX2	AR	Reduced Risk	
Zellweger Syndrome Spectrum (PEX6-Related)	PEX6	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 2+0 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.*3+80T>G (chr5:70,247.901T>G) variant allele in an individual with Ashkenazi Jewish or Asian ancestry is typically indicative of a duplication of SMN1. When present in an Ashkenazi Jewish or Asian individual with two copies of SMN1, c.*3+80T>G is likely indicative of a silent (2+0) carrier. In individuals with two copies of SMN1 with African American, Hispanic or Caucasian ancestry, the presence or absence of c.*3+80T>G significantly increases or decreases, respectively, the likelihood of being a silent 2+0 silent carrier.

Pathogenic or likely pathogenic sequence variants in exon 7 may be detected during testing for the c.*3+80T>G variant allele; these will be reported if confirmed to be located in SMN1 using locus-specific Sanger primers

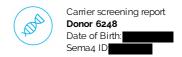
Pathogenic or likely pathogenic sequence variants in exon 7 may be detected during testing for the c.*3+80T>G variant allele; these will be reported if confirmed to be located in SMN1 using locus-specific Sanger primers.

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 SureSelectTMQXT 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 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 $\Delta\Delta$ Ct formula.

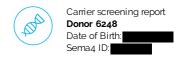
Long-Range PCR (Analytical Detection Rate >99%)

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.

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

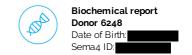
Duchenne Muscular Dystrophy:

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 6248

Date of Birth

Sema4 ID
Client ID:

Indication: Encounter of male for testing for genetic disease carrier status for procreative management

Specimen Information

Specimen Type: Blood
Date Collected: 03/02/2021
Date Received: 03/03/2021
Final Report: 03/14/2021



Tay-Sachs Disease Enzyme

Results and Interpretation

Non-carrier

(Z31.440)

Table 1: List of assays performed with detailed results

Specimen Hex A% Total		Total Hexosaminidase	Non-Carrier Range	Comment
Tay-Sachs WBC	58.2	2154 nmol/hr/mg	55.0-72.0	Non-Carrier
Tay-Sachs Plasma	70.2	332 nmol/hr/ml	58.0-72.0	Non-Carrier

Expected Carrier Ranges: Hex A% <54% (Serum/Plasma), Hex A% <50% (WBC)

Interpretation

The test was performed in the patient's plasma and white blood cells (WBC). The Hex A% activities are both within the non-carrier range. These findings are consistent with the patient being a non-carrier for Tay-Sachs disease.

Test description

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. It is estimated that less than 2% of Tay-Sachs carriers have non-carrier levels of 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, such as pseudodeficiency alleles, may occur if benign variants interfere with the enzymatic assay. False negative results may occur if both HEXA and HEXB variants are present in the same individual.

Please note this test was developed and its performance characteristics were determined by Mount Sinai Genomics, Inc and were considered acceptable for patient testing. It has not been cleared or approved by the FDA. The FDA has determined that such clearance or approval is not necessary.

Chunli Yu, M.D., Laboratory Director

Church ffr

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





Patient Information:
6248, Donor
DOB:
Sex: M
MR#: 6248
Patient#

Partner Information: Not Tested

Physician:
Seitz, Suzanne
ATTN: Seitz, Suzanne
Fairfax Cryobank
3015 Williams Drive
Fairfax. VA 22031

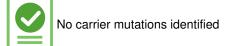
Laboratory:
Fulgent Therapeutics LLC
CAP#: 8042697
CLIA#: 05D2043189
Laboratory Director:
Dr. Amar Jariwala

Report Date: Jan 29,2025

Accession:

Test#: Specimen Type: DNA Collected: Jan 20,2025 Accession: N/A

FINAL RESULTS



TEST PERFORMED

Single Gene Carrier Screening: GHRHR

(1 Gene Panel: *GHRHR*; 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)

Patient: 6248, Donor; Sex: M; DOB: MR#: 6248 Accession#:

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GENES TESTED:

Custom Beacon Carrier Screening Panel - Gene

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

GHRHR

METHODS:

Genomic DNA was isolated from the submitted specimen indicated above (if cellular material was submitted). DNA was barcoded, and enriched for the coding exons of targeted genes using hybrid capture technology. Prepared DNA libraries were then sequenced using a Next Generation Sequencing technology. Following alignment to the human genome reference sequence (assembly GRCh37), variants were detected in regions of at least 10x coverage. For this specimen, 100.00% and 100.00% of coding regions and splicing junctions of genes listed had been sequenced with coverage of at least 10x and 20x, respectively, by NGS or by Sanger sequencing. The remaining regions did not have 10x coverage, and were not evaluated. Variants were interpreted manually using locus specific databases, literature searches, and other molecular biological principles. To minimize false positive results, any variants that do not meet internal quality standards are confirmed by Sanger sequencing. Variants classified as pathogenic, likely pathogenic, or risk allele which are located in the coding regions and nearby intronic regions (+/- 20bp) of the genes listed above are reported. Variants outside these intervals may be reported but are typically not guaranteed. When a single pathogenic or likely pathogenic variant is identified in a clinically relevant gene with autosomal recessive inheritance, the laboratory will attempt to ensure 100% coverage of coding sequences either through NGS or Sanger sequencing technologies ("fill-in"). All genes listed were evaluated for large deletions and/or duplications. However, single exon deletions or duplications will not be detected in this assay, nor will copy number alterations in regions of genes with significant pseudogenes. Putative deletions or duplications are analyzed using Fulgent Germline proprietary pipeline for this specimen. Bioinformatics: The Fulgent Germline v2019.2 pipeline was used to analyze this specimen.

LIMITATIONS:

General Limitations

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

Patient: 6248, Donor; Sex: M; DOB: MR#: 6248





Gene Specific Notes and Limitations

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

SIGNATURE:

Dr. Harry Gao, DABMG, FACMG on 1/29/2025

- Gao

Laboratory Director, Fulgent

DISCLAIMER:

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

Patient: 6248, Donor; Sex: M;

DOB: ; MR#: 6248

Accession#: PAGE 3 of 4





To view the supplemental table describing the carrier frequencies, detection rates, and residual risks associated with the genes tested on any Beacon panel, please visit the following link:

Beacon Expanded Carrier Screening Supplemental Table



Patient: 6248, Donor; Sex: M; DOB: MR#: 6248