



Donor 6073

Genetic Testing Summary

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

Last Updated: 05/04/23

Donor Reported Ancestry: German, Irish

Jewish Ancestry: No

Genetic Test*	Result	Comments/Donor's Residual Risk**
Chromosome analysis (karyotype)	Normal male karyotype	No evidence of clinically significant chromosome abnormalities
Hemoglobin evaluation	Normal hemoglobin fractionation and MCV/MCH results	Reduced risk to be a carrier for sickle cell anemia, beta thalassemia, alpha thalassemia trait (aa/-- and a-/a-) and other hemoglobinopathies
Cystic Fibrosis (CF) carrier screening	Negative by gene sequencing in the CFTR gene	1/440
Spinal Muscular Atrophy (SMA) carrier screening	Negative for deletions of exon 7 in the SMN1 gene	1/894
Expanded Genetic Disease Carrier Screening Panel attached- 283 diseases by gene sequencing	Carrier: Non-Syndromic Hearing Loss (GJB2)	Partner testing recommended before using this donor.
Special Testing		
Maple Syrup Urine Disease Type II (DBT)	Negative by gene sequencing in the DBT gene	1/16,000
Short Chain Acyl-CoA Dehydrogenase Deficiency (ACADS)	Negative by gene sequencing in the ACADS gene	1/11,000
Gene: CCDC103	Negative by gene sequencing	See attached report.

*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 6073
Date of Birth: [REDACTED]
Sema4 ID: [REDACTED]
Client ID: [REDACTED]
Indication: Carrier Testing

Specimen Information

Specimen Type: Blood
Date Collected: 02/05/2020
Date Received: 02/06/2020
Final Report: 02/20/2020

Referring Provider

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

Expanded Carrier Screen (283) Minus TSE
Number of genes tested: 283

SUMMARY OF RESULTS AND RECOMMENDATIONS

⊕ Positive	⊖ Negative
<p>Carrier of Non-Syndromic Hearing Loss (GJB2-Related) (AR) Associated gene(s): <i>GJB2</i> Variant(s) Detected: c.35delG, p.G12VfsX2, 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.

Interpretation of positive results

Non-Syndromic Hearing Loss (*GJB2*-Related) (AR)

Results and Interpretation

A heterozygous (one copy) pathogenic frameshift variant, c.35delG, p.G12VfsX2, was detected in the *GJB2* gene (NM_004004.5). When this variant is present in trans with a pathogenic variant, it is considered to be causative for non-syndromic hearing loss (*GJB2*-related). Therefore, this individual is expected to be at least a carrier for non-syndromic hearing loss (*GJB2*-related). Heterozygous carriers are not expected to exhibit symptoms of this disease.

What is Non-Syndromic Hearing Loss (*GJB2*-Related)?

Non-syndromic hearing loss (*GJB2*-related) is an autosomal recessive disorder that is caused by pathogenic variants in the gene *GJB2*. It is found in individuals of many different ethnicities, but it more prevalent in individuals of Ashkenazi Jewish descent, as well as Caucasians and Asians. Patients with this form of hearing loss do not experience any other disease manifestations. Hearing loss is usually present from birth and does not progress in severity over time. The level of hearing loss can vary between patients from mild to profound. Patients with two inactivating variants are more likely to have profound hearing loss, whereas patients with two non-inactivating variants are more likely to have mild hearing loss. However, the variability that exists between patients means that it may not be possible to predict the severity of an individual's hearing loss based on their genotype. Life expectancy is not reduced.

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 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.

Xingwu Lu, Ph.D., FACMG, Assistant Laboratory 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				
Non-Syndromic Hearing Loss (<i>GJB2</i> -Related)	<i>GJB2</i>	AR	Carrier	c.35delG, p.G12VfsX2, Pathogenic, Heterozygous (one copy)



⊖ Negative

3-Beta-Hydroxysteroid Dehydrogenase Type II Deficiency	<i>HSD3B2</i>	AR	Reduced Risk
3-Methylcrotonyl-CoA Carboxylase Deficiency (MCCC1-Related)	<i>MCCC1</i>	AR	Reduced Risk
3-Methylcrotonyl-CoA Carboxylase Deficiency (MCCC2-Related)	<i>MCCC2</i>	AR	Reduced Risk
3-Methylglutaconic Aciduria, Type III	<i>OPA3</i>	AR	Reduced Risk
3-Phosphoglycerate Dehydrogenase Deficiency	<i>PHGDH</i>	AR	Reduced Risk
6-Pyruvoyl-Tetrahydropterin Synthase Deficiency	<i>PTS</i>	AR	Reduced Risk
Abetalipoproteinemia	<i>MTTP</i>	AR	Reduced Risk
Achromatopsia (CNGB3-related)	<i>CNGB3</i>	AR	Reduced Risk
Acrodermatitis Enteropathica	<i>SLC39A4</i>	AR	Reduced Risk
Acute Infantile Liver Failure	<i>TRMU</i>	AR	Reduced Risk
Acyl-CoA Oxidase I Deficiency	<i>ACOX1</i>	AR	Reduced Risk
Adenosine Deaminase Deficiency	<i>ADA</i>	AR	Reduced Risk
Adrenoleukodystrophy, X-Linked	<i>ABCD1</i>	XL	Reduced Risk
Aicardi-Goutieres Syndrome (SAMHD1-Related)	<i>SAMHD1</i>	AR	Reduced Risk
Alpha-Mannosidosis	<i>MAN2B1</i>	AR	Reduced Risk
Alpha-Thalassemia	<i>HBA1/HBA2</i>	AR	Reduced Risk <i>HBA1</i> Copy Number: 2 <i>HBA2</i> Copy Number: 2 No pathogenic copy number variants detected <i>HBA1/HBA2</i> Sequencing: Negative
Alpha-Thalassemia Mental Retardation Syndrome	<i>ATRX</i>	XL	Reduced Risk
Alport Syndrome (COL4A3-Related)	<i>COL4A3</i>	AR	Reduced Risk
Alport Syndrome (COL4A4-Related)	<i>COL4A4</i>	AR	Reduced Risk
Alport Syndrome (COL4A5-Related)	<i>COL4A5</i>	XL	Reduced Risk
Alstrom Syndrome	<i>ALMS1</i>	AR	Reduced Risk
Andermann Syndrome	<i>SLC12A6</i>	AR	Reduced Risk
Argininosuccinic Aciduria	<i>ASL</i>	AR	Reduced Risk
Aromatase Deficiency	<i>CYP19A1</i>	AR	Reduced Risk
Arthrogryposis, Mental Retardation, and Seizures	<i>SLC35A3</i>	AR	Reduced Risk
Asparagine Synthetase Deficiency	<i>ASNS</i>	AR	Reduced Risk
Aspartylglycosaminuria	<i>AGA</i>	AR	Reduced Risk
Ataxia With Isolated Vitamin E Deficiency	<i>TTPA</i>	AR	Reduced Risk
Ataxia-Telangiectasia	<i>ATM</i>	AR	Reduced Risk
Autosomal Recessive Spastic Ataxia of Charlevoix-Saguenay	<i>SACS</i>	AR	Reduced Risk
Bardet-Biedl Syndrome (BBS10-Related)	<i>BBS10</i>	AR	Reduced Risk



Bardet-Biedl Syndrome (<i>BBS12</i> -Related)	<i>BBS12</i>	AR	Reduced Risk
Bardet-Biedl Syndrome (<i>BBS1</i> -Related)	<i>BBS1</i>	AR	Reduced Risk
Bardet-Biedl Syndrome (<i>BBS2</i> -Related)	<i>BBS2</i>	AR	Reduced Risk
Bare Lymphocyte Syndrome, Type II	<i>CIITA</i>	AR	Reduced Risk
Barter Syndrome, Type 4A	<i>BSND</i>	AR	Reduced Risk
Bernard-Soulier Syndrome, Type A1	<i>GP1BA</i>	AR	Reduced Risk
Bernard-Soulier Syndrome, Type C	<i>GP9</i>	AR	Reduced Risk
Beta-Globin-Related Hemoglobinopathies	<i>HBB</i>	AR	Reduced Risk
Beta-Ketothiolase Deficiency	<i>ACAT1</i>	AR	Reduced Risk
Bilateral Frontoparietal Polymicrogyria	<i>GPR56</i>	AR	Reduced Risk
Biotinidase Deficiency	<i>BTD</i>	AR	Reduced Risk
Bloom Syndrome	<i>BLM</i>	AR	Reduced Risk
Canavan Disease	<i>ASPA</i>	AR	Reduced Risk
Carbamoylphosphate Synthetase I Deficiency	<i>CPS1</i>	AR	Reduced Risk
Carnitine Palmitoyltransferase IA Deficiency	<i>CPT1A</i>	AR	Reduced Risk
Carnitine Palmitoyltransferase II Deficiency	<i>CPT2</i>	AR	Reduced Risk
Carpenter Syndrome	<i>RAB23</i>	AR	Reduced Risk
Cartilage-Hair Hypoplasia	<i>RMRP</i>	AR	Reduced Risk
Cerebral Creatine Deficiency Syndrome 1	<i>SLC6A8</i>	XL	Reduced Risk
Cerebral Creatine Deficiency Syndrome 2	<i>GAMT</i>	AR	Reduced Risk
Cerebrotendinous Xanthomatosis	<i>CYP27A1</i>	AR	Reduced Risk
Charcot-Marie-Tooth Disease, Type 4D	<i>NDRG1</i>	AR	Reduced Risk
Charcot-Marie-Tooth Disease, Type 5 / Arts Syndrome	<i>PRPS1</i>	XL	Reduced Risk
Charcot-Marie-Tooth Disease, X-Linked	<i>GJB1</i>	XL	Reduced Risk
Choreoacanthocytosis	<i>VPS13A</i>	AR	Reduced Risk
Choroideremia	<i>CHM</i>	XL	Reduced Risk
Chronic Granulomatous Disease (<i>CYBA</i> -Related)	<i>CYBA</i>	AR	Reduced Risk
Chronic Granulomatous Disease (<i>CYBB</i> -Related)	<i>CYBB</i>	XL	Reduced Risk
Citrin Deficiency	<i>SLC25A13</i>	AR	Reduced Risk
Citrullinemia, Type 1	<i>ASS1</i>	AR	Reduced Risk
Cohen Syndrome	<i>VPS13B</i>	AR	Reduced Risk
Combined Malonic and Methylmalonic Aciduria	<i>ACSF3</i>	AR	Reduced Risk
Combined Oxidative Phosphorylation Deficiency 1	<i>GFM1</i>	AR	Reduced Risk
Combined Oxidative Phosphorylation Deficiency 3	<i>TSFM</i>	AR	Reduced Risk
Combined Pituitary Hormone Deficiency 2	<i>PROP1</i>	AR	Reduced Risk
Combined Pituitary Hormone Deficiency 3	<i>LHX3</i>	AR	Reduced Risk



Combined SAP Deficiency	PSAP	AR	Reduced Risk	
Congenital Adrenal Hyperplasia due to 17-Alpha-Hydroxylase Deficiency	CYP17A1	AR	Reduced Risk	
Congenital Adrenal Hyperplasia due to 21-Hydroxylase Deficiency	CYP21A2	AR	Reduced Risk	CYP21A2 copy number: 2 CYP21A2 sequencing: Negative
Congenital Amegakaryocytic Thrombocytopenia	MPL	AR	Reduced Risk	
Congenital Disorder of Glycosylation, Type Ia	PMM2	AR	Reduced Risk	
Congenital Disorder of Glycosylation, Type Ib	MPI	AR	Reduced Risk	
Congenital Disorder of Glycosylation, Type Ic	ALG6	AR	Reduced Risk	
Congenital Insensitivity to Pain with Anhidrosis	NTRK1	AR	Reduced Risk	
Congenital Myasthenic Syndrome (CHRNE-Related)	CHRNE	AR	Reduced Risk	
Congenital Myasthenic Syndrome (RAPSN-Related)	RAPSN	AR	Reduced Risk	
Congenital Neutropenia (HAX1-Related)	HAX1	AR	Reduced Risk	
Congenital Neutropenia (VPS45-Related)	VPS45	AR	Reduced Risk	
Corneal Dystrophy and Perceptive Deafness	SLC4A11	AR	Reduced Risk	
Corticosterone Methyloxidase Deficiency	CYP11B2	AR	Reduced Risk	
Cystic Fibrosis	CFTR	AR	Reduced Risk	
Cystinosis	CTNS	AR	Reduced Risk	
D-Bifunctional Protein Deficiency	HSD17B4	AR	Reduced Risk	
Deafness, Autosomal Recessive 77	LOXHD1	AR	Reduced Risk	
Duchenne Muscular Dystrophy / Becker Muscular Dystrophy	DMD	XL	Reduced Risk	
Dyskeratosis Congenita (RTEL1-Related)	RTEL1	AR	Reduced Risk	
Dystrophic Epidermolysis Bullosa	COL7A1	AR	Reduced Risk	
Ehlers-Danlos Syndrome, Type VIIC	ADAMTS2	AR	Reduced Risk	
Ellis-van Creveld Syndrome (EVC-Related)	EVC	AR	Reduced Risk	
Emery-Dreifuss Myopathy 1	EMD	XL	Reduced Risk	
Enhanced S-Cone Syndrome	NR2E3	AR	Reduced Risk	
Ethylmalonic Encephalopathy	ETHE1	AR	Reduced Risk	
Fabry Disease	GLA	XL	Reduced Risk	
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	<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, cbIE 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	<i>EDA</i>	XL	Reduced Risk
Hypophosphatasia	<i>ALPL</i>	AR	Reduced Risk
Inclusion Body Myopathy 2	<i>GNE</i>	AR	Reduced Risk
Infantile Cerebral and Cerebellar Atrophy	<i>MED17</i>	AR	Reduced Risk
Isovaleric Acidemia	<i>IVD</i>	AR	Reduced Risk
Joubert Syndrome 2	<i>TMEM216</i>	AR	Reduced Risk
Joubert Syndrome 7 / Meckel Syndrome 5 / COACH Syndrome	<i>RPGRIP1L</i>	AR	Reduced Risk
Junctional Epidermolysis Bullosa (<i>LAMA3</i> -Related)	<i>LAMA3</i>	AR	Reduced Risk
Junctional Epidermolysis Bullosa (<i>LAMB3</i> -Related)	<i>LAMB3</i>	AR	Reduced Risk
Junctional Epidermolysis Bullosa (<i>LAMC2</i> -Related)	<i>LAMC2</i>	AR	Reduced Risk
Krabbe Disease	<i>GALC</i>	AR	Reduced Risk
Lamellar Ichthyosis, Type 1	<i>TGM1</i>	AR	Reduced Risk
Leber Congenital Amaurosis 10 and Other CEP290-Related Ciliopathies	<i>CEP290</i>	AR	Reduced Risk
Leber Congenital Amaurosis 13	<i>RDH12</i>	AR	Reduced Risk
Leber Congenital Amaurosis 2 / Retinitis Pigmentosa 20	<i>RPE65</i>	AR	Reduced Risk
Leber Congenital Amaurosis 5	<i>LCA5</i>	AR	Reduced Risk
Leber Congenital Amaurosis 8 / Retinitis Pigmentosa 12 / Pigmented Paravenous Chorioretinal Atrophy	<i>CRB1</i>	AR	Reduced Risk
Leigh Syndrome, French-Canadian Type	<i>LRPPRC</i>	AR	Reduced Risk
Lethal Congenital Contracture Syndrome 1 / Lethal Arthrogryposis with Anterior Horn Cell Disease	<i>GLE1</i>	AR	Reduced Risk
Leukoencephalopathy with Vanishing White Matter	<i>EIF2B5</i>	AR	Reduced Risk
Limb-Girdle Muscular Dystrophy, Type 2A	<i>CAPN3</i>	AR	Reduced Risk
Limb-Girdle Muscular Dystrophy, Type 2B	<i>DYSF</i>	AR	Reduced Risk
Limb-Girdle Muscular Dystrophy, Type 2C	<i>SGCG</i>	AR	Reduced Risk
Limb-Girdle Muscular Dystrophy, Type 2D	<i>SGCA</i>	AR	Reduced Risk
Limb-Girdle Muscular Dystrophy, Type 2E	<i>SGCB</i>	AR	Reduced Risk
Limb-Girdle Muscular Dystrophy, Type 2I	<i>FKRP</i>	AR	Reduced Risk
Lipoamide Dehydrogenase Deficiency	<i>DLD</i>	AR	Reduced Risk
Lipoid Adrenal Hyperplasia	<i>STAR</i>	AR	Reduced Risk
Lipoprotein Lipase Deficiency	<i>LPL</i>	AR	Reduced Risk



Long-Chain 3-Hydroxyacyl-CoA Dehydrogenase Deficiency	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 (NDUFAF5-Related)	NDUFAF5	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	GNPTAB	AR	Reduced Risk
Mucopolipidosis III Gamma	GNPTG	AR	Reduced Risk
Mucopolipidosis 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



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
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>GRHRP</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>SMARCAL1</i>	AR	Reduced Risk	
Segawa Syndrome	<i>TH</i>	AR	Reduced Risk	
Sjogren-Larsson Syndrome	<i>ALDH3A2</i>	AR	Reduced Risk	
Smith-Lemli-Opitz Syndrome	<i>DHCR7</i>	AR	Reduced Risk	
Spinal Muscular Atrophy	<i>SMN1</i>	AR	Reduced Risk	<i>SMN1</i> copy number: 2 <i>SMN2</i> copy number: >=3 c.'3+80T>G: Negative
Spondylthoracic 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	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 <i>FKTN</i> -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 (<i>PEX10</i> -Related)	PEX10	AR	Reduced Risk
Zellweger Syndrome Spectrum (<i>PEX1</i> -Related)	PEX1	AR	Reduced Risk
Zellweger Syndrome Spectrum (<i>PEX2</i> -Related)	PEX2	AR	Reduced Risk
Zellweger Syndrome Spectrum (<i>PEX6</i> -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 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 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 arrayCGH platform, quantitative PCR, or MLPA (depending on CNV size and gene content). While this algorithm is designed to pick up deletions and duplications of 2 or more exons in length, potentially pathogenic single-exon CNVs will be confirmed and reported, if detected.

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

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



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

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

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

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

Residual Risk Calculations

Carrier frequencies and detection rates for each ethnicity were calculated through the combination of internal curations of >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.



RESULTS RECIPIENT
GENETICS & IVF INSTITUTE
 Attn: Suzanne Seitz
 3015 Williams Dr
 Fairfax, VA 22031
 Phone: (703) 698-7355
 Fax: (703) 698-1137
 NPI: 1972005890
 Report Date: 03/25/2021

MALE
DONOR 6073
 DOB: [REDACTED]
 Ethnicity: Northern European
 Sample Type: EDTA Blood
 Date of Collection: 03/09/2021
 Date Received: 03/11/2021
 Date Tested: 03/24/2021
 Barcode: [REDACTED]
 Indication: Egg or sperm donor,
 Family history

FEMALE
 N/A

Foresight® Carrier Screen

NEGATIVE

ABOUT THIS TEST

The **Myriad Foresight Carrier Screen** utilizes sequencing, maximizing coverage across all DNA regions tested, to help you learn about your chance to have a child with a genetic disease.

RESULTS SUMMARY

Risk Details	DONOR 6073	Partner
Panel Information	Foresight Carrier Screen Custom Panel 12762 (2 conditions tested)	N/A
All conditions tested A complete list of all conditions tested can be found on page 4.	<input type="checkbox"/> NEGATIVE No disease-causing mutations were detected.	N/A

CLINICAL NOTES

- None

NEXT STEPS

- If necessary, patients can discuss residual risks with their physician or a genetic counselor.

Methods and Limitations

DONOR 6073 [Foresight Carrier Screen]: Sequencing with copy number analysis (Assay(s): DTS v3.2).

Sequencing with copy number analysis

High-throughput sequencing and read-depth-based copy number analysis are used to analyze the genes listed in the Conditions Tested section of the report. Except where otherwise noted, the region of interest (ROI) comprises the indicated coding regions and 20 non-coding bases flanking each region. In a minority of cases where genomic features (e.g., long homopolymers) compromise calling fidelity, the affected non-coding bases are excluded from the ROI. The ROI is sequenced to a minimum acceptable read depth, and the sequences are compared to a reference genomic sequence (Genome Reference Consortium Human Build 37 [GRCh37]/hg19). On average, 99% of all bases in the ROI are sequenced at a read depth that is greater than the minimum read depth. Sequence variants may not be detected in areas of lower sequence coverage. Insertions and deletions may not be detected as accurately as single-nucleotide variants. Select genes or regions for which pseudogenes or other regions of homology impede reliable variant detection may be assayed using alternate technology, or they may be excluded from the ROI. *CFTR* and *DMD* testing includes analysis for exon-level deletions and duplications with an average sensitivity of ~99%. Only exon-level deletions are assayed for other genes on the panel and such deletions are detected with a sensitivity of $\geq 75\%$. Selected founder deletions may be detected at slightly higher sensitivity. Affected exons and/or breakpoints of copy number variants are estimated from junction reads, where available, or using the positions of affected probes. Only exons known to be included in the region affected by a copy number variant are provided in the variant nomenclature. In some cases, the copy number variant may be larger or smaller than indicated. If *GJB2* is tested, large upstream deletions involving the *GJB6* and/or *CRYL1* genes that may affect the expression of *GJB2* are also analyzed.

Interpretation of reported variants

The classification and interpretation of all variants identified in this assay reflects the current state of Myriad's scientific understanding at the time this report was issued. Variants are classified according to internally defined criteria, which are compatible with the ACMG Standards and Guidelines for the Interpretation of Sequence Variants (PMID: 25741868). Variants that have been determined by Myriad to be disease-causing or likely disease-causing (i.e. pathogenic or likely pathogenic) are reported. Benign variants, variants of uncertain clinical significance (VUS), and variants not directly associated with the specified disease phenotype(s) are not reported. Variant classification and interpretation may change for a variety of reasons, including but not limited to, improvements to classification techniques, availability of additional scientific information, and observation of a variant in more patients. If the classification of one or more variants identified in this patient changes, an updated report reflecting the new classification generally will not be issued. If an updated report is issued, the variants reported may change based on their current classification. This can include changes to the variants displayed in gene specific 'variants tested' sections. Healthcare providers may contact Myriad directly to request updated variant classification information specific to this test result.

Limitations

The MWH Foresight Carrier Screen is designed to detect and report germline (constitutional) alterations. Mosaic (somatic) variation may not be detected, and if it is detected, it may not be reported. If more than one variant is detected in a gene, additional studies may be necessary to determine if those variants lie on the same chromosome or different chromosomes (phase). This test is not designed to detect sex-chromosome copy number variations. If present, sex-chromosome abnormalities may significantly reduce test sensitivity for X-linked conditions. Variant interpretation and residual and reproductive risk estimations assume a normal karyotype and may be different for individuals with abnormal karyotypes. The test does not fully address all inherited forms of intellectual disability, birth defects, or heritable diseases. Furthermore, not all forms of genetic variation are detected by this assay (i.e., duplications [except in specified genes], chromosomal rearrangements, structural abnormalities, etc.). Additional testing may be appropriate for some individuals. Pseudogenes and other regions of homology may interfere with this analysis. In an unknown number of cases, other genetic variation may interfere with variant detection. Rare carrier states where complementary changes exist between the chromosomes may not be detected by the assay. Other possible sources of diagnostic error include sample mix-up, trace contamination, bone marrow transplantation, blood transfusions, and technical or analytical errors.

Detection rates are determined using published scientific literature and/or reputable databases, when available, to estimate the fraction of disease alleles, weighted by frequency, that the methodology is predicted to be able or unable to detect. Detection rates are approximate and only account for analytical sensitivity. Certain variants that have been previously described in the literature may not be reported, if there is insufficient evidence for pathogenicity. Detection rates do not account for the disease specific rates of *de novo* variation.



RESULTS RECIPIENT
GENETICS & IVF INSTITUTE
Attn: Suzanne Seitz
NPI: 1972005890
Report Date: 03/25/2021

MALE
DONOR 6073
DOB: [REDACTED]
Ethnicity: Northern European
Barcode: [REDACTED]

FEMALE
N/A

This test was developed, and its performance characteristics determined by, Myriad Women's Health, Inc. It has not been cleared or approved by the US Food and Drug Administration (FDA). The FDA does not require this test to go through premarket 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 of 1988 (CLIA) as qualified to perform high-complexity clinical testing. These results are adjunctive to the ordering physician's evaluation. CLIA Number: #05D1102604.

Incidental Findings

Unless otherwise indicated, these results and interpretations are limited to the specific disease panel(s) requested by the ordering healthcare provider. In some cases, standard data analyses may identify genetic findings beyond the region(s) of interest specified by the test, and such findings may not be reported. These findings may include genomic abnormalities with major, minor, or no, clinical significance.

If you have questions or would like more information about any of the test methods or limitations, please contact (888) 268-6795.

Resources

GENOME CONNECT | <http://www.genomeconnect.org>

Patients can share their reports using research registries such as Genome Connect, an online research registry building a genetics and health knowledge base. Genome Connect provides patients, physicians, and researchers an opportunity to share genetic information to support the study of the impact of genetic variation on health conditions.

SENIOR LABORATORY DIRECTOR

Karla R. Bowles, PhD, FACMG, CGMB

Report content approved by Lulu Mao, PhD, DABMGG on Mar 25, 2021



RESULTS RECIPIENT
GENETICS & IVF INSTITUTE
Attn: Suzanne Seitz
NPI: 1972005890
Report Date: 03/25/2021

MALE
DONOR 6073
DOB: [REDACTED]
Ethnicity: Northern European
Barcode: [REDACTED]

FEMALE
N/A

Conditions Tested

Maple Syrup Urine Disease Type II - Gene: DBT. Autosomal Recessive. Sequencing with copy number analysis. Exons: NM_001918:1-11. **Detection Rate:** Northern European 97%.

Short-chain Acyl-CoA Dehydrogenase Deficiency - Gene: ACADS. Autosomal Recessive. Sequencing with copy number analysis. Exons: NM_000017:1-10. **Detection Rate:** Northern European >99%.

Risk Calculations

Below are the risk calculations for all conditions tested. Negative results do not rule out the possibility of being a carrier. Residual risk is an estimate of each patient's post-test likelihood of being a carrier, while the reproductive risk represents an estimated likelihood that the patients' future children could inherit each disease. These risks are inherent to all carrier-screening tests, may vary by ethnicity, are predicated on a negative family history, and are present even given a negative test result. Inaccurate reporting of ethnicity may cause errors in risk calculation. In addition, average carrier rates are estimated using incidence or prevalence data from published scientific literature and/or reputable databases, where available, and are incorporated into residual risk calculations for each population/ethnicity. When population-specific data is not available for a condition, average worldwide incidence or prevalence is used. Further, incidence and prevalence data are only collected for the specified phenotypes (which include primarily the classic or severe forms of disease) and may not include alternate or milder disease manifestations associated with the gene. Actual incidence rates, prevalence rates, and carrier rates, and therefore actual residual risks, may be higher or lower than the estimates provided. Carrier rates, incidence/prevalence, and/or residual risks are not provided for some genes with biological or heritable properties that would make these estimates inaccurate. A '+' symbol indicates a positive result. See the full clinical report for interpretation and details. The reproductive risk presented is based on a hypothetical pairing with a partner of the same ethnic group.

Disease	DONOR 6073 Residual Risk	Reproductive Risk
Maple Syrup Urine Disease Type II	1 in 16,000	< 1 in 1,000,000
Short-chain Acyl-CoA Dehydrogenase Deficiency	1 in 11,000	< 1 in 1,000,000

Patient	Sample	Referring Doctor
Patient Name: Donor 6073 Date of Birth: [REDACTED] Reference #: Indication: Donor of other specified organs or tissues (Z52.89) Test Type: Chromosome Analysis, Blood	Specimen Type: Peripheral Blood Lab #: Date Collected: 2/5/2020 Date Received: 2/6/2020 Final Report: 2/22/2020	[REDACTED] Fairfax Cryobank, Inc. [REDACTED] [REDACTED] [REDACTED]

CYTOGENETIC ANALYSIS

Results

Staining: **G-bands by trypsin using Giemsa (GTG)** Chromosome count: **46** Cells captured: **5**
 Band level: **400-550** Cells analyzed: **20** Cells karyotyped: **2**

Karyotype: **46,XY**

Interpretation

Cytogenetic analysis revealed the presence of a **normal male** karyotype in peripheral blood lymphocytes. This analysis does not show any evidence of a clinically significant numerical or structural chromosome abnormality.

The standard procedures used in this analysis do not routinely detect microdeletions, small rearrangements or low level mosaicism.

This case has been reviewed and electronically signed by Arvind Babu, Ph.D., FACMG, Laboratory Director
 Laboratory Medical Consultant: Bryn Webb, M.D.

If the ordering provider has questions about this report, please contact Sema4 at 800-298-6470, option 2 to speak with a genetic counselor or email gc@sema4.com

Performing Laboratory information:

QUEST DIAGNOSTICS/NICHOLS SJC, 33608 ORTEGA HWY, SAN JUAN CAPISTRANO, CA 92675-2042
 Laboratory Director: IRINA MARAMICA, MD PHD, CLIA: 05D063352



Patient Information	Specimen Information	Client Information
ID 6073, DONOR DOB: [REDACTED] AGE: [REDACTED] Gender: M Phone: NG Patient ID: [REDACTED]	Specimen: [REDACTED] Requisition: [REDACTED] Lab Ref #: [REDACTED] Collected: 02/05/2020 Received: 02/07/2020 / 20:38 EST Reported: 02/11/2020 / 16:42 EST	Client #: 41578 1000 GENOMICS, SEMA4 SEMA4 1428 MADISON AVE 2ND FL ATRAN BLDG RM 25 NEW YORK, NY 10029

Test Name	In Range	Out Of Range	Reference Range	Lab
HEMOGLOBINOPATHY EVAL INTERPRETATION				TBR
	Normal Pattern			
HEMOGLOBIN A	96.8		>96.0 Percent	
HEMOGLOBIN F	<1.0		<2.0 Percent	
HEMOGLOBIN A2	2.2		1.8-3.5 Percent	
HEMOGLOBIN S	0.0		0.0-0.0 Percent	
HEMOGLOBIN C	0.0		0.0-0.0 Percent	
HEMOGLOBIN VARIANT	0.0		0.0-0.0 Percent	
HEMOGLOBINOPATHY INDICES				TBR
RBC	5.04		4.20-5.80 Million/uL	
HEMOGLOBIN	15.8		13.2-17.1 g/dL	
HEMATOCRIT	47.2		38.5-50.0 %	
MCV	93.7		80.0-100.0 fL	
MCH	31.3		27.0-33.0 pg	
RDW	12.5		11.0-15.0 %	

PERFORMING SITE:

TBR Quest Diagnostics, One Malcolm Avenue, Teterboro, NJ 07608 Laboratory Director: Lawrence Tsao, M.D., CLIA: 31D0696246



Patient Information:

6073, Donor

DOB: [REDACTED]

Sex: M

MR#: 6073

Patient#: [REDACTED]

Accession:

[REDACTED]

Test# [REDACTED]

Order#: [REDACTED]

Ext Test#: [REDACTED] 0

Ext Order#: [REDACTED]

Specimen Type: DNA

Collected: Not provided

Received Date: Apr 14,2023

Authorized Date: Apr 15,2023

Physician:

Seitz, Suzanne

ATTN: Seitz, Suzanne

Fairfax Cryobank

3015 Williams Drive

Fairfax, VA 22031

Phone:

Fax:

Laboratory:

Fulgent Genetics

CAP#: 8042697

CLIA#: 05D2043189

Laboratory Director:

Dr. Hanlin (Harry) Gao

Report Date: **Apr 24,2023**

Final Report

TEST PERFORMED

CCDC103 Single Gene

(1 Gene Panel: *CCDC103*; gene sequencing with deletion and duplication analysis)

RESULTS:

No clinically significant sequence or copy-number variants were identified in the submitted specimen.

A negative result does not rule out the possibility of a genetic predisposition nor does it rule out any pathogenic mutations of the sort not queried by this test or in areas not reliably assessed by this test.

INTERPRETATION:

Notes and Recommendations:

- As requested, this report only includes variants classified as Pathogenic, Likely Pathogenic, or Risk Allele at the time of analysis. If detected, this report does not include variants classified as of uncertain significance.
- Gene specific notes and limitations may be present. See below.
- These results should be interpreted in the context of this individual's clinical findings, biochemical profile, and family history.
- Genetic counseling is recommended. Available genetic counselors and additional resources can be found at the National Society of Genetic Counselors (NSGC; <https://www.nsgc.org>)
- Guide to Interpreting Genomic Reports: A Genomics Toolkit (CSER Consortium; February 2017) (<https://www.genome.gov/For-Health-Professionals/Provider-Genomics-Education-Resources#hlep>)

GENES TESTED:

CCDC103 Single Gene

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

CCDC103

Gene Specific Notes and Limitations

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

METHODS:



Genomic DNA was isolated from the submitted specimen indicated above (if cellular material was submitted). DNA was barcoded, and enriched for the coding exons of targeted genes using hybrid capture technology. Prepared DNA libraries were then sequenced using a Next Generation Sequencing technology. Following alignment to the human genome reference sequence (assembly GRCh37), variants were detected in regions of at least 10x coverage. For this specimen, 100.00% and 100.00% of coding regions and splicing junctions of genes listed had been sequenced with coverage of at least 10x and 20x, respectively, by NGS or by Sanger sequencing. The remaining regions did not have 10x coverage, and were not evaluated. Variants were interpreted manually using locus specific databases, literature searches, and other molecular biological principles. To minimize false positive results, any variants that do not meet internal quality standards are confirmed by Sanger sequencing. Variants classified as pathogenic, likely pathogenic, or risk allele which are located in the coding regions and nearby intronic regions (+/- 20bp) of the genes listed above are reported. Variants outside these intervals may be reported but are typically not guaranteed. When a single pathogenic or likely pathogenic variant is identified in a clinically relevant gene with autosomal recessive inheritance, the laboratory will attempt to ensure 100% coverage of coding sequences either through NGS or Sanger sequencing technologies ("fill-in"). All genes listed were evaluated for large deletions and/or duplications. However, single exon deletions or duplications will not be detected in this assay, nor will copy number alterations in regions of genes with significant pseudogenes. Putative deletions or duplications identified by NGS are confirmed by an orthogonal method (qPCR or MLPA), unless exceeding an internally specified and validated quality score, beyond which deletions and duplications are considered real without further confirmation. New York patients: diagnostic findings are confirmed by Sanger, MLPA, or qPCR; exception SNV variants in genes for which confirmation of NGS results has been performed ≥ 10 times may not be confirmed if identified with high quality by NGS. Bioinformatics: The Fulgent Germline v2019.2 pipeline was used to analyze this specimen.

LIMITATIONS:

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

SIGNATURE:



Zhenbin Chen, Ph.D., CGMS, FACMG on 4/24/2023 08:02 PM PDT
Electronically signed

DISCLAIMER:

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