



## Donor 5556

### Genetic Testing Summary

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

Last Updated: 08/09/24

Donor Reported Ancestry: Irish, German

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	<b>Carrier: Congenital Disorder of Glycosylation Type 1A (PMM2)</b> Negative for other genes sequenced.	Partner testing is recommended before using this donor.
<b>Special Testing</b>		
Genes: POLG, TRPM1, CYP11B1	Negative by gene sequencing	

\*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	Sample	Referring Doctor
<b>Patient Name:</b> Donor 5556 <b>Date of Birth:</b> [REDACTED] <b>Reference #:</b> [REDACTED] <b>Indication:</b> Carrier Testing <b>Test Type:</b> Expanded Carrier Screen (283) Minus TSE	<b>Specimen Type:</b> Blood <b>Lab #:</b> [REDACTED] <b>Date Collected:</b> 1/22/2019 <b>Date Received:</b> 1/23/2019 <b>Final Report:</b> 2/6/2019	[REDACTED] <b>Fairfax Cryobank, Inc.</b> [REDACTED] [REDACTED] [REDACTED]

## RESULT SUMMARY

### THIS PATIENT WAS TESTED FOR 283 DISEASES.

Please see Table 1 for list of diseases tested.

#### POSITIVE for congenital disorder of glycosylation, type Ia

A heterozygous (one copy) pathogenic variant, c.422G>A, p.R141H, was detected in the *PMM2* gene

#### NEGATIVE for the remaining diseases

#### 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. In addition, 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 for congenital disorder of glycosylation, type Ia

A heterozygous (one copy) pathogenic missense variant, c.422G>A, p.R141H, was detected in the *PMM2* gene (NM\_000303.2). When this variant is present in trans with a pathogenic variant, it is considered to be causative for congenital disorder of glycosylation, type Ia. Therefore, this individual is expected to be at least a carrier for congenital disorder of glycosylation, type Ia. Heterozygous carriers are not expected to exhibit symptoms of this disease.

#### What is congenital disorder of glycosylation, type Ia?

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Congenital disorder of glycosylation, type Ia is an autosomal recessive syndrome caused by pathogenic variants in the gene *PMM2*. While patients have been reported from multiple ethnicities, this disease is more common in the Ashkenazi Jewish and Caucasian populations. This disease may present in infancy, childhood or adolescence, and the clinical manifestations are highly variable. In infants, the disease may present as failure to thrive as a result of feeding problems; later, the disease may manifest as encephalopathy, hypotonia, delayed language and motor development, intellectual disability, stroke-like episodes, and retinitis pigmentosa. Severely affected individuals may die in early childhood, but more mildly affected individuals may survive into adulthood with variable intellectual disability, spinal abnormalities, endocrine dysfunction and coagulopathy. Several specific variants have been associated with milder or more severe disease, and therefore the disease severity may be predicted in some patients.

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 <http://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.

## TEST SPECIFIC RESULTS

### Alpha-thalassemia

#### **NEGATIVE for alpha-thalassemia**

*HBA1* copy number: 2

*HBA2* copy number: 2

No pathogenic copy number variants detected

*HBA1* and *HBA2* sequence analysis: No pathogenic or likely pathogenic variants identified

Reduced risk of being an alpha-thalassemia carrier (aa/aa)

**Genes analyzed:** *HBA1* (NM\_000558.4) and *HBA2* (NM\_000517.4)

**Inheritance:** Autosomal Recessive

### **Recommendations**

Individuals of Asian, African, Hispanic and Mediterranean ancestry should also be screened for hemoglobinopathies by CBC and hemoglobin electrophoresis.

### **Interpretation**

No pathogenic or likely pathogenic copy number variants or sequence variants were detected in this patient, suggesting that four copies of the alpha-globin gene are present (aa/aa). Typically, individuals have four functional alpha-globin genes: 2 copies of *HBA1* and 2 copies of *HBA2*, whose expression is regulated by a cis-

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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.

This individual was negative for all *HBA* deletions, duplications and variants that were tested. These negative results reduce but do not eliminate the possibility that this individual is a carrier. See *Table of Residual Risks Based on Ethnicity*. With individuals of mixed ethnicity, it is recommended to use the highest residual risk estimate.

**Table of Residual Risks Based on Ethnicity**

Ethnicity	Carrier Frequency	Detection Rate	Residual Risk
Caucasian	1 in 500	95%	1 in 10,000
African American	1 in 30	95%	1 in 580
Asian	1 in 20	95%	1 in 380
Worldwide	1 in 25	95%	1 in 480

**Congenital Adrenal Hyperplasia (21-Hydroxylase Deficiency)**

**NEGATIVE for congenital adrenal hyperplasia (due to 21-hydroxylase deficiency)**

*CYP21A2* copy number: 2

No pathogenic copy number variants detected

No pathogenic sequence variants detected in *CYP21A2*

Reduced risk of being a congenital adrenal hyperplasia carrier

**Genes analyzed:** *CYP21A2* (NM\_000500.6)

**Inheritance:** Autosomal Recessive

**Recommendations**

Consideration of residual risk by ethnicity (see below) after a negative carrier screen is recommended, especially in the case of a positive family history of congenital adrenal hyperplasia.

**Interpretation**

This individual was negative for all pathogenic *CYP21A2* copy number variants that were tested, and no pathogenic or likely pathogenic variants were identified by sequence analysis. These negative results reduce but do not eliminate the possibility that this individual is a carrier. See *Table of Residual Risks Based on Ethnicity*. With individuals of mixed ethnicity, it is recommended to use the highest residual risk estimate.

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**Table of Residual Risk Based On Ethnicity - Classic Congenital Adrenal Hyperplasia Due to 21-Hydroxylase Deficiency**

Ethnicity	Carrier Frequency	Detection Rate	Residual Risk
Ashkenazi Jewish	1 in 40	>95%	1 in 780
Caucasian	1 in 67	>95%	1 in 1300
Worldwide	1 in 60	>95%	1 in 1200

**Table of Residual Risk Based On Ethnicity - Non-Classic Congenital Adrenal Hyperplasia Due to 21-Hydroxylase Deficiency**

Ethnicity	Carrier Frequency	Detection Rate	Residual Risk
Ashkenazi Jewish	1 in 7	>95%	1 in 120
Caucasian	1 in 11	>95%	1 in 200
Worldwide	1 in 16	>95%	1 in 300

**Fragile X syndrome**

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. Sequencing of the *FMR1* gene by next generation sequencing did not identify any clinically significant variants.

**Spinal Muscular Atrophy**

**NEGATIVE for spinal muscular atrophy**

*SMN1* Copy Number: 2

*SMN2* Copy Number: 1

c.\*3+80T>G: Negative

**Negative copy number result**

**Decreased risk of being an *SMN1* silent (2+0) carrier (see *SMA Table*)**

**Genes analyzed:** *SMN1* (NM\_000344.3) and *SMN2* (NM\_017411.3)

**Inheritance:** Autosomal Recessive

**Recommendations**

Consideration of residual risk by ethnicity after a negative carrier screen is recommended, especially in the case of a positive family history for spinal muscular atrophy.

**Interpretation**

This patient is negative for loss of *SMN1* copy number. Complete loss of *SMN1* is causative in spinal muscular

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atrophy (SMA). Two copies of *SMN1* were detected in this individual, which significantly reduces the risk of being an SMA carrier. Parallel testing to assess the presence of an *SMN1* duplication allele was also performed to detect a single nucleotide polymorphism (SNP), c.\*3+80T>G, in intron 7 of the *SMN1* gene. This individual was found to be negative for this change and is therefore, at a decreased risk of being a silent (2+0) carrier, see *SMA Table* for residual risk estimates based on ethnicity.

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

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

\*Residual risk with two copies *SMN1* detected using dosage sensitive methods. The presence of three or more copies of *SMN1* reduces the risk of being an *SMN1* carrier between 5 - 10 fold, depending on ethnicity. **FOR INDIVIDUALS WITH MIXED ETHNICITY, USE HIGHEST RESIDUAL RISK ESTIMATE**

^ Parental follow-up will be requested for confirmation

This case has been reviewed and electronically signed by Lisa Edelmann, Ph.D., FACMG, Laboratory Director

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

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## Test Methods and Comments

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

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

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

### Genotyping (Analytical Detection Rate >99%)

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

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

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

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

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

For congenital adrenal hyperplasia, the copy number of the *CYP21A2* gene was analyzed. This analysis can detect large deletions 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



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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



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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.

**Table 1. List of genes and diseases tested.**

Please see <http://go.sema4.com/residualrisk> for specific detection rates and residual risk by ethnicity.

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Gene	Disease
<b>ACADM</b>	Medium Chain Acyl-CoA Dehydrogenase Deficiency
<b>ABCB11</b>	Progressive Familial Intrahepatic Cholestasis, Type 2
<b>ABCC8</b>	Familial Hyperinsulinism (ABCC8-Related)
<b>ABCD1</b>	Adrenoleukodystrophy, X-Linked
<b>ACAD9</b>	Mitochondrial Complex I Deficiency (ACAD9-Related)
<b>ACADVL</b>	Very Long Chain Acyl-CoA Dehydrogenase Deficiency
<b>ACAT1</b>	Beta-Ketothiolase Deficiency
<b>ACOX1</b>	Acyl-CoA Oxidase I Deficiency
<b>ACSF3</b>	Combined Malonic and Methylmalonic Aciduria
<b>ADA</b>	Adenosine Deaminase Deficiency
<b>ADAMTS2</b>	Ehlers-Danlos Syndrome, Type VIIC
<b>AGA</b>	Aspartylglycosaminuria
<b>AGL</b>	Glycogen Storage Disease, Type III
<b>AGPS</b>	Rhizomelic Chondrodysplasia Punctata, Type 3
<b>AGXT</b>	Primary Hyperoxaluria, Type 1
<b>AIRE</b>	Polyglandular Autoimmune Syndrome, Type 1
<b>ALDH3A2</b>	Sjogren-Larsson Syndrome
<b>ALDOB</b>	Hereditary Fructose Intolerance
<b>ALG6</b>	Congenital Disorder of Glycosylation, Type Ic
<b>ALMS1</b>	Alstrom Syndrome
<b>ALPL</b>	Hypophosphatasia
<b>AMT</b>	Glycine Encephalopathy (AMT-Related)
<b>AQP2</b>	Nephrogenic Diabetes Insipidus, Type II
<b>ARSA</b>	Metachromatic Leukodystrophy
<b>ARSB</b>	Mucopolysaccharidosis type VI
<b>ASL</b>	Argininosuccinic Aciduria
<b>ASNS</b>	Asparagine Synthetase Deficiency
<b>ASPA</b>	Canavan Disease
<b>ASS1</b>	Citrullinemia, Type 1
<b>ATM</b>	Ataxia-Telangiectasia
<b>ATP6V1B1</b>	Renal Tubular Acidosis and Deafness
<b>ATP7A</b>	Menkes Disease
<b>ATP7B</b>	Wilson Disease
<b>ATRX</b>	Alpha-Thalassemia Mental Retardation Syndrome
<b>BBS1</b>	Bardet-Biedl Syndrome (BBS1-Related)
<b>BBS10</b>	Bardet-Biedl Syndrome (BBS10-Related)
<b>BBS12</b>	Bardet-Biedl Syndrome (BBS12-Related)
<b>BBS2</b>	Bardet-Biedl Syndrome (BBS2-Related)
<b>BCKDHA</b>	Maple Syrup Urine Disease, Type 1a
<b>BCKDHB</b>	Maple Syrup Urine Disease, Type 1b
<b>BCS1L</b>	GRACILE Syndrome and Other BCS1L-Related Disorders
<b>BLM</b>	Bloom Syndrome
<b>BSND</b>	Bartter Syndrome, Type 4A
<b>BTD</b>	Biotinidase Deficiency
<b>CAPN3</b>	Limb-Girdle Muscular Dystrophy, Type 2A
<b>CBS</b>	Homocystinuria (CBS-Related)
<b>CDH23</b>	Usher Syndrome, Type ID
<b>CEP290</b>	Leber Congenital Amaurosis 10 and Other CEP290-Related Ciliopathies
<b>CERKL</b>	Retinitis Pigmentosa 26

Gene	Disease
<b>CFTR</b>	Cystic Fibrosis
<b>CHM</b>	Choroideremia
<b>CHRNE</b>	Congenital Myasthenic Syndrome (CHRNE-Related)
<b>CIITA</b>	Bare Lymphocyte Syndrome, Type II
<b>CLN3</b>	Neuronal Ceroid-Lipofuscinosis (CLN3-Related)
<b>CLN5</b>	Neuronal Ceroid-Lipofuscinosis (CLN5-Related)
<b>CLN6</b>	Neuronal Ceroid-Lipofuscinosis (CLN6-Related)
<b>CLN8</b>	Neuronal Ceroid-Lipofuscinosis (CLN8-Related)
<b>CLRN1</b>	Usher Syndrome, Type III
<b>CNGB3</b>	Achromatopsia
<b>COL27A1</b>	Steel Syndrome
<b>COL4A3</b>	Alport Syndrome (COL4A3-Related)
<b>COL4A4</b>	Alport Syndrome (COL4A4-Related)
<b>COL4A5</b>	Alport Syndrome (COL4A5-Related)
<b>COL7A1</b>	Dystrophic Epidermolysis Bullosa
<b>CPS1</b>	Carbamoylphosphate Synthetase I Deficiency
<b>CPT1A</b>	Carnitine Palmitoyltransferase IA Deficiency
<b>CPT2</b>	Carnitine Palmitoyltransferase II Deficiency
<b>CRB1</b>	Leber Congenital Amaurosis 8 / Retinitis Pigmentosa 12 / Pigmented Paravenous Chorioretinal Atrophy
<b>CTNS</b>	Cystinosis
<b>CTSK</b>	Pycnodysostosis
<b>CYBA</b>	Chronic Granulomatous Disease (CYBA-related)
<b>CYBB</b>	Chronic Granulomatous Disease (CYBB-related)
<b>CYP11B2</b>	Corticosterone Methyloxidase Deficiency
<b>CYP17A1</b>	Congenital Adrenal Hyperplasia due to 17-Alpha-Hydroxylase Deficiency
<b>CYP21A2</b>	Classic Congenital Adrenal Hyperplasia due to 21-Hydroxylase Deficiency
<b>CYP19A1</b>	Aromatase Deficiency
<b>CYP27A1</b>	Cerebrotendinous Xanthomatosis
<b>DCLRE1C</b>	Omenn Syndrome / Severe Combined Immunodeficiency, Athabaskan-Type
<b>DHCR7</b>	Smith-Lemli-Opitz Syndrome
<b>DHDDS</b>	Retinitis Pigmentosa 59
<b>DLG</b>	Lipoamide Dehydrogenase Deficiency
<b>DMD</b>	Duchenne Muscular Dystrophy / Becker Muscular Dystrophy
<b>DNAH5</b>	Primary Ciliary Dyskinesia (DNAH5-Related)
<b>DNAI1</b>	Primary Ciliary Dyskinesia (DNAI1-Related)
<b>DNAI2</b>	Primary Ciliary Dyskinesia (DNAI2-related)
<b>DYSF</b>	Limb-Girdle Muscular Dystrophy, Type 2B
<b>EDA</b>	Hypohidrotic Ectodermal Dysplasia 1
<b>EIF2B5</b>	Leukoencephalopathy with Vanishing White Matter
<b>EMD</b>	Emery-Dreifuss Myopathy 1
<b>ESCO2</b>	Roberts Syndrome
<b>ETFA</b>	Glutaric Acidemia, Type IIa
<b>ETFDH</b>	Glutaric Acidemia, Type IIc
<b>ETHE1</b>	Ethylmalonic Encephalopathy
<b>EVC</b>	Ellis-van Creveld Syndrome (EVC-Related)
<b>EYS</b>	Retinitis Pigmentosa 25
<b>F11</b>	Factor XI Deficiency
<b>F9</b>	Factor IX Deficiency
<b>FAH</b>	Tyrosinemia, Type I

Gene	Disease
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Gene	Disease
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Patient: Donor 5556

DOB: [REDACTED]

Lab #: [REDACTED]

<b>FAM161A</b>	Retinitis Pigmentosa 28
<b>FANCA</b>	Fanconi Anemia, Group A
<b>FANCC</b>	Fanconi Anemia, Group C
<b>FANCG</b>	Fanconi Anemia, Group G
<b>FH</b>	Fumarase Deficiency
<b>FKRP</b>	Limb-Girdle Muscular Dystrophy, Type 2I
<b>FKTN</b>	Walker-Warburg Syndrome and Other FKTN-Related Dystrophies
<b>FMR1</b>	Fragile X Syndrome
<b>G6PC</b>	Glycogen Storage Disease, Type Ia
<b>GAA</b>	Glycogen Storage Disease, Type II
<b>GALC</b>	Krabbe Disease
<b>GALK1</b>	Galactokinase Deficiency
<b>GALT</b>	Galactosemia
<b>GAMT</b>	Cerebral Creatine Deficiency Syndrome 2
<b>GBA</b>	Gaucher Disease
<b>GBE1</b>	Glycogen Storage Disease, Type IV / Adult Polyglucosan Body Disease
<b>GCDH</b>	Glutaric Acidemia, Type I
<b>GFM1</b>	Combined Oxidative Phosphorylation Deficiency 1
<b>GJB1</b>	Charcot-Marie-Tooth Disease, X-Linked
<b>GJB2†</b>	Non-Syndromic Hearing Loss (GJB2-Related)
<b>GLA</b>	Fabry Disease
<b>GLB1</b>	Mucopolysaccharidosis Type IVb / GM1 Gangliosidosis
<b>GLDC</b>	Glycine Encephalopathy (GLDC-Related)
<b>GLE1</b>	Lethal Congenital Contracture Syndrome 1 / Lethal Arthrogyriposis with Anterior Horn Cell Disease
<b>GNE</b>	Inclusion Body Myopathy 2
<b>GNPTAB</b>	Mucopolipidosis II / IIIA
<b>GNPTG</b>	Mucopolipidosis III Gamma
<b>GNS</b>	Mucopolysaccharidosis Type IIID
<b>GP1BA</b>	Bernard-Soulier Syndrome, Type A1
<b>GP9</b>	Bernard-Soulier Syndrome, Type C
<b>GPR56</b>	Bilateral Frontoparietal Polymicrogyria
<b>GRHPR</b>	Primary Hyperoxaluria, Type 2
<b>HADHA</b>	Long-Chain 3-Hydroxyacyl-CoA Dehydrogenase Deficiency
<b>HAX1</b>	Congenital Neutropenia (HAX1-Related)
<b>HBA1/HBA2</b>	Alpha-Thalassemia
<b>HBB</b>	Beta-Globin-Related Hemoglobinopathies
<b>HEXA</b>	Tay-Sachs Disease
<b>HEXB</b>	Sandhoff Disease
<b>HFE2</b>	Hemochromatosis, Type 2A
<b>HGSNAT</b>	Mucopolysaccharidosis Type IIIC
<b>HLCS</b>	Holocarboxylase Synthetase Deficiency
<b>HMGCL</b>	HMG-CoA Lyase Deficiency
<b>HOGA1</b>	Primary Hyperoxaluria, Type 3
<b>HPS1</b>	Hermansky-Pudlak Syndrome, Type 1
<b>HPS3</b>	Hermansky-Pudlak Syndrome, Type 3
<b>HSD17B4</b>	D-Bifunctional Protein Deficiency
<b>HSD3B2</b>	3-Beta-Hydroxysteroid Dehydrogenase Type II Deficiency
<b>HYAL1</b>	Mucopolysaccharidosis type IX
<b>HYLS1</b>	Hydroletharus Syndrome
<b>IDS</b>	Mucopolysaccharidosis Type II

<b>IDUA</b>	Mucopolysaccharidosis Type I
<b>IKBKAP</b>	Familial Dysautonomia
<b>IL2RG</b>	X-Linked Severe Combined Immunodeficiency
<b>IVD</b>	Isovaleric Acidemia
<b>KCNJ11</b>	Familial Hyperinsulinism (KCNJ11-Related)
<b>LAMA3</b>	Junctional Epidermolysis Bullosa (LAMA3-Related)
<b>LAMB3</b>	Junctional Epidermolysis Bullosa (LAMB3-Related)
<b>LAMC2</b>	Junctional Epidermolysis Bullosa (LAMC2-Related)
<b>LCA5</b>	Leber Congenital Amaurosis 5
<b>LDLR</b>	Familial Hypercholesterolemia
<b>LDLRAP1</b>	Familial Autosomal Recessive Hypercholesterolemia
<b>LHX3</b>	Combined Pituitary Hormone Deficiency 3
<b>LIFR</b>	Stuve-Wiedemann Syndrome
<b>LIPA</b>	Wolman Disease / Cholesteryl Ester Storage Disease
<b>LOXHD1</b>	Deafness, Autosomal Recessive 77
<b>LPL</b>	Lipoprotein Lipase Deficiency
<b>LRPPRC</b>	Leigh Syndrome, French-Canadian Type
<b>MAN2B1</b>	Alpha-Mannosidosis
<b>MCCC1</b>	3-Methylcrotonyl-CoA Carboxylase Deficiency (MCCC1-Related)
<b>MCCC2</b>	3-Methylcrotonyl-CoA Carboxylase Deficiency (MCCC2-Related)
<b>MCOLN1</b>	Mucopolipidosis IV
<b>MED17</b>	Infantile Cerebral and Cerebellar Atrophy
<b>MEFV</b>	Familial Mediterranean Fever
<b>MESP2</b>	Spondylothoracic Dysostosis
<b>MFSD8</b>	Neuronal Ceroid-Lipofuscinosis (MFSD8-Related)
<b>MKS1</b>	Meckel syndrome 1 / Bardet-Biedl Syndrome 13
<b>MLC1</b>	Megalencephalic Leukoencephalopathy with Subcortical Cysts
<b>MMAA</b>	Methylmalonic Acidemia (MMAA-Related)
<b>MMAB</b>	Methylmalonic Acidemia (MMAB-Related)
<b>MMACHC</b>	Methylmalonic Aciduria and Homocystinuria, Cobalamin C Type
<b>MMADHC</b>	Methylmalonic Aciduria and Homocystinuria, Cobalamin D Type
<b>MPI</b>	Congenital Disorder of Glycosylation, Type Ib
<b>MPL</b>	Congenital Amegakaryocytic Thrombocytopenia
<b>MPV17</b>	Mitochondrial DNA Depletion Syndrome 6 / Navajo Neurohepatopathy
<b>MTHFR</b>	Homocystinuria due to MTHFR Deficiency
<b>MTM1</b>	Myotubular Myopathy 1
<b>MTRR</b>	Homocystinuria, cbIE Type
<b>MTTP</b>	Abetalipoproteinemia
<b>MUT</b>	Methylmalonic Acidemia (MUT-Related)
<b>MYO7A</b>	Usher Syndrome, Type IB
<b>NAGLU</b>	Mucopolysaccharidosis Type IIIB
<b>NAGS</b>	N-Acetylglutamate Synthase Deficiency
<b>NBN</b>	Nijmegen Breakage Syndrome
<b>NDRG1</b>	Charcot-Marie-Tooth Disease, Type 4D
<b>NDUFAF5</b>	Mitochondrial Complex I Deficiency (NDUFAF5-Related)
<b>NDUFS6</b>	Mitochondrial Complex I Deficiency (NDUFS6-Related)
<b>NEB</b>	Nemaline Myopathy 2
<b>NPC1</b>	Niemann-Pick Disease, Type C (NPC1-Related)
<b>NPC2</b>	Niemann-Pick Disease, Type C (NPC2-Related)
<b>NPHS1</b>	Nephrotic Syndrome (NPHS1-Related) / Congenital Finnish Nephrosis

**Patient:** Donor 5556

**DOB:** [REDACTED]

**Lab #:** [REDACTED]

Gene	Disease
<b>NPHS2</b>	Nephrotic Syndrome (NPHS2-Related) / Steroid-Resistant Nephrotic Syndrome
<b>NR2E3</b>	Enhanced S-Cone Syndrome
<b>NTRK1</b>	Congenital Insensitivity to Pain with Anhidrosis
<b>OAT</b>	Ornithine Aminotransferase Deficiency
<b>OPA3</b>	3-Methylglutaconic Aciduria, Type III
<b>OTC</b>	Ornithine Transcarbonylase Deficiency
<b>PAH</b>	Phenylalanine Hydroxylase Deficiency
<b>PCCA</b>	Propionic Acidemia (PCCA-Related)
<b>PCCB</b>	Propionic Acidemia (PCCB-Related)
<b>PCDH15</b>	Usher Syndrome, Type IF
<b>PDHA1</b>	Pyruvate Dehydrogenase E1-Alpha Deficiency
<b>PDHB</b>	Pyruvate Dehydrogenase E1-Beta Deficiency
<b>PEX1</b>	Zellweger Syndrome Spectrum (PEX1-Related)
<b>PEX10</b>	Zellweger Syndrome Spectrum (PEX10-Related)
<b>PEX2</b>	Zellweger Syndrome Spectrum (PEX2-Related)
<b>PEX6</b>	Zellweger Syndrome Spectrum (PEX6-Related)
<b>PEX7</b>	Rhizomelic Chondrodysplasia Punctata, Type 1
<b>PFKM</b>	Glycogen Storage Disease, Type VII
<b>PHGDH</b>	3-Phosphoglycerate Dehydrogenase Deficiency
<b>PKHD1</b>	Polycystic Kidney Disease, Autosomal Recessive
<b>PMM2</b>	Congenital Disorder of Glycosylation, Type Ia
<b>POMGNT1</b>	Muscle-Eye-Brain Disease and Other POMGNT1-Related Congenital Muscular Dystrophy-Dystroglycanopathies
<b>PPT1</b>	Neuronal Ceroid-Lipofuscinosis (PPT1-Related)
<b>PROP1</b>	Combined Pituitary Hormone Deficiency 2
<b>PRPS1</b>	Charcot-Marie-Tooth Disease, Type 5 / Arts syndrome
<b>PSAP</b>	Combined SAP Deficiency
<b>PTS</b>	6-Pyruvoyl-Tetrahydropterin Synthase Deficiency
<b>PUS1</b>	Mitochondrial Myopathy and Sideroblastic Anemia 1
<b>PYGM</b>	Glycogen Storage Disease, Type V
<b>RAB23</b>	Carpenter Syndrome
<b>RAG2</b>	Omenn Syndrome (RAG2-Related)
<b>RAPSN</b>	Congenital Myasthenic Syndrome (RAPSN-Related)
<b>RARS2</b>	Pontocerebellar Hypoplasia, Type 6
<b>RDH12</b>	Leber Congenital Amaurosis 13
<b>RMRP</b>	Cartilage-Hair Hypoplasia
<b>RPE65</b>	Leber Congenital Amaurosis 2 / Retinitis pigmentosa 20
<b>RPGRIP1L</b>	Joubert Syndrome 7 / Meckel Syndrome 5 / COACH Syndrome
<b>RS1</b>	X-Linked Juvenile Retinoschisis
<b>RTEL1</b>	Dyskeratosis Congenita (RTEL1-Related)
<b>SACS</b>	Autosomal Recessive Spastic Ataxia of Charlevoix-Saguenay
<b>SAMHD1</b>	Aicardi-Goutières Syndrome (SAMHD1-Related)
<b>SEPSECS</b>	Progressive Cerebello-Cerebral Atrophy

Gene	Disease
<b>SGCA</b>	Limb-Girdle Muscular Dystrophy, Type 2D
<b>SGCB</b>	Limb-Girdle Muscular Dystrophy, Type 2E
<b>SGCG</b>	Limb-Girdle Muscular Dystrophy, Type 2C
<b>SGSH</b>	Mucopolysaccharidosis Type IIIA
<b>SLC12A3</b>	Gitelman Syndrome
<b>SLC12A6</b>	Andermann Syndrome
<b>SLC17A5</b>	Salla Disease
<b>SLC22A5</b>	Primary Carnitine Deficiency
<b>SLC25A13</b>	Citrin Deficiency
<b>SLC25A15</b>	Hyperornithinemia-Hyperammonemia-Homocitrullinuria Syndrome
<b>SLC26A2</b>	Sulfate Transporter-Related Osteochondrodysplasia
<b>SLC26A4</b>	Pendred Syndrome
<b>SLC35A3</b>	Arthrogyposis, Mental Retardation, and Seizures
<b>SLC37A4</b>	Glycogen Storage Disease, Type Ib
<b>SLC39A4</b>	Acrodermatitis Enteropathica
<b>SLC4A11</b>	Corneal Dystrophy and Perceptive Deafness
<b>SLC6A8</b>	Cerebral Creatine Deficiency Syndrome 1
<b>SLC7A7</b>	Lysinuric Protein Intolerance
<b>SMARCA1</b>	Schimke Immunoosseous Dysplasia
<b>SMN1</b>	Spinal Muscular Atrophy
<b>SMPD1</b>	Niemann-Pick Disease (SMPD1-Related)
<b>STAR</b>	Lipoid Adrenal Hyperplasia
<b>SUMF1</b>	Multiple Sulfatase Deficiency
<b>TCIRG1</b>	Osteopetrosis 1
<b>TECPR2</b>	Hereditary Spastic Paraparesis 49
<b>TFR2</b>	Hemochromatosis, Type 3
<b>TGM1</b>	Lamellar Ichthyosis, Type 1
<b>TH</b>	Segawa Syndrome
<b>TMEM216</b>	Joubert Syndrome 2
<b>TPP1</b>	Neuronal Ceroid-Lipofuscinosis (TPP1-Related)
<b>TRMU</b>	Acute Infantile Liver Failure
<b>TSM</b>	Combined Oxidative Phosphorylation Deficiency 3
<b>TTPA</b>	Ataxia With Isolated Vitamin E Deficiency
<b>TYMP</b>	Myoneurogastrointestinal Encephalopathy
<b>USH1C</b>	Usher Syndrome, Type IC
<b>USH2A</b>	Usher Syndrome, Type IIA
<b>VPS13A</b>	Choreoacanthocytosis
<b>VPS13B</b>	Cohen Syndrome
<b>VPS45</b>	Congenital Neutropenia (VPS45-Related)
<b>VRK1</b>	Pontocerebellar Hypoplasia, Type 1A
<b>VSX2</b>	Microphthalmia / Anophthalmia
<b>WNT10A</b>	Odonto-Onycho-Dermal Dysplasia / Schopf-Schulz-Passarge Syndrome

† Please note that GJB2 testing includes testing for the two upstream deletions, del(GJB6-D13S1830) and del(GJB6-D13S1854) (PMID: 11807148 and 15994881)

**Patient Information**

Name: Donor 5556  
 Date of Birth: [REDACTED]  
 Sema4 ID: [REDACTED]  
 Client ID: [REDACTED]  
 Indication: Carrier Screening

**Specimen Information**

Specimen Type: Purified DNA  
 Date Collected: 08/24/2022  
 Date Received: 08/25/2022  
 Final Report: 09/08/2022

**Referring Provider**

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

Custom Carrier Screen (1 gene)  
 with Personalized Residual Risk

**SUMMARY OF RESULTS AND RECOMMENDATIONS**

⊖ Negative

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

AR=Autosomal recessive; XL=X-linked

**Recommendations**

- Consideration of residual risk by ethnicity after a negative carrier screen is recommended for the other diseases on the panel, especially in the case of a positive family history for a specific disorder. Please note that residual risks for X-linked diseases (including full repeat expansions for Fragile X syndrome) may not be accurate for males and the actual residual risk is likely to be lower.

**Test description**

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



Alice Tanner, Ph.D., M.S., CGC, FACMG, Laboratory Director  
 Laboratory Medical Consultant: George A. Diaz, M.D., Ph.D

## Genes and diseases tested

The personalized residual risks listed below are specific to this individual. The complete residual risk table is available at [go.sema4.com/residualrisk](https://go.sema4.com/residualrisk)

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

Disease	Gene	Inheritance Pattern	Status	Detailed Summary
<span style="color: green;">⊖</span> <b>Negative</b>				
<b>Mitochondrial DNA Depletion Syndrome 4A and 4B and other <i>POLG</i>-Related Disorders</b>	<i>POLG</i>	AR	Reduced Risk	<b>Personalized Residual Risk:</b> 1 in 320

*AR*=Autosomal recessive; *XL*=X-linked

## Test methods and comments

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

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

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

### Genotyping (Analytical Detection Rate >99%)

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

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

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

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

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

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

For spinal muscular atrophy (SMA), the copy numbers of the *SMN1* and *SMN2* genes were analyzed. The individual dosage of exons 7 and 8 as well as the combined dosage of exons 1, 4, 6 and 8 of *SMN1* and *SMN2* were assessed. Copy number gains and losses can be detected with this assay. Depending on ethnicity, 6 - 29 % of carriers will not be identified by dosage sensitive methods as this testing cannot detect individuals with two copies (duplication) of the *SMN1* gene on one chromosome and loss of *SMN1* (deletion) on the other chromosome (silent 2+0 carrier) or individuals that carry an intragenic mutation in *SMN1*. Please also note that 2% of individuals diagnosed with SMA have a



causative *SMN1* variant that occurred de novo, and therefore cannot be picked up by carrier screening in the parents. Analysis of *SMN1* is performed in association with short-read sequencing of exons 2a-7, followed by confirmation using long-range PCR (described below).

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

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

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

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

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

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

**Exceptions:** *ABCD1* (NM\_000033.3) exons 8 and 9; *ACADSB* (NM\_001609.3) chr10:124,810,695-124,810,707 (partial exon 9); *ADA* (NM\_000022.2) exon 1; *ADAMTS2* (NM\_014244.4) exon 1; *AGPS* (NM\_003659.3) chr2:178,257,512-178,257,649 (partial exon 1); *ALDH7A1* (NM\_001182.4) chr5:125,911,150-125,911,163 (partial exon 7) and chr5:125,896,807-125,896,821 (partial exon 10); *ALMS1* (NM\_015120.4) chr2:73,612,990-73,613,041 (partial exon 1); *APOPT1* (NM\_032374.4) chr14:104,040,437-104,040,455 (partial exon 3); *CDAN1* (NM\_138477.2) exon 2; *CEP152* (NM\_014985.3) chr15:49,061,146-49,061,165 (partial exon 14) and exon 22; *CEP290* (NM\_025114.3) exon 5, exon 7, chr12:88,519,017-88,519,039 (partial exon 13), chr12:88,514,049-88,514,058 (partial exon 15), chr12:88,502,837-88,502,841 (partial exon 23), chr12:88,481,551-88,481,589 (partial exon 32), chr12:88,471,605-88,471,700 (partial exon 40); *CFTR* (NM\_000492.3) exon 10; *COL4A4* (NM\_000092.4) chr2:227,942,604-227,942,619 (partial exon 25); *COX10* (NM\_001303.3) exon 6; *CYP11B1* (NM\_000497.3) exons 3-7; *CYP11B2* (NM\_000498.3) exons 3-7; *DNAI2* (NM\_023036.4) chr17:72,308,136-72,308,147 (partial exon 12); *DOK7* (NM\_173660.4) chr4:3,465,131-3,465,161 (partial exon 1) and exon 2; *DUOX2* (NM\_014080.4) exons 6-8; *EIF2AK3* (NM\_004836.5) exon 8; *EVC* (NM\_153717.2) exon 1; *F5* (NM\_000130.4) chr1:169,551,662-169,551,679 (partial exon 2); *FH* (NM\_000143.3) exon 1; *GAMT* (NM\_000156.5) exon 1; *GLDC* (NM\_000170.2) exon 1; *GNPTAB* (NM\_024312.4) chr17:4,837,000-4,837,400 (partial exon 2); *GNPTG* (NM\_032520.4) exon 1; *GHR* (NM\_000163.4) exon 3; *GYS2* (NM\_021957.3) chr12:21,699,370-21,699,409 (partial exon 12); *HGSNAT* (NM\_152419.2) exon 1; *IDS* (NM\_000202.6) exon 3; *ITGB4* (NM\_000213.4) chr17:73,749,976-73,750,060 (partial exon 33); *JAK3* (NM\_000215.3) chr19:17,950,462-17,950,483 (partial exon 10); *LIFR* (NM\_002310.5) exon 19; *LMBRD1* (NM\_018368.3) chr6:70,459,226-70,459,257 (partial exon 5), chr6:70,447,828-70,447,836 (partial exon 7) and exon 12; *LYST* (NM\_000081.3) chr1:235,944,158-235,944,176 (partial exon 16) and chr1:235,875,350-235,875,362 (partial exon 43); *MLYCD* (NM\_012213.2) chr16:83,933,242-83,933,282 (partial exon 1); *MTR* (NM\_000254.2) chr1:237,024,418-237,024,439 (partial exon 20) and chr1:237,038,019-237,038,029 (partial exon 24); *NBEAL2* (NM\_015175.2) chr3:47,021,385-47,021,407 (partial exon 1); *NEB* (NM\_001271208.1) exons 82-105; *NPC1* (NM\_000271.4) chr18:21,123,519-21,123,538 (partial exon 14); *NPHP1* (NM\_000272.3) chr2:110,937,251-110,937,263 (partial exon 3); *OCRL* (NM\_000027.3) chrX:128,674,450-128,674,460 (partial exon 1); *PHKB* (NM\_000293.2) exon 1 and chr16:47,732,498-47,732,504 (partial exon 30); *PIGN* (NM\_176787.4) chr18:59,815,547-59,815,576 (partial exon 8); *PIP5K1C* (NM\_012398.2) exon 1 and chr19:363,7602-363,7616 (partial exon 17); *POU1F1* (NM\_000306.3) exon 5; *PTPRC* (NM\_002838.4) exons 11 and 23; *PUS1* (NM\_025215.5) chr12:132,414,446-132,414,532 (partial exon 2); *RPGRIP1L* (NM\_015272.2) exon 23; *SGSH* (NM\_000199.3) chr17:78,194,022-78,194,072 (partial exon 1); *SLC6A8* (NM\_005629.3) exons 3 and 4; *ST3GAL5* (NM\_003896.3) exon 1; *SURF1* (NM\_003172.3) chr9:136,223,269-136,223,307 (partial exon 1); *TRPM6* (NM\_017662.4) chr9:77,362,800-77,362,811 (partial exon 31); *TSEN54* (NM\_020734.6.2) exon 1; *TYR* (NM\_000372.4) exon 5; *VWF* (NM\_000552.3) exons 24-26, chr12:6,125,675-6,125,684 (partial exon 30), chr12:6,121,244-6,121,265 (partial exon 33), and exon 34.

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



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

#### Next Generation Sequencing for *SMN1*

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

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

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

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

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

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

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

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

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

#### Residual Risk Calculations

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

## Personalized Residual Risk Calculations

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

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

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

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

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

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

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

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

## SELECTED REFERENCES

### Carrier Screening

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### 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.



Akler G et al. Towards a unified approach for comprehensive reproductive carrier screening in the Ashkenazi, Sephardi, and Mizrahi Jewish populations. *Mol Genet Genomic Med.* 2020 Feb 8(2):e1053.

**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	SPECIMEN INFORMATION	PROVIDER INFORMATION
5556, Donor ID#: 5556 DOB: [REDACTED] Sex: Male	Type: DNA Collected: August 24, 2022 Received: August 26, 2022 PG ID: [REDACTED]	Harvey Stern, MD, PhD Suzanne Seitz, MS Fairfax Cyrobank

**MOLECULAR GENETICS REPORT:**  
Custom Panel with CNV Detection

**SUMMARY OF RESULTS: Negative**

**RESULTS AND INTERPRETATIONS:**

In this patient, for the relevant gene, we found no sequence variants.

This patient is apparently negative for copy number variants (CNVs) within the genomic regions of this test.

These results should be interpreted in the context of clinical findings, family history and other laboratory data.

All genetic tests have limitations. See limitations and other information for this test on the following page(s).

**NOTES:**

1) Since this test is performed using exome capture probes, a reflex to any of our exome-based tests is available (PGxome, PGxome Custom Panels).

2) As requested, only variants that are currently interpreted as pathogenic or likely pathogenic have been reported. It is possible that there are one or more variants of uncertain significance in the genes of this panel that have not been included on this report.

**GENE ANALYZED:** *TRPM1*

**SUMMARY STATISTICS:**

Pipeline	Version	Average NGS Coverage	Fraction Bases Covered with NGS
Infinity_Pipeline	2.0.3	199x	100.0%

Minimum NGS coverage is  $\geq 20x$  for all coding exons and +/-10bp of flanking DNA.

Electronically signed on September 08, 2022 by:  
Angela Gruber, PhD  
Human Molecular Geneticist

Electronically signed and reported on September 08, 2022 by:  
Diane Allingham-Hawkins, PhD, FCCMG, FACMG  
Laboratory Director

**SUPPLEMENTAL INFORMATION v.22.06**

**Limitations and Other Test Notes:** Interpretation of the test results is limited by the information that is currently available. Better interpretation should be possible in the future as our knowledge about human genetics and genetic disorders improves.

When Next Generation Sequencing (NGS) or Sanger sequencing does not reveal any difference from the reference sequence, or when a sequence variant is homozygous, we cannot be certain that we were able to detect both patient alleles. Occasionally, a patient may carry an allele which does not capture or amplify due for example to a large deletion or insertion.

Copy number variants (CNVs) of four exons or more in size are detected with sensitivity approaching 100% through analysis of NGS data. However, sensitivity for detection of CNVs smaller than four exons is lower (~75%).

Unless otherwise indicated, coverage includes all coding exons of the gene(s) analyzed plus 10 bases of flanking noncoding DNA in all available transcripts along with other non-coding regions in which pathogenic variants have been identified at PreventionGenetics or reported elsewhere.

In most cases, we are unable to determine the phase of sequence variants.

Our ability to detect minor sequence variants due to somatic mosaicism is limited. Sequence variants that are present in less than 15% of the patient's nucleated cells may not be detected.

Unless present within coding regions, runs of mononucleotide repeats (eg (A)n or (T)n) with n >8 in the reference sequence) are generally not analyzed because of strand slippage during amplification.

Unless otherwise indicated, DNA sequence data is obtained from a specific cell type (often leukocytes from whole blood). Test reports contain no information about the DNA sequence in other cell types.

We cannot be certain that the reference sequences are correct. Genome build hg19, GRCh37 (Feb2009) is currently used as our reference in nearly all cases.

We have confidence in our ability to track a specimen once it has been received by PreventionGenetics. However, we take no responsibility for any specimen labeling errors that occur before the sample arrives at PreventionGenetics.

Genetic counseling to help to explain test results to the patients and to discuss reproductive options is recommended.

**Test Methods:** We use NGS technologies to cover the coding regions of the targeted genes plus 10 bases of non-coding DNA flanking each exon. As required, genomic DNA is extracted from the specimen. The DNA corresponding to these regions is captured using hybridization probes. Captured DNA is sequenced using Illumina's Reversible Dye Terminator (RDT) platform NovaSeq 6000 using 150 by 150 bp paired end reads (Illumina, San Diego, CA, USA).

The following quality control metrics are generally achieved: >98% of target bases are covered at >20x, and mean coverage of target bases >100x. Data analysis is performed using internally developed software. Where available, specified genes for which the enhance option is selected are backfilled with Sanger sequencing to achieve 100% coverage.

For Sanger sequencing, Polymerase Chain Reaction (PCR) is used to amplify the necessary exons plus additional flanking non-coding sequence. After purification of the PCR products, cycle sequencing is carried out using the

Applied Biosystems Incorporated (ABI) Big Dye Terminator v.3.1 kit. PCR products are resolved by electrophoresis on an ABI 3730xl capillary sequencer. In most cases, cycle sequencing is performed separately in both the forward and reverse directions; in some cases, sequencing is performed twice in either the forward or reverse directions.

CNVs are also detected from NGS data. We utilize a CNV calling algorithm that compares mean read depth and distribution for each target in the test sample against multiple matched controls. Neighboring target read depth and distribution and zygosity of any variants within each target region are used to reinforce CNV calls. On occasion, it will not be technically possible to confirm a smaller CNV called by NGS. In these instances, the CNV will not be included on the report. Exome-wide CNV is available as an add-on order for tests performed on an exome-backbone.

All differences from the reference sequences (sequence variants) are assigned to one of seven interpretation categories (Pathogenic, Likely Pathogenic, Variant of Uncertain Significance, Likely Benign, Benign, Risk, and Pseudodeficiency) per ACMG Guidelines (Richards et al. 2015. PubMed ID: 25741868). Rare and undocumented synonymous variants are nearly always classified as likely benign if there is no indication that they alter protein sequence or disrupt splicing. Benign and Likely Benign variants are not listed in the reports but are available upon request. Risk and pseudodeficiency variants may not be listed on the report but are available upon request.

Human Genome Variation Society (HGVS) recommendations are used to describe sequence variants (<http://www.hgvs.org>).

**Regulatory Information:** These results should be used in the context of available clinical findings, and should not be used as the sole basis for treatment. This test was developed and its performance characteristics determined by PreventionGenetics. US Food and Drug Administration (FDA) does not require this test to go through premarket FDA review. This laboratory is certified under the Clinical Laboratory Improvement Amendments of 1988 (CLIA) as qualified to perform high complexity clinical laboratory testing.

If the results of this test will be utilized as part of a clinical study in the European Union, please note this test is intended for performance evaluation only. For all other testing within the European Union, this test is intended for research use only.





Patient Information:

5556, Donor

DOB: [REDACTED]

Sex: M

MR#: 5556

Patient#: [REDACTED]

Partner Information:

Not Tested

Physician:

Seitz, Suzanne

ATTN: Seitz, Suzanne

Fairfax Cryobank

3015 Williams Drive

Fairfax, VA 22031

Laboratory:

Fulgent Therapeutics LLC

CAP#: 8042697

CLIA#: 05D2043189

Laboratory Director:

Lawrence M. Weiss, MD

Report Date: Jul 31, 2024

Accession:

[REDACTED]

Test#: [REDACTED]

Specimen Type: DNA

Collected: Not Provided

Accession:

N/A

## FINAL RESULTS



No carrier mutations identified

## TEST PERFORMED

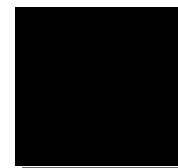
### Single Gene Carrier Screening: CYP11B1

(1 Gene Panel: *CYP11B1*; gene sequencing with deletion and duplication analysis)

## INTERPRETATION:

### Notes and Recommendations:

- No carrier mutations were identified in the submitted specimen. A negative result does not rule out the possibility of a genetic predisposition nor does it rule out any pathogenic mutations in areas not assessed by this test or in regions that were covered at a level too low to reliably assess. Also, it does not rule out mutations that are of the sort not queried by this test; see Methods and Limitations for more information. A negative result reduces, but does not eliminate, the chance to be a carrier for any condition included in this screen. Please see the supplemental table for details.
- This carrier screening test does not screen for all possible genetic conditions, nor for all possible mutations in every gene tested. This report does not include variants of uncertain significance; only variants classified as pathogenic or likely pathogenic at the time of testing, and considered relevant for reproductive carrier screening, are reported. Please see the gene specific notes for details. Please note that the classification of variants can change over time.
- Patients may wish to discuss any carrier results with blood relatives, as there is an increased chance that they are also carriers. These results should be interpreted in the context of this individual's clinical findings, biochemical profile, and family history.
- Gene specific notes and limitations may be present. See below.
- Genetic counseling is recommended. Available genetic counselors and additional resources can be found at the National Society of Genetic Counselors (NSGC; <https://www.nsgc.org>)



## GENES TESTED:

### Custom Beacon Carrier Screening Panel - Gene

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

*CYP11B1*

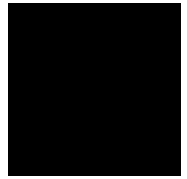
## METHODS:

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

## LIMITATIONS:

### General Limitations

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



### Gene Specific Notes and Limitations

CYP11B1: The current testing method is not able to reliably detect certain pathogenic variants in this gene due to the interference by highly homologous regions. This analysis is not designed to detect or rule-out copy-neutral chimeric CYP11B1/CYP11B2 gene.

### SIGNATURE:

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

**Dr. Harry Gao, DABMG, FACMG** on 7/31/2024  
Laboratory Director, Fulgent

### DISCLAIMER:

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

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To view the supplemental table describing the carrier frequencies, detection rates, and residual risks associated with the genes on this test please visit the following link:

[Beacon Expanded Carrier Screening Supplemental Table](#)



Patient: 5556, Donor; Sex: M;  
DOB: [REDACTED] MR#: 5556

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