



Client/Sending Facility:
Seattle Sperm Bank

4915 25th Ave Ne Ste 204
SEATTLE, WA 98105
Ph: (206)588-1484
Fax: (206) 466-4696 WAB-55

LCLS Specimen Number: 166-129-0284-0

Patient Name: 12193, DONOR

Date of Birth: [REDACTED]

Gender: M

Patient ID:

Lab Number: (J17-2249 L

Indications: DONOR

Account Number: [REDACTED]

Ordering Physician: J OLLIFFE

Specimen Type: BLOOD

Client Reference:

Date Collected: 06/15/2017

Date Received: 06/16/2017

Date Reported: 07/01/2017

Test: Chromosome, Blood, Routine

Cells Counted: 15

Cells Analyzed: 5

Cells Karyotyped: 2

Band Resolution: 500

CYTOGENETIC RESULT: 46,XY

INTERPRETATION: NORMAL MALE KARYOTYPE

Cytogenetic analysis of PHA stimulated cultures has revealed a MALE karyotype with an apparently normal GTG banding pattern in all cells observed.

This result does not exclude the possibility of subtle rearrangements below the resolution of cytogenetics or congenital anomalies due to other etiologies.

Chromosome analysis performed by Dianon Pathology CLIA 07D0644713.
1 Forest Parkway Shelton CT, 06484. Laboratory Director, James B Amberson, MD.

TO:

Seattle Sperm Bank

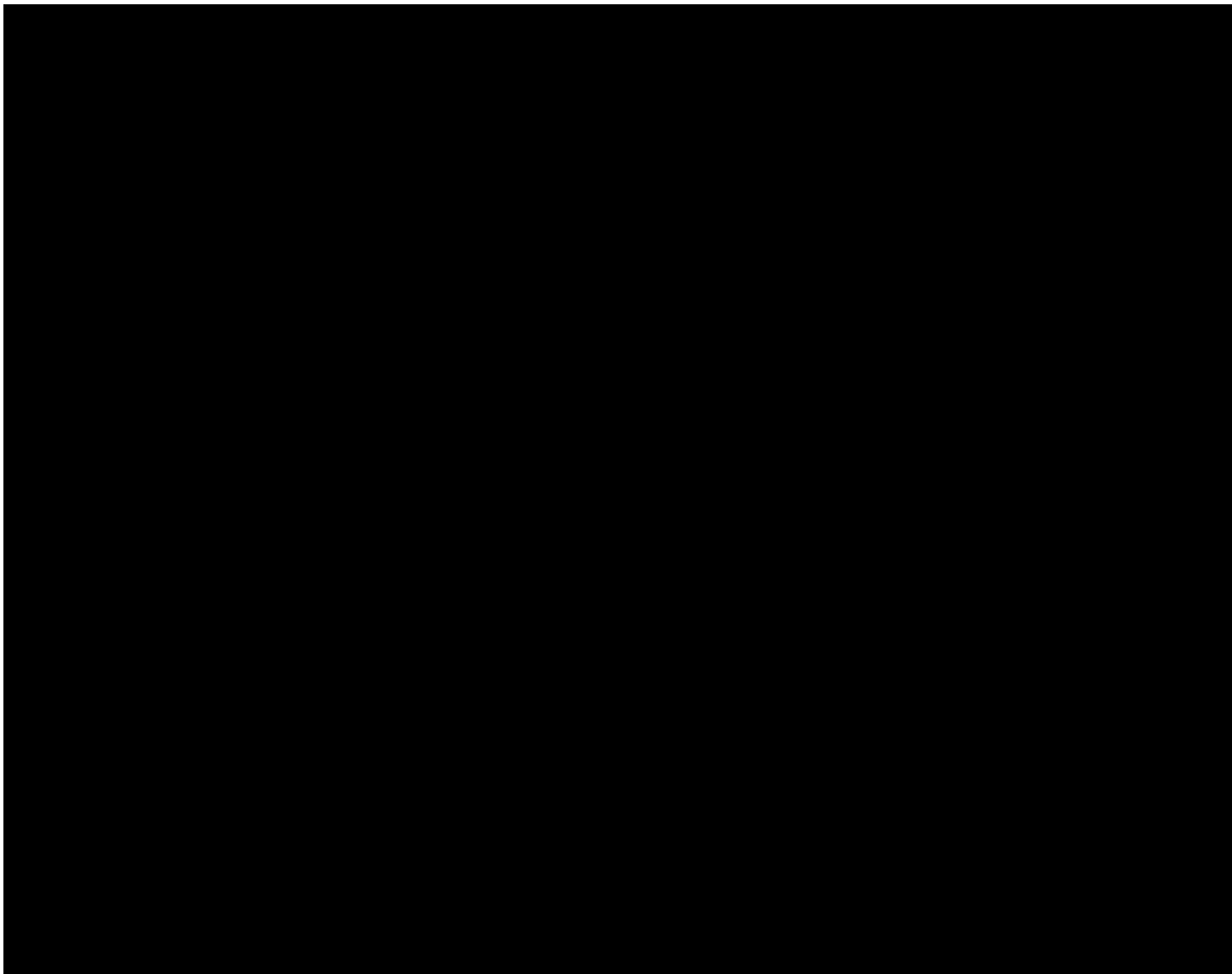


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Hiba Risheg, PhD., FACMG

Patricia Kandalaft, MD
Medical Director
Peter Papenhausen, PhD
National Director of Cytogenetics

Technical component performed by Laboratory Corporation of America Holdings,
550 17th Ave. Suite 200, SEATTLE, WA, 98122-5789 (800) 676-8033

Professional Component performed by LabCorp/Dynacare CLIA 50D0632667, 550 17th Ave. Suite 200, Seattle WA 98122-5789. Medical Director, Patricia Kandalaft, MD
Integrated Genetics is a brand used by Esoterix Genetic Laboratories, LLC, a wholly-owned subsidiary of Laboratory Corporation of America Holdings.

This document contains private and confidential health information protected by state and federal law.

RESULTS RECIPIENT
SEATTLE SPERM BANK
 Attn: Dr. Jeffrey Olliffe
 4915 25th Ave NE, Suite 204W
 Seattle, WA 98105
 Phone: (206) 588-1484
 Fax: (206) 466-4696
 NPI: 1306838271
 Report Date: 06/23/2017

MALE
DONOR 12193
DOB: [REDACTED]
 Ethnicity: Mixed or Other
 Caucasian
 Sample Type: EDTA Blood
 Date of Collection: 06/15/2017
 Date Received: 06/16/2017
 Date Tested: 06/22/2017
 Barcode: 11004212184405
 Indication: Egg or sperm donor

FEMALE
 N/A

Family Prep Screen

POSITIVE: CARRIER

ABOUT THIS TEST

The Counsyl Family Prep Screen (version 2.0) 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 12193	Partner
Panel Information	Family Prep Screen 2.0 Universal Panel Minus X-Linked (102 conditions tested)	N/A
<p>POSITIVE: CARRIER GJB2-related DFNB1 Nonsyndromic Hearing Loss and Deafness Reproductive Risk: 1 in 130 Inheritance: Autosomal Recessive</p>	<p>CARRIER* NM_004004.5(GJB2):c.35delG(aka p. G12Vfs*2) heterozygote</p>	<p>The reproductive risk presented is based on a hypothetical pairing with a partner of the same ethnic group. Carrier testing should be considered. See "Next Steps".</p>
<p>POSITIVE: CARRIER PEX1-related Zellweger Syndrome Spectrum Reproductive Risk: 1 in 450 Inheritance: Autosomal Recessive</p>	<p>CARRIER* NM_000466.2(PEX1):c.1952_1960dup9 (W653_M654insTVW) heterozygote †</p>	<p>The reproductive risk presented is based on a hypothetical pairing with a partner of the same ethnic group. Carrier testing should be considered. See "Next Steps".</p>

†Likely to have a negative impact on gene function.
 *Carriers generally do not experience symptoms.

No disease-causing mutations were detected in any other gene tested. A complete list of all conditions tested can be found on page 8.

CLINICAL NOTES

- None

NEXT STEPS

- Carrier testing should be considered for the diseases specified above for the patient's partner, as both parents must be carriers before a child is at high risk of developing the disease.
- Genetic counseling is recommended and patients may wish to discuss any positive results with blood relatives, as there is an increased chance that they are also carriers.

POSITIVE: CARRIER

GJB2-related DFNB1 Nonsyndromic Hearing Loss and Deafness

Reproductive risk: 1 in 130
 Risk before testing: 1 in 4,200

Gene: GJB2 | Inheritance Pattern: Autosomal Recessive

Patient	DONOR 12193	No partner tested
Result	👤 Carrier	N/A
Variation(s)	NM_004004.5(GJB2):c.35delG(aka p.G12Vfs*2) heterozygote	N/A
Methodology	Sequencing	N/A
Interpretation	This individual is a carrier of GJB2-related DFNB1 nonsyndromic hearing loss and deafness. Carriers generally do not experience symptoms.	N/A
Detection rate	98%	N/A
Exons tested	NM_004004:1-2.	N/A

What is GJB2-related DFNB1 Nonsyndromic Hearing Loss and Deafness?

DFNB1 nonsyndromic hearing loss and deafness is an inherited condition in which a person has mild to severe hearing loss from birth. It is caused by mutations in GJB2 (which encodes the protein connexin 26) and GJB6 (which encodes connexin 30). The condition is not progressive, meaning that it does not worsen over time.

The word “nonsyndromic” refers to the fact that there are no other symptoms or systems of the body involved with the disease. Unlike some other forms of hearing loss, DFNB1 nonsyndromic hearing loss and deafness does not affect balance or movement.

The degree of hearing loss is difficult to predict based on which genetic mutation one has. Even if members of the same family are affected by DFNB1 nonsyndromic hearing loss and deafness, the degree of hearing loss may vary among them.

How common is GJB2-related DFNB1 Nonsyndromic Hearing Loss and Deafness?

In the United States, the United Kingdom, France, Australia, and New Zealand, approximately 14 in 100,000 people have DFNB1 nonsyndromic hearing loss and deafness. Roughly 1 in 33 people are carriers of the mutation that causes the condition.

How is GJB2-related DFNB1 Nonsyndromic Hearing Loss and Deafness treated?

People with DFNB1 nonsyndromic hearing loss and deafness may show improvement by using hearing aids. For people with profound deafness, cochlear implants may also be helpful. They may also want to consider enrolling in an educational program for the hearing impaired.



RESULTS RECIPIENT
SEATTLE SPERM BANK
Attn: Dr. Jeffrey Olliffe
NPI: 1306838271
Report Date: 06/23/2017

MALE
DONOR 12193
DOB: [REDACTED]
Ethnicity: Mixed or Other
Caucasian
Barcode: 11004212184405

FEMALE
N/A

What is the prognosis for a person with GJB2-related DFNB1 Nonsyndromic Hearing Loss and Deafness?

While a person with GJB2-related DFNB1 nonsyndromic hearing loss and deafness will have mild to severe hearing loss, it does not affect lifespan and does not affect any other part of the body.

POSITIVE: CARRIER
PEX1-related Zellweger Syndrome Spectrum

Reproductive risk: 1 in 450
 Risk before testing: 1 in 50,000

Gene: PEX1 | Inheritance Pattern: Autosomal Recessive

Patient	DONOR 12193	No partner tested
Result	👤 Carrier	N/A
Variants	NM_000466.2(PEX1):c.1952_1960dup9(W653_M654insTWW) heterozygote †	N/A
Methodology	Sequencing	N/A
Interpretation	This individual is a carrier of PEX1-related Zellweger syndrome spectrum. Carriers generally do not experience symptoms.	N/A
Detection rate	>99%	N/A
Exons tested	NM_000466:1-24.	N/A

†Likely to have a negative impact on gene function.

What is PEX1-related Zellweger Syndrome Spectrum?

PEX1-related Zellweger syndrome spectrum (ZSS) is an inherited disease that impairs the proper functioning of the body's peroxisomes, a cellular structure that normally breaks down fatty acids and other metabolic waste products.

As indicated by the word "spectrum," people with ZSS vary widely in the type and severity of their symptoms. The disease is generally grouped into three subtypes: Zellweger syndrome (the most severe), neonatal adrenoleukodystrophy (intermediate severity) and infantile Refsum disease (the mildest form). Each is described below. Individuals with ZSS usually show symptoms of the disease as newborns or as children.

While specific genetic mutations cannot fully predict which form of the disease a person will inherit, some genetic mutations are more closely associated with milder or more severe symptoms. Please consult a healthcare professional for more information.

Zellweger Syndrome (ZS)

ZS is the most severe form of ZSS. Infants with ZS usually die before their first birthday without reaching many mental or physical milestones.

Infants born with ZS have developmental delay leading to severe mental retardation. They often have seizures and typically have facial deformities such as a high forehead, abnormal ear lobes, a large "soft spot" on the top of their heads, and a small chin. In some, the lack of muscle tone is so severe that the infant cannot move and may not be able to suck or swallow. They often show poor feeding. Their livers are usually enlarged and their skin and the whites of their eyes may have a yellowish tinge (jaundice.) Some have bleeding in their digestive tract. Bone deformities are also common.

Neonatal Adrenoleukodystrophy (NALD) and Infantile Refsum Disease (IRD)

The symptoms of NALD and IRD are similar to that of ZS, but typically less severe, with NALD being more severe than IRD. Symptoms in these children often begin in late infancy or early childhood and may progress more slowly.

Infants and children with NALD or IRD may have developmental delays leading to mild to severe mental retardation. Hearing loss and vision impairment typically grow worse over time and may lead to blindness and/or deafness. Many people with the disease have liver problems and some have developed episodes of spontaneous bleeding, particularly around the brain. Some children with the disease learn to walk, while others lack the muscle tone needed for such movement. Similarly many children with the disease learn to talk, though some do not.

How common is PEX1-related Zellweger Syndrome Spectrum?

ZSS affects 1 in 50,000 infants.

How is PEX1-related Zellweger Syndrome Spectrum treated?

There is no cure for ZSS and there is no standard way to treat it. Physicians can address certain symptoms as they arise, such as prescribing medication for seizures. Children with milder forms of the disease may benefit from hearing aids, glasses, and/or surgery to remove cataracts. In those who reach school age, special education is likely necessary. Modifications to the child's diet may also be recommended.

In children with severe forms of the disease, the main goal of treatment is to protect the child from infections and breathing problems.

What is the prognosis for a person with PEX1-related Zellweger Syndrome Spectrum?

ZSS usually reduces a person's lifespan. One study showed that children with NALD or IRD who survive the first year of life have a 77% chance of reaching school age. These children will all have some degree of learning disabilities or mental retardation. Most people with NALD survive into childhood while those with IRD can live into their teens or 20s, and perhaps even longer.

The prognosis for an infant with ZS is poor. Most die within the first year of life without reaching any physical or mental milestones.

Methods and Limitations

DONOR 12193 [Family Prep Screen 2.0]: sequencing, targeted genotyping, spinal muscular atrophy, and analysis of homologous regions.

Sequencing

High-throughput sequencing is used to analyze the listed exons, as well as selected intergenic and intronic regions, of the genes in the Conditions Tested section of the report. These regions are sequenced to high coverage and the sequences are compared to standards and references of normal variation. Mutations may not be detected in areas of lower sequence coverage. On average, more than 99% of all bases in the exons listed for each gene are sequenced at the minimum read depth. Variants discovered in other exons of these genes will also be reported if they meet quality control criteria. Triplet repeats and large deletions and duplications may not be detected. Small insertions and deletions may not be as accurately determined as single nucleotide variants. Genes that have closely related pseudogenes are not well analyzed by this method.

Detection rates are calculated by estimating from literature the fraction of disease alleles that the methodology is unable to detect.

All variants that are a recognized cause of the disease will be reported. In addition, variants that have not previously been established as a recognized cause of disease may be identified. In these cases, only variants classified as "predicted" or "likely" pathogenic are reported. Predicted/likely pathogenic variants are described elsewhere in the report as "predicted/likely to have a negative impact on gene function". In general, predicted pathogenic variants are those which are predicted to be pathogenic based on the nature of the sequence change, while likely pathogenic variants are evaluated by reviewing reports of allele frequencies in cases and controls, functional studies, variant annotation and effect prediction, and segregation studies. Benign variants, variants of uncertain significance, and variants not directly associated with the intended disease phenotype are not reported. Literature citations validating reported variants are available upon request.

Targeted genotyping

Targeted DNA mutation analysis is used to determine the genotypes of the listed variants in the Conditions Tested section of the report.

Spinal muscular atrophy

Targeted copy number analysis is used to determine the copy number of exon 7 of the *SMN1* gene relative to other genes. Other mutations may interfere with this analysis. Some individuals with two copies of *SMN1* are carriers with two *SMN1* genes on one chromosome and a *SMN1* deletion on the other chromosome. This is more likely in individuals who have 2 copies of the *SMN1* gene and are positive for the g.27134T>G SNP, which affects the reported residual risk; Ashkenazi Jewish or Asian patients with this genotype have a high post-test likelihood of being carriers for SMA and are reported as carriers.

Analysis of homologous regions

A combination of high-throughput sequencing, read depth-based copy number analysis, and targeted genotyping is used to determine the number of functional gene copies and/or the presence of selected loss of function mutations in certain genes that have homology to other regions. The precise breakpoints of large deletions in these genes cannot be determined, but are estimated from copy number analysis. High numbers of pseudogene copies may interfere with this analysis.

If *CYP21A2* is tested, patients who have one or more additional copies of the *CYP21A2* gene and a loss of function mutation may not actually be a carrier of 21-hydroxylase-deficient congenital adrenal hyperplasia (CAH). Because the true incidence of non-classic CAH is unknown, the residual carrier and reproductive risk numbers on the report are only based on published incidences for classic CAH. However, the published prevalence of non-classic CAH is highest in individuals of Ashkenazi Jewish, Hispanic, Italian, and Yugoslav descent. Therefore, the residual and reproductive risks are likely an underestimate of overall chances for 21-hydroxylase-deficient CAH, especially in the aforementioned populations, as they do not account for non-classic CAH. If *HBA1/HBA2* are tested, some individuals with four alpha globin genes may be carriers, with three genes on one chromosome and a deletion on the other chromosome. This and similar, but rare, carrier states, where complementary changes exist in both the gene and a pseudogene, may not be detected by the assay.

Limitations

In an unknown number of cases, nearby genetic variants may interfere with mutation detection. Other possible sources of diagnostic error include sample mix-up, trace contamination, bone marrow transplantation, blood transfusions and technical errors. This test is designed to detect and report germline alterations. While somatic variants present at low levels may be detected, these 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. The test does not fully address all inherited forms of intellectual disability, birth defects and genetic disease. A family history of any of these conditions may warrant additional evaluation. Furthermore, not all mutations will be identified in the genes analyzed and additional testing may be beneficial for some patients. For example, individuals of African, Southeast Asian, and Mediterranean ancestry are at increased risk for being carriers for hemoglobinopathies, which can be identified by CBC and hemoglobin electrophoresis or HPLC (*ACOG Practice Bulletin No. 78. Obstet. Gynecol. 2007;109:229-37*).

This test was developed and its performance characteristics determined by Counsyl, 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**.

LAB DIRECTORS



H. Peter Kang, MD, MS, FCAP

Conditions Tested

- 21-hydroxylase-deficient Congenital Adrenal Hyperplasia** - Gene: CYP21A2. Autosomal Recessive. Analysis of Homologous Regions. Variants (13): CYP21A2 deletion, CYP21A2 duplication, CYP21A2 triplication, G111Vfs*21, I173N, L308FfsX6, P31L, Q319*, Q319*+CYP21A2dup, R357W, V281L, [I237N;V238E;M240K], c.293-13C>G. Detection Rate: Mixed or Other Caucasian 96%.
- ABCC8-related Hyperinsulinism** - Gene: ABCC8. Autosomal Recessive. Sequencing. Exons: NM_000352:1-39. Detection Rate: Mixed or Other Caucasian >99%.
- Achromatopsia** - Gene: CNGB3. Autosomal Recessive. Sequencing. Exons: NM_019098:1-18. Detection Rate: Mixed or Other Caucasian >99%.
- Alkaptonuria** - Gene: HGD. Autosomal Recessive. Sequencing. Exons: NM_000187:1-14. Detection Rate: Mixed or Other Caucasian >99%.
- Alpha Thalassemia** - Genes: HBA1, HBA2. Autosomal Recessive. Analysis of Homologous Regions. Variants (13): -(alpha)20.5, --BRIT, --MEDI, --MEDII, --SEA, --THAI or --FIL, -alpha3.7, -alpha4.2, HBA1+HBA2 deletion, Hb Constant Spring, anti3.7, anti4.2, del H5-40. Detection Rate: Unknown due to rarity of disease.
- Alpha-1 Antitrypsin Deficiency** - Gene: SERPINA1. Autosomal Recessive. Sequencing. Exons: NM_000295:2-5. Detection Rate: Mixed or Other Caucasian >99%.
- Alpha-mannosidosis** - Gene: MAN2B1. Autosomal Recessive. Sequencing. Exons: NM_000528:1-15,17-24. Detection Rate: Mixed or Other Caucasian >99%.
- Alpha-sarcoglycanopathy** - Gene: SGCA. Autosomal Recessive. Sequencing. Exons: NM_000023:1-9. Detection Rate: Mixed or Other Caucasian 99%.
- Andermann Syndrome** - Gene: SLC12A6. Autosomal Recessive. Sequencing. Exons: NM_133647:1-25. Detection Rate: Mixed or Other Caucasian >99%.
- ARSACS** - Gene: SACS. Autosomal Recessive. Sequencing. Exons: NM_014363:2-10. Detection Rate: Mixed or Other Caucasian 97%.
- Aspartylglycosaminuria** - Gene: AGA. Autosomal Recessive. Sequencing. Exons: NM_000027:1-9. Detection Rate: Mixed or Other Caucasian >99%.
- Ataxia with Vitamin E Deficiency** - Gene: TTPA. Autosomal Recessive. Sequencing. Exons: NM_000370:1-5. Detection Rate: Mixed or Other Caucasian >99%.
- Ataxia-telangiectasia** - Gene: ATM. Autosomal Recessive. Sequencing. Exons: NM_000051:2-63. Detection Rate: Mixed or Other Caucasian 92%.
- Bardet-Biedl Syndrome, BBS1-related** - Gene: BBS1. Autosomal Recessive. Sequencing. Exons: NM_024649:1-17. Detection Rate: Mixed or Other Caucasian >99%.
- Bardet-Biedl Syndrome, BBS10-related** - Gene: BBS10. Autosomal Recessive. Sequencing. Exons: NM_024685:1-2. Detection Rate: Mixed or Other Caucasian >99%.
- Beta-sarcoglycanopathy** - Gene: SGCB. Autosomal Recessive. Sequencing. Exons: NM_000232:1-6. Detection Rate: Mixed or Other Caucasian >99%.
- Biotinidase Deficiency** - Gene: BTD. Autosomal Recessive. Sequencing. Exons: NM_000060:1-4. Detection Rate: Mixed or Other Caucasian >99%.
- Bloom Syndrome** - Gene: BLM. Autosomal Recessive. Sequencing. Exons: NM_000057:2-22. Detection Rate: Mixed or Other Caucasian 96%.
- Canavan Disease** - Gene: ASPA. Autosomal Recessive. Sequencing. Exons: NM_000049:1-6. Detection Rate: Mixed or Other Caucasian 94%.
- Carnitine Palmitoyltransferase IA Deficiency** - Gene: CPT1A. Autosomal Recessive. Sequencing. Exons: NM_001876:2-19. Detection Rate: Mixed or Other Caucasian 98%.
- Carnitine Palmitoyltransferase II Deficiency** - Gene: CPT2. Autosomal Recessive. Sequencing. Exons: NM_000098:1-5. Detection Rate: Mixed or Other Caucasian >99%.
- Cartilage-hair Hypoplasia** - Gene: RMRP. Autosomal Recessive. Sequencing. Exon: NR_003051:1. Detection Rate: Mixed or Other Caucasian >99%.
- Citrullinemia Type 1** - Gene: ASS1. Autosomal Recessive. Sequencing. Exons: NM_000050:3-16. Detection Rate: Mixed or Other Caucasian >99%.
- CLN3-related Neuronal Ceroid Lipofuscinosis** - Gene: CLN3. Autosomal Recessive. Sequencing. Exons: NM_001042432:2-16. Detection Rate: Mixed or Other Caucasian >99%.
- CLN5-related Neuronal Ceroid Lipofuscinosis** - Gene: CLN5. Autosomal Recessive. Sequencing. Exons: NM_006493:1-4. Detection Rate: Mixed or Other Caucasian 98%.
- Cohen Syndrome** - Gene: VPS13B. Autosomal Recessive. Sequencing. Exons: NM_017890:2-62. Detection Rate: Mixed or Other Caucasian 90%.
- Congenital Disorder of Glycosylation Type Ia** - Gene: PMM2. Autosomal Recessive. Sequencing. Exons: NM_000303:1-8. Detection Rate: Mixed or Other Caucasian >99%.
- Congenital Disorder of Glycosylation Type Ib** - Gene: MPI. Autosomal Recessive. Sequencing. Exons: NM_002435:1-8. Detection Rate: Mixed or Other Caucasian >99%.
- Congenital Finnish Nephrosis** - Gene: NPHS1. Autosomal Recessive. Sequencing. Exons: NM_004646:2-23,26-27,29. Detection Rate: Mixed or Other Caucasian >99%.
- Costeff Optic Atrophy Syndrome** - Gene: OPA3. Autosomal Recessive. Sequencing. Exons: NM_025136:1-2. Detection Rate: Mixed or Other Caucasian >99%.
- Cystic Fibrosis** - Gene: CFTR. Autosomal Recessive. Sequencing. Exons: NM_000492:1-27. IVS8-5T allele analysis is only reported in the presence of the R117H mutation. Detection Rate: Mixed or Other Caucasian 97%.
- Cystinosis** - Gene: CTNS. Autosomal Recessive. Sequencing. Exons: NM_004937:3-12. Detection Rate: Mixed or Other Caucasian >99%.
- D-bifunctional Protein Deficiency** - Gene: HSD17B4. Autosomal Recessive. Sequencing. Exons: NM_000414:1-24. Detection Rate: Mixed or Other Caucasian 94%.
- Dihydropyrimidine Dehydrogenase Deficiency** - Gene: DPYD. Autosomal Recessive. Sequencing. Exons: NM_000110:1-23. Detection Rate: Mixed or Other Caucasian 93%.
- Factor XI Deficiency** - Gene: F11. Autosomal Recessive. Sequencing. Exons: NM_000128:2-15. Detection Rate: Mixed or Other Caucasian >99%.
- Familial Dysautonomia** - Gene: IKBKAP. Autosomal Recessive. Sequencing. Exons: NM_003640:2-37. Detection Rate: Mixed or Other Caucasian >99%.
- Familial Mediterranean Fever** - Gene: MEFV. Autosomal Recessive. Sequencing. Exons: NM_000243:1-10. Detection Rate: Mixed or Other Caucasian >99%.
- Fanconi Anemia Type C** - Gene: FANCC. Autosomal Recessive. Sequencing. Exons: NM_000136:2-15. Detection Rate: Mixed or Other Caucasian >99%.
- FKTN-related Disorders** - Gene: FKTN. Autosomal Recessive. Sequencing. Exons: NM_001079802:3-11. Detection Rate: Mixed or Other Caucasian >99%.
- Galactosemia** - Gene: GALT. Autosomal Recessive. Sequencing. Exons: NM_000155:1-11. Detection Rate: Mixed or Other Caucasian >99%.
- Gaucher Disease** - Gene: GBA. Autosomal Recessive. Analysis of Homologous Regions. Variants (10): D409V, D448H, IVS2+1G>A, L444P, N370S, R463C, R463H, R496H, V394L, p.L29Afs*18. Detection Rate: Mixed or Other Caucasian 60%.
- GJB2-related DFNB1 Nonsyndromic Hearing Loss and Deafness** - Gene: GJB2. Autosomal Recessive. Sequencing. Exons: NM_004004:1-2. Detection Rate: Mixed or Other Caucasian 98%.
- Glutaric Acidemia Type 1** - Gene: GCDH. Autosomal Recessive. Sequencing. Exons: NM_000159:2-12. Detection Rate: Mixed or Other Caucasian >99%.
- Glycogen Storage Disease Type Ia** - Gene: G6PC. Autosomal Recessive. Sequencing. Exons: NM_000151:1-5. Detection Rate: Mixed or Other Caucasian >99%.
- Glycogen Storage Disease Type Ib** - Gene: SLC37A4. Autosomal Recessive. Sequencing. Exons: NM_001164277:3-11. Detection Rate: Mixed or Other Caucasian >99%.
- Glycogen Storage Disease Type III** - Gene: AGL. Autosomal Recessive. Sequencing. Exons: NM_000642:2-34. Detection Rate: Mixed or Other Caucasian >99%.
- Glycogen Storage Disease Type V** - Gene: PYGM. Autosomal Recessive. Sequencing. Exons: NM_005609:1-20. Detection Rate: Mixed or Other Caucasian >99%.
- GRACILE Syndrome** - Gene: BCS1L. Autosomal Recessive. Sequencing. Exons: NM_004328:3-9. Detection Rate: Mixed or Other Caucasian >99%.
- HADHA-related Disorders** - Gene: HADHA. Autosomal Recessive. Sequencing. Exons: NM_000182:1-20. Detection Rate: Mixed or Other Caucasian >99%.
- Hb Beta Chain-related Hemoglobinopathy (Including Beta Thalassemia and Sickle Cell Disease)** - Gene: HBB. Autosomal Recessive. Sequencing. Exons: NM_000518:1-3. Detection Rate: Mixed or Other Caucasian 96%.
- Hereditary Fructose Intolerance** - Gene: ALDOB. Autosomal Recessive. Sequencing. Exons: NM_000035:2-9. Detection Rate: Mixed or Other Caucasian >99%.
- Herlitz Junctional Epidermolysis Bullosa, LAMA3-related** - Gene: LAMA3. Autosomal Recessive. Sequencing. Exons: NM_000227:1-16,18-38. Detection Rate: Mixed or Other Caucasian >99%.

Herlitz Junctional Epidermolysis Bullosa, LAMB3-related - Gene: LAMB3. Autosomal Recessive. Sequencing. Exons: NM_000228:2-23. Detection Rate: Mixed or Other Caucasian >99%.

Herlitz Junctional Epidermolysis Bullosa, LAMC2-related - Gene: LAMC2. Autosomal Recessive. Sequencing. Exons: NM_005562:1-23. Detection Rate: Mixed or Other Caucasian >99%.

Hexosaminidase A Deficiency (Including Tay-Sachs Disease) - Gene: HEXA. Autosomal Recessive. Sequencing. Exons: NM_000520:1-14. Detection Rate: Mixed or Other Caucasian >99%.

Homocystinuria Caused by Cystathionine Beta-synthase Deficiency - Gene: CBS. Autosomal Recessive. Sequencing. Exons: NM_000071:3-17. Detection Rate: Mixed or Other Caucasian >99%.

Hypophosphatasia, Autosomal Recessive - Gene: ALPL. Autosomal Recessive. Sequencing. Exons: NM_000478:2-12. Detection Rate: Mixed or Other Caucasian >99%.

Inclusion Body Myopathy 2 - Gene: GNE. Autosomal Recessive. Sequencing. Exons: NM_001128227:3-12. Detection Rate: Mixed or Other Caucasian >99%.

Isovaleric Acidemia - Gene: IVD. Autosomal Recessive. Sequencing. Exons: NM_000225:1-12. Detection Rate: Mixed or Other Caucasian >99%.

Joubert Syndrome 2 - Gene: TMEM216. Autosomal Recessive. Sequencing. Exons: NM_001173990:1-5. Detection Rate: Mixed or Other Caucasian >99%.

Krabbe Disease - Gene: GALC. Autosomal Recessive. Sequencing. Exons: NM_000153:1-17. Detection Rate: Mixed or Other Caucasian >99%.

Lipoamide Dehydrogenase Deficiency - Gene: DLD. Autosomal Recessive. Sequencing. Exons: NM_000108:1-14. Detection Rate: Mixed or Other Caucasian >99%.

Maple Syrup Urine Disease Type 1B - Gene: BCKDHB. Autosomal Recessive. Sequencing. Exons: NM_183050:1-10. Detection Rate: Mixed or Other Caucasian >99%.

Medium Chain Acyl-CoA Dehydrogenase Deficiency - Gene: ACADM. Autosomal Recessive. Sequencing. Exons: NM_000016:1-12. Detection Rate: Mixed or Other Caucasian >99%.

Megalencephalic Leukoencephalopathy with Subcortical Cysts - Gene: MLC1. Autosomal Recessive. Sequencing. Exons: NM_015166:2-12. Detection Rate: Mixed or Other Caucasian >99%.

Metachromatic Leukodystrophy - Gene: ARSA. Autosomal Recessive. Sequencing. Exons: NM_000487:1-8. Detection Rate: Mixed or Other Caucasian >99%.

Mucopolisaccharidosis IV - Gene: MCOLN1. Autosomal Recessive. Sequencing. Exons: NM_020533:1-14. Detection Rate: Mixed or Other Caucasian >99%.

Mucopolysaccharidosis Type I - Gene: IDUA. Autosomal Recessive. Targeted Genotyping. Variants (2): Q70*, W402*. Detection Rate: Mixed or Other Caucasian 67%.

Muscle-eye-brain Disease - Gene: POMGNT1. Autosomal Recessive. Sequencing. Exons: NM_017739:2-22. Detection Rate: Mixed or Other Caucasian 90%.

NEB-related Nemaline Myopathy - Gene: NEB. Autosomal Recessive. Sequencing. Exons: NM_001271208:3-80,117-183. Detection Rate: Mixed or Other Caucasian 91%.

Niemann-Pick Disease Type C - Gene: NPC1. Autosomal Recessive. Sequencing. Exons: NM_000271:1-25. Detection Rate: Mixed or Other Caucasian 96%.

Niemann-Pick Disease, SMPD1-associated - Gene: SMPD1. Autosomal Recessive. Sequencing. Exons: NM_000543:1-6. Detection Rate: Mixed or Other Caucasian >99%.

Nijmegen Breakage Syndrome - Gene: NBN. Autosomal Recessive. Sequencing. Exons: NM_002485:1-16. Detection Rate: Mixed or Other Caucasian >99%.

Northern Epilepsy - Gene: CLN8. Autosomal Recessive. Sequencing. Exons: NM_018941:2-3. Detection Rate: Mixed or Other Caucasian >99%.

PCDH15-related Disorders - Gene: PCDH15. Autosomal Recessive. Sequencing. Exons: NM_033056:2-33. Detection Rate: Mixed or Other Caucasian 85%.

Pendred Syndrome - Gene: SLC26A4. Autosomal Recessive. Sequencing. Exons: NM_000441:2-21. Detection Rate: Mixed or Other Caucasian >99%.

PEX1-related Zellweger Syndrome Spectrum - Gene: PEX1. Autosomal Recessive. Sequencing. Exons: NM_000466:1-24. Detection Rate: Mixed or Other Caucasian >99%.

Phenylalanine Hydroxylase Deficiency - Gene: PAH. Autosomal Recessive. Sequencing. Exons: NM_000277:1-13. Detection Rate: Mixed or Other Caucasian 98%.

PKHD1-related Autosomal Recessive Polycystic Kidney Disease - Gene: PKHD1. Autosomal Recessive. Sequencing. Exons: NM_138694:2-67. Detection Rate: Mixed or Other Caucasian 98%.

Polyglandular Autoimmune Syndrome Type 1 - Gene: AIRE. Autosomal Recessive. Sequencing. Exons: NM_000383:1-14. Detection Rate: Mixed or Other Caucasian >99%.

Pompe Disease - Gene: GAA. Autosomal Recessive. Sequencing. Exons: NM_000152:2-20. Detection Rate: Mixed or Other Caucasian 90%.

PPT1-related Neuronal Ceroid Lipofuscinosis - Gene: PPT1. Autosomal Recessive. Sequencing. Exons: NM_000310:1-9. Detection Rate: Mixed or Other Caucasian >99%.

Primary Carnitine Deficiency - Gene: SLC22A5. Autosomal Recessive. Sequencing. Exons: NM_003060:1-10. Detection Rate: Mixed or Other Caucasian >99%.

Primary Hyperoxaluria Type 1 - Gene: AGXT. Autosomal Recessive. Sequencing. Exons: NM_000030:1-11. Detection Rate: Mixed or Other Caucasian >99%.

Primary Hyperoxaluria Type 2 - Gene: GRHPR. Autosomal Recessive. Sequencing. Exons: NM_012203:1-9. Detection Rate: Mixed or Other Caucasian >99%.

PROP1-related Combined Pituitary Hormone Deficiency - Gene: PROP1. Autosomal Recessive. Sequencing. Exons: NM_006261:1-3. Detection Rate: Mixed or Other Caucasian >99%.

Pseudocholinesterase Deficiency - Gene: BCHE. Autosomal Recessive. Sequencing. Exons: NM_000055:2-4. Detection Rate: Mixed or Other Caucasian >99%.

Pycnodysostosis - Gene: CTSK. Autosomal Recessive. Sequencing. Exons: NM_000396:2-8. Detection Rate: Mixed or Other Caucasian >99%.

Rhizomelic Chondrodysplasia Punctata Type 1 - Gene: PEX7. Autosomal Recessive. Sequencing. Exons: NM_000288:1-10. Detection Rate: Mixed or Other Caucasian >99%.

Salla Disease - Gene: SLC17A5. Autosomal Recessive. Sequencing. Exons: NM_012434:1-11. Detection Rate: Mixed or Other Caucasian 93%.

Segawa Syndrome - Gene: TH. Autosomal Recessive. Sequencing. Exons: NM_000360:1-13. Detection Rate: Mixed or Other Caucasian 96%.

Short Chain Acyl-CoA Dehydrogenase Deficiency - Gene: ACADS. Autosomal Recessive. Sequencing. Exons: NM_000017:1-10. Detection Rate: Mixed or Other Caucasian >99%.

Sjogren-Larsson Syndrome - Gene: ALDH3A2. Autosomal Recessive. Sequencing. Exons: NM_000382:1-10. Detection Rate: Mixed or Other Caucasian 92%.

Smith-Lemli-Opitz Syndrome - Gene: DHCR7. Autosomal Recessive. Sequencing. Exons: NM_001360:3-9. Detection Rate: Mixed or Other Caucasian >99%.

Spinal Muscular Atrophy - Gene: SMN1. Autosomal Recessive. Spinal Muscular Atrophy. Variant (1): SMN1 copy number. Detection Rate: Mixed or Other Caucasian 95%.

Steroid-resistant Nephrotic Syndrome - Gene: NPHS2. Autosomal Recessive. Sequencing. Exons: NM_014625:1-8. Detection Rate: Mixed or Other Caucasian >99%.

Sulfate Transporter-related Osteochondrodysplasia - Gene: SLC26A2. Autosomal Recessive. Sequencing. Exons: NM_000112:2-3. Detection Rate: Mixed or Other Caucasian >99%.

TPP1-related Neuronal Ceroid Lipofuscinosis - Gene: TPP1. Autosomal Recessive. Sequencing. Exons: NM_000391:1-13. Detection Rate: Mixed or Other Caucasian >99%.

Tyrosinemia Type I - Gene: FAH. Autosomal Recessive. Sequencing. Exons: NM_000137:1-14. Detection Rate: Mixed or Other Caucasian >99%.

Usher Syndrome Type 3 - Gene: CLRN1. Autosomal Recessive. Sequencing. Exons: NM_174878:1-3. Detection Rate: Mixed or Other Caucasian >99%.

Very Long Chain Acyl-CoA Dehydrogenase Deficiency - Gene: ACADVL. Autosomal Recessive. Sequencing. Exons: NM_000018:1-20. Detection Rate: Mixed or Other Caucasian >99%.

Wilson Disease - Gene: ATP7B. Autosomal Recessive. Sequencing. Exons: NM_000053:1-21. Detection Rate: Mixed or Other Caucasian >99%.

Risk Calculations

Below are the risk calculations for all conditions tested. Since negative results do not completely rule out the possibility of being a carrier, the **residual risk** represents the patient's post-test likelihood of being a carrier and the **reproductive risk** represents the likelihood the patient's 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 after a negative test result. Inaccurate reporting of ethnicity may cause errors in risk calculation. The reproductive risk presented is based on a hypothetical pairing with a partner of the same ethnic group.

†Indicates a positive result. See the full clinical report for interpretation and details.

Disease	DONOR 12193 Residual Risk	Reproductive Risk
21-hydroxylase-deficient Congenital Adrenal Hyperplasia	1 in 1,400	1 in 310,000
ABCC8-related Hyperinsulinism	1 in 11,000	< 1 in 1,000,000
Achromatopsia	1 in 8,600	< 1 in 1,000,000
Alkaptonuria	< 1 in 50,000	< 1 in 1,000,000
Alpha Thalassemia	Alpha globin status: aa/aa.	Not calculated
Alpha-1 Antitrypsin Deficiency	1 in 3,400	1 in 460,000
Alpha-mannosidosis	1 in 35,000	< 1 in 1,000,000
Alpha-sarcoglycanopathy	1 in 31,000	< 1 in 1,000,000
Andermann Syndrome	< 1 in 50,000	< 1 in 1,000,000
ARSACS	< 1 in 18,000	< 1 in 1,000,000
Aspartylglycosaminuria	< 1 in 50,000	< 1 in 1,000,000
Ataxia with Vitamin E Deficiency	< 1 in 50,000	< 1 in 1,000,000
Ataxia-telangiectasia	1 in 2,100	< 1 in 1,000,000
Bardet-Biedl Syndrome, BBS1-related	1 in 16,000	< 1 in 1,000,000
Bardet-Biedl Syndrome, BBS10-related	1 in 16,000	< 1 in 1,000,000
Beta-sarcoglycanopathy	< 1 in 50,000	< 1 in 1,000,000
Biotinidase Deficiency	1 in 12,000	< 1 in 1,000,000
Bloom Syndrome	< 1 in 12,000	< 1 in 1,000,000
Canavan Disease	< 1 in 7,700	< 1 in 1,000,000
Carnitine Palmitoyltransferase IA Deficiency	< 1 in 31,000	< 1 in 1,000,000
Carnitine Palmitoyltransferase II Deficiency	< 1 in 50,000	< 1 in 1,000,000
Cartilage-hair Hypoplasia	< 1 in 50,000	< 1 in 1,000,000
Citrullinemia Type 1	1 in 12,000	< 1 in 1,000,000
CLN3-related Neuronal Ceroid Lipofuscinosis	1 in 22,000	< 1 in 1,000,000
CLN5-related Neuronal Ceroid Lipofuscinosis	< 1 in 23,000	< 1 in 1,000,000
Cohen Syndrome	< 1 in 5,200	< 1 in 1,000,000
Congenital Disorder of Glycosylation Type Ia	1 in 16,000	< 1 in 1,000,000
Congenital Disorder of Glycosylation Type Ib	< 1 in 50,000	< 1 in 1,000,000
Congenital Finnish Nephrosis	< 1 in 50,000	< 1 in 1,000,000
Costeff Optic Atrophy Syndrome	< 1 in 50,000	< 1 in 1,000,000
Cystic Fibrosis	1 in 910	1 in 99,000
Cystinosis	1 in 22,000	< 1 in 1,000,000
D-bifunctional Protein Deficiency	1 in 2,900	< 1 in 1,000,000
Dihydropyrimidine Dehydrogenase Deficiency	1 in 1,400	1 in 570,000
Factor XI Deficiency	< 1 in 50,000	< 1 in 1,000,000
Familial Dysautonomia	< 1 in 50,000	< 1 in 1,000,000
Familial Mediterranean Fever	< 1 in 50,000	< 1 in 1,000,000
Fanconi Anemia Type C	1 in 16,000	< 1 in 1,000,000
FKTN-related Disorders	< 1 in 50,000	< 1 in 1,000,000
Galactosemia	1 in 8,600	< 1 in 1,000,000
Gaucher Disease	1 in 280	1 in 120,000
GJB2-related DFNB1 Nonsyndromic Hearing Loss and Deafness	p.G12Vfs*2 heterozygote †	1 in 130
Glutaric Acidemia Type 1	1 in 10,000	< 1 in 1,000,000
Glycogen Storage Disease Type Ia	1 in 18,000	< 1 in 1,000,000
Glycogen Storage Disease Type Ib	1 in 35,000	< 1 in 1,000,000
Glycogen Storage Disease Type III	1 in 16,000	< 1 in 1,000,000
Glycogen Storage Disease Type V	1 in 16,000	< 1 in 1,000,000
GRACILE Syndrome	< 1 in 50,000	< 1 in 1,000,000

Disease	DONOR 12193 Residual Risk	Reproductive Risk
HADHA-related Disorders	1 in 15,000	< 1 in 1,000,000
Hb Beta Chain-related Hemoglobinopathy (Including Beta Thalassemia and Sickle Cell Disease)	1 in 1,200	1 in 240,000
Hereditary Fructose Intolerance	1 in 8,000	< 1 in 1,000,000
Herlitz Junctional Epidermolysis Bullosa, LAMA3-related	< 1 in 50,000	< 1 in 1,000,000
Herlitz Junctional Epidermolysis Bullosa, LAMB3-related	< 1 in 50,000	< 1 in 1,000,000
Herlitz Junctional Epidermolysis Bullosa, LAMC2-related	< 1 in 50,000	< 1 in 1,000,000
Hexosaminidase A Deficiency (Including Tay-Sachs Disease)	1 in 30,000	< 1 in 1,000,000
Homocystinuria Caused by Cystathionine Beta-synthase Deficiency	1 in 25,000	< 1 in 1,000,000
Hypophosphatasia, Autosomal Recessive	1 in 16,000	< 1 in 1,000,000
Inclusion Body Myopathy 2	< 1 in 50,000	< 1 in 1,000,000
Isovaleric Acidemia	1 in 25,000	< 1 in 1,000,000
Joubert Syndrome 2	< 1 in 50,000	< 1 in 1,000,000
Krabbe Disease	1 in 15,000	< 1 in 1,000,000
Lipoamide Dehydrogenase Deficiency	< 1 in 50,000	< 1 in 1,000,000
Maple Syrup Urine Disease Type 1B	1 in 25,000	< 1 in 1,000,000
Medium Chain Acyl-CoA Dehydrogenase Deficiency	1 in 5,900	< 1 in 1,000,000
Megalencephalic Leukoencephalopathy with Subcortical Cysts	< 1 in 50,000	< 1 in 1,000,000
Metachromatic Leukodystrophy	1 in 20,000	< 1 in 1,000,000
Mucopolidosis IV	< 1 in 50,000	< 1 in 1,000,000
Mucopolysaccharidosis Type 1	1 in 480	1 in 300,000
Muscle-eye-brain Disease	< 1 in 5,000	< 1 in 1,000,000
NEB-related Nemaline Myopathy	< 1 in 5,500	< 1 in 1,000,000
Niemann-Pick Disease Type C	1 in 5,400	< 1 in 1,000,000
Niemann-Pick Disease, SMPD1-associated	1 in 25,000	< 1 in 1,000,000
Nijmegen Breakage Syndrome	1 in 16,000	< 1 in 1,000,000
Northern Epilepsy	< 1 in 50,000	< 1 in 1,000,000
PCDH15-related Disorders	1 in 2,300	< 1 in 1,000,000
Pendred Syndrome	1 in 7,000	< 1 in 1,000,000
PEX1-related Zellweger Syndrome Spectrum	NM_000466.2(PEX1):c.1952_1960dup9 (W653_M654insTVW) heterozygote †	1 in 450
Phenylalanine Hydroxylase Deficiency	1 in 3,000	1 in 600,000
PKHD1-related Autosomal Recessive Polycystic Kidney Disease	1 in 4,100	1 in 990,000
Polyglandular Autoimmune Syndrome Type 1	1 in 14,000	< 1 in 1,000,000
Pompe Disease	1 in 1,600	< 1 in 1,000,000
PPT1-related Neuronal Ceroid Lipofuscinosis	< 1 in 50,000	< 1 in 1,000,000
Primary Carnitine Deficiency	< 1 in 50,000	< 1 in 1,000,000
Primary Hyperoxaluria Type 1	1 in 35,000	< 1 in 1,000,000
Primary Hyperoxaluria Type 2	< 1 in 50,000	< 1 in 1,000,000
PROP1-related Combined Pituitary Hormone Deficiency	1 in 11,000	< 1 in 1,000,000
Pseudocholinesterase Deficiency (Mild Condition)	1 in 2,700	1 in 300,000
Pycnodysostosis	< 1 in 50,000	< 1 in 1,000,000
Rhizomelic Chondrodysplasia Punctata Type 1	1 in 16,000	< 1 in 1,000,000
Salla Disease	< 1 in 7,500	< 1 in 1,000,000
Segawa Syndrome	< 1 in 13,000	< 1 in 1,000,000
Short Chain Acyl-CoA Dehydrogenase Deficiency	1 in 16,000	< 1 in 1,000,000
Sjogren-Larsson Syndrome	1 in 3,100	< 1 in 1,000,000
Smith-Lemli-Opitz Syndrome	1 in 4,900	1 in 970,000
Spinal Muscular Atrophy	NM_000344.3(SMN1):g.27134T= homozygote SMN1: 2 copies	1 in 110,000
Steroid-resistant Nephrotic Syndrome	1 in 770	
Sulfate Transporter-related Osteochondrodysplasia	1 in 40,000	< 1 in 1,000,000
TPP1-related Neuronal Ceroid Lipofuscinosis	1 in 11,000	< 1 in 1,000,000
Tyrosinemia Type 1	1 in 30,000	< 1 in 1,000,000
Tyrosinemia Type I	1 in 17,000	< 1 in 1,000,000
Usher Syndrome Type 3	< 1 in 50,000	< 1 in 1,000,000
Very Long Chain Acyl-CoA Dehydrogenase Deficiency	1 in 8,800	< 1 in 1,000,000
Wilson Disease	1 in 8,600	< 1 in 1,000,000