REFERENCE LABORATORY GENETICS

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CarrierRef®
CARRIER TESTING

Request No.:	-		
Client:	-		
Analysis code:	15048		
Patient Name:	-		
Date of Birth:	-	Patient Ref.:	-
Gender:	Male	Sample Type:	Blood
Sample Arrival Date:	25/01/2021	Date of Result:	19/02/2021

SUMMARY OF RESULTS: MUTATIONS IDENTIFIED

CONDITION and GENE	INHERITANCE	
Congenital nephrotic syndrome, type 2 *NPHS2*	Autosomal Recessive, Digenic NPHS1	Carrier Mutation: c.686G>A (p.Arg229Gln)

Reproductive Risk and following considerations:

Reproductive Risk has been detected. Consider partner carrier testing

INTERPRETATION

The variant in the *NPHS2* gene, p.Arg229Gln, is only pathogenic under certain circumstances. Please see below for details.

Notes and Recommendations:

The test results indicate that this individual is a CARRIER. Genetic counseling is strongly recommended to discuss reproductive risk and prenatal testing options.

- Based on these results, you are positive for carrier mutations in 1 gene. The risk estimates for Autosomal Recessive diseases given below are quantified based on general population carrier frequencies. Carrier screening for the reproductive partner is recommended to accurately assess this risk:
- There is a 1/1156 chance of having a child affected with Congenital nephrotic syndrome, type 2, a *NPHS2*-related condition.
- Testing for copy number changes in the *SMN1* gene was performed to screen for your carrier status for Spinal Muscular Atrophy. 2 copies of the *SMN1* gene were detected. These results are within the normal range for non-carriers. See Limitations section for more information.
- This carrier screening test does not screen for all possible genetics conditions, nor for all possible mutations in every gene tested. Individuals with negative test results may still have up to a 3-4% risk to have a child with a birth defect due to genetic and/or environmental factors.
- Patients may wish to discuss any carrier results with blood relatives, as there is an increased chance that they are also carriers.

CONGENITAL NEPHROTIC SYNDROME, TYPE 2

PATIENT	-
Result	Carrier
Variant Details	*NPHS2* (NM_014625.3) c.686G>A (p.Arg229Gln)
Methodology	NGS

What is Congenital nephrotic syndrome, type 2?

Congenital nephrotic syndrome is a condition that begins in infancy and typically leads to irreversible kidney failure by early childhood. Children with congenital nephrotic syndrome begin to have symptoms of the condition between birth and 3 months. In this disease the kidneys are unable to filter waste from the blood. Signs and symptoms of this condition are excessive protein in the urine, increased cholesterol in the blood, and swelling/retention of fluid throughout the body. Affected individuals may also have low blood cell counts, a weakened immune system, and anemia as a result of kidney failure.

What is my risk to have an affected child?

Congenital nephrotic syndrome, type 2 is inherited in an autosomal recessive manner. The risk for being a carrier for *NPHS2*-related Congenital nephrotic syndrome, type 2 is 1/289. Individuals of Finnish descent have an increased carrier risk of 1/50. If the patient and the partner are both carriers, the risk for an affected child is 1 in 4 (25%).

What is the prognosis/treatment?

With medical treatment kidney failure can be delayed but not entirely avoided. Children with congenital nephrotic syndrome typically develop end-stage renal disease between ages 2 and 8. Many of these patients will require dialysis and kidney transplantation. Affected infants are also prone to serious bacterial infection in the first year of life.

Which mutation has been detected?

The detected mutation was NM_014625.3:c.686G>A (p.Arg229Gln). While this variant, p.Arg229Gln, has been commonly reported in the general population, the disease penetrance of this allele is dependent on the specific *NPHS2* variants occurring in trans with this variant. It should be noted that this variant is only pathogenic under certain circumstances. This variant is not significantly associated with disease when homozygous or in the compound heterozygous state with variants in exons 1-6 of *NPHS2* (PubMed: 23800802, 18499321). However, this variant may be associated with disease when observed in trans with certain variants in exons 7 and 8 (PubMed: 24509478). This effect has been observed in multiple patients with late onset steroid resistant nephrotic syndrome. Functional studies of p.Arg229Gln in trans with another mutation in exons 7 or 8 have also shown a dominant-negative effect resulting in the mislocalization of the podocin protein (PubMed: 24509478). The laboratory classifies this mutation as likely pathogenic.

ANALYZED and INFORMED GENES

CarrierRef®. 277 genes tested (99.43% of coding bases at >20x). For more specific information on genes and calculation of residual risk see ADDITIONAL TABLE.

ABCA12	*CEP290*	*FAM161A*	*IDUA*	*PC*	*SLC26A3*
ABCA4	*CERKL*	*FANCA*	*IKBKAP*	*PCCA*	*SLC26A4*
ABCB11	*CFTR*	*FANCC*	*IVD*	*PCCB*	*SLC35A3*
ABCC8	*CHRNE*	*FANCG*	*KCNJ11*	*PCDH15*	*SLC37A4*
ACADM	*CHRNG*	*FH*	*LAMA3*	*PDHB*	*SLC39A4*
ACADS	*CIITA*	*FKRP*	*LAMB3*	*PEX1*	*SLC3A1*
ACADVL	*CLN5*	*FKTN*	*LAMC2*	*PEX10*	*SLC45A2*
ACAT1	*CLN6*	*G6PC*	*LCA5*	*PEX2*	*SLC4A11*
ACOX1	*CLN8*	*GAA*	*LHCGR*	*PEX6*	*SLC7A7*
ADA	*CLRN1*	*GALC*	*LIFR*	*PEX7*	*SLC7A9*
ADAMTS2	*COL4A3*	*GALK1*	*LIPA*	*PFKM*	*SMN1*
AGA	*COL4A4*	*GALNS*	*LOXHD1*	*PHGDH*	*SMPD1*
AGL	*COL7A1*	*GALT*	*LPL*	*PKHD1*	*SRD5A2*
AGXT	*CPT1A*	*GAMT*	*LRPPRC*	*PMM2*	*STAR*
AIRE	*CPT2*	*GBA*	*LYST*	*POLG*	*SUMF1*
ALDH3A2	*CTNS*	*GBE1*	*MAN2B1*	*POMGNT1*	*TAT*
ALDOB	*CTSC*	*GCDH*	*MCCC1*	*POR*	*TCIRG1*
ALG6	*CTSK*	*GDF5*	*MCCC2*	*PPT1*	*TECPR2*
ALPL	*CYBA*	*GJB2*	*MCOLN1*	*PROP1*	*TFR2*
AMH	*CYP11B1*	*GLB1*	*MED17*	*PTS*	*TGM1*
AMHR2	*CYP11B2*	*GLDC*	*MEFV*	*PUS1*	*TH*
AMT	*CYP17A1*	*GNE*	*MFSD8*	*PYGM*	*TMEM216*
ARG1	*CYP19A1*	*GNPTAB*	*MKS1*	*RAB23*	*TPP1*
ARSA	*CYP1B1*	*GNS*	*MLC1*	*RAG2*	*TRIM32*
ARSB	*CYP21A2*	*GRHPR*	*MLYCD*	*RAPSN*	*TRMU*
ASL	*CYP27A1*	*GUCY2D*	*MMAA*	*RARS2*	*TSEN54*
ASNS	*DBT*	*GUSB*	*MMAB*	*RDH12*	*TTC37*
ASPA	*DCLRE1C*	*HADHA*	*MMACHC*	*RLBP1*	*TTPA*
ASS1	*DHCR7*	*HADHB*	*MPI*	*RMRP*	*TYMP*
ATM	*DHDDS*	*HAX1*	*MPL*	*RPE65*	*TYR*
ATP6V1B1	*DLD*	*HBA1*	*MPV17*	*RTEL1*	*TYRP1*
ATP7B	*DNAI1*	*HBA2*	*MTTP*	*SACS*	*UGT1A1*
BBS1	*DNAI2*	*HBB*	*MUT*	*SEPSECS*	*USH1C*
BBS10	*DOK7*	*HEXA*	*MYO15A*	*SERPINA1*	*USH2A*
BBS12	*DYSF*	*HEXB*	*MYO7A*	*SGCA*	*VPS13A*
BBS2	*EIF2AK3*	*HFE2*	*NAGLU*	*SGCB*	*VPS13B*
BCHE	*EIF2B5*	*HGD*	*NBN*	*SGCD*	*VPS53*
BCKDHA	*ERCC6*	*HGSNAT*	*NDUFS6*	*SGCG*	*VRK1*
BCKDHB	*ERCC8*	*HLCS*	*NEB*	*SGSH*	*VSX2*
BCS1L	*ETFA*	*HMGCL*	*NPC1*	*SLC12A3*	*WRN*
BLM	*ETFB*	*HOGA1*	*NPC2*	*SLC12A6*	*XPA*
BRIP1	*ETFDH*	*HPS1*	*NPHS1*	*SLC17A5*	*XPC*
BSND	*ETHE1*	*HPS3*	*NPHS2*	*SLC22A5*	
BTD	*EVC*	*HPS4*	*NR2E3*	*SLC25A13*	
CAPN3	*EVC2*	*HSD17B3*	*NTRK1*	*SLC25A15*	
CBS	*EXOSC3*	*HSD17B4*	*OPA3*	*SLC25A20*	
CDH23	*FAH*	*HSD3B2*	*PAH*	*SLC26A2*	

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, variants were detected in regions of at least 10x coverage. For this specimen, 99.46% and 99.43% of coding regions and splicing junctions of genes listed had been sequenced with coverage of at least 10x and 20x respectively 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. All the variants with quality score less than 500 (roughly 40x of coverage for a heterozygous variant) will be confirmed by Sanger sequencing. Only variants classified as pathogenic, likely-pathogenic are reported. 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 (see Gene Specific Limitations below). Putative deletions or duplications identified are confirmed by an orthogonal method (qPCR or MLPA). If included in the panel, *FMR1* repeat analysis is performed by repeat-primed PCR (rpPCR) and amplicon length analysis. Methylation studies are not performed. Variants are classified using the ACMG Guidelines for Sequence Variant Interpretation (PubMed: 27993330) unless otherwise specified.

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 comingling 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. We use 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 LIMITATIONS

CFTR

Analysis of the intron 8 polymorphic region (e.g. IVS8-5T allele) is only performed if the p.Arg117His (R117H) mutation is detected. Single exon deletion/ duplication analysis is limited to deletions of previously reported exons: 1, 2, 3, 11, 19, 20, 21.

CYP11B1

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

CYP11B2

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

CYP21A2

Significant pseudogene interference and/or reciprocal exchanges between the *CYP21A2* gene and its pseudogene, *CYP21A1P*, have been known to occur and may impact results. As such, the relevance of variants reported in this gene must be interpreted clinically in the context of this individual's clinical findings, biochemical profile, and family history. Two specific variants - NM_000500.7:c.1174G>A (p.Ala392Thr) and NM_000500.7:c.188A>T (p.His63Leu) - are not typically evaluated for this test; both are very rare and are susceptible to technical interference, but they can be evaluated if there's an specfici request due to family history. The NM_000500.7:c.955C>T (p.Gln319Ter) variant is in the region with pseudogene interference, the probability of the variant in real copy is greater than 50%, and will be reported. The request for a confirmation test is recommended if the partner is tested positive in the same gene.

GALT
In general, the D2 "Duarte" allele is not reported if detected, but can be reported upon request. While this allele can cause positive newborn screening results, it is not known to cause clinical symptoms in any state. See GeneReviews for more information: https://www.ncbi.nlm.nih.gov/books/NBK1518

GBA
The current testing method may not be able to reliably detect certain pathogenic variants in the *GBA* gene due to homologous recombination between the pseudogene and the functional gene.

HBA1
The phase of heterozygous alterations in the *HBA1* gene and the *HBA2* gene cannot be determined, but can be confirmed through parental testing.

HBA2
The phase of heterozygous alterations in the *HBA1* gene and the *HBA2* gene cannot be determined, but can be confirmed through parental testing.

NEB
This gene contains a 32-kb triplicate region (exons 82-105) which is not amenable to sequencing and deletion/duplication analysis.

SMN1
The current testing method detects sequencing variants in exon 7 and copy number variations in exons 7-8 of the *SMN1* gene (NM_022874.2). Sequencing and deletion/duplication analysis are not performed on any other region in this gene. About 5%-8% of the population have two copies of *SMN1* on a single chromosome and a deletion on the other chromosome, known as a [2+0] configuration (PubMed: 20301526). The current testing method cannot directly detect carriers with a [2 +0] *SMN1* configuration, but can detect linkage between the silent carrier allele and certain population-specific single nucleotide changes. As a result, a negative result for carrier testing greatly reduces but does not eliminate the chance that a person is a carrier. The 3-copy *SMN1* state can be detected by this test and will be reported out if present.

UGT1A1
Common variants in the *UGT1A1* gene (population allele frequency >5%) are typically not reported as they do not cause a Mendelian condition.

SIGNATURE

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Gene	Inheritance	Condition	Ethnicity	Carrier frequency	Detection rate	Post test carrier probability*	Post-test probability of having an affected child**
ABCA12	AR	Congenital Ichthyosis: ABCA12	General	<1/500	98%	1/24951	<1/49902000
ABCA4	AR	Stargardt Disease	General	1/51	98%	1/2501	1/510204
ABCB11	AR	Progressive Familial Intrahepatic Cholestasis: Type 2	General	1/112	98%	1/5551	1/2486848
ABCC8	AR	Familial hyperinsulinism, ABCC8-related	General	1/112	98%	1/5551	1/2486848
			Ashkenazi Jewish	1/44	98%	1/2151	1/378576
			Finnish	1/25	98%	1/1201	1/120100
			Middle-Eastern	1/25	98%	1/1201	1/120100
ACADM	AR	Medium-chain acyl-CoA dehydrogenase (MCAD) deficiency	General	1/69	98%	1/3401	1/938676
			East Asian	1/198	99%	1/19701	1/15603192
			European	1/52	99%	1/5101	1/1061008
			Native American	1/43	96%	1/1051	1/180772
ACADS	AR	Short-chain acyl-coA dehydrogenase (SCAD) deficiency	General	1/85	99%	1/8401	1/2856340
			African	1/52	99%	1/5101	1/1061008
			African American	1/52	99%	1/5101	1/1061008
			Middle-Eastern	1/52	99%	1/5101	1/1061008
			European	1/76	99%	1/7501	1/2280304
			South Asian/Indian	1/51	99%	1/5001	1/1020204
ACADVL	AR	Very long-chain acyl-CoA dehydrogenase (VLCAD) deficiency	General	1/118	93%	1/1672	1/789184
			Middle-Eastern	1/74	93%	1/1044	1/309024
			Native American	1/61	93%	1/858	1/209352
			South Asian/Indian	1/73	93%	1/1030	1/300760
ACAT1	AR	3-ketothiolase deficiency	General	<1/500	98%	<1/24951	<1/49902000
ACOX1	AR	Peroxisomal acyl-CoA oxidase deficiency	General	<1/500	98%	<1/24951	<1/49902000
ADA	AR	Adenosine deaminase deficiency	General	1/224	93%	1/3187	1/2855552
ADAMTS2	AR	Ehlers-Danlos syndrome, Dermatosparaxis type VIIC	General	<1/500	98%	<1/24951	<1/49902000
			Ashkenazi Jewish	1/248	98%	1/12351	1/12252192
AGA	AR	Aspartylglucosaminuria	General	<1/500	98%	<1/24951	<1/49902000
			Finnish	1/71	98%	1/3501	1/994284
AGL	AR	Glycogen storage disease type III	General	1/158	95%	1/3141	1/1985112
			Faroese	1/28	95%	1/541	1/60592
			Inuit	1/25	95%	1/481	1/48100
			North African Jewish	1/37	95%	1/721	1/106708
AGXT	AR	Primary hyperoxaluria type 1	General	1/120	99%	1/11901	1/5712480
			European	1/173	99%	1/17201	1/11903092
AIRE	AR	Autoimmune polyendocrinopathy syndrome type I	General	1/150	98%	1/7451	1/4470600
			Finnish	1/79	98%	1/3901	1/1232716
ALDH3A2	AR	Sjögren-Larsson syndrome	General	1/250	98%	1/12451	1/12451000
ALDOB	AR	Hereditary fructose intolerance	General	1/122	99%	1/12101	1/5905288
			African American	1/250	99%	1/24901	1/24901000
			African	1/250	99%	1/24901	1/24901000
			European	1/67	99%	1/6601	1/1769068
			Middle-Eastern	1/97	99%	1/9601	1/3725188
ALG6	AR	Congenital disorder of glycosylation type Ic	General	<1/500	98%	<1/24951	<1/49902000
ALPL	AR	Hypophosphatasia	General	1/158	95%	1/3141	1/1985112
			European	1/274	95%	1/5461	1/5985256
			Mennonite	1/25	95%	1/481	1/48100
AMH	AR	Persistent Mullerian Duct Syndrome: Type I	General	<1/500	98%	<1/24951	<1/49902000
AMHR2	AR	Persistent Mullerian Duct Syndrome: Type II	General	<1/500	98%	<1/24951	<1/49902000
AMT	AR	Glycine Encephalopathy: AMT Related	General	1/373	98%	1/18601	1/27752692
			Finnish	1/117	98%	1/5801	1/2714868
ARG1	AR	Arginase deficiency	General	1/296	98%	1/14751	1/17465184
ARSA	AR	Metachromatic leukodystrophy	General	1/100	95%	1/1981	1/792400
			European	1/78	95%	1/1541	1/480792
ARSB	AR	Mucopolysaccharidosis type VI (Maroteaux-Lamy syndrome)	General	1/250	98%	1/12451	1/12451000
			Western Australian	1/283	98%	1/14101	1/15962332
ASL	AR	Argininosuccinate lyase deficiency	General	1/132	90%	1/1311	1/692208
ASNS	AR	Asparagine synthetase deficiency	General	<1/500	98%	<1/24951	<1/49902000
ASPA	AR	Canavan disease	General	1/300	97%	1/9968	1/11961600
			Ashkenazi Jewish	1/55	96%	1/1351	1/297220
ASS1	AR	Citrullinemia	General	1/119	96%	1/2951	1/1404676
			East Asian	1/132	96%	1/3276	1/1729728
ATM	AR	Ataxia-telangiectasia	General	1/100	92%	1/1239	1/495600
ATP6V1B1	AR	Renal tubular acidosis with deafness	General	<1/500	98%	<1/24951	<1/49902000
ATP7B	AR	Wilson disease	General	1/87	98%	1/4301	1/1496748
			European	1/42	98%	1/2051	1/344568
			Ashkenazi Jewish	1/70	98%	1/3451	1/966280
BBS1	AR, DG	Bardet-Biedl syndrome type 1	General	1/367	99%	1/36601	1/53730268
BBS10	AR, DG	Bardet-Biedl syndrome type 10	General	1/395	99%	1/39401	1/62253580
BBS12	AR, DG	Bardet-Biedl syndrome type 12	General	1/791	99%	1/79001	1/249959164
BBS2	AR, DG	Bardet-Biedl syndrome 2 (+)	General	1/621	99%	1/62001	1/154010484
			Ashkenazi Jewish	1/107	99%	1/10601	1/4537228
BBS2	AR, DG	Retinitis Pigmentosa 74 (+)	General	1/621	99%	1/62001	<1/10000000

Gene	Inheritance	Condition	Ethnicity	Carrier frequency	Detection rate	Post test carrier probability*	Post-test probability of having an affected child**
			Ashkenazi Jewish	1/107	99%	1/10601	1/4537228
BBS2	AR, DG	BBS2-related disorders	General	1/621	99%	1/62001	1/154010484
			Ashkenazi Jewish	1/107	99%	1/10601	1/4537228
BCHE	AR	Pseudocholinesterase Deficiency	General	1/28	99%	1/2701	1/302512
BCKDHA	AR	Maple syrup urine disease type Ia	General	1/321	98%	1/16001	1/20545284
			Mennonite	1/10	98%	1/451	1/18040
BCKDHB	AR	Maple syrup urine disease type Ib	General	1/364	98%	1/18151	1/26427856
			Ashkenazi Jewish	1/97	98%	1/4801	1/1862788
BCS1L	AR	Björnstad syndrome (+)	General	<1/500	98%	1/24951	<1/49902000
BCS1L	AR	GRACILE syndrome (+)	General	<1/500	98%	<1/24951	<1/49902000
BCS1L	AR	Mitochondrial complex III deficiency (+)	General	<1/500	98%	1/24951	<1/49902000
BCS1L	AR	BCS1L-related conditions	General	<1/500	98%	<1/24951	<1/49902000
BLM	AR	Bloom syndrome	General	1/800	87%	1/6147	1/19670400
			Ashkenazi Jewish	1/134	99%	1/13301	1/7129336
BRIP1	AR	Fanconi Anemia: Type J	General	<1/500	98%	<1/24951	<1/49902000
BSND	AR	Bartter syndrome	General	1/500	98%	1/24951	1/49902000
BTD	AR	Biotinidase deficiency	General	1/124	99%	1/12301	1/6101296
			European	1/71	99%	1/7001	1/1988284
			Latino	1/136	99%	1/13501	1/7344544
			Middle-Eastern	1/55	99%	1/5401	1/1188220
CAPN3	AR	Limb-girdle muscular dystrophy type 2A	General	<1/500	98%	<1/24951	<1/49902000
			European	1/103	98%	1/5101	1/2101612
CBS	AR	Homocystinuria due to cystathionine beta-synthase deficiency	General	1/224	99%	1/22301	1/19981696
			European	1/86	99%	1/8501	1/2924344
			Middle-Eastern	1/21	99%	1/2001	1/168084
CDH23	AR, DG	Usher syndrome, type 1D	General	1/285	90%	1/2841	1/3238740
CEP290	AR	Bardet-Biedl syndrome 14 (+)	General	1/190	98%	1/9451	1/7182760
CEP290	AR	Joubert syndrome 5 (+)	General	1/190	98%	1/9451	1/7182760
CEP290	AR	Leber congenital amaurosis 10 (+)	General	1/190	98%	1/9451	1/7182760
CEP290	AR	Meckel syndrome 4 (+)	General	1/190	98%	1/9451	1/7182760
CEP290	AR	Senior-Løken syndrome 6 (+)	General	1/190	98%	1/9451	1/7182760
CEP290	AR	CEP290-related disorders	General	1/190	98%	1/9451	1/7182760
CERKL	AR	Retinitis Pigmentosa 26	General	1/148	98%	1/7351	1/4351792
CFTR	AR	Cystic fibrosis	General	1/32	99%	1/3101	1/396928
			African American	1/61	99%	1/6001	1/1464244
			African	1/61	99%	1/6001	1/1464244
			Ashkenazi Jewish	1/24	99%	1/2301	1/220896
			European	1/25	99%	1/2401	1/240100
			East Asian	1/94	99%	1/9301	1/3497176
			Latino	1/58	99%	1/5701	1/1322632
CHRNE	AR	Congenital Myasthenic Syndrome, CHRNE-related	General	1/408	99%	1/40701	1/66424032
CHRNG	AR	Multiple pterygium syndrome	General	<1/500	98%	<1/24951	<1/49902000
CIITA	AR	Bare lymphocyte syndrome, type II	General	<1/500	98%	<1/24951	<1/49902000
CLN5	AR	Neuronal ceroid lipofuscinosis, CLN5-related	General	<1/500	95%	<1/9981	<1/19962000
			Finnish	1/115	95%	1/2281	1/1049260
CLN6	AR	Neuronal ceroid lipofuscinosis, CLN6-related	General	<1/500	92%	<1/6239	<1/12478000
CLN8	AR	Neuronal ceroid lipofuscinosis, CLN8-related	General	<1/500	95%	<1/9981	<1/19962000
			Finnish	1/135	95%	1/2681	1/1447740
CLRN1	AR	Usher syndrome, type 3A	General	1/500	98%	1/24951	1/49902000
			Ashkenazi Jewish	1/120	98%	1/5951	1/2856480
			Finnish	1/70	98%	1/3451	1/966280
COL4A3	AR, DG	Alport syndrome, COL4A3-related	General	1/267	98%	1/13301	1/14205468
			Ashkenazi Jewish	1/188	98%	1/9351	1/7031952
COL4A4	AR, DG	Alport syndrome, COL4A4-related	General	1/267	98%	1/13301	1/14205468
COL7A1	AR	Dystrophic epidermolysis bullosa	General	1/196	97%	1/6501	1/5096784
CPT1A	AR	Carnitine palmitoyltransferase IA deficiency	General	1/354	90%	1/3531	1/4999896
			Hutterite	1/16	90%	1/151	1/9664
CPT2	AR	Carnitine palmitoyltransferase II deficiency	General	<1/500	95%	<1/9981	<1/19962000
			Ashkenazi Jewish	1/51	95%	1/1001	1/204204
CTNS	AR	Cystinosis	General	1/158	99%	1/15701	1/9923032
			British	1/81	99%	1/8001	1/2592324
CTSC	AR	Papillon-Lefevre Syndrome	General	<1/500	98%	<1/24951	<1/49902000
CTSK	AR	Pycnodysostosis	General	<1/500	98%	<1/24951	<1/49902000
CYBA	AR	Chronic granulomatous disease	General	1/224	99%	1/22301	1/19981696
CYP11B1	AR	Congenital adrenal hyperplasia due to 11-beta-hydroxylase deficiency	General	1/158	98%	1/7851	1/4961832
			Morrocan Jewish	1/35	98%	1/1701	1/238140
CYP11B2	AR	Corticosterone methyloxidase deficiency	General	<1/500	98%	<1/24951	<1/49902000
CYP17A1	AR	Congenital adrenal hyperplasia due to 17-alpha-hydroxylase deficiency	General	1/500	98%	1/24951	<1/10000000

Gene	Inheritance	Condition	Ethnicity	Carrier frequency	Detection rate	Post test carrier probability*	Post-test probability of having an affected child**
CYP19A1	AR	Aromatase deficiency	General	<1/500	98%	<1/24951	<1/49902000
CYP1B1	AR	Primary congenital glaucoma	General	1/50	99%	1/4901	1/980200
CYP21A2	AR	Congenital adrenal hyperplasia due to 21- hydroxylase deficiency	General Inuit Middle-Eastern	1/61 1/9 1/35	99% 99% 99%	1/6001 1/801 1/3401	1/1464244 1/28836 1/476140
CYP27A1	AR	Cerebrotendinous xanthomatosis	General Morrocan Jewish	1/500 1/5	98% 98%	1/24951 1/201	1/49902000 1/4020
DBT	AR	Maple syrup urine disease type II	General	1/481	98%	1/24001	1/46177924
DCLRE1C	AR	Severe combined immunodeficiency with sensitivity to ionizing radiation	General	<1/500	98%	<1/24951	<1/49902000
DHCR7	AR	Smith-Lemli-Opitz syndrome	General African American African Ashkenazi Jewish	1/30 1/138 1/138 1/36	96% 96% 96% 96%	1/726 1/3426 1/3426 1/876	1/87120 1/1891152 1/1891152 1/126144
DHDDS	AR	Retinitis Pigmentosa 59	General Ashkenazi Jewish	1/296 1/118	98% 98%	1/14751 1/5851	1/17465184 1/2761672
DLD	AR	Dihydrolipoamide dehydrogenase deficiency	General Ashkenazi Jewish	1/500 1/107	98% 98%	1/24951 1/5301	1/49902000 1/2268828
DNAI1	AR	Primary ciliary dyskinesia, DNAI1-related	General	1/230	98%	1/11451	1/10534920
DNAI2	AR	Primary ciliary dyskinesia, DNAI2-related	General	1/447	98%	1/22301	1/39874188
DOK7	AR	Congenital Myasthenic Syndrome: DOK7 Related	General	1/472	98%	1/23551	1/44464288
DYSF	AR	Limb-girdle muscular dystrophy type 2B	General Japanese Libyan Jewish	<1/500 1/332 1/18	95% 95% 95%	1/9981 1/6621 1/341	<1/19962000 1/8792688 1/24552
EIF2AK3	AR	Wolcott-Rallison syndrome	General	<1/500	98%	<1/24951	<1/49902000
EIF2B5	AR	Leukoencephalopathy with vanishing white matter	General	<1/500	98%	<1/24951	<1/49902000
ERCC6	AR	Cockayne syndrome type B (+)	General Japanese	1/500 1/74	99% 99%	1/49901 1/7301	1/99802000 1/2161096
ERCC6	AR	De Sanctis-Cacchione syndrome (+)	General Japanese	1/500 1/74	99% 99%	1/49901 1/7301	1/99802000 1/2161096
ERCC6	AR	ERCC6-Related Disorders	General Japanese	1/500 1/74	99% 99%	1/49901 1/7301	1/99802000 1/2161096
ERCC8	AR	Cockayne syndrome type A	General	1/822	98%	1/41051	1/134975688
ETFA	AR	Glutaric aciduria IIA	General	1/500	98%	1/24951	1/49902000
ETFB	AR	Glutaric aciduria IIB	General	1/500	98%	1/24951	1/49902000
ETFDH	AR	Glutaric aciduria IIC	General East Asian	1/250 1/74	98% 98%	1/12451 1/3651	1/12451000 1/1080696
ETHE1	AR	Ethylmalonic encephalopathy	General	<1/500	98%	<1/24951	<1/49902000
EVC	AR	Ellis-van Creveld syndrome, EVC-related	General Amish	1/142 1/7	98% 98%	1/7051 1/301	1/4004968 1/8428
EVC2	AR	Ellis-van Creveld syndrome, EVC2-related	General Amish	1/240 1/7	98% 98%	1/11951 1/301	1/11472960 1/8428
EXOSC3	AR	Pontocerebellar hypoplasia type 1B	General	<1/500	98%	<1/24951	<1/49902000
FAH	AR	Tyrosinemia, type 1	General Ashkenazi Jewish Finnish French Canadian South Asian/Indian	1/99 1/150 1/122 1/66 1/172	95% 95% 95% 95% 95%	1/1961 1/2981 1/2421 1/1301 1/3421	1/776556 1/1788600 1/1181448 1/343464 1/2353648
FAM161A	AR	Retinitis Pigmentosa 28	General	1/296	98%	1/14751	1/17465184
FANCA	AR	Fanconi anemia group A	General	1/239	98%	1/11901	1/11377356
FANCC	AR	Fanconi anemia group C	General Ashkenazi Jewish	1/535 1/99	99% 99%	1/53401 1/9801	1/114278140 1/3881196
FANCG	AR	Fanconi anemia group G	General	1/632	90%	1/6311	1/15954208
FH	AR	Fumarase deficiency	General	<1/500	90%	<1/4991	<1/9982000
FKRP	AR	Muscular dystrophy-dystroglycanopathy, FKRP- related	General	1/158	98%	1/7851	1/4961832
FKTN	AR	FKTN-Related Disorders	General Ashkenazi Jewish Japanese	<1/500 1/150 1/82	99% 99% 99%	<1/49901 1/14901 1/8101	<1/99802000 1/8940600 1/2657128
FKTN	AR	Fukuyama congenital macular dystrophy (+)	General Ashkenazi Jewish Japanese	<1/500 1/150 1/82	99% 99% 99%	1/49901 1/14901 1/8101	<1/99802000 1/8940600 1/2657128
FKTN	AR	Muscular dystrophy-dystroglycanopathy, FKTN-related (+)	General Ashkenazi Jewish Japanese	<1/500 1/150 1/82	99% 99% 99%	<1/49901 1/14901 1/8101	<1/99802000 1/8940600 1/2657128
G6PC	AR	Glycogen Storage disease, type 1a	General Ashkenazi Jewish	1/177 1/64	95% 95%	1/3521 1/1261	1/2492868 1/322816
GAA	AR	Pompe disease	General African American African East Asian	1/100 1/60 1/60 1/112	98% 98% 98% 98%	1/4951 1/2951 1/2951 1/5551	1/1980400 1/708240 1/708240 1/2486848
GALC	AR	Krabbe disease	General	1/158	99%	1/15701	1/9923032

Gene	Inheritance	Condition	Ethnicity	Carrier frequency	Detection rate	Post test carrier probability*	Post-test probability of having an affected child**
			Israeli Druze	1/6	99%	1/501	1/12024
GALK1	AR	Galactokinase deficiency	General	1/110	95%	1/2181	1/959640
			Irish	1/64	95%	1/1261	1/322816
GALNS	AR	Mucopolysaccharidosis IVA (Morquio syndrome A)	General	1/224	97%	1/7434	1/6660864
GALT	AR	Galactosemia	General	1/110	95%	1/2181	1/959640
			African	1/94	95%	1/1861	1/699736
			African American	1/94	95%	1/1861	1/699736
GAMT	AR	Guanidinoacetate methyltransferase deficiency	General	1/371	99%	1/37001	1/54909484
GBA	AR	Gaucher disease	General	1/77	99%	1/7601	1/2341108
			African	1/35	99%	1/3401	1/476140
			African American	1/35	99%	1/3401	1/476140
			Ashkenazi Jewish	1/15	99%	1/1401	1/84060
GBE1	AR	Glycogen storage disease IV	General	1/387	99%	1/38601	1/59754348
GCDH	AR	Glutaric aciduria, type I	General	1/87	98%	1/4301	1/1496748
			Amish	1/9	98%	1/401	1/14436
GDF5	AR	Du Pan Syndrome	General	<1/500	98%	<1/24951	<1/49902000
GJB2	AR	Nonsyndromic hearing loss, GJB2-related	General	1/42	99%	1/4101	1/688968
			African	1/25	99%	1/2401	1/240100
			African American	1/25	99%	1/2401	1/240100
			Ashkenazi Jewish	1/21	99%	1/2001	1/168084
			European	1/33	99%	1/3201	1/422532
			Latino	1/100	99%	1/9901	1/3960400
			Middle-Eastern	1/83	99%	1/8201	1/2722732
			South Asian/Indian	1/148	99%	1/14701	1/8702992
GLB1	AR	Mucopolysaccharidosis type IVB (Morquio syndrome B) (+)	General	1/134	99%	1/13301	1/7129336
			Maltese	1/30	99%	1/2901	1/348120
			Roma	1/50	99%	1/4901	1/980200
GLB1	AR	GM1-gangliosidosis (+)	General	1/134	99%	1/13301	1/7129336
			Maltese	1/30	99%	1/2901	1/348120
			Roma	1/50	99%	1/4901	1/980200
GLB1	AR	GLB1-Related Disorders	General	1/134	99%	1/13301	1/7129336
			Maltese	1/30	99%	1/2901	1/348120
			Roma	1/50	99%	1/4901	1/980200
GLDC	AR	Glycine encephalopathy, GLDC-related	General	1/193	98%	1/9601	1/7411972
			British Columbia	1/125	99%	1/12401	1/6200500
			Canadian	1/117	99%	1/11601	1/5429268
			Finnish				
GNE	AR	Inclusion body myopathy type 2 (Nonaka myopathy)	General	<1/500	80%	<1/2496	<1/4992000
			Iranian Jewish	1/11	80%	1/51	1/2244
GNPTAB	AR	Mucolipidosis II alpha/beta (+)	General	<1/500	95%	<1/9981	<1/19962000
GNPTAB	AR	Mucolipidosis III alpha/beta (+)	General	<1/500	95%	<1/9981	<1/19962000
GNPTAB	AR	GNPTAB-Related Disorders	General	<1/500	95%	<1/9981	<1/19962000
GNS	AR	Mucopolysaccharidosis IIID (Sanfilippo syndrome D)	General	1/500	98%	1/24951	1/49902000
GRHPR	AR	Primary Hyperoxaluria type II	General	<1/500	99%	1/49901	<1/99802000
GUCY2D	AR	Leber Congenital amaurosis 1: GUCY2D-Related	General	<1/500	98%	<1/24951	<1/49902000
GUSB	AR	Mucopolysaccharidosis type VII (Sly syndrome)	General	1/250	98%	1/12451	1/12451000
HADHA	AR	Long-chain 3-hydroxyacyl-CoA dehydrogenase (LCHAD) deficiency (+)	General	<1/500	98%	<1/24951	<1/49902000
			Finnish	1/124	98%	1/6151	1/3050896
HADHA	AR	Trifunctional Protein Deficiency: HADHA related (+)	General	<1/500	98%	<1/24951	<1/49902000
			Finnish	1/124	98%	1/6151	1/3050896
HADHA	AR	HADHA-Related Disorders	General	<1/500	98%	<1/24951	<1/49902000
			Finnish	1/124	98%	1/6151	1/3050896
HADHB	AR	Mitochondrial Trifunctional Protein Deficiency: HADHB Related	General	<1/500	98%	<1/24951	<1/49902000
			Finnish	1/124	98%	1/6151	1/3050896
HAX1	AR	Severe Congenital Neutropenia, HAX1-related	General	1/224	98%	1/11151	1/9991296
HBA1	AR, DG	Alpha thalassemia	General	1/20	90%	1/191	1/15280
			African	1/3	90%	1/21	1/252
			African American	1/3	90%	1/21	1/252
			Ashkenazi Jewish	1/13	90%	1/121	1/6292
			East Asian	1/8	90%	1/71	1/2272
			Middle-Eastern	1/3	90%	1/21	1/252
			South Asian/Indian	1/5	90%	1/41	1/820
HBA2	AR, DG	Alpha thalassemia	General	1/20	90%	1/191	1/15280
			African	1/3	90%	1/21	1/252
			African American	1/3	90%	1/21	1/252
			Ashkenazi Jewish	1/13	90%	1/121	1/6292
			East Asian	1/8	90%	1/71	1/2272
			Middle-Eastern	1/3	90%	1/21	1/252
			South Asian/Indian	1/5	90%	1/41	1/820
HBB	AR	Beta thalassemia (+)	General	1/158	95%	1/3141	1/1985112
			African	1/10	95%	1/181	1/7240
			African American	1/10	95%	1/181	1/7240
			East Asian	1/50	95%	1/981	1/196200
			Latino	1/128	95%	1/2541	1/1300992
			Mediterranean	1/3	95%	1/41	1/492

Gene	Inheritance	Condition	Ethnicity	Carrier frequency	Detection rate	Post test carrier probability*	Post-test probability of having an affected child**
			South Asian/Indian	1/25	95%	1/481	1/48100
HBB	AR	Sickle cell disease (+)	General	1/158	95%	1/3141	1/1985112
			African	1/10	95%	1/181	1/7240
			African American	1/10	95%	1/181	1/7240
			East Asian	1/50	95%	1/981	1/196200
			Latino	1/128	95%	1/2541	1/1300992
			Mediterranean	1/3	95%	1/41	1/492
			South Asian/Indian	1/25	95%	1/481	1/48100
HBB	AR	Hemoglobinopathy: HbC (+)	General	1/158	95%	1/3141	1/1985112
			African	1/10	95%	1/181	1/7240
			African American	1/10	95%	1/181	1/7240
			East Asian	1/50	95%	1/981	1/196200
			Latino	1/128	95%	1/2541	1/1300992
			Mediterranean	1/3	95%	1/41	1/492
			South Asian/Indian	1/25	95%	1/481	1/48100
HBB	AR	HBB-related disorders	General	1/158	95%	1/3141	1/1985112
			African	1/10	95%	1/181	1/7240
			African American	1/10	95%	1/181	1/7240
			East Asian	1/50	95%	1/981	1/196200
			Latino	1/128	95%	1/2541	1/1300992
			Mediterranean	1/3	95%	1/41	1/492
			South Asian/Indian	1/25	95%	1/481	1/48100
HEXA	AR	Tay-Sachs disease	General	1/300	99%	1/29901	1/35881200
			Ashkenazi Jewish	1/27	99%	1/2601	1/280908
HEXB	AR	Sandhoff disease	General	1/600	98%	1/29951	1/71882400
HFE2	AR	Hemochromatosis, type 2A	General	1/500	99%	1/49901	1/99802000
HGD	AR	Alkaptonuria	General	1/250	90%	1/2491	1/2491000
HGSNAT	AR	Mucopolysaccharidosis type IIIC (Sanfilippo syndrome C)	General	1/434	98%	1/21651	1/37586136
			European	1/345	98%	1/17201	1/23737380
HLCS	AR	Holocarboxylase synthetase deficiency	General	1/500	98%	1/24951	1/49902000
HMGCL	AR	3-hydroxy-3-methylglutaryl-CoA lyase deficiency	General	<1/500	98%	<1/24951	<1/49902000
HOGA1	AR	Primary hyperoxaluria type III	General	1/184	99%	1/18301	1/13469536
HPS1	AR	Hermansky-Pudlak syndrome 1	General	1/354	98%	1/17651	1/24993816
			Puerto Rican	1/21	98%	1/1001	1/84084
HPS3	AR	Hermansky-Pudlak syndrome 3	General	1/354	98%	1/17651	1/24993816
HPS4	AR	Hermansky-Pudlak syndrome 4	General	<1/500	98%	<1/24951	<1/49902000
HSD17B3	AR	17-Beta-Hydroxysteroid dehydrogenase deficiency	General	1/192	98%	1/9551	1/7335168
			Palestinian	1/8	98%	1/351	1/11232
HSD17B4	AR	D-bifunctional protein deficiency	General	1/158	98%	1/7851	1/4961832
HSD3B2	AR	Congenital adrenal hyperplasia due to 3-beta- hydroxysteroid dehydrogenase 2 deficiency	General	<1/500	98%	1/24951	<1/10000000
IDUA	AR	Mucopolysaccharidosis, type I (Hurler syndrome)	General	<1/500	95%	<1/9981	<1/19962000
			European	1/153	95%	1/3041	1/1861092
IKBKAP	AR	Familial dysautonomia	General	1/300	99%	1/29901	1/35881200
			Ashkenazi Jewish	1/31	99%	1/3001	1/372124
IVD	AR	Isovaleric acidemia	General	1/167	90%	1/1661	1/1109548
			African	1/100	90%	1/991	1/396400
			African American	1/100	90%	1/991	1/396400
			European	1/115	90%	1/1141	1/524860
			East Asian	1/407	90%	1/4061	1/6611308
KCNJ11	AR	Permanent neonatal diabetes mellitus (+)	General	1/423	99%	1/42201	1/71404092
			European	1/232	99%	1/23101	1/21437728
KCNJ11	AR	Familial Hyperinsulinism, Type 2, KCNJ11 Related (+)	General	1/423	99%	1/42201	1/71404092
			European	1/232	99%	1/23101	1/21437728
KCNJ11	AR	KCNJ11-Related disorders	General	1/423	99%	1/42201	1/71404092
			European	1/232	99%	1/23101	1/21437728
LAMA3	AR	Junctional epidermolysis bullosa, LAMA3-related (+)	General	1/781	98%	1/39001	1/121839124
LAMA3	AR	Laryngo-onycho-cutaneous syndrome (+)	General	1/781	98%	1/39001	1/121839124
LAMA3	AR	LAMA3-Related Disorders	General	1/781	98%	1/39001	1/121839124
LAMB3	AR	Junctional epidermolysis bullosa, LAMB3-related	General	1/781	98%	1/39001	1/121839124
LAMC2	AR	Junctional epidermolysis bullosa, LAMC2-related	General	1/781	98%	1/39001	1/121839124
LCA5	AR	Leber congenital amaurosis 5	General	1/500	98%	1/24951	1/49902000
LHCGR	AR	Leydig Cell Hypoplasia (Luteinizing Hormone Resistance)	General	<1/500	98%	<1/24951	<1/49902000
LIFR	AR	Stuve-Wiedemann syndrome	General	<1/500	98%	<1/24951	<1/49902000
LIPA	AR	Lysosomal acid lipase deficiency	General	<1/500	99%	<1/49901	<1/99802000
			European	1/112	99%	1/11101	1/4973248
LOXHD1	AR	Nonsyndromic hearing loss, LOXHD1-related	General	1/500	98%	1/24951	1/49902000
			Ashkenazi Jewish	1/180	98%	1/8951	1/6444720
LPL	AR	Lipoprotein Lipase Deficiency	General	1/500	99%	1/49901	1/99802000
			French Canadian	1/46	99%	1/4501	1/828184
LRPPRC	AR	Leigh syndrome with Complex IV deficiency	General	1/447	98%	1/22301	1/39874188
			Faroese	1/21	98%	1/1001	1/84084

Gene	Inheritance	Condition	Ethnicity	Carrier frequency	Detection rate	Post test carrier probability*	Post-test probability of having an affected child**
			French Canadian	1/22	98%	1/1051	1/92488
LYST	AR	Chediak-Higashi syndrome	General	<1/500	90%	<1/4991	<1/9982000
MAN2B1	AR	Alpha-mannosidosis	General European	1/354 1/274	99% 99%	1/35301 1/27301	1/49986216 1/29921896
MCCC1	AR	3-Methylcrotonyl-CoA carboxylase 1 deficiency (3- MCC deficiency)	General	1/95	98%	1/4701	1/1786380
MCCC2	AR	3-Methylcrotonyl-CoA carboxylase 2 deficiency (3- MCC deficiency)	General	1/95	98%	1/4701	1/1786380
MCOLN1	AR	Mucolipidosis IV	General Ashkenazi Jewish	1/300 1/100	99% 99%	1/29901 1/9901	1/35881200 1/3960400
MED17	AR	Postnatal progressive microcephaly with seizures and brain atrophy	General	<1/500	99%	<1/49901	<1/99802000
MEFV	AR	Familial Mediterranean fever	General Mediterranean	1/20 1/7	99% 90%	1/1901 1/61	1/152080 1/1708
MFSD8	AR	Neuronal ceroid lipofuscinosis, MFSD8-related	General	<1/500	95%	<1/9981	<1/19962000
MKS1	AR	Meckel syndrome 1 (+)	General Finnish	1/260 1/47	98% 98%	1/12951 1/2301	1/13469040 1/432588
MKS1	AR	Bardet-Biedl syndrome 13 (+)	General Finnish	1/260 1/47	98% 98%	1/12951 1/2301	1/13469040 1/432588
MKS1	AR	Joubert syndrome 28 (+)	General Finnish	1/260 1/47	98% 98%	1/12951 1/2301	1/13469040 1/432588
MKS1	AR	MKS1-Related Disorders	General Finnish	1/260 1/47	98% 98%	1/12951 1/2301	1/13469040 1/432588
MLC1	AR	Megalencephalic leukoencephalopathy with subcortical cysts	General	<1/500	97%	<1/16634	<1/33268000
MLYCD	AR	Malonyl-CoA Decarboxylase Deficiency	General	<1/500	98%	<1/24951	<1/49902000
MMAA	AR	Methylmalonic aciduria, cblA type	General	1/301	97%	1/10001	1/12041204
MMAB	AR	Methylmalonic aciduria, cblB type	General	1/435	98%	1/21701	1/37759740
MMACHC	AR	Methylmalonic aciduria and homocystinuria, cblC type	General	1/134	90%	1/1331	1/713416
MPI	AR	Congenital disorder of glycosylation type Ib	General	<1/500	98%	<1/24951	<1/49902000
MPL	AR	Congenital amegakaryocytic thrombocytopenia	General Ashkenazi Jewish	1/102 1/55	98% 98%	1/5051 1/2701	1/2060808 1/594220
MPV17	AR	Hepatocerebral mitochondrial DNA depletion syndrome, MPV17-related	General Native American	<1/500 1/20	96% 96%	1/12476 1/476	<1/24952000 1/38080
MTTP	AR	Abetalipoproteinemia	General Ashkenazi Jewish	<1/500 1/180	98% 98%	<1/24951 1/8951	<1/49902000 1/6444720
MUT	AR	Methylmalonic acidemia, MUT-related	General East Asian Middle-Eastern	1/195 1/53 1/52	96% 96% 96%	1/4851 1/1301 1/1276	1/3783780 1/275812 1/265408
MYO15A	AR	Nonsyndromic Hearing Loss and Deafness: MYO15A Related	General Balinese Pakistani	1/500 1/6 1/77	98% 98% 98%	1/24951 1/251 1/3801	1/49902000 1/6024 1/1170708
MYO7A	AR	Non-syndromic hearing loss, MYO7A-related (+)	General East Asian	1/206 1/62	98% 98%	1/10521 1/3051	1/8669304 1/756648
MYO7A	AR	Usher syndrome, type 1B (+)	General East Asian	1/206 1/62	98% 98%	1/10251 1/3051	1/8446824 1/756648
MYO7A	AR	MYO7A-Related Disorders	General East Asian	1/206 1/62	98% 98%	1/10251 1/3051	1/8446824 1/756648
NAGLU	AR	Mucopolysaccharidosis type IIIB (Sanfilippo syndrome B)	General European East Asian	<1/500 1/346 1/298	99% 99% 99%	<1/49901 1/34501 1/29701	<1/99802000 1/47749384 1/35403592
NBN	AR	Nijmegen breakage syndrome	General	1/158	99%	1/15701	1/9923032
NDUFS6	AR	Mitochondrial complex I deficiency (Leigh syndrome), NDUFS6-related	General	<1/500	98%	<1/24951	<1/49902000
NEB	AR	Nemaline myopathy	General Amish Ashkenazi Jewish Finnish	1/112 1/11 1/108 1/112	98% 98% 98% 98%	1/5551 1/501 1/5351 1/5551	1/2486848 1/22044 1/2311632 1/2486848
NPC1	AR	Niemann-Pick disease, type C1	General	1/194	90%	1/1931	1/1498456
NPC2	AR	Niemann-Pick disease, type C2	General	1/194	99%	1/19301	1/14977576
NPHS1	AR, DG	Congenital nephrotic syndrome, type 1	General Finnish	1/289 1/50	98% 98%	1/14401 1/2451	1/16647556 1/490200
NPHS2	AR, DG	Congenital nephrotic syndrome, type 2	General Finnish	1/289 1/50	98% 98%	1/14401 1/2451	1/16647556 1/490200
NR2E3	AR	Enhanced S-cone syndrome (+)	General	1/209	98%	1/10401	1/8695236
NR2E3	AR	Retinitis Pigmentosa 37 (+)	General	1/209	98%	1/10401	1/8695236
NR2E3	AR	NR2E3-related conditions	General	1/209	98%	1/10401	1/8695236
NTRK1	AR	Congenital insensitivity to pain with anhidrosis	General	<1/500	99%	<1/49901	<1/99802000
OPA3	AR	Costeff syndrome	General Iraqi Jewish	<1/500 1/50	98% 98%	<1/24951 1/2451	<1/10000000 1/490200
PAH	AR	Phenylalanine hydroxylase deficiency (Phenylketonuria)	General	1/93	99%	1/9201	1/3422772

Gene	Inheritance	Condition	Ethnicity	Carrier frequency	Detection rate	Post test carrier probability*	Post-test probability of having an affected child**
			European Middle-Eastern South East Asian	1/63 1/74 1/59	99% 99% 99%	1/6201 1/7301 1/5801	1/1562652 1/2161096 1/1369036
PC	AR	Pyruvate carboxylase deficiency	General	1/250	95%	1/4981	1/4981000
PCCA	AR	Propionic acidemia, PCCA-related	General Native American	1/224 1/85	96% 96%	1/5576 1/2101	1/4996096 1/714340
PCCB	AR	Propionic acidemia, PCCB-related	General Native American	1/224 1/85	99% 99%	1/22301 1/8401	1/19981696 1/2856340
PCDH15	AR, DG	Non-syndromic hearing loss, PCDH15-related (+)	General Ashkenazi Jewish	1/395 1/72	98% 98%	1/19701 1/3551	1/31127580 1/1022688
PCDH15	AR, DG	Usher syndrome, type 1F (+)	General Ashkenazi Jewish	1/395 1/72	98% 98%	1/19701 1/3551	1/31127580 1/1022688
PCDH15	AR, DG	PCDH15-Related Disorders	General Ashkenazi Jewish	1/395 1/72	98% 98%	1/19701 1/3551	1/31127580 1/1022688
PDHB	AR	Pyruvate dehydrogenase E1-beta deficiency	General	<1/500	98%	<1/24951	<1/49902000
PEX1	AR	Zellweger syndrome, PEX1-related	General	1/147	95%	1/2921	1/1717548
PEX10	AR	Zellweger syndrome, PEX10-related	General Japanese	1/500 1/354	95% 95%	1/9981 1/7061	1/19962000 1/9998376
PEX2	AR	Zellweger syndrome, PEX2-related	General Ashkenazi Jewish	1/500 1/123	95% 95%	1/9981 1/2441	1/19962000 1/1200972
PEX6	AR	Zellweger syndrome, PEX6-related	General	1/280	95%	1/5581	1/6250720
PEX7	AR	Rhizomelic chondrodysplasia punctata, type 1	General	1/158	99%	1/15701	1/9923032
PFKM	AR	Glycogen storage disease VII	General	<1/500	98%	<1/24951	<1/49902000
PHGDH	AR	Phosphoglycerate dehydrogenase deficiency	General Ashkenazi Jewish	<1/500 1/280	98% 98%	<1/24951 1/13951	<1/49902000 1/15625120
PKHD1	AR	Polycystic kidney disease, PKHD1-related	General Ashkenazi Jewish	1/70 1/107	98% 98%	1/3451 1/5301	1/966280 1/2268828
PMM2	AR	Congenital disorder of glycosylation type 1a	General Ashkenazi Jewish European	<1/500 1/57 1/71	99% 99% 99%	<1/49901 1/5601 1/7001	<1/99802000 1/1277028 1/1988284
POLG	AR	Alpers-Huttenlocher syndrome (+)	General	1/113	95%	1/2241	1/1012932
POLG	AR	Progressive external ophthalmoplegia (+)	General	1/113	95%	1/2241	1/1012932
POLG	AR	Ataxia neuropathy spectrum (+)	General	1/113	95%	1/2241	1/1012932
POLG	AR	POLG-Related Disorders	General	1/113	95%	1/2241	1/1012932
POLG	AR	Myocerebrohepatopathy syndrome (+)	General	1/113	95%	1/2241	1/1012932
POMGNT1	AR	Muscular dystrophy-dystroglycanopathy (+)	General Finnish	1/462 1/111	98% 98%	1/23051 1/5501	1/42598248 1/2442444
POMGNT1	AR	Retinitis Pigmentosa 76 (+)	General Finnish	1/462 1/111	98% 98%	1/23051 1/5501	1/42598248 1/2442444
POMGNT1	AR	POMGNT1-related disorders	General Finnish	1/462 1/111	98% 98%	1/23051 1/5501	1/42598248 1/2442444
POR	AR	Antley-Bixler Syndrome	General	1/159	98%	1/7901	1/5025036
PPT1	AR	Neuronal ceroid lipofuscinosis, PPT1-related	General European Finnish	1/368 1/488 1/75	98% 98% 98%	1/18351 1/24351 1/3701	1/27012672 1/47533152 1/1110300
PROP1	AR	Combined pituitary hormone deficiency 2	General	1/45	98%	1/2201	1/396180
PTS	AR	Tetrahydrobiopterin deficiency	General	1/354	96%	1/8826	<1/10000000
PUS1	AR	Mitochondrial myopathy and sideroblastic anemia 1	General	<1/500	98%	<1/24951	<1/49902000
PYGM	AR	Glycogen storage disease type V	General European	<1/500 1/206	99% 99%	<1/49901 1/20501	<1/99802000 1/16892824
RAB23	AR	Carpenter syndrome	General	<1/500	98%	<1/24951	<1/49902000
RAG2	AR	Omenn syndrome, RAG2-related	General	1/137	98%	1/6801	1/3726948
RAPSN	AR	Congenital myasthenic syndrome, RAPSN-related (+)	General	<1/500	99%	<1/49901	<1/99802000
RAPSN	AR	Fetal akinesia deformation sequence (+)	General	<1/500	99%	<1/49901	<1/99802000
RAPSN	AR	RAPSN-Related Disorders	General	<1/500	99%	<1/49901	<1/99802000
RARS2	AR	Pontocerebellar hypoplasia type 6	General	<1/500	98%	<1/24951	<1/49902000
RDH12	AR	Leber congenital amaurosis type 13	General European	<1/500 1/456	98% 98%	<1/24951 1/22751	<1/49902000 1/41497824
RLBP1	AR	Retinal dystrophy: RLBP1-Related	General European	1/296 1/84	98% 98%	1/14751 1/4151	1/17465184 1/1394736
RMRP	AR	Anauxetic dysplasia (+)	General Amish Finnish	<1/500 1/16 1/76	99% 99% 99%	<1/49901 1/1501 1/7501	<1/99802000 1/96064 1/2280304
RMRP	AR	Cartilage-hair hypoplasia (+)	General Amish Finnish	<1/500 1/16 1/76	99% 99% 99%	<1/49901 1/1501 1/7501	<1/99802000 1/96064 1/2280304
RMRP	AR	Metaphyseal dysplasia without hypotrichosis (+)	General Amish Finnish	<1/500 1/16 1/76	99% 99% 99%	<1/49901 1/1501 1/7501	<1/99802000 1/96064 1/2280304

Gene	Inheritance	Condition	Ethnicity	Carrier frequency	Detection rate	Post test carrier probability*	Post-test probability of having an affected child**
RMRP	AR	RMRP-related conditions	General	<1/500	99%	1/49901	<1/99802000
			Amish	1/16	99%	1/1501	1/96064
			Finnish	1/76	99%	1/7501	1/2280304
RMRP	AR	Cartilage-Hair Hypoplasia Anauxetic Dysplasia Spectrum Disorder (+)	General	<1/500	99%	<1/49901	<1/99802000
			Amish	<1/500	99%	<1/49901	<1/99802000
			Finnish	<1/500	99%	<1/49901	<1/99802000
RPE65	AR	Leber congenital amaurosis 2 (+)	General	1/228	98%	1/11351	1/10352112
RPE65	AR	Retinitis Pigmentosa 20 (+)	General	1/228	98%	1/11351	1/10352112
RPE65	AR	RPE65-Related Disorders	General	1/228	98%	1/11351	1/10352112
RTEL1	AR	Dyskeratosis congenita type 5	General	1/500	99%	1/49901	1/99802000
			Ashkenazi Jewish	1/203	99%	1/20201	1/16403212
SACS	AR	Autosomal Recessive Spastic Ataxia of Charlevoix-Saguenay	General	<1/500	95%	<1/9981	<1/19962000
			French Canadian	1/19	95%	1/361	1/27436
SEPSECS	AR	Pontocerebellar hypoplasia, type 2D	General	<1/500	98%	<1/24951	<1/49902000
SERPINA1	AR	Alpha-1-Antitrypsin Deficiency	General	1/33	95%	1/641	1/84612
			European	1/19	95%	1/361	1/27436
SGCA	AR	Limb-girdle muscular dystrophy, type 2D	General	<1/500	98%	<1/24951	<1/49902000
			European	1/288	98%	1/14351	1/16532352
			Finnish	1/150	98%	1/7451	1/4470600
SGCB	AR	Limb-girdle muscular dystrophy, type 2E	General	1/500	98%	1/24951	1/49902000
			European	1/406	98%	1/20251	1/32887624
SGCD	AR	Limb-girdle muscular dystrophy, type 2F	General	<1/500	98%	<1/24951	<1/49902000
SGCG	AR	Limb-girdle muscular dystrophy, type 2C	General	1/381	98%	1/19001	1/28957524
			Moroccan	1/250	98%	1/12451	1/12451000
			Roma/Gypsy	1/96	98%	1/4751	1/1824384
SGSH	AR	Mucopolysaccharidosis IIIA (Sanfilippo syndrome A)	General	1/454	98%	1/22651	1/41134216
			European	1/253	98%	1/12601	1/12752212
SLC12A3	AR	Gitelman syndrome	General	1/100	98%	1/4951	1/1980400
SLC12A6	AR	Andermann syndrome	General	<1/500	98%	<1/24951	<1/49902000
			French Canadian	1/23	99%	1/2201	1/202492
SLC17A5	AR	Sialic acid storage disorder	General	<1/500	91%	<1/5545	<1/11090000
			Finnish	1/100	91%	1/1101	1/440400
SLC22A5	AR	Systemic primary carnitine deficiency	General	1/129	76%	1/534	1/275544
			African	1/86	76%	1/355	1/122120
			African American	1/86	76%	1/355	1/122120
			East Asian	1/77	76%	1/318	1/97944
			Faroese	1/9	76%	1/34	1/1224
			Pacific Islander	1/37	76%	1/151	1/22348
			South Asian/Indian	1/51	76%	1/209	1/42636
SLC25A13	AR	Citrin deficiency	General	<1/500	95%	<1/9981	<1/19962000
			East Asian	1/65	95%	1/1281	1/333060
SLC25A15	AR	Hyperornithinemia-hyperammonemia-homocitrullinemia syndrome (Triple H syndrome)	General	<1/500	99%	<1/49901	<1/99802000
			French Canadian	1/37	99%	1/3601	1/532948
SLC25A20	AR	Carnitine-acylcarnitine translocase deficiency	General	<1/500	98%	<1/24951	<1/49902000
SLC26A2	AR	Achondrogenesis, type IB (+)	General	1/158	90%	1/1571	1/992872
			Finnish	1/50	90%	1/491	1/98200
SLC26A2	AR	Atelosteogenesis II (+)	General	1/158	90%	1/1571	1/992872
			Finnish	1/50	90%	1/491	1/98200
SLC26A2	AR	Diastrophic dysplasia (+)	General	1/158	90%	1/1571	1/992872
			Finnish	1/50	90%	1/491	1/98200
SLC26A2	AR	Multiple epiphyseal dysplasia 4 (+)	General	1/158	90%	1/1571	1/992872
			Finnish	1/50	90%	1/491	1/98200
SLC26A2	AR	SLC26A2-Related Conditions	General	1/158	90%	1/1571	1/992872
			Finnish	1/50	90%	1/491	1/98200
SLC26A3	AR	Congenital secretory chloride diarrhea	General	<1/500	98%	<1/24951	<1/49902000
			Middle-Eastern	1/57	98%	1/2801	1/638628
SLC26A4	AR	Pendred syndrome	General	1/80	98%	1/3951	1/1264320
			African	1/76	98%	1/3751	1/1140304
			African American	1/76	98%	1/3751	1/1140304
			European	1/88	98%	1/4351	1/1531552
			East Asian	1/74	98%	1/3651	1/1080696
SLC35A3	AR	Arthrogryposis, mental retardation and seizures	General	<1/500	98%	<1/24951	<1/49902000
			Ashkenazi Jewish	1/453	98%	1/22601	1/40953012
SLC37A4	AR	Glycogen storage disease, type Ib	General	1/158	95%	1/3141	1/1985112
			Ashkenazi Jewish	1/71	95%	1/1401	1/397884
SLC39A4	AR	Acrodermatitis enteropathica	General	<1/500	98%	<1/24951	<1/49902000
SLC3A1	AR, DG	Cystinuria: type I	General	1/50	98%	1/2451	1/490200
			European	1/42	98%	1/2051	1/344568
SLC45A2	AR	Oculocutaneous Albinism: Type IV	General	1/159	98%	1/7901	1/5025036
			Japanese	1/146	98%	1/7251	1/4234584
SLC4A11	AR	Corneal endothelial dystrophy	General	<1/500	98%	<1/24951	<1/49902000
SLC7A7	AR	Lysinuric protein intolerance	General	<1/500	95%	<1/9981	<1/19962000
			Finnish	1/122	95%	1/2421	1/1181448

Gene	Inheritance	Condition	Ethnicity	Carrier frequency	Detection rate	Post test carrier probability*	Post-test probability of having an affected child**
			Japanese	1/119	95%	1/2361	1/1123836
SLC7A9	AR, DG	Cystinuria: Non-type I	General	1/42	98%	1/2051	1/344568
SMN1	AR	Spinal Muscular Atrophy	General African African American Ashkenazi Jewish European East Asian Latino	1/54 1/72 1/72 1/67 1/47 1/59 1/68	91% 71% 71% 91% 95% 93% 90%	1/590 1/246 1/246 1/734 1/921 1/830 1/671	1/127440 1/70848 1/70848 1/196712 1/173148 1/195880 1/182512
SMPD1	AR	Niemann-Pick disease, type A/B	General Ashkenazi Jewish Latino	1/250 1/115 1/106	95% 95% 95%	1/4981 1/2281 1/2101	1/4981000 1/1049260 1/890824
SRD5A2	AR	5-alpha-reductase deficiency	General	<1/500	98%	<1/24951	<1/49902000
STAR	AR	Lipoid congenital adrenal hyperplasia	General	<1/500	98%	<1/24951	<1/49902000
SUMF1	AR	Multiple sulfatase deficiency	General Ashkenazi Jewish	1/500 1/320	98% 98%	1/24951 1/15951	1/49902000 1/20417280
TAT	AR	Tyrosinemia, type II	General	1/250	98%	1/12451	1/12451000
TCIRG1	AR	Osteopetrosis, TCIRG1-related	General	1/250	98%	1/12451	1/12451000
TECPR2	AR	Spastic paraplegia 49	General	<1/500	98%	<1/24951	<1/49902000
TFR2	AR	Hemochromatosis, type 3	General	<1/500	98%	<1/24951	<1/49902000
TGM1	AR	Congenital ichthyosis	General	1/224	95%	1/4461	1/3997056
TH	AR	Segawa syndrome	General	1/224	98%	1/11151	1/9991296
TMEM216	AR	Joubert syndrome 2 (+)	General Ashkenazi Jewish	1/141 1/92	98% 98%	1/7001 1/4551	1/3948564 1/1674768
TMEM216	AR	Meckel syndrome 2 (+)	General Ashkenazi Jewish	1/141 1/92	98% 98%	1/7001 1/4551	1/3948564 1/1674768
TMEM216	AR	TMEM216-Related Disorders	General Ashkenazi Jewish	1/141 1/92	98% 98%	1/7001 1/4551	1/3948564 1/1674768
TPP1	AR	Neuronal ceroid lipofuscinosis, TPP1-related	General French Canadian	1/252 1/53	97% 97%	1/8368 1/1734	1/8434944 1/367608
TRIM32	AR	Bardet-Biedl syndrome 11 (+)	General Hutterite	<1/500 1/12	98% 98%	<1/24951 1/551	<1/49902000 1/26448
TRIM32	AR	Limb-girdle muscular dystrophy, type 2H (+)	General Hutterite	<1/500 1/12	98% 98%	<1/24951 1/551	<1/49902000 1/26448
TRIM32	AR	TRIM32-Related Disorders	General Hutterite	<1/500 1/12	98% 98%	<1/24951 1/551	<1/49902000 1/26448
TRMU	AR	Liver failure, acute infantile	General Yemenite Jewish	<1/500 1/34	98% 98%	<1/24951 1/1651	<1/49902000 1/224536
TSEN54	AR	Pontocerebellar hypoplasia, TSEN54-related	General	1/250	98%	1/12451	1/12451000
TTC37	AR	Trichohepatoenteric syndrome	General	1/500	98%	1/24951	1/49902000
TTPA	AR	Ataxia with isolated vitamin E deficiency	General European	<1/500 1/267	98% 90%	<1/24951 1/2661	<1/49902000 1/2841948
TYMP	AR	Mitochondrial neurogastrointestinal encephalopathy (MNGIE) disease	General	<1/500	98%	<1/24951	<1/49902000
TYR	AR	Oculocutaneous Albinsim: Type I	General	1/100	98%	1/4951	1/1980400
TYRP1	AR	Oculocutaneous Albinsim: Type 3	General African	<1/500 1/47	98% 98%	<1/24951 1/2301	<1/49902000 1/432588
UGT1A1	AR	Crigler-Najjar syndrome	General	<1/500	98%	<1/24951	<1/49902000
USH1C	AR	Non-syndromic hearing loss, USH1C-related (+)	General French Canadian	1/353 1/227	90% 90%	1/3521 1/2261	1/4971652 1/2052988
USH1C	AR	Usher syndrome, type IC (+)	General French Canadian	1/353 1/227	90% 90%	1/3521 1/2261	1/4971652 1/2052988
USH1C	AR	USH1C-Related Disorders	General French Canadian	1/353 1/227	90% 90%	1/3521 1/2261	1/4971652 1/2052988
USH2A	AR	Usher syndrome, type 2A	General European	1/126 1/73	96% 96%	1/3126 1/1801	1/1575504 1/525892
VPS13A	AR	Choreoacanthocytosis	General	<1/500	98%	<1/24951	<1/49902000
VPS13B	AR	Cohen syndrome	General	<1/500	98%	<1/24951	<1/49902000
VPS53	AR	Pontocerebellar hypoplasia VPS53 Related	General Morrocan Jewish	<1/500 1/37	98% 98%	<1/24951 1/1801	<1/49902000 1/266548
VRK1	AR	Pontocerebellar hypoplasia type 1A VRK1 Related	General	<1/500	98%	<1/24951	<1/49902000
VSX2	AR	Microphthalmia with or without coloboma	General	1/91	98%	1/4501	1/1638364
WRN	AR	Werner Syndrome	General European Japanese	1/308 1/112 1/71	98% 98% 98%	1/15351 1/5551 1/3501	1/18912432 1/2486848 1/994284
XPA	AR	Xeroderma pigmentosum, group A	General Japanese	1/500 1/74	99% 99%	1/49901 1/7301	1/99802000 1/2161096
XPC	AR	Xeroderma pigmentosum, group C	General	1/500	99%	1/49901	1/99802000

*For genes that have tested negative

Gene	Inheritance Condition	Ethnicity	Carrier frequency	Detection rate	Post test carrier probability*	Post-test probability of having an affected child**

**For genes that have tested negative and reproductive couple not tested.
Abbrevations: AR, autosomal recessive, XL, X-Linked, DG, digenic