



FINAL RESULTS



No carrier mutations identified

TEST PERFORMED

Sonic Beacon Expanded Carrier Screen v2.0 - Male

(361 Gene Panel; gene sequencing
with deletion and duplication analysis)

INTERPRETATION:

Notes and Recommendations:

- No carrier mutations were identified in the submitted specimens. A negative result does not rule out the possibility of a genetic predisposition nor does it rule out any pathogenic mutations in areas not assessed by this test or in regions that were covered at a level too low to reliably assess. A soft call does not rule out mutations that are of the sort not queried by this test; see Methods and Limitations for more information.
- Testing for copy number changes in the *SMN1* gene was performed to screen for the carrier status of Spina Muscular Atrophy. The results for this individual are within the normal range for non-carriers. See Limitations section for more information.
- This carrier screening test does not screen for all possible genetic 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 their doctor, as there is an increased chance that they are also carriers. These results should be interpreted in the context of this individual's clinical findings, biochemical profile, and family history.
- Gene specific notes and mutations may be present. See below.
- This report does not include variants of uncertain significance.
- Genetic counseling is recommended. Contact your physician about the available options for genetic counseling.



GENES TESTED:

ABCA12	ABCA3	ABCA4	ABCB11	ABCC8	ACAD9
ACADVL	ACAT1	ACOX1	ACSF3	ADA	ADAMTS2
ADGRG1	ADK	AGA	AGL	AGPS	AGXT
AHI1	AIPL1	ALDH3A2	ALDOB	ALG6	ALMS1
ALPL	AMT	AQP2	ARG1	ARL13B	ARSA
ARSB	ASL	ASNS	ASPA	ASS1	ATM
ATP6V1B1	ATP7B	BBS1	BBS10	BBS12	BBS2
BCKDHA	BCKDHB	BCS1L	BLM	BSND	CAPN3
CASQ2	CBS	CC2D2A	CCDC103	CCDC39	CCDC88C
CDH23	CEP290	CFTR	CHRNE	CHRNA3	CHST6
CIITA	CLN3	CLN5	CLN6	CLN8	CLRN1
CNGB3	COL27A1	COL4A3	COL4A4	COL7A1	COX15
CPS1	CPT1A	CPT2	CRB1	CRYL1	CTNS
CTSA	CTSC	CTSD	CTSK	CYBA	CYP11A1
CYP11B1	CYP11B2	CYP17A1	CYP1B1	CYP21A2	CYP27A1
DBT	DCLRE1C	DDX11	DHCR7	DHDDS	DLD
DNAH5	DNAI1	DNAI2	DUOX2	DUOXA2	DYNC2H1
DYSF	EIF2AK3	EIF2B5	ELP1	ERCC2	ERCC5
ERCC6	ERCC8	ESCO2	ETFA	ETFB	ETFDH
ETHE1	EVC	EVC2	EXOSC3	F2	F5
FAH	FAM126A	FAM161A	FANCA	FANCC	FANCG
FH	FKRP	FKTN	FOXRED1	FTCD	FUCA1
G6PC	GAA	GALC	GALNS	GALT	GAMT
GBA	GBE1	GCDH	GDAP1	GDF5	GFM1
GJB2	GJB6	GLB1	GLDC	GLE1	GNE
GNPTAB	GNPTG	GNS	GSS	GUCY2D	GUSB
HADHA	HADHB	HAX1	HBA1	HBA2	HBB
HEXA	HEXB	HGSNAT	HJV	HLCS	HMGCL
HOGA1	HPS1	HPS3	HPS4	HSD17B4	HSD3B2
HYLS1	IDUA	IVD	IYD	JAK3	KCNJ11
LAMA2	LAMA3	LAMB3	LAMC2	LCA5	LDLRAP1
LHX3	LIFR	LIPA	LMBRD1	LOXHD1	LPL
LRP2	LRPPRC	LYST	MAN2B1	MANBA	MCOLN1
MCPH1	MED17	MESP2	MFSD8	MKS1	MLC1
MLYCD	MMAA	MMAB	MMACHC	MMADHC	MPI
MPL	MPV17	MTHFR	MTMR2	MTRR	MTTP
MUT	MVK	MYO7A	NAGA	NAGLU	NAGS
NBN	NDRG1	NDUFAF2	NDUFAF5	NDUFS4	NDUFS6
NDUFS7	NDUFV1	NEB	NEU1	NPC1	NPC2
NPHP1	NPHS1	NPHS2	NTRK1	OAT	OCA2
OPA3	OTOF	P3H1	PAH	PANK2	PC
PCCA	PCCB	PCDH15	PCNT	PDHB	PEX1
PEX10	PEX12	PEX2	PEX26	PEX6	PEX7
PFKM	PHGDH	PHYH	PKHD1	PLA2G6	PLOD1
PMM2	POLG	POLR1C	POMGNT1	POMT1	POMT2
POR	PPT1	PRF1	PROP1	PSAP	PTS
PUS1	QDPR	RAB23	RAG1	RAG2	RAPSN



RARS2	RAX	RDH12	RMRP	RNASEH2B	RPE65
RPGRIP1L	RTEL1	SACS	SAMD9	SAMHD1	SCO2
SEPSECS	SERPINA1	SGCA	SGCB	SGCD	SGCG
SGSH	SH3TC2	SLC12A6	SLC17A5	SLC19A3	SLC1A4
SLC22A5	SLC25A13	SLC25A15	SLC26A2	SLC26A3	SLC35A3
SLC37A4	SLC39A4	SLC45A2	SLC46A1	SLC5A5	SLC7A7
SMARCAL1	SMN1	SMPD1	SPG11	SPINK5	STAR
SUMF1	SURF1	TCIRG1	TCTN2	TECPR2	TF
TG	TGM1	TH	TMEM216	TPO	TPP1
TRDN	TRIM32	TRMU	TSEN54	TSFM	TSHB
TTC37	TTPA	TYMP	TYR	TYRP1	UGT1A1
USH1C	USH1G	USH2A	VPS13A	VPS13B	VPS45
VPS53	VRK1	VSX2	WHRN	WRN	XPA
XPC	ZFYVE26				

METHODS:

Genomic DNA was isolated from the submitted specimen indicated above (if cellular material was submitted). DNA was barcoded, and enriched for the coding exons of targeted genes using hybrid capture technology. Prepared DNA libraries were then sequenced using a Next Generation Sequencing technology. Following alignment to the human genome reference sequence (assembly GRCh37), variants were detected in regions of at least 10x coverage. For this specimen, 99.55% and 99.50% of coding regions and splicing junctions of genes tested had been sequenced with coverage of at least 10x and 20x, respectively, by NGS or by Sanger sequencing. The remaining regions did not have 10x coverage, and were not evaluated. Variants were interpreted manually using locus specific databases, literature searches, and other molecular biology computational resources. To minimize false positive results, any variants that do not meet internal quality standards are confirmed by Sanger sequencing. Variants classified as pathogenic, likely pathogenic, or risk allele which are located in the coding regions and nearby intronic regions (+/- 20bp) of the genes tested above are reported. Variants outside these intervals may be reported but are typically not guaranteed. When a single pathogenic or likely pathogenic variant is identified in a clinically relevant gene with autosomal recessive inheritance, the laboratory will attempt to ensure 100% coverage of coding sequences either through NGS or Sanger sequencing technologies ("full"). All genes tested were evaluated for large deletions and/or duplications. However, single exon deletions or duplications will not be detected in this assay, nor will copy number alterations in regions of genes with significant pseudogenes. Putative deletions or duplications are analyzed using Fulgent Germ line proprietary pipeline for this specimen. New York patients: diagnostic findings are confirmed by Sanger, MLPA, or qPCR; except on SNV variants in genes for which confirmation of NGS results has been performed ≥ 10 times may not be confirmed definitively with high quality by NGS. Bioinformatics: The Fulgent Germ line v2019.2 pipeline was used to analyze this specimen.

LIMITATIONS:

General Limitations

These test results and variant interpretation are based on the proper identification of the submitted specimen, accuracy of any stated family relationships, and use of the correct human reference sequences at the queried locus. In very rare instances, errors may result due to mix-up or co-mingling of specimens. Positive results do not imply that there are no other contributors, genetic or otherwise, to future pregnancies, and negative results do not rule out the genetic risk to a pregnancy. Offcial gene names change over time. Fulgent uses the most up to date gene names based on HUGO Gene Nomenclature Committee (<https://www.genenames.org>) recommendations. If the gene name on report does not match that of ordered gene, please contact the laboratory and details can be provided. Result interpretation is based on the available clinical and family history information for this individual, collected published information, and a mutation 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 analyses can identify alterations of genomic regions which include one or more genes (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 analyses has not been performed in regions that have been sequenced by Sanger.

Gene Specific Notes and Limitations

CFTR: Analyses of the non-8 polymorphic region (e.g. IVS8-5T alleles) is only performed if the p.Arg117 (R117) mutation is detected. Single exon deletion/duplication analyses is limited to deletions of previously reported exons: 1, 2, 3, 11, 19, 20, 21. **CRYL1:** As mutations in the CRYL1 gene are not known to be associated with any clinical condition, sequence variants in this gene are not analyzed. However, to increase copy number detection sensitivity for large deletions including this gene and a neighboring gene on the same chromosome (GJB6, also known as connexin 30), this gene was evaluated for copy number variation. **CYP11B1:** The current sequencing method is not able to reliably detect certain pathogenic variants in this gene due to the interference by highly homozygous regions. This analysis is not designed to detect or rule-out copy-number changes in the CYP11B1/CYP11B2 gene. **CYP11B2:** The current sequencing method is not able to reliably detect certain pathogenic variants in this gene due to the interference by highly homozygous regions. This analysis is not designed to detect or rule-out copy-number changes in the 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 variant reports in this gene must be interpreted carefully in the context of the clinical findings, biochemical profile, and family history of each patient. The variants c.188A>T (p.S63Leu), c.844G>T (p.V282Leu), c.1174G>A (p.A392Thr), and c.1360C>T (p.P454Ser) in CYP21A2 will not be routinely reported as these variants are primarily associated with non-classic congenital adrenal hyperplasia and mild disease penetrance. Additionally, the variant c.955C>T (p.G319Ter) in the region with pseudogene interference, and the probability of this variant occurring in the real gene is greater than 50%. When observed, this variant will be reported as a possible carrier without LR-PCR. The confirmation test is recommended for the second reproductive partner's test positive for variants in CYP21A2. **DUOX2:** The current sequencing method is not able to reliably detect variants in exons 6-8 of the DUOX2 gene (NM 014080.5) due to significant interference by the highly homozygous gene, DUOX1. **F5:** The common Factor 5 "Leiden" allele is not typically reported; its mild risk allele may be reported upon request. **GALT:** In general, the D2 "Duar" 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 (PubMed: 25473725, 30593450). **GBA:** The current sequencing method may not be able to reliably detect certain pathogenic variants in the GBA gene due to homozygous recombination between the pseudogene and the functional gene. **HBA1:** The phase of the heterozygous alterations in the HBA1 gene cannot be determined, but can be confirmed through parental testing. **HBA2:** The phase of the heterozygous alterations in the HBA2 gene cannot be determined, but can be confirmed through parental testing. **MTHFR:** As recommended by ACMG, the two common polymorphisms in the MTHFR gene - c.1286A>C (p.G429A, also known as c.1298A>C) and c.665C>T (p.A222V, also known as c.677C>T) - are not reported in this test due to lack of sufficient clinical utility or merging (PubMed: 23288205). **NEB:** This gene contains a 32-kb repeat region (exons 82-105) which is not amenable to sequencing and deletion/duplication analyses. **NPHS2:** If detected, the variant NM 014625.3:c.686G>A (p.Arg229Gln) will not be reported as this variant is not significantly associated with disease when homozygous or in the compound heterozygous state with variants in exons 1-6 of NPHS2. **SERPINA1:** If detected the variant NM 000295.5:c.863A>T (p.G288V) will not be reported as this variant is associated with mild disease penetrance and is not associated with severe early onset disease. **SMN1:** The current sequencing method detects sequence variants in exon 7 and copy number variations in exons 7-8 of the SMN1 gene (NM 022874.2). Sequencing and deletion/duplication analyses 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 sequencing method cannot reliably detect carriers with a [2+0] SMN1 configuration, but can detect linkage between the 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. Only abnormal results will be reported. **TRDN:** Due to high GC content of certain exons, copy number analyses may have reduced sensitivity for pathogenic deletions/duplications of TRDN. Confirmation of pathogenic deletions/duplications are limited to individuals with a positive personal history of cardiac arrhythmia and/or individuals carrying a pathogenic/likely pathogenic sequence variant. **UGT1A1:** Common variants in the UGT1A1 gene (population allele frequency >5%) are typically not reported as they do not cause a Mendelian condition. **WRN:** Due to the interference by highly homozygous regions within the WRN gene, our current sequencing method has less sensitivity to detect variants in exons 10-11 of WRN (NM 000553.6).

SIGNATURE:

Donor MQ191022



DISCLAIMER:

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

Supplemental Table

Gene	Condition	Inheritance	Ethnicity	Carrier Rate	Detection Rate	Post test Carrier Probability*	Residual Risk*
<i>ABCA12</i>	Congenital ichthyosis ABCA 2 related	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>ABCA3</i>	Surfactant metabolism dysfunction pulmonary 3	AR	General Population	in 6	99%	in 50	in 5 336 464
<i>ABCA4</i>	Stargardt disease	AR	General Population	in 5	98%	in 2 50	in 5 0 204
<i>ABCB11</i>	Progressive familial intrahepatic cholestasis	AR	General Population	in 2	98%	in 5 55	in 2 486 848
<i>ABCC8</i>	Familial hyperinsulinism	AR	General Population	in 2	98%	in 5 55	in 2 486 848
			Ashkenazi Jewish Population	in 44	98%	in 2 5	in 378 576
			Finnish Population	in 25	98%	in 20	in 20 00
			Middle Eastern Population	in 25	98%	in 20	in 20 00
<i>ACAD9</i>	Acyl CoA dehydrogenase 9 (ACAD9) deficiency	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>ACADVL</i>	Very long chain acyl CoA dehydrogenase (VLCAD) deficiency	AR	General Population	in 8	93%	in 672	in 789 84
			Middle Eastern Population	in 74	93%	in 044	in 309 024
			Native American Population	in 6	93%	in 858	in 209 352
			South Asian/ ndian Population	in 73	93%	in 030	in 300 760
<i>ACAT1</i>	3 ketothiolase deficiency	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>ACOX1</i>	Peroxisomal acyl CoA oxidase deficiency	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>ACSF3</i>	Combined malonic and methylmalonic aciduria	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>ADA</i>	Adenosine deaminase deficiency	AR	General Population	in 224	93%	in 3 87	in 2 855 552
<i>ADAMTS2</i>	Ehlers Danlos syndrome dermatosparaxis type	AR	General Population	< in 500	98%	in 24 95	< in 0 million
			Ashkenazi Jewish Population	in 248	98%	in 2 35	< in 0 million
<i>ADGRG1</i>	Bilateral frontoparietal polymicrogyria	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>ADK</i>	Hypermethioninemia due to adenosine kinase deficiency	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>AGA</i>	Aspartylglucosaminuria	AR	General Population	< in 500	98%	in 24 95	< in 0 million
			Finnish Population	in 7	98%	in 3 50	in 994 284
<i>AGL</i>	Glycogen storage disease type	AR	General Population	in 58	95%	in 3 4	in 985 2
			Faroeese Population	in 28	95%	in 54	in 60 592
			nut Population	in 25	95%	in 48	in 48 00
			North African Jewish Population	in 37	95%	in 72	in 06 708
<i>AGPS</i>	Rhizomelic chondrodysplasia punctata type 3	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>AGXT</i>	Primary hyperoxaluria type	AR	General Population	in 20	99%	in 90	in 5 7 2 480
			Caucasian / European Population	in 73	99%	in 7 20	< in 0 million
<i>AHI1</i>	Joubert syndrome AH related	AR	General Population	in 448	99%	in 44 70	< in 0 million
<i>AIP1</i>	Childhood onset severe retinal dystrophy A PL related	AR	General Population	in 409	99%	in 40 80	< in 0 million
<i>ALDH3A2</i>	Sjögren Larsson syndrome	AR	General Population	in 250	98%	in 2 45	< in 0 million
<i>ALDOB</i>	Hereditary fructose intolerance	AR	General Population	in 22	99%	in 2 0	in 5 905 288
			African/African American Population	in 250	99%	in 24 90	< in 0 million
			Caucasian / European Population	in 67	99%	in 6 60	in 769 068
			Middle Eastern Population	in 97	99%	in 9 60	in 3 725 88
<i>ALG6</i>	Congenital disorder of glycosylation type c	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>ALMS1</i>	Alstrom syndrome	AR	General Population	in 500	98%	in 24 95	< in 0 million
<i>ALPL</i>	Hypophosphatasia	AR	General Population	in 58	95%	in 3 4	in 985 2
			Caucasian / European Population	in 274	95%	in 5 46	in 5 985 256
			Mennonite Population	in 25	95%	in 48	in 48 00
<i>AMT</i>	Glycine encephalopathy	AR	General Population	in 373	98%	in 8 60	< in 0 million
			Finnish Population	in 7	98%	in 5 80	in 2 7 4 868
<i>AQP2</i>	Nephrogenic diabetes insipidus	AR	General Population	< in 500	95%	in 9 98	< in 0 million
			Finnish Population	in 69	95%	in 3 36	in 2 272 036
<i>ARG1</i>	Arginase deficiency	AR	General Population	in 296	98%	in 4 75	< in 0 million
<i>ARL13B</i>	Joubert syndrome ARL 3B related	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>ARSA</i>	Metachromatic leukodystrophy	AR	General Population	in 00	99%	in 9 90	in 3 960 400
			Caucasian / European Population	in 78	99%	in 7 70	in 2 402 7 2
			Yemenite Jewish Population	in 75	99%	in 7 40	in 2 220 300
<i>ARSB</i>	Mucopolysaccharidosis type V (Maroteaux Lamy syndrome)	AR	General Population	in 250	98%	in 2 45	< in 0 million
			Western Australian Population	in 283	98%	in 4 0	< in 0 million
<i>ASL</i>	Argininosuccinate lyase deficiency	AR	General Population	in 32	90%	in 3	in 692 208
<i>ASNS</i>	Asparagine synthetase deficiency	AR	General Population	< in 500	99%	in 49 90	< in 0 million
			ranian Jewish Population	in 80	99%	in 7 90	in 2 528 320
<i>ASPA</i>	Canavan disease	AR	General Population	in 300	97%	in 9 968	< in 0 million
			Ashkenazi Jewish Population	in 55	96%	in 35	in 297 220
<i>ASS1</i>	Citrullinemia	AR	General Population	in 9	96%	in 2 95	in 404 676
			East Asian Population	in 32	96%	in 3 276	in 729 728

Supplemental Table

Gene	Condition	Inheritance	Ethnicity	Carrier Rate	Detection Rate	Post test Carrier Probability*	Residual Risk*
<i>ATM</i>	Ataxia telangiectasia	AR	General Population	in 00	92%	in 239	in 495 600
<i>ATP6V1B1</i>	Renal tubular acidosis with deafness	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>ATP7B</i>	Wilson disease	AR	General Population Caucasian / European Population Ashkenazi Jewish Population	in 87 in 42 in 70	98% 98% 98%	in 4 30 in 2 05 in 3 45	in 496 748 in 344 568 in 966 280
<i>BBS1</i>	Bardet Biedl syndrome type	AR	General Population	in 367	99%	in 36 60	< in 0 million
<i>BBS10</i>	Bardet Biedl syndrome type 0	AR	General Population	in 395	99%	in 39 40	< in 0 million
<i>BBS12</i>	Bardet Biedl syndrome type 2	AR	General Population	in 79	99%	in 79 00	< in 0 million
<i>BBS2</i>	Bardet Biedl syndrome 2	AR	General Population Ashkenazi Jewish Population	in 62 in 07	99% 99%	in 62 00 in 0 60	< in 0 million in 4 537 228
<i>BBS2</i>	Retinitis Pigmentosa 74	AR	General Population Ashkenazi Jewish Population	in 62 in 07	99% 99%	in 62 00 in 0 60	< in 0 million in 4 537 228
<i>BCKDHA</i>	Maple syrup urine disease type a	AR	General Population Mennonite Population	in 32 in 0	98% 98%	in 6 00 in 45	< in 0 million in 8 040
<i>BCKDHB</i>	Maple syrup urine disease type b	AR	General Population Ashkenazi Jewish Population	in 364 in 97	98% 98%	in 8 5 in 4 80	< in 0 million in 862 788
<i>BCS1L</i>	Björnstad syndrome	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>BCS1L</i>	GRAC LE syndrome	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>BCS1L</i>	Mitochondrial complex deficiency	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>BLM</i>	Bloom syndrome	AR	General Population Ashkenazi Jewish Population	in 800 in 34	87% 99%	in 6 47 in 3 30	< in 0 million in 7 29 336
<i>BSND</i>	Bartter syndrome	AR	General Population	in 500	98%	in 24 95	< in 0 million
<i>CAPN3</i>	Limb girdle muscular dystrophy type 2A	AR	General Population Caucasian / European Population	< in 500 in 03	98% 98%	in 24 95 in 5 0	< in 0 million in 2 0 6 2
<i>CASQ2</i>	Catecholaminergic polymorphic ventricular tachycardia	AR	General Population	in 224	99%	in 22 30	< in 0 million
<i>CBS</i>	Homocystinuria due to cystathionine beta synthase deficiency	AR	General Population Caucasian / European Population Middle Eastern Population	in 224 in 86 in 2	99% 99% 99%	in 22 30 in 8 50 in 2 00	< in 0 million in 2 924 344 in 68 084
<i>CC2D2A</i>	Joubert syndrome 9	AR	General Population	in 20	99%	in 20 00	in 6 080 804
<i>CCDC103</i>	Primary ciliary dyskinesia type 7	AR	General Population	in 3 6	98%	in 5 75	< in 0 million
<i>CCDC39</i>	Primary ciliary dyskinesia type 4	AR	General Population	in 2	98%	in 0 50	in 8 862 844
<i>CCDC88C</i>	Congenital hydrocephalus	AR	General Population	in 37	99%	in 3 60	in 7 453 348
<i>CDH23</i>	Usher syndrome type D	AR	General Population	in 285	90%	in 2 84	in 364
<i>CEP290</i>	Joubert syndrome 5	AR	General Population	in 90	98%	in 9 45	in 7 82 760
<i>CEP290</i>	Leber congenital amaurosis 0	AR	General Population	in 90	98%	in 9 45	in 7 82 760
<i>CEP290</i>	Bardet Biedl syndrome 4	AR	General Population	in 90	98%	in 9 45	in 7 82 760
<i>CEP290</i>	CEP290 related disorders	AR	General Population	in 90	98%	in 9 45	in 7 82 760
<i>CEP290</i>	Senior Løken syndrome 6	AR	General Population	in 90	98%	in 9 45	in 7 82 760
<i>CEP290</i>	Meckel syndrome 4	AR	General Population	in 90	98%	in 9 45	in 7 82 760
<i>CFTR</i>	Cystic Fibrosis	AR	General Population African/African American Population Ashkenazi Jewish Population Caucasian / European Population East Asian Population Latino Population	in 32 in 6 in 24 in 25 in 94 in 58	99% 99% 99% 99% 99% 99%	in 3 0 in 6 00 in 2 30 in 2 40 in 9 30 in 5 70	in 396 928 in 464 244 in 220 896 in 240 00 in 3 497 76 in 322 632
<i>CHRNE</i>	Congenital myasthenic syndrome	AR	General Population	in 408	99%	in 40 70	< in 0 million
<i>CHRNA3</i>	Multiple pterygium syndrome	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>CHST6</i>	Macular corneal dystrophy CHST6 related	AR	General Population	in 79	99%	in 7 80	in 2 465 6
<i>CIITA</i>	Bare lymphocyte syndrome type	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>CLN3</i>	Neuronal ceroid lipofuscinosis	AR	General Population Finnish Population	in 230 in 72	98% 98%	in 45 in 3 55	< in 0 million in 022 688
<i>CLN5</i>	Neuronal ceroid lipofuscinosis CLN5 related	AR	General Population Finnish Population	< in 500 in 5	95% 95%	in 9 98 in 2 28	< in 0 million in 049 260
<i>CLN6</i>	Neuronal ceroid lipofuscinosis CLN6 related	AR	General Population	< in 500	92%	in 6 239	< in 0 million
<i>CLN8</i>	Neuronal ceroid lipofuscinosis CLN8 related	AR	General Population Finnish Population	< in 500 in 35	95% 95%	in 9 98 in 2 68	< in 0 million in 447 740
<i>CLRN1</i>	Usher syndrome type 3A	AR	General Population Ashkenazi Jewish Population Finnish Population	in 500 in 20 in 70	98% 98% 98%	in 24 95 in 5 95 in 3 45	< in 0 million in 2 856 480 in 966 280
<i>CNGB3</i>	Achromatopsia	AR	General Population Micronesian Population	in 87 in 2	99% 99%	in 8 60 in 0	in 2 993 48 in 808

Supplemental Table

Gene	Condition	Inheritance	Ethnicity	Carrier Rate	Detection Rate	Post test Carrier Probability*	Residual Risk*
COL27A1	Steel syndrome	AR	General Population	< in 500	98%	in 24 95	< in 0 million
COL4A3	Alport syndrome COL4A3 related	AR	General Population	in 267	98%	in 3 30	< in 0 million
			Ashkenazi Jewish Population	in 88	98%	in 9 35	in 7 03 952
COL4A4	Alport syndrome COL4A4 related	AR	General Population	in 267	98%	in 3 30	< in 0 million
COL7A1	Dystrophic epidermolysis bullosa	AR	General Population	in 96	97%	in 6 50	in 5 096 784
COX15	Mitochondrial complex V deficiency	AR	General Population	< in 500	99%	in 49 90	< in 0 million
CPS1	Carbamoylphosphate synthetase deficiency	AR	General Population	in 570	98%	in 28 45	< in 0 million
CPT1A	Carnitine palmitoyltransferase A deficiency	AR	General Population	in 354	90%	in 3 53	in 4 999 896
			Hutterite Population	in 6	90%	in 5	in 9 664
CPT2	Carnitine palmitoyltransferase deficiency	AR	General Population	< in 500	95%	in 9 98	< in 0 million
			Ashkenazi Jewish Population	in 5	95%	in 00	in 204 204
CRB1	Leber congenital amaurosis 8	AR	General Population	in 04	98%	in 5 5	in 2 42 8 6
CRB1	Retinitis pigmentosa 2	AR	General Population	in 04	98%	in 5 5	in 2 42 8 6
CRYL1	GJB6 CRYL related nonsyndromic hearing loss	UK	General Population	in 423	99%	in 42 20	< in 0 million
CTNS	Cystinosis	AR	General Population	in 58	99%	in 5 70	in 9 923 032
			British Population	in 8	99%	in 8 00	in 2 592 324
			Moroccan Jewish Population	in 00	99%	in 9 90	in 3 960 400
CTSA	Galactosialidosis	AR	General Population	< in 500	99%	in 49 90	< in 0 million
CTSC	Papillon Lefevre syndrome	AR	General Population	< in 500	98%	in 24 95	< in 0 million
CTSD	Neuronal ceroid lipofuscinosis CTSD related	AR	General Population	< in 500	99%	in 49 90	< in 0 million
CTSK	Pycnodysostosis	AR	General Population	< in 500	98%	in 24 95	< in 0 million
CYBA	Chronic granulomatous disease	AR	General Population	in 224	99%	in 22 30	< in 0 million
CYP11A1	Congenital adrenal insufficiency	AR	General Population	in 4	99%	in 30	in 5 53 256
CYP11B1	Congenital adrenal hyperplasia due to beta hydroxylase deficiency	AR	General Population	in 58	98%	in 7 85	in 4 96 832
			Moroccan Jewish Population	in 35	98%	in 70	in 238 40
CYP11B2	Corticosterone methyloxidase deficiency	AR	General Population	< in 500	98%	in 24 95	< in 0 million
CYP17A1	Congenital adrenal hyperplasia due to 17 alpha hydroxylase deficiency	AR	General Population	in 500	98%	in 24 95	< in 0 million
CYP11B1	Primary congenital glaucoma	AR	General Population	in 50	99%	in 4 90	in 980 200
CYP21A2	Congenital adrenal hyperplasia due to 21 hydroxylase deficiency	AR	General Population	in 6	99%	in 6 00	in 464 244
			nuit Population	in 9	99%	in 80	in 28 836
			Middle Eastern Population	in 35	99%	in 3 40	in 476 40
CYP27A1	Cerebrotendinous xanthomatosis	AR	General Population	in 500	98%	in 24 95	< in 0 million
			Moroccan Jewish Population	in 5	98%	in 20	in 4 020
DBT	Maple syrup urine disease type 1	AR	General Population	in 48	98%	in 24 00	< in 0 million
DCLRE1C	Severe combined immunodeficiency with sensitivity to ionizing radiation	AR	General Population	< in 500	98%	in 24 95	< in 0 million
DDX11	Warsaw breakage syndrome	AR	General Population	< in 500	99%	in 49 90	< in 0 million
			Ashkenazi Jewish Population	in 68	99%	in 6 70	in 822 672
DHCR7	Smith Lemli Opitz syndrome	AR	General Population	in 30	96%	in 726	in 87 20
			African/African American Population	in 38	96%	in 3 426	in 89 52
			Ashkenazi Jewish Population	in 36	96%	in 876	in 26 44
DHDDS	Retinitis pigmentosa 59	AR	General Population	in 296	98%	in 4 75	< in 0 million
			Ashkenazi Jewish Population	in 8	98%	in 5 85	in 2 76 672
DLD	Dihydropyrimidinase deficiency	AR	General Population	in 500	98%	in 24 95	< in 0 million
			Ashkenazi Jewish Population	in 07	98%	in 5 30	in 2 268 828
DNAH5	Primary ciliary dyskinesia DNAH5 related	AR	General Population	in 42	98%	in 7 05	in 4 004 968
			Ashkenazi Jewish Population	in 3	99%	in 20	in 5 062 852
DNAI1	Primary ciliary dyskinesia DNAI1 related	AR	General Population	in 230	98%	in 45	< in 0 million
DNAI2	Primary ciliary dyskinesia DNAI2 related	AR	General Population	in 447	98%	in 22 30	< in 0 million
DUOX2	Congenital hypothyroidism DUOX2 related	AR	General Population	in 366	9%	in 4 057	in 5 938 797
DUOX2	Congenital hypothyroidism DUOX2 related	AR	General Population	< in 500	99%	in 49 90	< in 0 million
DYNC2H1	Short rib thoracic dysplasia 3 with or without polydactyly	AR	General Population	in 68	98%	in 3 35	in 924 876
DYSF	Limb girdle muscular dystrophy type 2B	AR	General Population	< in 500	95%	in 9 98	< in 0 million
			Japanese Population	in 332	95%	in 6 62	in 8 792 688
			Libyan Jewish Population	in 8	95%	in 34	in 24 552
EIF2AK3	Wolcott Rallison Syndrome	AR	General Population	< in 500	98%	in 24 95	< in 0 million
EIF2B5	Leukoencephalopathy with vanishing white matter	AR	General Population	< in 500	98%	in 24 95	< in 0 million
ELP1	Familial Dysautonomia	AR	General Population	in 300	99%	in 29 90	< in 0 million
			Ashkenazi Jewish Population	in 3	99%	in 3 00	in 372 24



Supplemental Table

Gene	Condition	Inheritance	Ethnicity	Carrier Rate	Detection Rate	Post test Carrier Probability*	Residual Risk*
<i>ERCC2</i>	Xeroderma pigmentosum group D	AR	General Population	in 65	99%	in 6 40	in 664 260
<i>ERCC2</i>	Photosensitive trichothiodystrophy	AR	General Population	in 65	99%	in 6 40	in 664 260
<i>ERCC2</i>	Cerebrooculofacioskeletal syndrome 2	AR	General Population	in 65	99%	in 6 40	in 664 260
<i>ERCC5</i>	Xeroderma Pigmentosa group G	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>ERCC6</i>	De Sanctis Cacchione syndrome	AR	General Population Japanese Population	in 500 in 74	99% 99%	in 49 90 in 7 30	< in 0 million in 2 6 096
<i>ERCC6</i>	Cockayne syndrome type B	AR	General Population Japanese Population	in 500 in 74	99% 99%	in 49 90 in 7 30	< in 0 million in 2 6 096
<i>ERCC8</i>	Cockayne syndrome type A	AR	General Population	in 822	98%	in 4 05	< in 0 million
<i>ESCO2</i>	Roberts syndrome	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>ETFA</i>	Glutaric aciduria A	AR	General Population	in 500	98%	in 24 95	< in 0 million
<i>ETFB</i>	Glutaric aciduria B	AR	General Population	in 500	98%	in 24 95	< in 0 million
<i>ETFDH</i>	Glutaric aciduria C	AR	General Population East Asian Population	in 250 in 74	98% 98%	in 2 45 in 3 65	< in 0 million in 080 696
<i>ETHE1</i>	Ethylmalonic encephalopathy	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>EVC</i>	Weyers acrofacial dysostosis EVC related	AR	General Population Amish Population	in 42 in 7	98% 98%	in 7 05 in 30	in 4 004 968 in 8 428
<i>EVC</i>	Ellis van Creveld syndrome EVC related	AR	General Population Amish Population	in 42 in 7	98% 98%	in 7 05 in 30	in 4 004 968 in 8 428
<i>EVC2</i>	Weyers acrofacial dysostosis EVC2 related	AR	General Population Amish Population	in 240 in 7	98% 98%	in 95 in 30	< in 0 million in 8 428
<i>EVC2</i>	Ellis van Creveld syndrome EVC2 related	AR	General Population Amish Population	in 240 in 7	98% 98%	in 95 in 30	< in 0 million in 8 428
<i>EXOSC3</i>	Pontocerebellar hypoplasia type B	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>F2</i>	Prothrombin related conditions	AR	General Population Caucasian / European Population	in 33 in 4	99% 99%	in 3 20 in 30	in 422 532 in 4 8 6
<i>F5</i>	Factor V deficiency	AR	General Population Caucasian / European Population Latino Population African/African American Population East Asian Population Native American Population	in 36 in 9 in 45 in 83 in 222 in 80	99% 99% 99% 99% 99% 99%	in 3 50 in 80 in 4 40 in 8 20 in 22 0 in 7 90	in 504 44 in 36 876 in 792 80 in 2 722 732 < in 0 million in 2 528 320
<i>FAH</i>	Tyrosinemia type	AR	General Population Ashkenazi Jewish Population Finnish Population French Canadian Population South Asian/ ndian Population	in 99 in 50 in 22 in 66 in 72	95% 95% 95% 95% 95%	in 96 in 2 98 in 2 42 in 30 in 3 42	in 776 556 in 788 600 in 8 448 in 343 464 in 2 353 648
<i>FAM126A</i>	Hypomyelinating leukodystrophy type 5	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>FAM161A</i>	Retinitis pigmentosa 28	AR	General Population	in 296	98%	in 4 75	< in 0 million
<i>FANCA</i>	Fanconi anemia group A	AR	General Population Moroccan Jewish ndian Jewish Population	in 239 in 00 in 27	99% 99% 99%	in 23 80 in 9 90 in 2 60	< in 0 million in 3 960 400 in 280 908
<i>FANCC</i>	Fanconi anemia group C	AR	General Population Ashkenazi Jewish Population	in 535 in 99	99% 99%	in 53 40 in 9 80	< in 0 million in 3 88 96
<i>FANCG</i>	Fanconi anemia group G	AR	General Population	in 632	90%	in 6 3	< in 0 million
<i>FH</i>	Fumarase deficiency	AR	General Population Ashkenazi Jewish Population	< in 500 in 99	99% 99%	in 49 90 in 9 80	< in 0 million in 3 88 96
<i>FKRP</i>	Muscular dystrophy dystroglycanopathy FKRP related	AR	General Population	in 58	98%	in 7 85	in 4 96 832
<i>FKTN</i>	Muscular dystrophy dystroglycanopathy FKTN related	AR	General Population Ashkenazi Jewish Population Japanese Population	< in 500 in 50 in 82	99% 99% 99%	in 49 90 in 4 90 in 8 0	< in 0 million in 8 940 600 in 2 657 28
<i>FKTN</i>	Fukuyama congenital muscular dystrophy	AR	General Population Ashkenazi Jewish Population Japanese Population	< in 500 in 50 in 82	99% 99% 99%	in 49 90 in 4 90 in 8 0	< in 0 million in 8 940 600 in 2 657 28
<i>FOXRED1</i>	Mitochondrial complex deficiency	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>FTCD</i>	Glutamate formiminotransferase deficiency	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>FUCA1</i>	Fucosidosis	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>G6PC</i>	Glycogen storage disease type a	AR	General Population Ashkenazi Jewish Population	in 77 in 64	95% 95%	in 3 52 in 26	in 2 492 868 in 322 8 6
<i>GAA</i>	Pompe disease	AR	General Population African/African American Population East Asian Population Ashkenazi Jewish Population	in 00 in 60 in 2 in 76	98% 98% 98% 99%	in 4 95 in 2 95 in 5 55 in 7 50	in 980 400 in 708 240 in 2 486 848 in 2 280 304



Supplemental Table							
Gene	Condition	Inheritance	Ethnicity	Carrier Rate	Detection Rate	Post test Carrier Probability*	Residual Risk*
<i>GALC</i>	Krabbe disease	AR	General Population Israeli Druze Population	in 58 in 6	99% 99%	in 5 70 in 50	in 9 923 032 in 2 024
<i>GALNS</i>	Mucopolysaccharidosis VA (Morquio syndrome A)	AR	General Population	in 224	97%	in 7 434	in 6 660 864
<i>GALT</i>	Galactosemia	AR	General Population African/African American Population Ashkenazi Jewish Population	in 0 in 94 in 27	99% 99% 99%	in 0 90 in 9 30 in 2 60	in 4 796 440 in 3 497 76 in 6 40 308
<i>GAMT</i>	Guanidinoacetate methyltransferase deficiency	AR	General Population	in 37	99%	in 37 00	< in 0 million
<i>GBA</i>	Gaucher disease	AR	General Population African/African American Population Ashkenazi Jewish Population	in 77 in 35 in 5	99% 99% 99%	in 7 60 in 3 40 in 40	in 2 34 08 in 476 40 in 84 060
<i>GBE1</i>	Glycogen storage disease V	AR	General Population	in 387	99%	in 38 60	< in 0 million
<i>GCDH</i>	Glutaric aciduria type	AR	General Population Amish Population	in 87 in 9	98% 98%	in 4 30 in 40	in 496 748 in 4 436
<i>GDAP1</i>	Charcot Marie Tooth disease GDAP related	AR	General Population	in 52	99%	in 5 0	in 9 8 408
<i>GDF5</i>	Du Pan Syndrome	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>GFM1</i>	Combined oxidative phosphorylation deficiency GFM related	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>GJB2</i>	Nonsyndromic hearing loss GJB2 related	AR	General Population African/African American Population Ashkenazi Jewish Population Caucasian / European Population Latino Population Middle Eastern Population South Asian/ ndian Population	in 42 in 25 in 2 in 33 in 00 in 83 in 48	99% 99% 99% 99% 99% 99% 99%	in 4 0 in 2 40 in 2 00 in 3 20 in 9 90 in 8 20 in 4 70	in 688 968 in 240 00 in 68 084 in 422 532 in 3 960 400 in 2 722 732 in 8 702 992
<i>GJB6</i>	GJB6 CRYL related nonsyndromic hearing loss	AR	General Population	in 423	99%	in 42 20	< in 0 million
<i>GLB1</i>	GM gangliosidosis	AR	General Population Maltese Population Roma Population	in 34 in 30 in 50	99% 99% 99%	in 3 30 in 2 90 in 4 90	in 7 29 336 in 348 20 in 980 200
<i>GLB1</i>	Mucopolysaccharidosis type VB (Morquio syndrome B)	AR	General Population Maltese Population Roma Population	in 34 in 30 in 50	99% 99% 99%	in 3 30 in 2 90 in 4 90	in 7 29 336 in 348 20 in 980 200
<i>GLDC</i>	Glycine encephalopathy GLDC related	AR	General Population British Columbia Canadian Population Finnish Population	in 93 in 25 in 7	98% 99% 99%	in 9 60 in 2 40 in 60	in 7 4 972 in 6 200 500 in 5 429 268
<i>GLE1</i>	Lethal congenital contracture syndrome	AR	General Population Finnish Population	< in 500 in 80	98% 98%	in 24 95 in 3 95	< in 0 million in 264 320
<i>GNE</i>	Inclusion body myopathy type 2 (Nonaka myopathy)	AR	General Population Iranian Jewish Population	< in 500 in	99% 99%	in 49 90 in 00	in 99 802 000 in 44 044
<i>GNPTAB</i>	Mucopolipidosis alpha/beta	AR	General Population	< in 500	95%	in 9 98	< in 0 million
<i>GNPTAB</i>	Mucopolipidosis alpha/beta	AR	General Population	< in 500	95%	in 9 98	< in 0 million
<i>GNPTG</i>	Mucopolipidosis gamma	AR	General Population	< in 500	95%	in 9 98	< in 0 million
<i>GNS</i>	Mucopolysaccharidosis D (Sanfilippo syndrome D)	AR	General Population	in 500	98%	in 24 95	< in 0 million
<i>GSS</i>	Glutathione synthetase deficiency	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>GUCY2D</i>	Leber congenital amaurosis	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>GUSB</i>	Mucopolysaccharidosis type V	AR	General Population	in 250	98%	in 2 45	< in 0 million
<i>HADHA</i>	Trifunctional protein deficiency	AR	General Population Finnish Population	< in 500 in 24	98% 98%	in 24 95 in 6 5	< in 0 million in 3 050 896
<i>HADHA</i>	Long chain 3 hydroxyacyl CoA dehydrogenase (LCHAD) deficiency	AR	General Population Finnish Population	< in 500 in 24	98% 98%	in 24 95 in 6 5	< in 0 million in 3 050 896
<i>HADHB</i>	Trifunctional protein deficiency	AR	General Population Finnish Population	< in 500 in 24	98% 98%	in 24 95 in 6 5	< in 0 million in 3 050 896
<i>HAX1</i>	Severe congenital neutropenia HAX related	AR	General Population	in 224	98%	in 5	in 9 99 296
<i>HBA1</i>	Alpha thalassemia	AR	General Population General Population Southeast Asian Population Southeast Asian Population Mediterranean Population Mediterranean Population African/African American Population	in 8 in 000 ≤ in 7 ≤ in 4 ≤ in 6 in 500 in 30	98% 98% 98% 98% 98% 98% 98%	in 860 in 860 ≤ in 305 ≤ in 305 ≤ in 229 ≤ in 229 in 45	in 3 440 364 in 3 440 364 ≤ in 7 228 ≤ in 7 228 ≤ in 457 556 ≤ in 457 556 in 5 804 000



Supplemental Table

Gene	Condition	Inheritance	Ethnicity	Carrier Rate	Detection Rate	Post test Carrier Probability*	Residual Risk*
<i>HBA2</i>	Alpha thalassemia	AR	General Population	in 8	98%	in 860	in 3 440 364
			General Population	in 000	98%	in 860	in 3 440 364
			Southeast Asian Population	≤ in 7	98%	≤ in 305	≤ in 7 228
			Southeast Asian Population	≤ in 4	98%	≤ in 305	≤ in 7 228
			Mediterranean Population	≤ in 6	98%	≤ in 229	≤ in 457 556
			Mediterranean Population	in 500	98%	≤ in 229	≤ in 457 556
<i>HBB</i>	Sickle cell disease	AR	African/African American Population	in 30	98%	in 45	in 5 804 000
			General Population	in 58	95%	in 3 4	in 985 2
			African/African American Population	in 0	95%	in 8	in 7 240
			East Asian Population	in 50	95%	in 98	in 96 200
			Latino Population	in 28	95%	in 2 54	in 300 992
			Mediterranean Population	in 3	95%	in 4	in 492
<i>HBB</i>	Hemoglobin C disease	AR	South Asian/ ndian Population	in 25	95%	in 48	in 48 00
			General Population	in 58	95%	in 3 4	in 985 2
			African/African American Population	in 0	95%	in 8	in 7 240
			East Asian Population	in 50	95%	in 98	in 96 200
			Latino Population	in 28	95%	in 2 54	in 300 992
			Mediterranean Population	in 3	95%	in 4	in 492
<i>HBB</i>	Beta thalassemia	AR	South Asian/ ndian Population	in 25	95%	in 48	in 48 00
			General Population	in 58	95%	in 3 4	in 985 2
			African/African American Population	in 0	95%	in 8	in 7 240
			East Asian Population	in 50	95%	in 98	in 96 200
			Latino Population	in 28	95%	in 2 54	in 300 992
			Mediterranean Population	in 3	95%	in 4	in 492
<i>HEXA</i>	Tay Sachs disease	AR	South Asian/ ndian Population	in 25	95%	in 48	in 48 00
			General Population	in 300	99%	in 29 90	< in 0 million
			Ashkenazi Jewish Population	in 27	99%	in 2 60	in 280 908
<i>HEXB</i>	Sandhoff disease	AR	Moroccan Jewish Population	in 0	99%	in 0 90	in 4 796 440
			General Population	in 600	98%	in 29 95	< in 0 million
			General Population	in 434	98%	in 2 65	< in 0 million
<i>HGSNAT</i>	Mucopolysaccharidosis type C (Sanfilippo syndrome C)	AR	Caucasian / European Population	in 345	98%	in 7 20	< in 0 million
			General Population	in 500	99%	in 49 90	< in 0 million
<i>HJV</i>	Hemochromatosis type 2A	AR	General Population	in 500	99%	in 49 90	< in 0 million
<i>HLCS</i>	Holocarboxylase synthetase deficiency	AR	General Population	in 500	98%	in 24 95	< in 0 million
<i>HMGCL</i>	3 hydroxy 3 methylglutaryl CoA lyase deficiency	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>HOGA1</i>	Primary hyperoxaluria type	AR	General Population	in 84	99%	in 8 30	< in 0 million
<i>HPS1</i>	Hermansky Pudlak syndrome	AR	General Population	in 354	98%	in 7 65	< in 0 million
			Puerto Rican Population	in 2	98%	in 00	in 84 084
<i>HPS3</i>	Hermansky Pudlak syndrome 3	AR	General Population	in 354	98%	in 7 65	< in 0 million
<i>HPS4</i>	Hermansky Pudlak syndrome 4	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>HSD17B4</i>	D bifunctional protein deficiency	AR	General Population	in 58	98%	in 7 85	in 4 96 832
<i>HSD3B2</i>	Congenital adrenal hyperplasia due to 3 beta hydroxysteroid dehydrogenase 2 deficiency	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>HYLS1</i>	Hydroletharus syndrome	AR	General Population	< in 500	98%	in 24 95	< in 0 million
			Finnish Population	in 50	98%	in 2 45	in 490 200
<i>IDUA</i>	Mucopolysaccharidosis type (Hurler syndrome)	AR	General Population	< in 500	95%	in 9 98	< in 0 million
			Caucasian / European Population	in 53	95%	in 3 04	in 86 092
<i>IVD</i>	sovaleric Acidemia	AR	General Population	in 67	90%	in 66	in 09 548
			African/African American Population	in 00	90%	in 99	in 396 400
			Caucasian / European Population	in 5	90%	in 4	in 524 860
			East Asian Population	in 407	90%	in 4 06	in 6 6 308
<i>IYD</i>	Thyroid dysmorphogenesis YD related	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>JAK3</i>	Severe combined immunodeficiency JAK3 related	AR	General Population	in 299	99%	in 29 80	< in 0 million
<i>KCNJ11</i>	Congenital hyperinsulinism	AR	General Population	in 423	99%	in 42 20	< in 0 million
			Caucasian / European Population	in 232	99%	in 23 0	< in 0 million
<i>KCNJ11</i>	Permanent neonatal diabetes mellitus	AR	General Population	in 423	99%	in 42 20	< in 0 million
			Caucasian / European Population	in 232	99%	in 23 0	< in 0 million
<i>LAMA2</i>	Muscular dystrophy LAMA2 related	AR	General Population	< in 500	99%	in 49 90	< in 0 million
			Caucasian / European Population	in 25	99%	in 2 40	in 6 200 500
<i>LAMA3</i>	Junctional epidermolysis bullosa LAMA3 related	AR	General Population	in 78	98%	in 39 00	< in 0 million
<i>LAMA3</i>	Laryngo onycho cutaneous syndrome	AR	General Population	in 78	98%	in 39 00	< in 0 million
<i>LAMB3</i>	Junctional epidermolysis bullosa LAMB3 related	AR	General Population	in 78	98%	in 39 00	< in 0 million
<i>LAMC2</i>	Junctional epidermolysis bullosa LAMC2 related	AR	General Population	in 78	98%	in 39 00	< in 0 million
<i>LCA5</i>	Leber congenital amaurosis 5	AR	General Population	in 500	98%	in 24 95	< in 0 million

Supplemental Table

Gene	Condition	Inheritance	Ethnicity	Carrier Rate	Detection Rate	Post test Carrier Probability*	Residual Risk*
<i>LDLRAP1</i>	Familial Hypercholesterolemia	AR	General Population	in 8	99%	in 70	in 22 432
			Amish Population	in 2	99%	in 0	in 808
			Caucasian / European Population	in 7	99%	in 60	in 6 828
			French Canadian Population	in 8	99%	in 70	in 22 432
<i>LHX3</i>	Combined pituitary hormone deficiency 3	AR	General Population	in 45	98%	in 2 20	in 396 80
<i>LIFR</i>	Stuve Wiedemann syndrome	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>LIPA</i>	Lysosomal acid lipase deficiency	AR	General Population	< in 500	99%	in 49 90	< in 0 million
			Caucasian / European Population	in 2	99%	in 0	in 4 973 248
			Iranian Jewish Population	in 26	99%	in 2 50	in 260 04
<i>LMBRD1</i>	Methylmalonic aciduria and homocystinuria cblF type	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>LOXHD1</i>	Nonsyndromic hearing loss LOXHD related	AR	General Population	in 500	98%	in 24 95	< in 0 million
			Ashkenazi Jewish Population	in 80	98%	in 8 95	in 6 444 720
<i>LPL</i>	Familial lipoprotein lipase deficiency	AR	General Population	in 500	99%	in 49 90	< in 0 million
			French Canadian Population	in 46	99%	in 4 50	in 828 84
<i>LRP2</i>	Donnai Barrow syndrome	AR	General Population	in 2 4	99%	in 0 65	in 9 7 256
<i>LRPPRC</i>	Leigh syndrome with Complex V deficiency	AR	General Population	in 447	98%	in 22 30	< in 0 million
			Faroese Population	in 2	98%	in 00	in 84 084
			French Canadian Population	in 22	98%	in 05	in 92 488
<i>LYST</i>	Chediak Higashi syndrome	AR	General Population	< in 500	90%	in 4 99	in 9 982 000
<i>MAN2B1</i>	Alpha Mannosidosis	AR	General Population	in 354	99%	in 35 30	< in 0 million
			Caucasian / European Population	in 274	99%	in 27 30	< in 0 million
<i>MANBA</i>	Beta Mannosidosis	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>MCOLN1</i>	Mucopolipidosis V	AR	General Population	in 300	99%	in 29 90	< in 0 million
			Ashkenazi Jewish Population	in 00	99%	in 9 90	in 3 960 400
<i>MCPH1</i>	Primary microcephaly recessive	AR	General Population	in 47	99%	in 4 60	in 8 585 388
<i>MED17</i>	Postnatal Progressive Microcephaly with Seizures and Brain Atrophy	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>MED17</i>	Postnatal Progressive Microcephaly with Seizures and Brain Atrophy	AR	Bukharan/Kurdish Jewish Population	in 20	99%	in 90	in 52 080
			General Population	< in 500	98%	in 24 95	< in 0 million
<i>MESP2</i>	Spondylocostal dysostosis	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>MFSD8</i>	Neuronal ceroid lipofuscinosis MFSD8 related	AR	General Population	< in 500	95%	in 9 98	< in 0 million
<i>MKS1</i>	Bardet Biedl syndrome 3	AR	General Population	in 260	98%	in 2 95	< in 0 million
			Finnish Population	in 47	98%	in 2 30	in 432 588
<i>MKS1</i>	Joubert syndrome 28	AR	General Population	in 260	98%	in 2 95	< in 0 million
			Finnish Population	in 47	98%	in 2 30	in 432 588
<i>MKS1</i>	Meckel syndrome	AR	General Population	in 260	98%	in 2 95	< in 0 million
			Finnish Population	in 47	98%	in 2 30	in 432 588
<i>MLC1</i>	Megalencephalic leukoencephalopathy with subcortical cysts	AR	General Population	< in 500	99%	in 49 90	< in 0 million
			Libyan Jewish Population	in 40	99%	in 3 90	in 624 60
<i>MLYCD</i>	Malonyl CoA decarboxylase deficiency	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>MMAA</i>	Methylmalonic aciduria cblA type	AR	General Population	in 30	97%	in 0 00	< in 0 million
<i>MMAB</i>	Methylmalonic aciduria cblB type	AR	General Population	in 435	98%	in 2 70	< in 0 million
<i>MMACHC</i>	Methylmalonic aciduria and homocystinuria cblC type	AR	General Population	in 34	90%	in 33	in 7 3 4 6
<i>MMADHC</i>	Methylmalonic aciduria and homocystinuria cblD type	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>MPI</i>	Congenital disorder of glycosylation type b	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>MPL</i>	Congenital amegakaryocytic thrombocytopenia	AR	General Population	in 02	98%	in 5 05	in 2 060 808
			Ashkenazi Jewish Population	in 55	98%	in 2 70	in 594 220
<i>MPV17</i>	Hepatocerebral mitochondrial DNA depletion syndrome MPV 7 related	AR	General Population	< in 500	96%	in 2 476	< in 0 million
			Native American Population	in 20	96%	in 476	in 38 080
<i>MTHFR</i>	Homocystinuria MTHFR related	AR	General Population	in 224	98%	in 5	in 9 99 296
<i>MTMR2</i>	Charcot Marie Tooth disease type 4B	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>MTRR</i>	Homocystinuria megaloblastic anemia cobalamin E type	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>MTTP</i>	Abetalipoproteinemia	AR	General Population	< in 500	98%	in 24 95	< in 0 million
			Ashkenazi Jewish Population	in 80	98%	in 8 95	in 6 444 720
<i>MUT</i>	Methylmalonic acidemia MUT related	AR	General Population	in 95	96%	in 4 85	in 3 783 780
			East Asian Population	in 53	96%	in 30	in 275 8 2
			Middle Eastern Population	in 52	96%	in 276	in 265 408
<i>MUT</i>	Methylmalonic aciduria methylmalonyl CoA mutase deficiency	AR	General Population	in 00	99%	in 9 90	in 3 960 400
<i>MVK</i>	Hyperimmunoglobulinemia D syndrome	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>MVK</i>	Mevalonate kinase deficiency	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>MYO7A</i>	Usher syndrome type B	AR	General Population	in 206	98%	in 0 25	in 8 446 824
			East Asian Population	in 62	98%	in 3 05	in 756 648



Supplemental Table

Gene	Condition	Inheritance	Ethnicity	Carrier Rate	Detection Rate	Post test Carrier Probability*	Residual Risk*
<i>MYO7A</i>	Non syndromic hearing loss MYO7A related	AR	General Population East Asian Population	in 206 in 62	98% 98%	in 0.25 in 3.05	in 8.446.824 in 756.648
<i>NAGA</i>	Schindler disease types and 3	AR	General Population	in 94	99%	in 9.30	in 3.497.76
<i>NAGLU</i>	Mucopolysaccharidosis type B (Sanfilippo syndrome B)	AR	General Population Caucasian / European Population East Asian Population	< in 500 in 346 in 298	99% 99% 99%	in 49.90 in 34.50 in 29.70	< in 0 million < in 0 million < in 0 million
<i>NAGS</i>	N acetylglutamate synthase deficiency	AR	General Population	< in 500	98%	in 24.95	< in 0 million
<i>NBN</i>	Nijmegen breakage syndrome	AR	General Population	in 58	99%	in 5.70	in 9.923.032
<i>NDRG1</i>	Charcot Marie Tooth disease type 4D	AR	General Population	in 22	98%	in 0.5	in 92.488
<i>NDUFAF2</i>	Mitochondrial complex deficiency	AR	General Population	< in 500	99%	in 49.90	< in 0 million
<i>NDUFAF5</i>	Mitochondrial complex deficiency (Leigh syndrome)	AR	General Population Ashkenazi Jewish Population	in 447 in 290	98% 98%	in 22.30 in 4.45	< in 0 million < in 0 million
<i>NDUFS4</i>	Mitochondrial complex deficiency	AR	General Population	< in 500	99%	in 49.90	< in 0 million
<i>NDUFS4</i>	Mitochondrial complex deficiency	AR	General Population Hutterite Population	< in 500 in 27	99% 99%	in 49.90 in 2.60	< in 0 million in 280.908
<i>NDUFS6</i>	Mitochondrial complex deficiency (Leigh syndrome)	AR	General Population Bukharan/Kurdish Jewish Population	< in 500 in 24	99% 99%	in 49.90 in 2.30	< in 0 million in 220.896
<i>NDUFS7</i>	Mitochondrial complex deficiency	AR	General Population	< in 500	99%	in 49.90	< in 0 million
<i>NDUFV1</i>	Mitochondrial complex deficiency nuclear type 4	AR	General Population	< in 500	99%	in 49.90	< in 0 million
<i>NEB</i>	Nemaline myopathy	AR	General Population Amish Population Ashkenazi Jewish Population Finnish Population	in 2 in in 08 in 2	98% 98% 98% 98%	in 5.55 in 50 in 5.35 in 5.55	in 2.486.848 in 22.044 in 2.3.632 in 2.486.848
<i>NEU1</i>	Sialidosis type and	AR	General Population	< in 500	99%	in 49.90	< in 0 million
<i>NPC1</i>	Niemann Pick disease type C	AR	General Population	in 94	90%	in 93	in 498.456
<i>NPC2</i>	Niemann Pick disease type C2	AR	General Population	in 94	99%	in 9.30	< in 0 million
<i>NPHP1</i>	Joubert syndrome 4	AR	General Population Finnish Population	in 480 in 24	98% 98%	in 23.95 in 6.5	< in 0 million in 3.050.896
<i>NPHP1</i>	Nephronophthisis	AR	General Population Finnish Population	in 480 in 24	98% 98%	in 23.95 in 6.5	< in 0 million in 3.050.896
<i>NPHP1</i>	NPHP related disorders	AR	General Population Finnish Population	in 480 in 24	98% 98%	in 23.95 in 6.5	< in 0 million in 3.050.896
<i>NPHP1</i>	Senior Løken syndrome	AR	General Population Finnish Population	in 480 in 24	98% 98%	in 23.95 in 6.5	< in 0 million in 3.050.896
<i>NPHS1</i>	Congenital nephrotic syndrome type	AR	General Population Finnish Population	in 289 in 50	98% 98%	in 4.40 in 2.45	< in 0 million in 490.200
<i>NPHS2</i>	Congenital nephrotic syndrome type 2	AR	General Population Finnish Population	in 289 in 50	98% 98%	in 4.40 in 2.45	< in 0 million in 490.200
<i>NTRK1</i>	Congenital insensitivity to pain with anhidrosis	AR	General Population	< in 500	99%	in 49.90	< in 0 million
<i>OAT</i>	Gyrate atrophy of choroid and retina	AR	General Population	< in 500	98%	in 24.95	< in 0 million
<i>OCA2</i>	Oculocutaneous albinism type	AR	General Population	in 00	98%	in 4.95	in 980.400
<i>OCA2</i>	Oculocutaneous albinism type	AR	General Population	in 76	99%	in 7.50	in 2.280.304
<i>OPA3</i>	Costeff syndrome	AR	General Population raqi Jewish Population	< in 500 in 50	98% 98%	in 24.95 in 2.45	< in 0 million in 490.200
<i>OTOF</i>	Nonsyndromic hearing loss OTOF related	AR	General Population Spanish Population	< in 500 in 06	99% 99%	in 49.90 in 0.50	< in 0 million in 4.452.424
<i>P3H1</i>	Osteogenesis imperfecta type V	AR	General Population West African Population African American Population	< in 500 in 67 in 250	99% 99% 99%	in 49.90 in 6.60 in 24.90	< in 0 million in 769.068 < in 0.000.000
<i>PAH</i>	Phenylalanine Hydroxylase deficiency (Phenylketonuria)	AR	General Population Caucasian / European Population Middle Eastern Population South East Asian	in 93 in 63 in 74 in 59	99% 99% 99% 99%	in 9.20 in 6.20 in 7.30 in 5.80	in 3.422.772 in 562.652 in 2.6.096 in 369.036
<i>PANK2</i>	Pantothenate kinase associated neurodegeneration	AR	General Population	in 289	99%	in 28.80	< in 0 million
<i>PC</i>	Pyruvate carboxylase deficiency	AR	General Population	in 250	95%	in 4.98	in 4.98.000
<i>PCCA</i>	Propionic acidemia PCCA related	AR	General Population Native American Population	in 224 in 85	96% 96%	in 5.576 in 2.0	in 4.996.096 in 7.4.340
<i>PCCB</i>	Propionic acidemia PCCB related	AR	General Population Native American Population	in 224 in 85	99% 99%	in 22.30 in 8.40	< in 0 million in 2.856.340
<i>PCDH15</i>	Non syndromic hearing loss PCDH 5 related	AR	General Population Ashkenazi Jewish Population	in 395 in 72	98% 98%	in 9.70 in 3.55	in 78.804 in 4.204

Supplemental Table

Gene	Condition	Inheritance	Ethnicity	Carrier Rate	Detection Rate	Post test Carrier Probability*	Residual Risk*
<i>PCDH15</i>	Usher syndrome type F	AR	General Population Ashkenazi Jewish Population	in 395 in 72	98% 98%	in 9 70 in 3 55	in 78 804 in 4 204
<i>PCNT</i>	Microcephalic osteodysplastic primordial dwarfism type	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>PDHB</i>	Pyruvate dehydrogenase E beta deficiency	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>PEX1</i>	Zellweger syndrome PEX related	AR	General Population	in 47	95%	in 2 92	in 7 7 548
<i>PEX10</i>	Zellweger syndrome PEX 0 related	AR	General Population Japanese Population	in 500 in 354	95% 95%	in 9 98 in 7 06	< in 0 million in 9 998 376
<i>PEX12</i>	Zellweger syndrome PEX 2 related	AR	General Population	in 373	95%	in 7 44	< in 0 million
<i>PEX2</i>	Zellweger syndrome PEX2 related	AR	General Population Ashkenazi Jewish Population	in 500 in 23	95% 95%	in 9 98 in 2 44	< in 0 million in 200 972
<i>PEX26</i>	Zellweger syndrome	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>PEX6</i>	Zellweger syndrome PEX6 related	AR	General Population Yemenite Jewish Population	in 280 in 8	99% 99%	in 27 90 in 70	< in 0 million in 22 472
<i>PEX7</i>	Rhizomelic chondrodysplasia punctata type	AR	General Population	in 58	99%	in 5 70	in 9 923 032
<i>PFKM</i>	Glycogen storage disease V	AR	General Population Ashkenazi Jewish Population	< in 500 in 20	99% 99%	in 49 90 in 90	< in 0 million in 5 7 2 480
<i>PHGDH</i>	Phosphoglycerate dehydrogenase deficiency	AR	General Population Ashkenazi Jewish Population	< in 500 in 280	98% 98%	in 24 95 in 3 95	< in 0 million in 0 million
<i>PHYH</i>	Refsum disease	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>PKHD1</i>	Polycystic kidney disease PKHD related	AR	General Population Ashkenazi Jewish Population	in 70 in 07	98% 98%	in 3 45 in 5 30	in 966 280 in 2 268 828
<i>PLA2G6</i>	Infantile neuroaxonal dystrophy	AR	General Population	in 500	97%	in 6 634	< in 0 million
<i>PLOD1</i>	Ehlers Danlos syndrome with kyphoscoliosis PLOD related	AR	General Population	in 59	99%	in 5 80	< in 0 million
<i>PMM2</i>	Congenital disorder of glycosylation type a	AR	General Population Ashkenazi Jewish Population Caucasian / European Population	< in 500 in 57 in 7	99% 99% 99%	in 49 90 in 5 60 in 7 00	< in 0 million in 277 028 in 988 284
<i>POLG</i>	Ataxia neuropathy spectrum	AR	General Population	in 3	95%	in 2 24	in 0 2 932
<i>POLG</i>	Progressive external ophthalmoplegia	AR	General Population	in 3	95%	in 2 24	in 0 2 932
<i>POLG</i>	Mycocerebrohepatopathy syndrome	AR	General Population	in 3	95%	in 2 24	in 0 2 932
<i>POLG</i>	POLG related disorders	AR	General Population	in 3	95%	in 2 24	in 0 2 932
<i>POLG</i>	Alpers Huttenlocher syndrome	AR	General Population	in 3	95%	in 2 24	in 0 2 932
<i>POLR1C</i>	Hypomyelinating Leukodystrophy POLR C related	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>POLR1C</i>	Treacher Collins syndrome POLR C related	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>POMGNT1</i>	Muscular dystrophy dystroglycanopathy	AR	General Population Finnish Population	in 462 in	98% 98%	in 23 05 in 5 50	< in 0 million in 2 442 444
<i>POMGNT1</i>	Retinitis pigmentosa 76	AR	General Population Finnish Population	in 462 in	98% 98%	in 23 05 in 5 50	< in 0 million in 2 442 444
<i>POMT1</i>	Muscular dystrophy dystroglycanopathy POMT related	AR	General Population	in 290	99%	in 28 90	< in 0 million
<i>POMT2</i>	Muscular dystrophy dystroglycanopathy POMT2 related	AR	General Population	in 37	99%	in 37 00	< in 0 million
<i>POR</i>	Antley Bixler syndrome	AR	General Population	in 59	98%	in 7 90	in 5 025 036
<i>PPT1</i>	Neuronal ceroid lipofuscinosis PPT related	AR	General Population Caucasian / European Population Finnish Population	in 368 in 488 in 75	98% 98% 98%	in 8 35 in 24 35 in 3 70	< in 0 million in 0 million in 0 300
<i>PRF1</i>	Hemophagocytic lymphohistiocytosis familial 2	AR	General Population	in 49	99%	in 4 80	in 8 82 396
<i>PROP1</i>	Combined pituitary hormone deficiency 2	AR	General Population	in 45	98%	in 2 20	in 396 80
<i>PSAP</i>	Metachromatic leukodystrophy due to saposin b deficiency	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>PTS</i>	Tetrahydrobiopterin deficiency	AR	General Population	in 354	96%	in 8 826	< in 0 million
<i>PUS1</i>	Mitochondrial myopathy and sideroblastic anemia	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>QDPR</i>	Tetrahydrobiopterin deficiency QDPR related	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>RAB23</i>	Carpenter syndrome	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>RAG1</i>	Omenn syndrome RAG related	AR	General Population	in 290	98%	in 4 45	in 6 763 60
<i>RAG2</i>	Omenn syndrome RAG2 related	AR	General Population	in 37	98%	in 6 80	in 3 726 948
<i>RAPSN</i>	Congenital myasthenic syndrome RAPSN related	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>RAPSN</i>	Fetal akinesia deformation sequence	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>RARS2</i>	Pontocerebellar hypoplasia type 6	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>RAX</i>	Microphthalmia isolated 3	AR	General Population	in 289	99%	in 28 80	< in 0 million

Supplemental Table

Gene	Condition	Inheritance	Ethnicity	Carrier Rate	Detection Rate	Post test Carrier Probability*	Residual Risk*
<i>RDH12</i>	Leber congenital amaurosis type 3	AR	General Population Caucasian / European Population	< in 500 in 456	98% 98%	in 24 95 in 22 75	< in 0 million < in 0 million
<i>RMRP</i>	Metaphyseal dysplasia without hypotrichosis	AR	General Population Amish Population Finnish Population	< in 500 in 6 in 76	99% 99% 99%	in 49 90 in 50 in 7 50	< in 0 million in 96 064 in 2 280 304
<i>RMRP</i>	Cartilage Hair Hypoplasia Anauxetic Dysplasia Spectrum Disorder	AR	General Population Amish Population Finnish Population	< in 500 in 6 in 76	99% 99% 99%	in 49 90 in 49 90 in 49 90	< in 0 million < in 0 million < in 0 million
<i>RMRP</i>	Anauxetic dysplasia	AR	General Population Amish Population Finnish Population	< in 500 in 6 in 76	99% 99% 99%	in 49 90 in 50 in 7 50	< in 0 million in 96 064 in 2 280 304
<i>RMRP</i>	Cartilage hair hypoplasia	AR	General Population Amish Population Finnish Population	< in 500 in 6 in 76	99% 99% 99%	in 49 90 in 50 in 7 50	< in 0 million in 96 064 in 2 280 304
<i>RNASEH2B</i>	Aicardi Goutieres syndrome 2	AR	General Population	in 2 7	99%	in 0 80	in 9 375 268
<i>RPE65</i>	Retinitis pigmentosa 20	AR	General Population	in 228	98%	in 35	< in 0 million
<i>RPE65</i>	Leber congenital amaurosis 2	AR	General Population	in 228	98%	in 35	< in 0 million
<i>RPGRIP1L</i>	COACH syndrome	AR	General Population	in 259	98%	in 2 90	< in 0 million
<i>RPGRIP1L</i>	Joubert syndrome 7	AR	General Population	in 259	98%	in 2 90	< in 0 million
<i>RPGRIP1L</i>	Meckel syndrome 5	AR	General Population	in 259	98%	in 2 90	< in 0 million
<i>RTEL1</i>	Dyskeratosis congenita type 5	AR	General Population Ashkenazi Jewish Population	in 500 in 203	99% 99%	in 49 90 in 20 20	< in 0 million < in 0 million
<i>SACS</i>	Autosomal recessive spastic ataxia of Charlevoix Saguenay	AR	General Population French Canadian Population	< in 500 in 9	95% 95%	in 9 98 in 36	< in 0 million in 27 436
<i>SAMD9</i>	Normophosphatemic Familial Tumoral Calcinosis	AR	General Population Yemeni Jewish Population	< in 500 in 25	99% 99%	in 49 90 in 2 40	< in 0 million in 240 00
<i>SAMHD1</i>	Aicardi Goutieres syndrome	AR	General Population	< in 500	95%	in 9 98	< in 0 million
<i>SCO2</i>	Mitochondrial complex V deficiency	AR	General Population	in 50	99%	in 4 90	in 8 940 600
<i>SEPSECS</i>	Pontocerebellar hypoplasia type 2D	AR	General Population Moroccan/ raqi Jewish Population	< in 500 in 44	99% 99%	in 49 90 in 4 30	< in 0 million in 756 976
<i>SERPINA1</i>	Alpha antitrypsin deficiency	AR	General Population Caucasian / European Population	in 33 in 9	95% 95%	in 64 in 36	in 84 6 2 in 27 436
<i>SGCA</i>	Limb girdle muscular dystrophy type 2D	AR	General Population Caucasian / European Population Finnish Population	< in 500 in 288 in 50	98% 98% 98%	in 24 95 in 4 35 in 7 45	< in 0 million < in 0 million in 4 470 600
<i>SGCB</i>	Limb girdle muscular dystrophy type 2E	AR	General Population Caucasian / European Population	in 500 in 406	98% 98%	in 24 95 in 20 25	< in 0 million < in 0 million
<i>SGCD</i>	Limb girdle muscular dystrophy type 2F	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>SGCG</i>	Limb girdle muscular dystrophy type 2C	AR	General Population Moroccan Population Roma / Gypsy Population	in 38 in 250 in 96	98% 98% 98%	in 9 00 in 2 45 in 4 75	< in 0 million < in 0 million in 824 384
<i>SGSH</i>	Mucopolysaccharidosis A (Sanfilippo syndrome A)	AR	General Population Caucasian / European Population	in 454 in 253	98% 98%	in 22 65 in 2 60	< in 0 million < in 0 million
<i>SH3TC2</i>	Charcot Marie Tooth disease SH3TC2 related	AR	General Population	in 69	99%	in 6 80	in 877 076
<i>SLC12A6</i>	Andermann syndrome	AR	General Population French Canadian Population	< in 500 in 23	98% 99%	in 24 95 in 2 20	< in 0 million in 202 492
<i>SLC17A5</i>	Sialic acid storage disorder	AR	General Population Finnish Population	< in 500 in 00	9 % 9 %	in 5 545 in 0	< in 0 million in 440 400
<i>SLC19A3</i>	Refsum disease	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>SLC19A3</i>	Biotin responsive basal ganglia disease	AR	General Population	in 09	99%	in 5 40	in 2 354 836
<i>SLC1A4</i>	Spastic tetraplegia thin corpus callosum and progressive microcephaly syndrome	AR	General Population Ashkenazi Jewish Population	< in 500 in 06	99% 99%	in 49 90 in 0 50	< in 0 million in 4 452 424
<i>SLC22A5</i>	Systemic primary carnitine deficiency	AR	General Population African/African American Population East Asian Population Faroese Population Pacific Islander Population South Asian/ Indian Population	in 29 in 86 in 77 in 9 in 37 in 5	99% 99% 99% 99% 99% 99%	in 2 80 in 8 50 in 7 60 in 80 in 3 60 in 5 00	in 6 605 3 6 in 2 924 344 in 2 34 08 in 28 836 in 532 948 in 020 204
<i>SLC25A13</i>	Citrin deficiency	AR	General Population East Asian Population	< in 500 in 65	95% 95%	in 9 98 in 28	< in 0 million in 333 060
<i>SLC25A15</i>	Hyperornithinemia hyperammonemia homocitrullinemia syndrome (Triple H syndrome)	AR	General Population French Canadian Population	< in 500 in 37	99% 99%	in 49 90 in 3 60	< in 0 million in 532 948



Supplemental Table							
Gene	Condition	Inheritance	Ethnicity	Carrier Rate	Detection Rate	Post test Carrier Probability*	Residual Risk*
<i>SLC26A2</i>	Diastrophic dysplasia	AR	General Population Finnish Population	in 58 in 50	90% 90%	in 57 in 49	in 992 872 in 98 200
<i>SLC26A2</i>	Achondrogenesis type B	AR	General Population Finnish Population	in 58 in 50	90% 90%	in 57 in 49	in 992 872 in 98 200
<i>SLC26A2</i>	Multiple epiphyseal dysplasia	AR	General Population Finnish Population	in 58 in 50	90% 90%	in 57 in 49	in 992 872 in 98 200
<i>SLC26A2</i>	Atelosteogenesis	AR	General Population Finnish Population	in 58 in 50	90% 90%	in 57 in 49	in 992 872 in 98 200
<i>SLC26A3</i>	Congenital secretory chloride diarrhea	AR	General Population Middle Eastern Population	< in 500 in 57	98% 98%	in 24 95 in 2 80	< in 0 million in 638 628
<i>SLC35A3</i>	Arthrogryposis intellectual disability and seizures	AR	General Population Ashkenazi Jewish Population	< in 500 in 453	98% 98%	in 24 95 in 22 60	< in 0 million < in 0 million
<i>SLC37A4</i>	Glycogen storage disease type b	AR	General Population Ashkenazi Jewish Population	in 58 in 7	95% 95%	in 3 4 in 40	in 985 2 in 397 884
<i>SLC39A4</i>	Acrodermatitis enteropathica	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>SLC45A2</i>	Oculocutaneous albinism type V	AR	General Population Japanese Population	in 59 in 46	98% 98%	in 7 90 in 7 25	in 5 025 036 in 4 234 584
<i>SLC46A1</i>	Hereditary folate malabsorption	AR	General Population Puerto Rican Population	< in 500 in 500	99% 99%	in 49 90 in 49 90	< in 0 million < in 0 million
<i>SLC5A5</i>	Thyroid dysmorphogenesis SLC5A5 related	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>SLC7A7</i>	Lysinuric protein intolerance	AR	General Population Finnish Population Japanese Population	< in 500 in 22 in 9	95% 95% 95%	in 9 98 in 2 42 in 2 36	< in 0 million in 8 448 in 23 836
<i>SMARCA1</i>	Schimke immunosseous dysplasia	AR	General Population	in 500	90%	in 4 99	in 9 982 000
<i>SMN1</i>	Spinal muscular atrophy	AR	General Population African/African American Population Ashkenazi Jewish Population Caucasian / European Population East Asian Population Latino Population Sephardic Jewish Population	in 54 in 72 in 67 in 47 in 59 in 68 in 34	9 % 7 % 9 % 95% 93% 90% 96%	in 590 in 246 in 734 in 92 in 830 in 67 in 826	in 27 440 in 70 848 in 96 7 2 in 73 48 in 95 880 in 82 5 2 in 2 336
<i>SMPD1</i>	Niemann Pick disease type A/B	AR	General Population Ashkenazi Jewish Population Latino Population	in 250 in 5 in 06	95% 95% 95%	in 4 98 in 2 28 in 2 0	in 4 98 000 in 049 260 in 890 824
<i>SPG11</i>	SPG related Neuromuscular Disorders	AR	General Population	in 59	99%	in 5 80	< in 0 million
<i>SPINK5</i>	Netherton syndrome	AR	General Population Ashkenazi Jewish Population	in 224 in 7	99% 99%	in 23 30 in 60	< in 0 million in 08 868
<i>STAR</i>	Lipoid congenital adrenal hyperplasia	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>SUMF1</i>	Multiple sulfatase deficiency	AR	General Population Ashkenazi Jewish Population	in 500 in 320	98% 98%	in 24 95 in 5 95	< in 0 million < in 0 million
<i>SURF1</i>	Charcot Marie Tooth disease SURF related	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>SURF1</i>	Leigh syndrome SURF related	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>TCIRG1</i>	Osteopetrosis TC RG related	AR	General Population	in 250	98%	in 2 45	< in 0 million
<i>TCTN2</i>	Meckel syndrome 8	AR	General Population Ethiopian Jewish Population Yemenite Jewish Population	< in 500 in 42 in 78	99% 99% 99%	in 49 90 in 4 0 in 7 70	< in 0 million in 688 968 in 2 402 7 2
<i>TCTN2</i>	Joubert syndrome 24	AR	General Population	< in 500	99%	in 49 90	< in 0 million
<i>TECPR2</i>	Spastic paraplegia 49	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>TF</i>	Atransferrinemia	AR	General Population	in 6	99%	in 50	in 5 336 464
<i>TG</i>	Thyroid dysmorphogenesis TG related	AR	General Population	in 24	99%	in 24 00	< in 0 million
<i>TGM1</i>	Congenital ichthyosis	AR	General Population	in 224	95%	in 4 46	in 3 997 056
<i>TH</i>	Segawa syndrome	AR	General Population	in 224	98%	in 5	in 9 99 296
<i>TMEM216</i>	Joubert syndrome 2	AR	General Population Ashkenazi Jewish Population	in 4 in 92	98% 98%	in 7 00 in 4 55	in 3 948 564 in 674 768
<i>TMEM216</i>	Meckel syndrome 2	AR	General Population Ashkenazi Jewish Population	in 4 in 92	98% 98%	in 7 00 in 4 55	in 3 948 564 in 674 768
<i>TPO</i>	Thyroid dysmorphogenesis TPO related	AR	General Population	in 373	99%	in 37 20	< in 0 million
<i>TPP1</i>	Neuronal ceroid lipofuscinosis TPP related	AR	General Population French Canadian Population	in 252 in 53	97% 97%	in 8 368 in 734	in 8 434 944 in 367 608
<i>TRDN</i>	Catecholaminergic polymorphic ventricular tachycardia	AR	General Population	in 354	98%	in 7 65	< in 0 million
<i>TRIM32</i>	Limb girdle muscular dystrophy type 2H	AR	General Population Hutterite Population	< in 500 in 2	98% 98%	in 24 95 in 55	< in 0 million in 26 448



Supplemental Table							
Gene	Condition	Inheritance	Ethnicity	Carrier Rate	Detection Rate	Post test Carrier Probability*	Residual Risk*
<i>TRIM32</i>	Bardet Biedl syndrome	AR	General Population Hutterite Population	< in 500 in 2	98% 98%	in 24 95 in 55	< in 0 million in 26 448
<i>TRMU</i>	Liver failure acute infantile	AR	General Population Yemeni Jewish Population	< in 500 in 34	98% 98%	in 24 95 in 65	< in 0 million in 224 536
<i>TSEN54</i>	Pontocerebellar hypoplasia TSEN54 related	AR	General Population	in 250	98%	in 2 45	< in 0 million
<i>TSFM</i>	Combined oxidative phosphorylation deficiency TSFM related	AR	General Population Finnish Population	< in 500 in 80	98% 98%	in 24 95 in 3 95	< in 0 million in 264 320
<i>TSHB</i>	Congenital hypothyroidism TSHB related	AR	General Population	in 500	99%	in 49 90	< in 0 million
<i>TTC37</i>	Trichohepatoenteric syndrome	AR	General Population	in 500	98%	in 24 95	< in 0 million
<i>TPA</i>	Ataxia with isolated vitamin E deficiency	AR	General Population Caucasian / European Population	< in 500 in 267	98% 90%	in 24 95 in 2 66	< in 0 million in 2 84 948
<i>TYMP</i>	Mitochondrial neurogastrointestinal encephalopathy (MNGE) disease	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>TYR</i>	Oculocutaneous albinism types A and B	AR	General Population	in 20	99%	in 90	in 52 080
<i>TYRP1</i>	Oculocutaneous albinism type	AR	General Population African Population	< in 500 in 47	98% 98%	in 24 95 in 2 30	< in 0 million in 432 588
<i>UGT1A1</i>	Crigler Najjar syndrome	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>USH1C</i>	Usher syndrome type C	AR	General Population French Canadian Population	in 353 in 227	90% 90%	in 3 52 in 2 26	in 4 97 652 in 2 052 988
<i>USH1C</i>	Non syndromic hearing loss USH C related	AR	General Population French Canadian Population	in 353 in 227	90% 90%	in 3 52 in 2 26	in 4 97 652 in 2 052 988
<i>USH1G</i>	Usher syndrome type G	AR	General Population	in 434	99%	in 43 30	< in 0 million
<i>USH2A</i>	Usher syndrome type 2A	AR	General Population Caucasian / European Population Ashkenazi Jewish Population Iranian Jewish Population	in 26 in 73 in 35 in 60	96% 96% 99% 99%	in 3 26 in 80 in 3 40 in 5 90	in 575 504 in 525 892 in 476 40 in 4 6 240
<i>VPS13A</i>	Choreoacanthocytosis	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>VPS13B</i>	Cohen syndrome	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>VPS45</i>	Severe congenital neutropenia VPS45 related	AR	General Population	in 224	98%	in 5	in 9 99 296
<i>VPS53</i>	Pontocerebellar hypoplasia VPS53 related	AR	General Population Moroccan Jewish Population	< in 500 in 37	98% 98%	in 24 95 in 80	< in 0 million in 266 548
<i>VRK1</i>	Pontocerebellar hypoplasia type A	AR	General Population	< in 500	98%	in 24 95	< in 0 million
<i>VSX2</i>	Microphthalmia with or without coloboma	AR	General Population	in 9	98%	in 4 50	in 638 364
<i>WHRN</i>	Usher syndrome type 2D	AR	General Population	in 282	99%	in 28 0	< in 0 million
<i>WRN</i>	Werner syndrome	AR	General Population Caucasian / European Population Japanese Population	in 308 in 2 in 7	98% 98% 98%	in 5 35 in 5 55 in 3 50	< in 0 million in 2 486 848 in 994 284
<i>XPA</i>	Xeroderma pigmentosum group A	AR	General Population Japanese Population	in 500 in 74	99% 99%	in 49 90 in 7 30	< in 0 million in 2 6 096
<i>XPC</i>	Xeroderma pigmentosum group C	AR	General Population	in 500	99%	in 49 90	< in 0 million
<i>ZFYVE26</i>	Spastic paraplegia 5	AR	General Population	< in 500	98%	in 24 95	< in 0 million

* For genes that have tested negative

† The carrier frequency for a pathogenic variant is described in rows marked with a dagger symbol. Abbreviations: AR, autosomal recessive; XL, X-linked