Limitations Methodology and List of genes

The information in this document relates to the new version of the CarrierTest, which is performed by the GNTlabs by GENNET laboratory starting December 1, 2025.

1. Limitations, Methodology and Considerations

Like any laboratory test, CarrierTest has certain limitations. While it is a reliable screening method that provides valuable information on genetic carrier status, it cannot offer 100% certainty. The following considerations should be taken into account when interpreting the results.

2. General Considerations and Possible Sources of Uncertainty

The test result is valid assuming the sample belongs to the tested individual. CarrierTest is performed under strict laboratory quality standards; however, as with any medical test, a very rare possibility of sample mix-up or technical issue during collection, labeling, or processing can never be completely excluded.

3. Additional Information on Residual Risk

The CarrierTest is intended for healthy individuals who show no signs of a genetic disorder. The aim of the test is to reduce the risk of being a carrier, not to eliminate it entirely. The remaining (residual) risk of being a carrier after a negative CarrierTest result depends on the structure of the specific gene, the laboratory method used, and the carrier frequency in the European population, which may differ for individuals of other ethnic origins (see Table 2).
If a mutation is detected in one partner, the residual carrier risk of the other partner is used to calculate the risk of the offspring being affected.
The risk that both partners are carriers of a mutation in the same gene is very low after a negative CarrierTest result. For such a couple, the risk of having a child with an autosomal recessive disorder is therefore very low.
The risks of diseases arising from new mutations in germ cells or multigenic mutations may not be detected by this test.

4. Technical and Analytical Aspects

CarrierTest uses whole-exome sequencing (WES), which analyzes a virtual panel of the (primarily) coding regions of selected human DNA genes (refer to Table 2) with overlaps into introns up to 50 bp. This test is based on massive parallel sequencing technology using short reads (SBS sequencing, Illumina), which is primarily suitable for analyzing SNP and small InDel variants. The sequencing data for each sample is subject to quality control, which ensures that all evaluable samples will have a minimum of 55M paired-end reads (clusters) after the removal of optical and PCR duplicates. The technical parameters of this method do not guarantee 100% coverage of all target regions.

Detecting certain variants or gene parts may not be possible due to local sequence characteristics, high/low genomic complexity, or the presence of closely related pseudogenes. Variants in promoter or deep intronic regions (unless specified otherwise), repetitive expansions (trinucleotide, hexanucleotide, or other), structural variants like inversions and gene conversions, and low-level mosaic variants may not be detected by this technology.

Current research shows that for many genes, the pathogenic allele is not always caused by a single point mutation, but may be the result of the presence of multiple variants in the sequence of a single copy of the gene (in the cis position), in which case we refer to a complex allele. These individual variants do not significantly disrupt the function of the gene on their own, as they often occur at a high frequency in the population, but together they can disrupt the gene. The method used is not able to detect this rare situation where multiple variants occur in a single gene. A negative CarrierTest result or the finding of another pathogenic variant in a given gene therefore does not rule out the presence of a rare complex allele. This risk of false negative results applies to all tested genes. Pathogenic complex alleles have been described in genes such as *BTD*, *TYR, CFTR*, and others.

With the exception of specified genes or regions (see Table 1), CarrierTest does not analyze changes in the number of copies of genes or their parts (CNVs). The test is focused on germline mutations (mutations in germ cells). Somatic mutations are not examined. The test analyzes DNA and therefore does not investigate possible interactions between different genes or epigenetic factors.
For samples with lower quality (e.g., blood from patients with hematological disorders or highly degraded DNA), the quality of the NGS data may be reduced, which can lower the method's sensitivity for variant detection.

5. Variant Classification and Pathogenicity

CarrierTest is a screening method that only detects selected pathogenic variants of classes 4/5 (pathogenic/likely pathogenic). Variant pathogenicity is evaluated based on current scientific and clinical knowledge (ClinVar/ClinSign databases) and may change over time. Should the classification of a detected variant change, GNTlabs will inform about this fact and offer an updated interpretation. The test cannot rule out mutations in other (uncovered, unanalyzed, or unevaluated) genes. GNTlabs, at its own discretion and in line with its commitment to the highest quality results, verifies NGS findings usi complementary methods such as Sanger sequencing, long-range PCR, fragment analysis, or MLPA and StripAssay methods.

6. Conclusion

CarrierTest is a screening method used to reduce the risk of autosomal recessive hereditary diseases in offspring. If a disease caused by a disorder of one of the tested genes is suspected, this must be stated in the request form so that a targeted examination can be performed with an evaluation of all potentially pathogenic variants, including complex alleles. Despite meeting the highest scientific and analytical standards, a residual risk cannot be excluded.

7. Suggestion

The results of CarrierTest findings could be reviewed with a clinical geneticist, who may interpret the results for the patient and suggest possible treatment, monitoring, and preventive measures for the patient and their family.

Table 1: ***Notes on the analysis of selected genes***

Gene	Notes
AR	The current testing method does not evaluate CAG trinucleotide repeat expansions in this gene.
CFTR	Single exon deletion/duplication analysis is limited to deletions of previously reported exons: 1, 2, 3, 11, 19, 20, 21.
CYP21A2	The CarrierTest is only a screening method that detects common variants of the *CYP21A2* gene: c.293-13C>G; p.Arg357Trp and p.Val282Leu, which is associated with a milder phenotype. Due to the presence of a highly homologous pseudogene and gene rearrangements in the corresponding genomic region, this method does not detect the presence of a chimeric gene (occurs in 30% of patients), changes in the copy number of parts of *CYP21A2* or the entire gene, the frequent p.Ile173Asn mutation (11% of patients), and other pathogenic mutations of the *CYP21A2* gene.
DMD	Single exon deletion/duplication analysis is limited to regions repeatedly published in the UMD database (http://www.umd.be/DMD/W_DMD/).
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.
HBB	The test is optimized for the detection of small variants (SNVs and indels) in coding regions and adjacent intron-exon boundaries. Large deletions/duplications may not be reliably detected by this method due to high sequence homology and the presence of segmental duplications. For these types of variants, complementary testing using MLPA is recommended.
HFE	CarrierTest reports only the most common variant, p.Cys282Tyr.
SERPINA1	The carrier test focuses on the Glu366Lys mutation (PI*Z mutation) (rs28929474). Homozygotes for the Glu366Lys mutation (ZZ genotype) account for 95% of patients with AAT deficiency with a reduction in AAT production to 15% of normal values.
SMN1	The current testing method detects copy number variations in exons 8 of the *SMN1* gene (NM_022874.2). Sequencing and deletion/duplication analysis are not performed on any other regions in this gene. Approximately 5% to 8% of the population has two copies of *SMN1* on one chromosome and a deletion on the other, which is known as a [2+0] configuration (PubMed: 20301526). The current testing method cannot directly detect carriers with an *SMN1* [2+0] configuration.
TYR	Due to interference from highly homologous regions, our current testing method has reduced sensitivity for detecting variants in exons 4-5 of the *TYR* gene (NM_000372.5).

Table 2: ***List of genes analyzed within CarrierTest, associated diseases and residual risks***

Gene (RefSeq)	Disease/Syndrome	Ethnicity	Sensitivity	Carrier Rate	Residual Risk
ABCA3	ABCA3 Deficiency (ABCA3-related Pulmonary Surfactant Metabolism Dysfunction)	Caucasians	99%	1 in 100	1 in 10 000
		Finns	99%	1 in 500	1 in 50 000
		Ashkenazi	>95%	< 1 in 500	< 1 in 10 000
ABCC8	Congenital Hyperinsulinism (ABCC8-related)	Caucasians	99%	1 in 300	1 in 30 000
		Finns	99%	1 in 220	1 in 22 000
ABCD1	Adrenoleukodystrophy, X-linked	Ashkenazi	99%	1 in 75	1 in 7500
		General population (female)	99%	~1 in 20000	N/A
ACADM	Medium Chain Acyl-Coenzyme A Dehydrogenase (MCAD) Deficiency	Caucasians	99%	1 in 75	1 in 7 500
		Finns	99%	1 in 400	1 in 40 000
		Ashkenazi	99%	1 in 100	1 in 10 000
ACADS	Short Chain Acyl-CoA Dehydrogenase (SCAD) Deficiency	Caucasians	99%	1 in 110	1 in 11 000
		Finns	99%	<1 in 500	<1 in 50 000
		Ashkenazi	99%	1 in 20	1 in 2000
ACADVL	Very Long Chain Acyl-Coenzyme A Dehydrogenase (VLCAD) Deficiency	Caucasians	99%	1 in 120	1 in12 000
		Finns	99%	1 in 260	1 in 26 000
		Ashkenazi	99%	< 1 in 500	< 1 in 50 000
ACAT1	Beta-ketothiolase deficiency	General population	99%	<1 in 500	< 1 in 50 000
		Ashkenazi	97%	<1 in 500	<1 in 17 000
ADGRV1	Usher Syndrome Type 2C	Caucasians	98%	1 in 170	1 in 8 500
		Finns	98%	1 in 400	1 in 20 000
		Ashkenazi	98%	1 in 300	1 in 15 000
AGA	Aspartylglucosaminuria	General population	98%	< 1 in 500	1 in 25 000
		Finns	99%	1 in 36	1 in 3 500
AGL	Glycogen Storage Disease Type III	Caucasians	99%	1 in 160	1 in 16 000
		Finns	99%	<1 in 500	<1 in 50 000
		Ashkenazi	98%	<1 in 500	<1 in 25 000
AGXT	Primary Hyperoxaluria Type 1	Caucasians	97%	1 in 250	1 in 8 300
		Finns	99%	< 1 in 500	< 1 in 50 000
		Ashkenazi	99%	< 1 in 500	< 1 in 50 000
AHI1	Joubert Syndrome Type 3	Caucasians	99%	1 in 300	1 in 30 000
		Finns	99%	< 1 in 500	< 1 in 50 000
		Ashkenazi	99%	< 1 in 500	< 1 in 50 000
AIRE	Autoimmune Polyendocrinopathy with Candidiasis and Ectodermal Dysplasia	Caucasians	99%	1 in 150	1 in 15 000
		Finns	98%	1 in 90	1 in 4 500
		Ashkenazi	98%	<1 in 500	<1 in 25 000
ALDOB	Fructose Intolerance (Hereditary)	General population	99%	1 in 100	1 in 10 000

ALPL	Hypophosphatasia	Caucasians	99%	1 in 150	1 in 15 000
		Finns	99%	1 in 30	1 in 3 000
		Ashkenazi	99%	< 1 in 500	< 1 in 50 000
ANO10	Spinocerebellar Ataxia Type 10 (SCAR10)	General population	>95%	< 1 in 500	1 in 9981
ANXA5	N/A	General population	N/A	N/A	N/A
AR	Androgen Insensitivity Syndrome (X-linked)	General population (female)	70%	1 in 5000	N/A
ARSA	Metachromatic Leukodystrophy	General population	99%	1 in 100	1 in10 000
ASL	Argininosuccinic Acid Lyase Deficiency	General population	99%	1 in 130	1 in 13 000
ASPA	Canavan Disease	General population	99%	1 in 150	1 in 15 000
		Ashkenazi	99%	1 in 55	1 in 5 000
ASS1	Citrullinemia	General population	99%	1 in 120	1 in 12 000
ATM	Ataxia-Telangiectasia	General population	>95%	1 in 166	1 in 3301
ATP7B	Wilson Disease	General population	99%	1 in 90	1 in 9 000
		Finns	99%	1 in 200	1 in 20 000
		Ashkenazi	99%	1 in 67	1 in 6 700
BBS1	Bardet-Biedl Syndrome Type 1	Caucasians	99%	1 in 150	1 in 15 000
		Finns	99%	1 in 300	1 in 30 000
		Ashkenazi	99%	< 1 in 500	< 1 in 50 000
BBS2	Bardet-Biedl Syndrome Type 2	General population	99%	< 1 in 500	< 1 in 50 000
		Ashkenazi	99%	1 in 130	1 in 13 000
BCKDHB	Maple Syrup Urine Disease Type 1B	General population	99%	< 1 in 500	< 1 in 50 000
		Finns	99%	1 in 175	1 in 17 500
		Ashkenazi	99%	1 in 75	1 in 7 500
BLM	Bloom Syndrome	Caucasians	99%	1 in 330	1 in 33 000
		Finns	99%	< 1 in 500	< 1 in 50 000
		Ashkenazi	98%	1 in 100	1 in 5 000
BTD	Biotinidase Deficiency	General population	99%	1 in 120	1 in 12 000
CBS	Homocystinuria	Caucasians	99%	1 in 150	1 in 15 000
		Finns	99%	1 in 500	1 in 50 000
		Ashkenazi		1 in 330	1 in 33 000
CC2D2A	Joubert Syndrome Type 9	General population	98%	1 in 200	1 in 10 000
CCDC88C	Congenital hydrocephalus 1	Caucasians	98%	<1 in 500	< 1 in 25,000
CDH23	Hearing loss, retinis	Caucasians	99%	1 in 250	1 in 4981
		Finns	99%	< 1 in 500	< 1 in 50 000
		Ashkenazi	99%	< 1 in 500	< 1 in 50 000
CEP290	Joubert syndrome 5, Leber congenital amaurosis 10	General population	99%	1 in 166	1 in 16 000
CFTR	Cystic fibrosis	General population	98%	1 in 24	1 in 1 150
CLCN1	Congenital myotonia, autosomal recessive form	Caucasians	99%	1 in 140	1 in 14 000
		Finns	99%	1 in 25	1 in 2 500
		Ashkenazi	99%	1 in 130	1 in 13 000

CLRN1	Usher Syndrome Type 3A	Caucasians	98%	1 in 460	1 in 23 000
		Finns	99%	1 in 70	1 in 7 000
		Ashkenazi	99%	1 in 95	1 in 9 500
CNGB3	Achromatopsia (CNGB3-related)	Caucasians	97%	1 in 120	1 in 4 000
		Finns	97%	1 in 170	1 in 5 600
		Ashkenazi	99%	1 in 270	1 in 27 000
COL4A5	Alport Syndrome (X-linked)	General population (female)	99%	1 in 5000	N/A
COL7A1	Epidermolysis Bullosa (Recessive Dystrophic)	General population	99%	1 in 160	1 in 16 000
CPT2	Carnitine Palmitoyltransferase II Deficiency	Caucasians	99%	1 in 180	1 in 18 000
		Finns	99%	1 in 240	1 in 24 000
		Ashkenazi	99%	1 in 40	1 in 4000
CRB1	Leber Congenital Amaurosis (CRB1-related)	General population	99%	1 in 320	1 in 32 000
CTNS	Cystinosis	General population	98%	< 1 in 500	<1 in 25 000
CYP11A1	Congenital Lipoid Adrenal Hyperplasia	N/A	99%	< 1 in 500	< 1 in 50,000
CYP21A2	Congenital Adrenal Hyperplasia (CYP21A2-related)	Caucasians	88%	1 in 70	1 in 580
		Ashkenazi	90%	1 in 40	1 in 390
CYP27A1	Cerebrotendinous Xanthomatosis (CTX)	General population	99%	1 in 300	1 in 30 000
CYP27B1	Vitamin D Dependent Rickets Type 1A	General population	99%	< 1 in 500	<1 in 50 000
DHCR7	Smith-Lemli-Opitz Syndrome	Caucasians	99%	1 in 50	1 in 5 000
		Finns	99%	1 in 181	1 in 18 000
		Ashkenazi	99%	1 in 40	1 in 4 000
DHDDS	Retinitis Pigmentosa 59	General population	99%	< 1 in 500	<1 in 50 000
		Ashkenazi	99%	1 in 120	1 in 12 000
DLD	Dihydrolipoamide Dehydrogenase Deficiency	General population	99%	< 1 in 500	<1 in 50 000
		Ashkenazi	99%	1 in 60	1 in 6 000
DMD	Duchenne and Becker Muscular Dystrophy (X-linked)	General population (female)	90%	1 in 3000	1 in 30000
DNAJC30	Leber Hereditary Optic Neuropathy (DNAJC30-related)	General population	N/A	N/A	N/A
DYNC2H1	Short-rib Polydactyly Syndrome Type III	General population	99%	< 1 in 500	<1 in 50 000
ELP1	Familial Dysautonomia	General population	99%	< 1 in 500	<1 in 50 000
		Ashkenazi	99%	1 in 37	1 in 3 700
ERCC2	Xeroderma pigmentosum	Caucasians	99%	1 in 200	1 in 20 000
		Finns	99%	< 1 in 500	<1 in 50 000
		Ashkenazi	99%	1 in 100	1 in 10 000
EVC2	Ellis-van Creveld Syndrome	General population	99%	< 1 in 500	<1 in 50 000
F2	Prothrombin Thrombophilia (F2-related)	General population	99%	1 in 150	1 in 14900
F5	Factor V Leiden Thrombophilia (F5-related)	General population	N/A	N/A	N/A
F9	Factor IX deficiency (hemophilia B)	General population (female)	99%	~1 in 20000	N/A
FAH	Tyrosinemia Type I	General population	99%	1 in 200	1 in 3981
FANCA	Fanconi Anemia Type A	General population	99%	1 in 200	1 in 20 000

FANCC	Fanconi Anemia Type C	General population	98%	< 1 in 500	1 in 25 000
		Ashkenazi	99%	1 in 89	1 in 9 000
FKRP	Limb-Girdle Muscular Dystrophy Type 2I	General population	99%	1 in 250	1 in 25 000
FKTN	Walker-Warburg Syndrome (FKTN-related)	General population	98%	< 1 in 500	1 in 25 000
		Ashkenazi	97%	1 in 80	1 in 2 600
FMO3	Trimethylaminuria	General population	99%	1 in 204	1 in 20 000
G6PC	Glycogen Storage Disease Type 1A	General population	99%	1 in 150	1 in 15 000
		Ashkenazi	99%	1 in 70	1 in 7 000
GAA	Pompe Disease	General population	99%	1 in 100	1 in 10 000
GALT	Galactosemia	General population	99%	1 in 84	1 in 8 400
GBA	Gaucher Disease	General population	>95%	1 in 137	<1 in 2 700
		Ashkenazi	>95%	1 in 15	<1 in 280
GBE1	Glycogen Storage Disease Type IV	General population	99%	1 in 300	1 in 30 000
		Ashkenazi	99%	1 in 70	1 in 7 000
GCDH	Glutaric Acidemia Type 1	General population	99%	1 in 150	1 in 15 000
GJB2	Non-Syndromic Hearing Loss/Deafness (GJB2-related)	General population	99%	1 in 30	1 in 3 000
		Ashkenazi	99%	1 in 13	1 in 1 2100
GLA	Fabry Disease (X-linked)	General population (female)	99%	< 1 in 500	N/A
GLB1	GM1 Gangliosidosis	General population	99%	1 in 220	1 in 22 000
GLDC	Glycine Encephalopathy (Nonketotic Hyperglycinemia)	General population	99%	1 in 333	1 in 33 000
GNPTAB	Mucolipidosis Type II/III	General population	98%	1 in 250	1 in 12 500
GRIP1	Fraser syndrome	Caucasians	99%	< 1 in 500	< 1 in 50,000
HADHA	Long Chain 3-Hydroxyacyl-CoA Dehydrogenase (LCHAD) Deficiency	General population	99%	1 in 200	1 in 20 000
		Finns	99%	1 in 120	1 in 12000
HBB	Beta Thalassemia/Sickle Cell Disease	General population	99%	1 in 132	1 in 13 000
		Mediterranean	>95%	1 in 28	1 in 13 000
HEXA	Tay-Sachs Disease	General population	99%	1 in 200	1 in 20 000
		Ashkenazi	97%	1 in 30	1 in 581
HFE	Hemochromatosis (type I)	General population	100%	1 in 32	N/A
HPS1	Hermansky-Pudlak Syndrome Type 1	General population	98%	< 1 in 500	<1 in 25 000
HPS3	Hermansky-Pudlak Syndrome Type 3	General population	98%	< 1 in 500	1 in 25 000
		Ashkenazi	99%	1 in 250	1 in 25 000
HSD17B4	Peroxisomal Multifunctional Protein 2 Deficiency	General population	98%	< 1 in 500	1 in 25 000
CHRNE	Congenital Myasthenic Syndrome (CHRNE-related)	General population	>95%	< 1 in 500	<1 in 10 000
CHST6	Macular Corneal Dystrophy	General population	>95%	< 1 in 500	<1 in 10 000
IDUA	Mucopolysaccharidosis Type I (Hurler/Scheie Syndrome)	General population	99%	1 in 100	1 in 10 000
IL2RG	X-Linked Severe Combined Immunodeficiency (SCID)	General population (female)	99	1 in 25000	N/A
KERA	Cornea Plana 2	Finns	90%	1 in 122	1 in 1210
L1CAM	L1 Syndrome (X-linked)	General population (female)	>95%	N/A	N/A

LRP2	Donnai-Barrow Syndrome	Caucasians	98%	< 1 in 500	< 1 in 25,000
MCCC1	3-Methylcrotonyl-CoA Carboxylase 1 Deficiency	General population	99%	1 in120	1 in 12 000
MCCC2	3-Methylcrotonyl-CoA Carboxylase 2 Deficiency	General population	99%	1 in 120	1 in 12 000
MCOLN1	Mucolipidosis Type IV	General population	97%	<1 in 500	<1 in 16 500
		Ashkenazi	97%	1 in 96	1 in 3 200
MCPH1	Microcephaly (Primary)	Caucasians	99%	1 in 416	1 in 42,000
MEFV	Familial Mediterranean Fever	General population	99%	1 in 250	1 in 25 000
		Mediterranean	99%	1 in 10	1 in 1 000
		Ashkenazi	99%	1 in 10	1 in 1 000
MID1	Opitz G/BBB Syndrome (X-linked)	General population (female)	90%	N/A	N/A
MLC1	Megalencephalic Leukoencephalopathy with Subcortical Cysts	General population	99%	< 1 in 500	<1 in 50 000
		Ashkenazi	99%	1 in 200	1 in 20 000
MMACHC	Methylmalonic Acidemia and Homocystinuria (CblC type)	General population	98%	1 in 170	1 in 8 500
MMUT	Methylmalonic Acidemia (Mut-related)	General population	99%	1 in 330	1 in 33 000
MTM1	Myotubular Myopathy (X-linked)	General population (female)	99%	1 in 25000	N/A
MVK	Mevalonate Kinase Deficiency	General population	99%	1 in 250	1 in 25 000
MYO7A	Usher Syndrome Type 1B	General population	99%	1 in 147	1 in 14 700
NAGA	Alpha-N-Acetylgalactosaminidase Deficiency (Schindler Disease)	Caucasians	99%	1 in 115	1 in 11 500
		Finns	99%	1 in 350	1 in 35 000
		Ashkenazi	99%	< 1 in 500	<1 in 50 000
NBN	Nijmegen Breakage Syndrome	General population	99%	< 1 in 500	<1 in 50 000
		Easter Europeans	99%	1 in 120	1 in 12 000
NPC1	Niemann-Pick Disease Type C1	General population	99%	1 in 200	1 in 20 000
NPC2	Niemann-Pick Disease Type C2	General population	99%	< 1 in 500	<1 in 50 000
NPHS1	Congenital Nephrotic Syndrome (NPHS1-related)	General population	99%	1 in 300	1 in 30 000
		Finns	97%	1 in 38	1 in 1234
		Ashkenazi	99%	< 1 in 500	<1 in 50 000
OCA2	Oculocutaneous Albinism Type 2	General population	>95%	< 1 in 500	1 in 9981
OTC	Ornithine Transcarbamylase (OTC) Deficiency (X-linked)	General population (female)	99%	1 in 20000	N/A
PAH	Phenylketonuria (PKU)	Caucasians	99%	1 in 40	1 in 981
		Finns	99%	1 in 170	1 in 17 000
		Ashkenazi	99%	1 in 17	1 in 1 700
PCDH15	Usher Syndrome Type 1F	General population	98%	1 in 400	1 in 20 000
		Ashkenazi	99%	1 in 116	1 in 11 600
PEX1	Zellweger Syndrome Spectrum (PEX1-related)	General population	98%	1 in 200	1 in 10 000
PEX10	Zellweger Syndrome Spectrum (PEX10-related)	General population	98%	< 1 in 500	<1 in 25 000

PEX12	Zellweger Syndrome Spectrum (PEX12-related)	General population	98%	< 1 in 500	<1 in 25 000
PEX13	Zellweger Syndrome Spectrum (PEX13-related)	General population	98%	< 1 in 500	<1 in 25 000
PEX14	Zellweger Syndrome Spectrum (PEX14-related)	General population	98%	< 1 in 500	<1 in 25 000
PEX16	Zellweger Syndrome Spectrum (PEX16-related)	General population	99%	< 1 in 500	<1 in 50 000
PEX2	Zellweger Syndrome Spectrum (PEX2-related)	General population	99%	< 1 in 500	<1 in 50 000
PEX6	Zellweger Syndrome Spectrum (PEX6-related)	General population	>95%	< 1 in 500	1 in 10 000
PEX7	Zellweger Syndrome Spectrum (PEX7-related)	General population	>95%	< 1 in 500	1 in 10 000
PKHD1	Autosomal Recessive Polycystic Kidney Disease (ARPKD)	General population	99%	1 in 70	1 in 7 000
		Finns	99%	1 in 38	1 in 3 700
PLA2G6	Neurodegeneration with Brain Iron Accumulation (PLA2G6-related)	General population	>95%	< 1 in 500	<1 in 10 000
PMM2	Congenital Disorder of Glycosylation Type Ia (CDG-Ia)	General population	99%	1 in 60	1 in 6 000
POLG	Progressive External Ophthalmoplegia (POLG-related)	General population	>95%	1 in 200	1 in 4 000
PRF1	Hemophagocytic Lymphohistiocytosis Type 2	General population	98%	< 1 in 500	<1 in 25 000
RARS2	Pontocerebellar hypoplasia	Caucasians	98%	1 in 364	1 in 18,000
RNASEH2B	Aicardi-Goutieres Syndrome (RNASEH2B-related)	Caucasians	99%	1 in 195	1 in 19,000
RS1	Retinoschisis (X-linked)	General population (female)	>95%	< 1 in 500	1 in 9981
SCO2	Cytochrome c Oxidase Deficiency (SCO2-related)	Caucasians	98%	< 1 in 500	< 1 in 25,000
SERPINA1	Alpha-1 Antitrypsin Deficiency	General population	100%	1 in 32	N/A
SGSH	Mucopolysaccharidosis Type IIIA (Sanfilippo A)	General population	99%	1 in 230	1 in23 000
SLC19A3	Biotin-Responsive Basal Ganglia Disease	General population	99%	< 1 in 500	<1 in 50 000
SLC26A2	Diastrophic Dysplasia	General population	99%	1 in 140	1 in 14 000
		Finns	99%	1 in 75	1 in 7 500
SLC26A4	Pendred Syndrome/Non-Syndromic Deafness (DFNB4)	General population	99%	1 in 75	1 in 7 500
SLC37A4	Glycogen Storage Disease Type Ib	General population	99%	< 1 in 500	<1 in 50 000
SLC4A11	Congenital Hereditary Endothelial Dystrophy (CHED)	General population	99%	< 1 in 500	<1 in 50 000
SLC6A8	Cerebral creatine deficiency syndromes	General population (female)	99%	~1 in 5000	N/A
SMN1/SMN2	Spinal Muscular Atrophy (SMA)	General population	100%	1 in 40	N/A
SMPD1	Niemann-Pick Disease Type A/B	General population	99%	< 1 in 500	<1 in 50 000
		Ashkenazi	99%	1 in 80	1 in 8 000
TF	Atransferrinemia	Caucasians	98%	< 1 in 500	< 1 in 25,000

TGM1	Congenital Ichthyosis (TGM1-related)	General population	99%	1 in 300	1 in 30 000
TMEM216	Joubert Syndrome Type 2	General population	99%	< 1 in 500	<1 in 50 000
		Ashkenazi	99%	1 in 110	1 in 11 000
TPP1	Neuronal Ceroid Lipofuscinosis Type 2 (CLN2)	General population	99%	1 in 180	1 in 18 000
TYR	Oculocutaneous Albinism Type 1	General population	99%	1 in 200	1 in 20 000
		Ashkenazi	99%	1 in 21	1 in 2 100
UNC13D	Hemophagocytic Lymphohistiocytosis Type 3	Caucasians	98%	1 in 293	1 in 15,000
USH1C	Usher Syndrome Type 1C	General population	98%	< 1 in 500	<1 in 25 000
		Ashkenazi	97%	1 in 235	1 in 7 800
USH2A	Usher Syndrome Type 2A	General population	99%	1 in 55	1 in 5 500
XPC	Xeroderma Pigmentosum Group C	General population	98%	< 1 in 500	<1 in 25 000