INVITAE

INVITAE CARRIER SCREEN RESULTS

Patient name:	[redacted]	**Sample type:**	Blood	**Report date:**	22-AUG-2022
DOB:	[redacted]	**Sample collection date:**	04-AUG-2022	**Invitae #:**	[redacted]
Sex assigned at birth:	Male	**Sample accession date:**	11-AUG-2022	**Clinical team:**	Valerie Shaikly
Gender:	Man				
Patient ID (MRN):	BFA0153				

Reason for testing

Gamete donor

Test performed

Invitae Carrier Screen

- Invitae primary panel (CF, SMA)
- Add-on genes

RESULT: POSITIVE

This carrier test evaluated 175 gene(s) for genetic changes (variants) that are associated with an increased risk of having a child with a genetic condition. Knowledge of carrier status for one of these conditions may provide information that can be used to assist with family planning and/or preparation. Carrier screening is not intended for diagnostic purposes. To identify a potential genetic basis for a condition in the individual being tested, diagnostic testing for the gene(s) of interest is recommended.

This test shows the presence of clinically significant genetic change(s) in this individual in the gene(s) indicated below. No other clinically significant changes were identified in the remaining genes evaluated with this test.

RESULTS	GENE	VARIANT(S)	INHERITANCE	PARTNER TESTING RECOMMENDED
Carrier: CFTR-related conditions	CFTR	c.1210-34TG[12]T[5] (Intronic)	Autosomal recessive	Yes
Carrier: Isovaleric acidemia	IVD	c.157C>T (p.Arg53Cys)	Autosomal recessive	Yes

Next steps

- See the table above for recommendations regarding testing of this individual's reproductive partner.
- Even for genes that have a negative test result, there is always a small risk that an individual could still be a carrier. This is called “residual risk.” See the table below for residual risks, which presumes a negative family history of the conditions listed.
- Discussion with a physician and/or genetic counselor is recommended to further review the implications of this test result and to understand these results in the context of any family history of a genetic condition.
- All patients, regardless of result, may wish to consider additional screening for hemoglobinopathies by complete blood count (CBC) and hemoglobin electrophoresis, if this has not already been completed.
- Individuals can register their tests at **https://www.invitae.com/patients/** to access online results, educational resources, and next steps.

Laboratory Director: Neng Chen, PhD, FACMG, NYCQ, CGMB
Invitae 1400 16th Street, San Francisco, CA 94103 · clientservices@invitae.com · 800.436.3037

Clinical summary

RESULT: CARRIER

CFTR-related conditions

A single Pathogenic variant, c.1210-34TG[12]T[5] (Intronic), was identified in CFTR. This variant has unique interpretation considerations. See "What are CFTR-related conditions?" and Variant details for additional information.

What are CFTR-related conditions?

The c.1210-34TG[12]T[5] cystic fibrosis (CF) variant was identified in this individual. There are multiple forms of the 5T variant, which are classified by the number of TG repeats. Each form of the 5T variant is associated with a different degree of risk for CFTR-related symptoms when inherited in combination with a pathogenic variant from the other parent, ranging from a healthy individual to congenital absence of the vas deferens (CAVD) in males to an individual with mild/atypical CF. The combination of the c.1210-34TG[12]T[5] variant with a severe pathogenic CFTR variant from the other parent is associated with symptoms in the majority of individuals; however, most individuals who are homozygous for the c.1210-34TG[12]T[5] variant are asymptomatic (see Variant details section).

R117H is another change which can occur within CFTR as part of a complex allele with a 5T variant. If present, the R117H variant would be reported as a Result to Note.

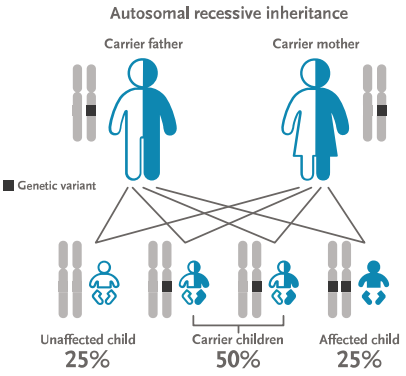
CFTR-related conditions encompass a spectrum of disorders that typically impact the respiratory and/or digestive systems, and cause male infertility. Cystic fibrosis (CF) is typically a childhood-onset disease in which abnormally thick mucus production can cause a variety of symptoms including recurrent respiratory infections and progressive lung disease, as well as nutritional deficiencies and poor growth due to deficiency of enzymes produced by the pancreas to digest food (pancreatic insufficiency). Symptoms range from mild to severe. Prognosis depends on the severity of symptoms as well as response to treatments; many affected individuals live well into adulthood. Milder forms of CFTR-related conditions include CAVD associated with male infertility, variable respiratory manifestations, and hereditary pancreatitis. Life span is not typically impacted with less severe CFTR-related conditions. Intellect is not affected with the various CFTR-related conditions. The combination of variants identified in an affected individual impacts the observed clinical features and severity of the symptoms. Additional genetic and environmental factors are believed to play a role in determining the risk of developing these complex CFTR-related conditions.

Additionally, individuals with a single disease-causing CFTR variant (heterozygous carriers) may have an approximately 4-10 fold increased risk for chronic pancreatitis, although the absolute risk of pancreatitis remains low (less than 1 in 100). Hereditary pancreatitis is characterized by recurrent episodes of acute inflammation of the pancreas (pancreatitis) beginning in childhood or adolescence, leading to chronic pancreatitis. Chronic pancreatitis is a risk factor for pancreatic cancer. Due to this potential increased risk for chronic pancreatitis, heterozygous carriers may consider follow-up with a medical provider.

Follow-up depends on each affected individual's specific situation, and discussion with a healthcare provider should be considered.

Next steps

Carrier testing for the reproductive partner is recommended.



If your partner tests positive:

In autosomal recessive inheritance, an individual must have disease-causing genetic changes in each copy of the CFTR gene to be affected. Carriers, who have a disease-causing genetic change in only one copy of the gene, typically do not have symptoms. When both reproductive partners are carriers of an autosomal recessive condition, there is a 25% chance for each child to have the condition.

If your partner tests negative:

A negative carrier test result reduces, but does not eliminate, the chance that a person may be a carrier. The risk that a person could still be a carrier, even after a negative test result, is called a residual risk. See the table below for your partner's hypothetical residual risk after testing negative for CFTR-related conditions. These values are provided only as a guide, are based on the detection rate for the condition as tested at Invitae, and assume a negative family history, the absence of symptoms, and vary based on the ethnic background of an individual. For genes associated with both dominant and recessive inheritance, the numbers provided apply to the recessive condition(s) associated with the gene.

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
CFTR-related conditions (AR) NM_000492.3	CFTR	African-American - classic CF	1 in 61	1 in 6000
		Ashkenazi Jewish - classic CF	1 in 29	1 in 2800
		Asian - classic CF	1 in 88	1 in 8700
		Caucasian - classic CF	1 in 28	1 in 2700
		Pan-ethnic - classic CF	1 in 45	1 in 4400
		Pan-ethnic - classic CF and CFTR-related disorders	1 in 9	1 in 800

RESULT: CARRIER

Isovaleric acidemia

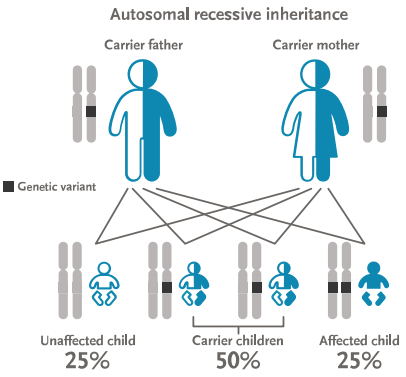
A single Pathogenic variant, c.157C>T (p.Arg53Cys), was identified in IVD.

What is isovaleric acidemia?

Isovaleric acidemia is condition in which the body cannot break down the amino acid, leucine. This causes a build up of leucine and other substances in the body, which affects multiple body systems. There are two main forms of isovaleric acidemia: acute neonatal and a chronic form. In the neonatal form, infants develop poor feeding, vomiting, lethargy, and seizures, which can progress to coma and death if left untreated. Those surviving the first episode generally have developmental delay. In the chronic form, individuals often present with poor growth (failure to thrive) and developmental delay, and intermittent worsening of symptoms often triggered by fasting or concurrent illness (decompensation). Affected individuals may have a characteristic "sweaty feet" body odor during an acute illness. Some affected individuals may never experience any overt signs or symptoms (asymptomatic). Prognosis depends on acute or chronic presentation and the severity of symptoms. Treatment may help prevent or reduce the severity of symptoms. Follow-up depends on each affected individual's specific situation, and discussion with a healthcare provider should be considered.

Next steps

Carrier testing for the reproductive partner is recommended.



If your partner tests positive:

In autosomal recessive inheritance, an individual must have disease-causing genetic changes in each copy of the IVD gene to be affected. Carriers, who have a disease-causing genetic change in only one copy of the gene, typically do not have symptoms. When both reproductive partners are carriers of an autosomal recessive condition, there is a 25% chance for each child to have the condition.

If your partner tests negative:

A negative carrier test result reduces, but does not eliminate, the chance that a person may be a carrier. The risk that a person could still be a carrier, even after a negative test result, is called a residual risk. See the table below for your partner's hypothetical residual risk after testing negative for isovaleric acidemia. These values are provided only as a guide, are based on the detection rate for the condition as tested at Invitae, and assume a negative family history, the absence of symptoms, and vary based on the ethnic background of an individual. For genes associated with both dominant and recessive inheritance, the numbers provided apply to the recessive condition(s) associated with the gene.

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
Isovaleric acidemia (AR) NM_002225.3	IVD	Pan-ethnic	1 in 250	1 in 24900

Results to note

FMR1

- Normal triplet repeats observed: 30

  CGG repeat ranges: normal (<45 CGG repeats), intermediate (45-54 CGG repeats), premutation (55-200 CGG repeats), full mutation (>200 CGG repeats).

SMN1

- Negative result. SMN1: 2 copies; c.*3+80T>G not detected.

Pseudodeficiency allele(s)

- Benign changes, c.1685T>C (p.Ile562Thr), known to be pseudodeficiency alleles, identified in the GALC gene. Pseudodeficiency alleles are not known to be associated with disease, including Krabbe disease.
- The presence of a pseudodeficiency allele does not impact this individual's risk to be a carrier. Individuals with pseudodeficiency alleles may exhibit false positive results on related biochemical tests, including newborn screening. However, pseudodeficiency alleles are not known to cause disease, even when there are two copies of the variant (homozygous) or when in combination with another disease-causing variant (compound heterozygous). Carrier testing for the reproductive partner is not indicated based on this result.

Variant details

CFTR, Intron 9, c.1210-34TG[12]T[5] (Intronic), heterozygous, PATHOGENIC

- This sequence change, also referred to as 5T;TG12 or TG12-5T in the literature, consists of 12 TG and 5 T sequence repeats on the same chromosome, and is located in intron 9 of the CFTR gene. It does not directly change the encoded amino acid sequence of the CFTR protein.
- The frequency data for this variant in the population databases is considered unreliable, as metrics indicate poor data quality at this position in the gnomAD database.
- The TG[12]T[5] allele has been observed in males with congenital bilateral absence of the vas deferens (CBAVD) and in both males and females with cystic fibrosis (CF) when present on the opposite chromosome (in trans) from a severe pathogenic CFTR variant (PMID: 14685937). When this allele is observed in trans with a severe pathogenic CFTR variant, the penetrance of CFTR-related conditions (CBAVD and/or non-classic CF) is expected to be high (>90%); however, the penetrance of classic CF is low (<20%) (PMID: 14685937, 27447098). Individuals who are homozygous for this variant, or who have this variant in combination with TG[11]T[5], are likely to be asymptomatic (PMID: 34196078).
- Algorithms developed to predict the effect of variants on protein structure and function are not available or were not evaluated for this variant.
- Experimental studies demonstrate that the 5T allele leads to exclusion of exon 10 (referred to as exon 9 in some publications) from the mRNA, which ultimately results in a non-functional CFTR protein (PMID: 7691356, 7684641, 10556281, 14685937, 21658649). Importantly, the number of TG repeats (11, 12 or 13) modifies the extent of exon 10 skipping when in cis with the 5T allele (PMID: 14685937, 10556281, 9435322). In a mini-gene assay, the percentage of CFTR mRNA without exon 10 was 54% for TG[11]T[5], 72% for TG[12]T[5] and 100% for TG[13]T[5] (PMID: 10556281).
- Algorithms developed to predict the effect of sequence changes on RNA splicing suggest that this variant is not likely to affect RNA splicing.
- For these reasons, this variant has been classified as Pathogenic.

IVD, Exon 2, c.157C>T (p.Arg53Cys), heterozygous, PATHOGENIC

- This sequence change replaces arginine, which is basic and polar, with cysteine, which is neutral and slightly polar, at codon 53 of the IVD protein (p.Arg53Cys). RNA analysis indicates that this missense change induces altered splicing and likely results in a shortened protein product.
- This variant is present in population databases (rs34695403, gnomAD 0.003%).

- This missense change has been observed in individuals with isovaleric acidemia (PMID: 10677295, 31442447; Invitae).
- This variant is also known as 148C>T (Arg21Cys).
- ClinVar contains an entry for this variant (Variation ID: 3567).
- Algorithms developed to predict the effect of missense changes on protein structure and function (SIFT, PolyPhen-2, Align-GVGD) all suggest that this variant is likely to be disruptive.
- Studies have shown that this missense change results in skipping of exon 2, but is expected to preserve the integrity of the reading-frame (PMID: 2063866, 10677295).
- For these reasons, this variant has been classified as Pathogenic.

Residual risk

This table displays residual risks after a negative result for each of the genes and corresponding disorders. The values provided assume a negative family history and the absence of symptoms for each disorder. For genes associated with both dominant and recessive inheritance, the numbers in this table apply to the recessive condition(s) associated with the gene, unless otherwise noted. Residual risk values are provided for disorders when carrier frequency is greater than 1 in 500. For disorders with carrier frequency equal to, or less than, 1 in 500, residual risk is considered to be reduced substantially. When provided, residual risk values are inferred from published carrier frequencies, and estimated detection rates are based on testing technologies used at Invitae. Residual risks are provided only as a guide for assessing approximate risk given a negative result; values will vary based on the ethnic background of an individual. For individuals of mixed ethnicity, it is recommended to use the highest residual risk estimate. For any genes marked with an asterisk*, refer to the Limitations section below for detailed coverage information. In the case of a sample-specific limitation, "N/A" indicates that a residual risk value could not be calculated. AR = autosomal recessive, XL = X-linked, AD = autosomal dominant.

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
3-hydroxy-3-methylglutaryl-CoA lyase deficiency (AR) NM_000191.2	HMGCL	Pan-ethnic	≤1 in 500	Reduced
		Portuguese	1 in 160	1 in 15900
ABCC8-related conditions (AR) NM_000352.4 When the mother is a noncarrier, but the father is a carrier, there is a residual risk for focal disease (1 in 540 for the Ashkenazi Jewish population; undetermined in other ethnic groups)	ABCC8	Ashkenazi Jewish	1 in 52	1 in 5100
		Finnish	1 in 100	1 in 9900
		Pan-ethnic	1 in 177	1 in 17600
Adenosine deaminase deficiency (AR) NM_000022.2	ADA	Pan-ethnic	1 in 224	1 in 2788
Alpha-mannosidosis (AR) NM_000528.3	MAN2B1	Pan-ethnic	1 in 354	1 in 35300
Alpha-thalassemia (AR) NM_000558.4, NM_000517.4	HBA1/ HBA2 *	African-American	1 in 30	1 in 291
		Asian	1 in 20	1 in 191
		Caucasian	≤1 in 500	Reduced
		Pan-ethnic	1 in 25	1 in 241
Alport syndrome (COL4A3-related) (AR) NM_000091.4	COL4A3	Ashkenazi Jewish	1 in 192	1 in 19100
		Caucasian	1 in 284	1 in 28300
		Pan-ethnic	1 in 354	1 in 35300
Alport syndrome (COL4A4-related) (AR) NM_000092.4	COL4A4	Pan-ethnic	1 in 353	1 in 35200
Alport syndrome (COL4A5-related) (XL) NM_000495.4	COL4A5 *	Pan-ethnic	≤1 in 500	Reduced
Alström syndrome (AR) NM_015120.4	ALMS1	Pan-ethnic	≤1 in 500	Reduced
Arginase deficiency (AR) NM_000045.3	ARG1	Pan-ethnic	1 in 274	1 in 27300
Argininosuccinate lyase deficiency (AR) NM_000048.3	ASL	Pan-ethnic	1 in 133	1 in 1321
Aspartylglucosaminuria (AR) NM_000027.3	AGA	Finnish	1 in 69	1 in 6800
		Pan-ethnic	≤1 in 500	Reduced
Ataxia with vitamin E deficiency (AR) NM_000370.3	TTPA	Italian	1 in 274	1 in 2731
		Pan-ethnic	≤1 in 500	Reduced
ATM-related conditions (AR) NM_000051.3	ATM	Pan-ethnic	1 in 100	1 in 9900
		Sephardic Jewish	1 in 69	1 in 6800
ATP7A-related conditions (XL) NM_000052.6	ATP7A	Pan-ethnic	≤1 in 500	Reduced
Autoimmune polyendocrinopathy with candidiasis and ectodermal dysplasia (AR) NM_000383.3	AIRE	Finnish	1 in 79	1 in 7800
		Pan-ethnic	1 in 150	1 in 14900
		Sardinian	1 in 60	1 in 5900
		Sephardic Jewish (Iranian)	1 in 48	1 in 4700
Autosomal recessive congenital ichthyosis (TGM1-related) (AR) NM_000359.2	TGM1	Norwegian	1 in 151	1 in 3000
		Pan-ethnic	1 in 224	1 in 4460

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
Autosomal recessive spastic ataxia of Charlevoix-Saguenay (AR) NM_014363.5	SACS	French Canadian (Saguenay-Lac-St-Jean)	1 in 21	1 in 2000
		Pan-ethnic	≤1 in 500	Reduced
Bardet-Biedl syndrome (BBS10-related) (AR) NM_024685.3	BBS10	Pan-ethnic	1 in 354	1 in 35300
Bardet-Biedl syndrome (BBS12-related) (AR) NM_152618.2	BBS12	Pan-ethnic	1 in 708	Reduced
BBS1-related conditions (AR) NM_024649.4	BBS1	Faroese	1 in 30	1 in 2900
		Pan-ethnic	1 in 330	1 in 32900
BBS2-related conditions (AR) NM_031885.3	BBS2	Ashkenazi Jewish	1 in 140	1 in 13900
		Pan-ethnic	1 in 560	Reduced
BCS1L-related conditions (AR) NM_004328.4	BCS1L	Caucasian	1 in 407	1 in 40600
		Finnish	1 in 108	1 in 10700
		Pan-ethnic	≤1 in 500	Reduced
Biopterin-deficient hyperphenylalaninemia (PTS-related) (AR) NM_000317.2	PTS	Chinese	1 in 122	1 in 12100
		Pan-ethnic	1 in 433	1 in 43200
Biotinidase deficiency (AR) NM_000060.3	BTD	Pan-ethnic	1 in 125	1 in 12400
Bloom syndrome (AR) NM_000057.3	BLM	Ashkenazi Jewish	1 in 100	1 in 9900
		Pan-ethnic	≤1 in 500	Reduced
Canavan disease (AR) NM_000049.2	ASPA	Ashkenazi Jewish	1 in 57	1 in 5600
		Pan-ethnic	1 in 159	1 in 15800
Carbamoyl phosphate synthetase I deficiency (AR) NM_001875.4	CPS1	Pan-ethnic	≤1 in 500	Reduced
Carnitine palmitoyltransferase I deficiency (AR) NM_001876.3	CPT1A	Hutterite	1 in 16	1 in 1500
		Pan-ethnic	≤1 in 500	Reduced
Carnitine palmitoyltransferase II deficiency (AR) NM_000098.2	CPT2	Ashkenazi Jewish	1 in 45	1 in 4400
		Pan-ethnic	1 in 182	1 in 18100
Cartilage-hair hypoplasia-anauxetic dysplasia spectrum disorders (AR) NR_003051.3	RMRP	Amish	1 in 10	1 in 900
		Finnish	1 in 76	1 in 7500
		Pan-ethnic	≤1 in 500	Reduced
Cerebrotendinous xanthomatosis (AR) NM_000784.3	CYP27A1	Pan-ethnic	1 in 112	1 in 5550
		Sephardic Jewish	1 in 76	1 in 3750
Citrullinemia type 1 (AR) NM_000050.4	ASS1	Pan-ethnic	1 in 120	1 in 2975
CLN3-related conditions (AR) NM_001042432.1	CLN3	Pan-ethnic	1 in 230	1 in 22900
CLRN1-related conditions (AR) NM_174878.2	CLRN1	Ashkenazi Jewish	1 in 120	1 in 11900
		Pan-ethnic	1 in 533	Reduced
Cobalamin C deficiency (AR) NM_015506.2	MMACHC	Pan-ethnic	1 in 123	1 in 12200
Cockayne syndrome A (AR) NM_000082.3	ERCC8	Pan-ethnic	1 in 514	Reduced
Cockayne syndrome B (AR) NM_000124.3	ERCC6	Pan-ethnic	1 in 377	1 in 37600
Cohen syndrome (AR) NM_017890.4	VPS13B	Amish (Ohio)	1 in 12	1 in 1100
		Pan-ethnic	≤1 in 500	Reduced
Combined pituitary hormone deficiency (PROP1-related) (AR) NM_006261.4	PROP1	Pan-ethnic	1 in 45	1 in 2200
Congenital adrenal hyperplasia due to 21-hydroxylase deficiency (AR) NM_000500.7	CYP21A2 *	Pan-ethnic	1 in 61	1 in 751
Congenital disorder of glycosylation type Ia (AR) NM_000303.2	PMM2	Ashkenazi Jewish	1 in 61	1 in 6000
		Caucasian	1 in 60	1 in 5900
		Pan-ethnic	1 in 190	1 in 18900
Congenital disorder of glycosylation type Ib (AR) NM_002435.2	MPI	Pan-ethnic	≤1 in 500	Reduced

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
Congenital disorder of glycosylation type Ic (AR) NM_013339.3	ALG6 *	Pan-ethnic	≤1 in 500	Reduced
Congenital nephrotic syndrome type 1 (AR) NM_004646.3	NPHS1	Finnish	1 in 46	1 in 4500
		Old Order Mennonite	1 in 12	1 in 1100
		Pan-ethnic	≤1 in 500	Reduced
Congenital nephrotic syndrome type 2 (AR) NM_014625.3	NPHS2	Pan-ethnic	≤1 in 500	Reduced
CYP11B1-related conditions (AR) NM_000497.3	CYP11B1	Pan-ethnic	1 in 194	1 in 19300
		Sephardic Jewish (Moroccan)	1 in 40	1 in 3900
Cystinosis (AR) NM_004937.2	CTNS	French Canadian (Saguenay-Lac-St-Jean)	1 in 39	1 in 3800
		Pan-ethnic	1 in 158	1 in 15700
		Sephardic Jewish (Moroccan)	1 in 100	1 in 9900
Dihydrolipoamide dehydrogenase deficiency (AR) NM_000108.4	DLD	Ashkenazi Jewish	1 in 107	1 in 5300
		Pan-ethnic	≤1 in 500	Reduced
DMD-related conditions (XL) NM_004006.2	DMD	Pan-ethnic	1 in 667	Reduced
DYSF-related conditions (AR) NM_003494.3	DYSF	Pan-ethnic	1 in 311	1 in 31000
		Sephardic Jewish (Libyan)	1 in 10	1 in 900
Dyskeratosis congenita spectrum disorders (RTEL1-related) (AR) NM_001283009.1	RTEL1	Ashkenazi Jewish	1 in 222	1 in 22100
		Pan-ethnic	≤1 in 500	Reduced
Ellis-van Creveld syndrome (EVC-related) (AR) NM_153717.2	EVC	Amish	1 in 8	1 in 700
		Pan-ethnic	1 in 220	1 in 21900
EVC2-related conditions (AR) NM_147127.4	EVC2	Pan-ethnic	1 in 199	1 in 19800
Fabry disease (XL) NM_000169.2	GLA	Pan-ethnic	≤1 in 500	Reduced
Familial dysautonomia (AR) NM_003640.3	ELP1	Ashkenazi Jewish	1 in 36	1 in 3500
		Pan-ethnic	≤1 in 500	Reduced
Familial Mediterranean fever (AR) NM_000243.2	MEFV	Armenian	1 in 8	1 in 71
		Ashkenazi Jewish	1 in 13	1 in 121
		Pan-ethnic	1 in 64	1 in 631
		Sephardic Jewish	1 in 14	1 in 131
		Turkish	1 in 8	1 in 71
Fanconi anemia type A (AR) NM_000135.2	FANCA	Afrikaner	1 in 83	1 in 8200
		Pan-ethnic	1 in 345	1 in 34400
		Sephardic Jewish	1 in 133	1 in 13200
		Spanish Roma	1 in 64	1 in 6300
Fanconi anemia type C (AR) NM_000136.2	FANCC	Ashkenazi Jewish	1 in 89	1 in 8800
		Pan-ethnic	1 in 417	1 in 41600
FMR1-related conditions including fragile X syndrome (XL) NM_002024.5	FMR1 *	Ashkenazi Jewish	1 in 58	1 in 5700
		Asian	≤1 in 500	Reduced
		Caucasian	1 in 187	1 in 18600
		Hispanic	≤1 in 500	Reduced
		Pan-ethnic	1 in 259	1 in 25800
Galactokinase deficiency galactosemia (AR) NM_000154.1	GALK1	Pan-ethnic	1 in 122	1 in 12100
		Roma	1 in 47	1 in 4600
Galactosemia (GALT-related) (AR) NM_000155.3	GALT	African-American	1 in 87	1 in 8600
		Ashkenazi Jewish	1 in 156	1 in 15500
		Irish Traveller	1 in 11	1 in 1000
		Pan-ethnic	1 in 100	1 in 9900
GBA-related conditions including Gaucher disease (AR) NM_001005741.2	GBA *	Ashkenazi Jewish	1 in 15	1 in 234
		Pan-ethnic	1 in 158	1 in 561
GJB2-related conditions (AR) NM_004004.5	GJB2	Ashkenazi Jewish	1 in 13	1 in 1200
		Pan-ethnic	1 in 50	1 in 4900
		Thai	1 in 9	1 in 800

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
GLB1-related conditions (AR) NM_000404.2	GLB1	Pan-ethnic	1 in 158	1 in 15700
		Roma	1 in 50	1 in 4900
		South Brazilian	1 in 58	1 in 5700
Glutaric acidemia type I (AR) NM_000159.3	GCDH	Amish	1 in 9	1 in 800
		Oji-Cree First Nations	1 in 9	1 in 800
		Pan-ethnic	1 in 87	1 in 8600
Glycine encephalopathy (AMT-related) (AR) NM_000481.3	AMT	Finnish	1 in 142	1 in 14100
		Pan-ethnic	1 in 325	1 in 32400
Glycine encephalopathy (GLDC-related) (AR) NM_000170.2	GLDC	Caucasian	1 in 141	1 in 14000
		Pan-ethnic	1 in 165	1 in 16400
Glycogen storage disease type Ia (AR) NM_000151.3	G6PC	Ashkenazi Jewish	1 in 71	1 in 1400
		Pan-ethnic	1 in 177	1 in 3520
Glycogen storage disease type II (Pompe disease) (AR) NM_000152.3	GAA	African-American	1 in 60	1 in 5900
		Ashkenazi Jewish	1 in 58	1 in 5700
		Asian	1 in 112	1 in 11100
		Pan-ethnic	1 in 100	1 in 9900
Glycogen storage disease type III (AR) NM_000642.2	AGL	Faroese	1 in 28	1 in 540
		Pan-ethnic	1 in 159	1 in 3160
		Sephardic Jewish (Moroccan)	1 in 34	1 in 660
GNE-related conditions (AR) NM_001128227.2	GNE	Pan-ethnic	1 in 179	1 in 17800
		Sephardic Jewish (Iranian)	1 in 10	1 in 900
GNPTAB-related conditions (AR) NM_024312.4	GNPTAB	Irish Traveller	1 in 15	1 in 1400
		Pan-ethnic	1 in 200	1 in 19900
HADHA-related conditions (AR) NM_000182.4	HADHA	Caucasian	1 in 250	1 in 24900
		Finnish	1 in 125	1 in 12400
		Pan-ethnic	1 in 350	1 in 34900
HBB-related hemoglobinopathies (AR) NM_000518.4	HBB	African-American	1 in 8	1 in 700
		Asian	1 in 54	1 in 5300
		Caucasian	1 in 373	1 in 37200
		Hispanic	1 in 17	1 in 1600
		Mediterranean	1 in 28	1 in 2700
		Pan-ethnic	1 in 49	1 in 4800
Hereditary fructose intolerance (AR) NM_000035.3	ALDOB	African-American	1 in 226	1 in 22500
		Middle Eastern	1 in 97	1 in 9600
		Pan-ethnic	1 in 122	1 in 12100
HGSNAT-related conditions (AR) NM_152419.2	HGSNAT	Pan-ethnic	≤1 in 500	Reduced
Holocarboxylase synthetase deficiency (AR) NM_000411.6	HLCS	Faroese	1 in 20	1 in 1900
		Japanese	1 in 158	1 in 15700
		Pan-ethnic	1 in 224	1 in 22300
Homocystinuria due to cystathionine beta-synthase deficiency (AR) NM_000071.2	CBS	Norwegian	1 in 40	1 in 3900
		Pan-ethnic	1 in 224	1 in 22300
		Qatari	1 in 21	1 in 2000
HSD17B4-related conditions (AR) NM_000414.3	HSD17B4	Pan-ethnic	1 in 158	1 in 15700
Hydrolethalus syndrome type 1 (AR) NM_145014.2	HYLS1	Finnish	1 in 40	1 in 3900
		Pan-ethnic	≤1 in 500	Reduced
Hypophosphatasia (AR) NM_000478.5	ALPL	Mennonite	1 in 25	1 in 480
		Pan-ethnic	1 in 150	1 in 2980
Joubert syndrome and related disorders (MKS1-related) (AR) NM_017777.3	MKS1	Finnish	1 in 47	1 in 920
		Pan-ethnic	1 in 260	1 in 5180
Joubert syndrome and related disorders (TMEM216-related) (AR) NM_001173990.2	TMEM216	Ashkenazi Jewish	1 in 92	1 in 9100
		Pan-ethnic	≤1 in 500	Reduced
Junctional epidermolysis bullosa (LAMC2-related) (AR) NM_005562.2	LAMC2	Pan-ethnic	≤1 in 500	Reduced

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
KCNJ11-related conditions (AR) NM_000525.3	KCNJ11	Pan-ethnic	≤1 in 500	Reduced
Krabbe disease (AR) NM_000153.3	GALC *	Druze	1 in 6	1 in 500
		Pan-ethnic	1 in 158	1 in 15700
LAMA2-related muscular dystrophy (AR) NM_000426.3	LAMA2	Pan-ethnic	1 in 87	1 in 8600
LAMA3-related conditions (AR) NM_000227.4	LAMA3	Pan-ethnic	≤1 in 500	Reduced
LAMB3-related conditions (AR) NM_000228.2	LAMB3	Pan-ethnic	1 in 317	1 in 31600
Limb-girdle muscular dystrophy (CAPN3-related) (AR) NM_000070.2	CAPN3	Pan-ethnic	1 in 134	1 in 13300
Limb-girdle muscular dystrophy type 2C (AR) NM_000231.2	SGCG	Caucasian	1 in 571	Reduced
		Japanese	1 in 374	1 in 37300
		Moroccan	1 in 250	1 in 24900
		Pan-ethnic	≤1 in 500	Reduced
		Roma	1 in 59	1 in 5800
Limb-girdle muscular dystrophy type 2D (AR) NM_000023.2	SGCA	Caucasian	1 in 286	1 in 28500
		Finnish	1 in 150	1 in 14900
		Pan-ethnic	≤1 in 500	Reduced
Limb-girdle muscular dystrophy type 2E (AR) NM_000232.4	SGCB	Caucasian	1 in 404	1 in 5038
		Pan-ethnic	≤1 in 500	Reduced
Lipoid congenital adrenal hyperplasia (AR) NM_000349.2	STAR	Korean	1 in 170	1 in 16900
		Pan-ethnic	≤1 in 500	Reduced
Lysosomal acid lipase deficiency (AR) NM_000235.3	LIPA	Caucasian	1 in 112	1 in 1850
		Pan-ethnic	1 in 359	1 in 5967
		Sephardic Jewish (Iranian)	1 in 33	1 in 534
Maple syrup urine disease type 1A (AR) NM_000709.3	BCKDHA	Mennonite	1 in 10	1 in 900
		Pan-ethnic	1 in 373	1 in 37200
Maple syrup urine disease type 1B (AR) NM_183050.2	BCKDHB	Ashkenazi Jewish	1 in 97	1 in 9600
		Pan-ethnic	1 in 346	1 in 34500
Maple syrup urine disease type 2 (AR) NM_001918.3	DBT	Pan-ethnic	≤1 in 500	Reduced
Medium-chain acyl-CoA dehydrogenase deficiency (AR) NM_000016.5	ACADM	Northern European	1 in 40	1 in 3900
		Pan-ethnic	1 in 66	1 in 6500
Megalencephalic leukoencephalopathy with subcortical cysts 1 (AR) NM_015166.3	MLC1	Pan-ethnic	≤1 in 500	Reduced
		Sephardic Jewish (Libyan)	1 in 40	1 in 3900
Metachromatic leukodystrophy (ARSA-related) (AR) NM_000487.5	ARSA	Navajo	1 in 40	1 in 780
		Pan-ethnic	1 in 100	1 in 1980
		Sephardic Jewish	1 in 46	1 in 900
Methylmalonic acidemia (MMAA-related) (AR) NM_172250.2	MMAA	Pan-ethnic	1 in 316	1 in 10500
Methylmalonic acidemia (MMAB-related) (AR) NM_052845.3	MMAB	Pan-ethnic	1 in 456	1 in 22750
Methylmalonic acidemia (MUT-related) (AR) NM_000255.3	MUT	Pan-ethnic	1 in 204	1 in 5075
Mitochondrial complex IV deficiency / Leigh syndrome, French Canadian type (AR) NM_133259.3	LRPPRC	French Canadian (Saguenay-Lac-St-Jean)	1 in 23	1 in 2200
		Pan-ethnic	≤1 in 500	Reduced
Mucolipidosis type III gamma (AR) NM_032520.4	GNPTG	Pan-ethnic	≤1 in 500	Reduced
Mucolipidosis type IV (AR) NM_020533.2	MCOLN1	Ashkenazi Jewish	1 in 100	1 in 9900
		Pan-ethnic	≤1 in 500	Reduced
Mucopolysaccharidosis type I (AR) NM_000203.4	IDUA	Pan-ethnic	1 in 148	1 in 4900
Mucopolysaccharidosis type II (XL) NM_000202.6	IDS *	Pan-ethnic	≤1 in 500	Reduced

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
Mucopolysaccharidosis type IIIA (AR) NM_000199.3	SGSH	Northern European	1 in 173	1 in 17200
		Pan-ethnic	1 in 215	1 in 21400
		Taiwanese	≤1 in 500	Reduced
Mucopolysaccharidosis type IIIB (AR) NM_000263.3	NAGLU	Pan-ethnic	1 in 224	1 in 22300
Muscular dystrophy-dystroglycanopathy (FKRP-related) (AR) NM_024301.4	FKRP	Norwegian	1 in 116	1 in 11500
		Pan-ethnic	1 in 158	1 in 15700
Muscular dystrophy-dystroglycanopathy (FKTN-related) (AR) NM_001079802.1	FKTN	Ashkenazi Jewish	1 in 80	1 in 7900
		Japanese	1 in 188	1 in 18700
		Pan-ethnic	≤1 in 500	Reduced
MYO7A-related conditions (AR) NM_000260.3	MYO7A	Pan-ethnic	1 in 200	1 in 3980
Nemaline myopathy 2 (AR) NM_001271208.1	NEB *	Ashkenazi Jewish	1 in 108	1 in 10700
		Pan-ethnic	1 in 158	1 in 3140
Neuronal ceroid lipofuscinosis type 1 (AR) NM_000310.3	PPT1	Finnish	1 in 70	1 in 3450
		Pan-ethnic	1 in 199	1 in 9900
Neuronal ceroid lipofuscinosis type 2 (AR) NM_000391.3	TPP1	Newfoundland	1 in 53	1 in 1734
		Pan-ethnic	1 in 250	1 in 8300
Neuronal ceroid lipofuscinosis type 5 (AR) NM_006493.2	CLN5	Finnish	1 in 115	1 in 11400
		Pan-ethnic	≤1 in 500	Reduced
Neuronal ceroid lipofuscinosis type 6 (AR) NM_017882.2	CLN6	Pan-ethnic	≤1 in 500	Reduced
Neuronal ceroid lipofuscinosis type 8 (AR) NM_018941.3	CLN8	Finnish	1 in 135	1 in 13400
		Pan-ethnic	≤1 in 500	Reduced
Niemann-Pick disease type C (NPC1-related) (AR) NM_000271.4	NPC1	Pan-ethnic	1 in 183	1 in 18200
Niemann-Pick disease type C (NPC2-related) (AR) NM_006432.3	NPC2	Pan-ethnic	1 in 871	Reduced
Niemann-Pick disease types A and B (AR) NM_000543.4	SMPD1	Ashkenazi Jewish	1 in 90	1 in 1780
		Pan-ethnic	1 in 250	1 in 4980
Nijmegen breakage syndrome (AR) NM_002485.4	NBN *	Eastern European	1 in 155	1 in 15400
		Pan-ethnic	≤1 in 500	Reduced
OPA3-related conditions (AR) NM_025136.3	OPA3	Pan-ethnic	≤1 in 500	Reduced
		Sephardic Jewish (Iraqi)	1 in 10	1 in 900
Ornithine transcarbamylase deficiency (XL) NM_000531.5	OTC	Pan-ethnic	≤1 in 500	Reduced
Osteopetrosis (TCIRG1-related) (AR) NM_006019.3	TCIRG1	Ashkenazi Jewish	1 in 350	1 in 34900
		Chuvash	1 in 30	1 in 2900
		Pan-ethnic	1 in 317	1 in 31600
PCDH15-related conditions (AR) NM_033056.3	PCDH15	Ashkenazi Jewish	1 in 78	1 in 7700
		Pan-ethnic	1 in 400	1 in 39900
PEX7-related conditions (AR) NM_000288.3	PEX7	Pan-ethnic	1 in 157	1 in 15600
Phenylalanine hydroxylase deficiency (AR) NM_000277.1	PAH	African-American	1 in 111	1 in 11000
		Ashkenazi Jewish	1 in 225	1 in 22400
		East Asian	1 in 50	1 in 1225
		Finnish	1 in 225	1 in 22400
		Irish	1 in 33	1 in 3200
		Japanese	1 in 200	1 in 19900
		Pan-ethnic	1 in 58	1 in 5700
		Turkish	1 in 26	1 in 2500
Polycystic kidney disease (PKHD1-related) (AR) NM_138694.3	PKHD1	Pan-ethnic	1 in 70	1 in 6900
POMGNT1-related conditions (AR) NM_017739.3	POMGNT1	Finnish	1 in 111	1 in 11000
		Pan-ethnic	≤1 in 500	Reduced
Primary carnitine deficiency (AR) NM_003060.3	SLC22A5	Faroese	1 in 9	1 in 800
		Japanese	1 in 100	1 in 9900

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
		Pan-ethnic	1 in 71	1 in 7000
Primary hyperoxaluria type 1 (AR) NM_000030.2	AGXT	Pan-ethnic	1 in 135	1 in 13400
Primary hyperoxaluria type 2 (AR) NM_012203.1	GRHPR	Pan-ethnic	≤1 in 500	Reduced
Primary hyperoxaluria type 3 (AR) NM_138413.3	HOGA1	Pan-ethnic	1 in 354	1 in 35300
Propionic acidemia (PCCA-related) (AR) NM_000282.3	PCCA	Arab	1 in 100	1 in 2475
		Pan-ethnic	1 in 224	1 in 5575
Propionic acidemia (PCCB-related) (AR) NM_000532.4	PCCB	Arab	1 in 100	1 in 9900
		Greenlandic Inuit	1 in 20	1 in 1900
		Pan-ethnic	1 in 224	1 in 22300
Pycnodysostosis (AR) NM_000396.3	CTSK	Pan-ethnic	1 in 438	1 in 43700
Pyruvate carboxylase deficiency (AR) NM_000920.3	PC	Algonquian Indian	1 in 10	1 in 180
		Pan-ethnic	1 in 250	1 in 4980
Roberts syndrome (AR) NM_001017420.2	ESCO2	Pan-ethnic	≤1 in 500	Reduced
Sandhoff disease (AR) NM_000521.3	HEXB	Metis (Saskatchewan)	1 in 15	1 in 1400
		Pan-ethnic	1 in 180	1 in 17900
Sialic acid storage diseases (AR) NM_012434.4	SLC17A5	Finnish	1 in 100	1 in 9900
		Pan-ethnic	≤1 in 500	Reduced
Sjögren-Larsson syndrome (AR) NM_000382.2	ALDH3A2	Pan-ethnic	≤1 in 500	Reduced
		Swedish	1 in 250	1 in 24900
SLC12A6-related conditions (AR) NM_133647.1	SLC12A6	French Canadian (Saguenay-Lac-St-Jean)	1 in 23	1 in 2200
		Pan-ethnic	≤1 in 500	Reduced
SLC26A2-related conditions (AR) NM_000112.3	SLC26A2	Finnish	1 in 75	1 in 1480
		Pan-ethnic	1 in 158	1 in 3140
SLC26A4-related conditions (AR) NM_000441.1	SLC26A4	Asian	1 in 74	1 in 7300
		Pan-ethnic	1 in 80	1 in 7900
SLC37A4-related conditions (AR) NM_001164277.1	SLC37A4	Pan-ethnic	1 in 354	1 in 7060
Smith-Lemli-Opitz syndrome (AR) NM_001360.2	DHCR7	African-American	1 in 339	1 in 33800
		Ashkenazi Jewish	1 in 41	1 in 4000
		Hispanic	1 in 135	1 in 13400
		Northern European	1 in 50	1 in 4900
		Pan-ethnic	1 in 71	1 in 7000
		Sephardic Jewish	1 in 68	1 in 6700
		Southern European	1 in 83	1 in 8200
Spastic paraplegia type 15 (AR) NM_015346.3	ZFYVE26	Pan-ethnic	≤1 in 500	Reduced
Spinal muscular atrophy (AR) NM_000344.3 Carrier residual risks listed are for 2 copy SMN1 results. Carrier residual risk for >2 copies are 5- to 10-fold lower.	SMN1 *	African-American	1 in 59	1 in 342
		Ashkenazi Jewish	1 in 62	1 in 1017
		Asian	1 in 50	1 in 701
		Caucasian	1 in 45	1 in 880
		Hispanic	1 in 48	1 in 784
		Pan-ethnic	1 in 49	1 in 800
Spondylocostal dysostosis (MESP2-related) (AR) NM_001039958.1	MESP2	Pan-ethnic	1 in 224	1 in 22300
		Puerto Rican	1 in 55	1 in 5400
Tay-Sachs disease (AR) NM_000520.4	HEXA	Ashkenazi Jewish	1 in 27	1 in 2600
		Asian	1 in 126	1 in 12500
		Caucasian	1 in 182	1 in 18100
		French Canadian	1 in 27	1 in 2600
		Irish	1 in 41	1 in 4000
		Pan-ethnic	1 in 250	1 in 24900
		Sephardic Jewish	1 in 125	1 in 12400

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
Tyrosine hydroxylase deficiency (AR) NM_199292.2	TH	Caucasian	1 in 224	1 in 22300
		Pan-ethnic	≤1 in 500	Reduced
Tyrosinemia type I (AR) NM_000137.2	FAH *	Ashkenazi Jewish	1 in 143	1 in 2840
		French Canadian	1 in 66	1 in 1300
		French Canadian (Saguenay-Lac-St-Jean)	1 in 16	1 in 300
		Pan-ethnic	1 in 125	1 in 2480
Tyrosinemia type II (AR) NM_000353.2	TAT	Pan-ethnic	1 in 250	1 in 24900
USH1C-related conditions (AR) NM_005709.3	USH1C *	French Canadian/Acadian	1 in 227	1 in 22600
		Pan-ethnic	1 in 353	1 in 3521
		Sephardic Jewish	1 in 125	1 in 1241
USH2A-related conditions (AR) NM_206933.2	USH2A	Caucasian	1 in 70	1 in 6900
		Pan-ethnic	1 in 112	1 in 11100
		Sephardic Jewish	1 in 36	1 in 3500
Very long-chain acyl-CoA dehydrogenase deficiency (AR) NM_000018.3	ACADVL	Pan-ethnic	1 in 100	1 in 9900
Wilson disease (AR) NM_000053.3	ATP7B	Ashkenazi Jewish	1 in 67	1 in 3300
		Canary Islander	1 in 25	1 in 1200
		Pan-ethnic	1 in 90	1 in 4450
		Sardinian	1 in 50	1 in 2450
		Sephardic Jewish	1 in 65	1 in 3200
X-linked adrenoleukodystrophy (XL) NM_000033.3	ABCD1	Pan-ethnic	1 in 16800	Reduced
		Sephardic Jewish	≤1 in 500	Reduced
X-linked juvenile retinoschisis (XL) NM_000330.3	RS1	Pan-ethnic	≤1 in 500	Reduced
X-linked myotubular myopathy (XL) NM_000252.2	MTM1	Pan-ethnic	≤1 in 500	Reduced
X-linked severe combined immunodeficiency (XL) NM_000206.2	IL2RG	Pan-ethnic	≤1 in 500	Reduced
Xeroderma pigmentosum complementation group A (AR) NM_000380.3	XPA	Japanese	1 in 100	1 in 9900
		Pan-ethnic	1 in 1667	Reduced
Xeroderma pigmentosum complementation group C (AR) NM_004628.4	XPC	Pan-ethnic	1 in 763	Reduced
		Tunisian	1 in 50	1 in 4900
Zellweger spectrum disorder (PEX1-related) (AR) NM_000466.2	PEX1	Pan-ethnic	1 in 144	1 in 14300
Zellweger spectrum disorder (PEX2-related) (AR) NM_000318.2	PEX2	Ashkenazi Jewish	1 in 227	1 in 22600
		Pan-ethnic	≤1 in 500	Reduced
Zellweger spectrum disorder (PEX6-related) (AR) NM_000287.3	PEX6	French Canadian	1 in 55	1 in 5400
		Pan-ethnic	1 in 294	1 in 29300
		Sephardic Jewish	1 in 18	1 in 1700
Zellweger spectrum disorder (PEX10-related) (AR) NM_153818.1	PEX10	Pan-ethnic	1 in 606	Reduced
Zellweger spectrum disorder (PEX12-related) (AR) NM_000286.2	PEX12	Pan-ethnic	1 in 409	1 in 40800

Methods

- Genomic DNA obtained from the submitted sample is enriched for targeted regions using a hybridization-based protocol, and sequenced using Illumina technology. Unless otherwise indicated, all targeted regions are sequenced with ≥50x depth or are supplemented with additional analysis. Reads are aligned to a reference sequence (GRCh37), and sequence changes are identified and interpreted in the context of a single clinically relevant transcript, indicated below. Enrichment and analysis focus on the coding sequence of the indicated transcripts, 10bp of flanking intronic sequence, and other specific genomic regions demonstrated to be causative of disease at the time of assay design. Promoters, untranslated

regions, and other non-coding regions are not otherwise interrogated. Exonic deletions and duplications are called using an in-house algorithm that determines copy number at each target by comparing the read depth for each target in the proband sequence with both mean read-depth and read-depth distribution, obtained from a set of clinical samples. Markers across the X and Y chromosomes are analyzed for quality control purposes and may detect deviations from the expected sex chromosome complement. Such deviations may be included in the report in accordance with internal guidelines. Invitae utilizes a classification methodology to identify next-generation sequencing (NGS)-detected variants that require orthogonal confirmation (Lincoln, et al. J Mol Diagn. 2019 Mar;21(2):318-329.). Pathogenic and Likely Pathogenic variants that do not meet the validated quality thresholds are confirmed. Confirmation technologies may include any of the following: Sanger sequencing, Pacific Biosciences SMRT sequencing, MLPA, MLPA-seq, Array CGH.Array CGH confirmation of NGS CNV calling performed by Invitae Corporation (1400 16th Street, San Francisco, CA 94103, #05D2040778). The following analyses are performed if relevant to the requisition. For GBA the reference genome has been modified to mask the sites of polymorphic paralog sequence variants (PSVs) in both the gene and pseudogene. For CYP21A2 and GBA, if one or more reportable variants, gene conversion, or fusion event is identified via our NGS pipeline (see Limitations), these variants are confirmed by PacBio sequencing of an amplicon generated by long-range PCR and subsequent short-range PCR. In some cases, it may not be possible to disambiguate between the gene and pseudogene. For HBA1/2, the reference genome has been modified to force some sequencing reads derived from HBA1 to align to HBA2, and variant calling algorithms are modified to support an expectation of 4 alleles in these regions. HBA1/2 copy number calling is performed by a custom hypothesis testing algorithm which generates diplotype calls. If sequence data for a sample does not support a unique high confidence match from among hypotheses tested, that sample is flagged for manual review. Copy number variation is only reported for coding sequence of HBA1 and HBA2 and the HS-40 region. This assay does not distinguish among the -α3.7 subtypes, and all -α3.7 variants are called as HBA1 deletions. This assay may not detect overlapping copy gain and copy loss events when the breakpoints of those events are similar. For FMR1, triplet repeats are detected by PCR with fluorescently labeled primers followed by capillary electrophoresis. Reference ranges: Normal: <45 CGG repeats, intermediate: 45-54 CGG repeats, premutation: 55-200 CGG repeats, full mutation: >200 CGG repeats. For alleles with 55-90 triplet repeats, the region surrounding the FMR1 repeat is amplified by PCR. The PCR amplicons are then processed through PacBio SMRTBell library prep and sequenced using PacBio long read technology. The number of AGG interruptions within the 55-90 triplet repeat is read directly from the resulting DNA sequences. Technical component of confirmatory sequencing is performed by Invitae Corporation (1400 16th Street, San Francisco, CA 94103, #05D2040778).

- The following transcripts were used in this analysis. If more than one transcript is listed for a single gene, variants were reported using the first transcript listed unless otherwise indicated in the report: ABCC8 (NM_000352.4), ABCD1 (NM_000033.3), ACADM (NM_000016.5), ACADVL (NM_000018.3), ADA (NM_000022.2), AGA (NM_000027.3), AGL (NM_000642.2), AGXT (NM_000030.2), AIRE (NM_000383.3), ALDH3A2 (NM_000382.2), ALDOB (NM_000035.3), ALG6 (NM_013339.3), ALMS1 (NM_015120.4), ALPL (NM_000478.5), AMT (NM_000481.3), ARG1 (NM_000045.3), ARSA (NM_000487.5), ASL (NM_000048.3), ASPA (NM_000049.2), ASS1 (NM_000050.4), ATM (NM_000051.3), ATP7A (NM_000052.6), ATP7B (NM_000053.3), BBS1 (NM_024649.4), BBS10 (NM_024685.3), BBS12 (NM_152618.2), BBS2 (NM_031885.3), BCKDHA (NM_000709.3), BCKDHB (NM_183050.2), BCS1L (NM_004328.4), BLM (NM_000057.3), BTD (NM_000060.3), CAPN3 (NM_000070.2), CBS (NM_000071.2), CFTR (NM_000492.3), CLN3 (NM_001042432.1), CLN5 (NM_006493.2), CLN6 (NM_017882.2), CLN8 (NM_018941.3), CLRN1 (NM_174878.2), COL4A3 (NM_000091.4), COL4A4 (NM_000092.4), COL4A5 (NM_000495.4), CPS1 (NM_001875.4), CPT1A (NM_001876.3), CPT2 (NM_000098.2), CTNS (NM_004937.2), CTSK (NM_000396.3), CYP11B1 (NM_000497.3), CYP21A2 (NM_000500.7), CYP27A1 (NM_000784.3), DBT (NM_001918.3), DHCR7 (NM_001360.2), DLD (NM_000108.4), DMD (NM_004006.2), DYSF (NM_003494.3), ELP1 (NM_003640.3), ERCC6 (NM_000124.3), ERCC8 (NM_000082.3), ESCO2 (NM_001017420.2), EVC (NM_153717.2), EVC2 (NM_147127.4), FAH (NM_000137.2), FANCA (NM_000135.2), FANCC (NM_000136.2), FKRP (NM_024301.4), FKTN (NM_001079802.1), FMR1 (NM_002024.5), G6PC (NM_000151.3), GAA (NM_000152.3), GALC (NM_000153.3), GALK1 (NM_000154.1), GALT (NM_000155.3), GBA (NM_001005741.2), GCDH (NM_000159.3), GJB2 (NM_004004.5), GLA (NM_000169.2), GLB1 (NM_000404.2), GLDC (NM_000170.2), GNE (NM_001128227.2), GNPTAB (NM_024312.4), GNPTG (NM_032520.4), GRHPR (NM_012203.1), HADHA (NM_000182.4), HBA1 (NM_000558.4), HBA2 (NM_000517.4), HBB (NM_000518.4), HEXA (NM_000520.4), HEXB (NM_000521.3), HGSNAT (NM_152419.2), HLCS (NM_000411.6), HMGCL (NM_000191.2), HOGA1 (NM_138413.3), HSD17B4 (NM_000414.3), HYLS1 (NM_145014.2), IDS (NM_000202.6), IDUA (NM_000203.4), IL2RG (NM_000206.2), IVD (NM_002225.3), KCNJ11 (NM_000525.3), LAMA2 (NM_000426.3), LAMA3 (NM_000227.4), LAMB3 (NM_000228.2), LAMC2 (NM_005562.2), LIPA (NM_000235.3), LRPPRC (NM_133259.3), MAN2B1 (NM_000528.3), MCOLN1 (NM_020533.2), MEFV (NM_000243.2), MESP2 (NM_001039958.1), MKS1 (NM_017777.3), MLC1 (NM_015166.3), MMAA (NM_172250.2), MMAB (NM_052845.3), MMACHC (NM_015506.2), MPI (NM_002435.2), MTM1 (NM_000252.2), MUT (NM_000255.3), MYO7A (NM_000260.3), NAGLU (NM_000263.3), NBN (NM_002485.4), NEB (NM_001271208.1), NPC1 (NM_000271.4), NPC2 (NM_006432.3), NPHS1 (NM_004646.3), NPHS2 (NM_014625.3), OPA3 (NM_025136.3), OTC (NM_000531.5), PAH (NM_000277.1), PC (NM_000920.3), PCCA (NM_000282.3), PCCB (NM_000532.4), PCDH15 (NM_033056.3), PEX1 (NM_000466.2), PEX10 (NM_153818.1), PEX12 (NM_000286.2), PEX2 (NM_000318.2), PEX6 (NM_000287.3), PEX7 (NM_000288.3), PKHD1 (NM_138694.3), PMM2 (NM_000303.2), POMGNT1 (NM_017739.3), PPT1 (NM_000310.3), PROP1 (NM_006261.4), PTS (NM_000317.2), RMRP (NR_003051.3), RS1 (NM_000330.3), RTEL1 (NM_001283009.1), SACS (NM_014363.5), SGCA (NM_000023.2), SGCB (NM_000232.4), SGCG (NM_000231.2), SGSH (NM_000199.3), SLC12A6 (NM_133647.1), SLC17A5 (NM_012434.4), SLC22A5 (NM_003060.3), SLC26A2 (NM_000112.3), SLC26A4 (NM_000441.1), SLC37A4 (NM_001164277.1), SMN1

(NM_000344.3), SMPD1 (NM_000543.4), STAR (NM_000349.2), TAT (NM_000353.2), TCIRG1 (NM_006019.3), TGM1 (NM_000359.2), TH (NM_199292.2), TMEM216 (NM_001173990.2), TPP1 (NM_000391.3), TTPA (NM_000370.3), USH1C (NM_005709.3), USH2A (NM_206933.2), VPS13B (NM_017890.4), XPA (NM_000380.3), XPC (NM_004628.4), ZFYVE26 (NM_015346.3).

- This report only includes variants that have a clinically significant association with the conditions tested as of the report date. Variants of uncertain significance, benign variants, and likely benign variants are not included in this report. However, if additional evidence becomes available to indicate that the clinical significance of a variant has changed, Invitae may update this report and provide notification.
- A PMID is a unique identifier referring to a published, scientific paper. Search by PMID at http://www.ncbi.nlm.nih.gov/pubmed.
- An rsID is a unique identifier referring to a single genomic position, and is used to associate population frequency information with sequence changes at that position. Reported population frequencies are derived from a number of public sites that aggregate data from large-scale population sequencing projects, including ExAC (http://exac.broadinstitute.org) and dbSNP (http://ncbi.nlm.nih.gov/SNP).

Disclaimer

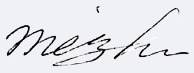
DNA studies do not constitute a definitive test for the selected condition(s) in all individuals. It should be realized that there are possible sources of error. Errors can result from trace contamination, rare technical errors, rare genetic variants that interfere with analysis, recent scientific developments, and alternative classification systems. This test should be one of many aspects used by the healthcare provider to help with a diagnosis and treatment plan, but it is not a diagnosis itself. This test was developed and its performance characteristics determined by Invitae. It has not been cleared or approved by the FDA. The laboratory is regulated under the Clinical Laboratory Improvement Act (CLIA) as qualified to perform high-complexity clinical tests (CLIA ID: 05D2040778). This test is used for clinical purposes. It should not be regarded as investigational or for research.

Limitations

- Based on validation study results, this assay achieves >99% analytical sensitivity and specificity for single nucleotide variants, insertions and deletions <15bp in length, and exon-level deletions and duplications. Invitae's methods also detect insertions and deletions larger than 15bp but smaller than a full exon but sensitivity for these may be marginally reduced. Invitae's deletion/duplication analysis determines copy number at a single exon resolution at virtually all targeted exons. However, in rare situations, single-exon copy number events may not be analyzed due to inherent sequence properties or isolated reduction in data quality. Certain types of variants, such as structural rearrangements (e.g. inversions, gene conversion events, translocations, etc.) or variants embedded in sequence with complex architecture (e.g. short tandem repeats or segmental duplications), may not be detected. Additionally, it may not be possible to fully resolve certain details about variants, such as mosaicism, phasing, or mapping ambiguity. Unless explicitly guaranteed, sequence changes in the promoter, non-coding exons, and other non-coding regions are not covered by this assay. Please consult the test definition on our website for details regarding regions or types of variants that are covered or excluded for this test. This report reflects the analysis of an extracted genomic DNA sample. While this test is intended to reflect the analysis of extracted genomic DNA from a referred patient, in very rare cases the analyzed DNA may not represent that individual's constitutional genome, such as in the case of a circulating hematolymphoid neoplasm, bone marrow transplant, blood transfusion, chimerism, culture artifact or maternal cell contamination.
- FMR1: Sizing accuracy is expected to be +/-1 for CGG repeat alleles less than or equal to 90 repeat units and +/-3 for CGG repeat alleles greater than 90 repeat units. If the two CGG repeats listed are the same, this may indicate that both alleles are the same size or that one allele is too small to be detected by this analysis. The number of AGG interruptions is only determined for females with triplet repeat sizes of 55-90. GBA: c.84dupG (p.Leu29Alafs*18), c.115+1G>A (Splice donor), c.222_224delTAC (p.Thr75del), c.475C>T (p.Arg159Trp), c.595_596delCT (p.Leu199Aspfs*62), c.680A>G (p.Asn227Ser), c.721G>A (p.Gly241Arg), c.754T>A (p.Phe252Ile), c.1226A>G (p.Asn409Ser), c.1246G>A (p.Gly416Ser), c.1263_1317del (p.Leu422Profs*4), c.1297G>T (p.Val433Leu), c.1342G>C (p.Asp448His), c.1343A>T (p.Asp448Val), c.1448T>C (p.Leu483Pro), c.1504C>T (p.Arg502Cys), c.1505G>A (p.Arg502His), c.1603C>T (p.Arg535Cys), c.1604G>A (p.Arg535His) variants only. Rarely, sensitivity to detect these variants may be reduced. When sensitivity is reduced, zygosity may be reported as "unknown". IDS: Detection of complex rearrangements not offered (PMID: 7633410, 20301451). SMN1: Systematic exon numbering is used for all genes, including SMN1, and for this reason the exon typically referred to as exon 7 in the literature (PMID: 8838816) is referred to as exon 8 in this report. This assay unambiguously detects SMN1 exon 8 copy number. The presence of the g.27134T>G variant (also known as c.*3+80T>G) is reported if SMN1 copy number = 2. SMN1 or SMN2: NM_000344.3:c.*3+80T>G variant only. CYP21A2: Analysis includes the most common variants (c.92C>T(p.Pro31Leu), c.293-13C>G (intronic), c.332_339delGAGACTAC (p.Gly111Valfs*21), c.518T>A (p.Ile173Asn), c.710T>A (p.Ile237Asn), c.713T>A (p.Val238Glu), c.719T>A

(p.Met240Lys), c.844G>T (p.Val282Leu), c.923dupT (p.Leu308Phefs*6), c.955C>T (p.Gln319*), c.1069C>T(p.Arg357Trp), c.1360C>T (p.Pro454Ser) and the 30Kb deletion) as well as select rare HGMD variants only (list available upon request). Full gene duplications are reported only in the presence of a pathogenic variant(s). When a duplication and a pathogenic variant(s) is identified, phase (cis/trans) cannot be determined. Full gene deletion analysis is not offered. Sensitivity to detect these variants, if they result from complex gene conversion/fusion events, may be reduced. COL4A5: Deletion/duplication analysis is not offered for exons 11-12. NBN: Deletion/duplication analysis is not offered for exons 15-16. USH1C: Deletion/duplication analysis is not offered for exons 5-6. FAH: Deletion/duplication analysis is not offered for exon 14. GALC: Deletion/duplication analysis is not offered for exon 6. HBA1/2: This assay is designed to detect deletions and duplications of HBA1 and/or HBA2, resulting from the -alpha20.5, --MED, --SEA, --FIL/--THAI, -alpha3.7, -alpha4.2, anti3.7 and anti4.2. Sensitivity to detect other copy number variants may be reduced. Detection of overlapping deletion and duplication events will be limited to combinations of events with significantly differing boundaries. In addition, deletion of the enhancer element HS-40 and the sequence variant, Constant Spring (NM_000517.4:c.427T>C), can be identified by this assay. HBA2: Sequencing analysis is not offered for exons 1-2. NEB: Deletion/duplication analysis is not offered for exons 82-105. NEB variants in this region with no evidence towards pathogenicity are not included in this report, but are available upon request. ALG6: Deletion/duplication analysis is not offered for exons 11-12.

This report has been reviewed and approved by:



Mei Zhu, Ph.D., FACMG
Clinical Molecular Geneticist