Reproductive Technologies, Inc. THE SPERM BANK OF CALIFORNIA

EXPANDED CARRIER SCREENING RESULTS DONOR 5984

Expanded carrier screening for 268 autosomal recessive conditions was completed by Invitae and reported on 03/02/2022.

The results were **NEGATIVE** for all 268 conditions.

Disease	Result	Residual risk to be a carrier
Cystic Fibrosis	Negative	1 in 2,700
Spinal Muscular Atrophy	Negative - 2 copies exon 7 Negative for c.*3+80T>G variant in exon 7	1 in 784
HBB Hemoglobinopathies	Negative	1 in 1,600
Alpha Thalassemia	Negative	1 in 241

Genetic screening tests can significantly reduce, but never completely eliminate, the chance that a person is a carrier for a particular disorder.

Please refer to the donor's Invitae expanded carrier test report for more information on the testing completed and the donor's results.

Please also see the Health Problems List for a summary of the information that this donor has provided to us regarding personal and family medical history.

Sincerely,

Janine Mash LCGC Certified Genetic Counselor San Francisco Genetic Counseling





Gender.	Patient name:5984 DONORDOB:Sex assigned at birth:MaleGender:Kale	Sample type: Sample collection date: Sample accession date: MRN:	Saliva 02/16/2022 02/17/2022	Report date: Invitae #: Clinical team:	03/02/2022 RQ3201247 Janine Mash Lorraine Bonner, MD
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Reason for testing

Gamete donor

Test performed

Invitae Comprehensive Carrier Screen without X-linked Disorders

- Primary Panel (CF, SMA)
- Add-on Comprehensive Carrier Screen without X-linked Disorders genes



RESULT: NEGATIVE

This carrier test evaluated 268 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.

This test did not identify any genetic changes in the gene(s) analyzed that are currently recognized as clinically significant. This negative result reduces, but does not eliminate, the chance that this individual is a carrier for conditions caused by any of the genes tested. This individual may still be a carrier for a genetic condition that is not evaluated by this test.

Next steps

- 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.



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)	HMGCL	Pan-ethnic	≤1 in 500	Reduced
NM_000191.2	HMGCL	Portuguese	1 in 160	1 in 15900
ABCB11-related conditions (AR) NM_003742.2	ABCB11	Pan-ethnic	1 in 100	1 in 9900
ABCC8-related conditions (AR)		Ashkenazi Jewish	1 in 52	1 in 5100
NM_000352.4 When the mother is a noncarrier, but the father is a		Finnish	1 in 100	1 in 9900
carrier, there is a residual risk for focal disease (1 in 540 for the Ashkenazi Jewish population; undetermined in other ethnic groups)	ABCC8	Pan-ethnic	1 in 177	1 in 17600
Abetalipoproteinemia (AR)	MTTP	Ashkenazi Jewish	1 in 131	1 in 13000
NM_000253.3	WITTE	Pan-ethnic	≤1 in 500	Reduced
Achromatopsia (CNGB3-related) (AR) NM_019098.4	CNGB3	Pan-ethnic	1 in 93	1 in 9200
ACOX1-related conditions (AR) NM_004035.6	ACOX1	Pan-ethnic	≤1 in 500	Reduced
Acrodermatitis enteropathica (AR) NM_130849.3	SLC39A4	Pan-ethnic	1 in 354	1 in 35300
Adenosine deaminase deficiency (AR) NM_000022.2	ADA	Pan-ethnic	1 in 224	1 in 2788
Aicardi-Goutieres syndrome 5 (AR) NM_015474.3	SAMHD1	Pan-ethnic	≤1 in 500	Reduced
Aldosterone synthase deficiency (AR)	CYP11B2	Pan-ethnic	≤1 in 500	Reduced
NM_000498.3	CTPTIBZ	Sephardic Jewish (Iranian)	1 in 30	1 in 2900
Alpha-mannosidosis (AR) NM_000528.3	MAN2B1	Pan-ethnic	1 in 354	1 in 35300
		African-American	1 in 30	1 in 291
Alpha-thalassemia (AR)	HBA1/	Asian	1 in 20	1 in 191
NM_000558.4, NM_000517.4	HBA2 *	Caucasian	≤1 in 500	Reduced
		Pan-ethnic	1 in 25	1 in 241
Algorithmum drama (COLAA2 related) (AD)		Ashkenazi Jewish	1 in 192	1 in 19100
Alport syndrome (COL4A3-related) (AR) NM_000091.4	COL4A3	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
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
Aromatase deficiency (AR) NM_031226.2	CYP19A1	Pan-ethnic	≤1 in 500	Reduced
Asparagine synthetase deficiency (AR) NM_133436.3	ASNS	Pan-ethnic	≤1 in 500	Reduced



DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
		Sephardic Jewish (Iranian)	1 in 80	1 in 7900
Aspartylglucosaminuria (AR)	AGA	Finnish	1 in 69	1 in 6800
NM_000027.3	AGA	Pan-ethnic	≤1 in 500	Reduced
Ataxia with vitamin E deficiency (AR)	TTPA	Italian	1 in 274	1 in 2731
NM_000370.3	IIFA	Pan-ethnic	≤1 in 500	Reduced
ATM-related conditions (AR)	ATM	Pan-ethnic	1 in 100	1 in 9900
NM_000051.3	ATM	Sephardic Jewish	1 in 69	1 in 6800
· · · · · · · · · · · · · · · · · · ·		Finnish	1 in 79	1 in 7800
Autoimmune polyendocrinopathy with candidiasis and ectodermal dysplasia (AR) NM_000383.3	AIRE	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	Norwegian	1 in 151	1 in 3000
TGM1-related) (AR) NM_000359.2	IGMI	Pan-ethnic	1 in 224	1 in 4460
Autosomal recessive spastic ataxia of Charlevoix- Saguenay (AR)	SACS	French Canadian (Saguenay-Lac-St- Jean)	1 in 21	1 in 2000
NM_014363.5		Pan-ethnic	≤1 in 500	Reduced
3ardet-Biedl syndrome (BBS10-related) (AR) NM_024685.3	BBS10	Pan-ethnic	1 in 354	1 in 35300
3ardet-Biedl syndrome (BBS12-related) (AR) NM_152618.2	BBS12	Pan-ethnic	1 in 708	Reduced
BBS1-related conditions (AR)	DDC1	Faroese	1 in 30	1 in 2900
VM_024649.4	BBS1	Pan-ethnic	1 in 330	1 in 32900
BS2-related conditions (AR)	BBS2	Ashkenazi Jewish	1 in 140	1 in 13900
IM_031885.3	BB27	Pan-ethnic	1 in 560	Reduced
		Caucasian	1 in 407	1 in 40600
BCS1L-related conditions (AR) NM_004328.4	BCS1L	Finnish	1 in 108	1 in 10700
NIVI_004528.4		Pan-ethnic	≤1 in 500	Reduced
Beta-ketothiolase deficiency (AR)	ACAT1	Caucasian	1 in 354	1 in 35300
IM_000019.3	ACATT	Pan-ethnic	≤1 in 500	Reduced
iopterin-deficient hyperphenylalaninemia (PTS-related)		Chinese	1 in 122	1 in 12100
AR) IM_000317.2	PTS	Pan-ethnic	1 in 433	1 in 43200
Bloom syndrome (AR)	BLM	Ashkenazi Jewish	1 in 100	1 in 9900
VM_000057.3	52.00	Pan-ethnic	≤1 in 500	Reduced
SND-related conditions (AR) NM_057176.2	BSND	Pan-ethnic	≤1 in 500	Reduced
Canavan disease (AR)	ASPA	Ashkenazi Jewish	1 in 57	1 in 5600
NM_000049.2	AJFA	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)	CPT1A	Hutterite	1 in 16	1 in 1500
NM_001876.3	CFIIA	Pan-ethnic	≤1 in 500	Reduced
Carnitine palmitoyltransferase II deficiency (AR)	CPT2	Ashkenazi Jewish	1 in 45	1 in 4400
VM_000098.2	CLIZ	Pan-ethnic	1 in 182	1 in 18100
Carpenter syndrome (RAB23-related) (AR) NM_183227.2	RAB23	Pan-ethnic	≤1 in 500	Reduced
Cartilage-hair hypoplasia-anauxetic dysplasia spectrum		Amish	1 in 10	1 in 900
lisorders (AR)	RMRP	Finnish	1 in 76	1 in 7500
IR_003051.3		Pan-ethnic	≤1 in 500	Reduced
DH23-related conditions (AR) IM_022124.5	CDH23	Pan-ethnic	1 in 202	1 in 4020
EP290-related conditions (AR) NM_025114.3	CEP290	Pan-ethnic	1 in 185	1 in 18400
Cerebrotendinous xanthomatosis (AR)		Pan-ethnic	1 in 112	1 in 5550
VM_000784.3	CYP27A1	Sephardic Jewish	1 in 76	1 in 3750
CERKL-related conditions (AR)	CED!//	Pan-ethnic	1 in 137	1 in 13600
NM_001030311.2	CERKL	Sephardic Jewish	1 in 24	1 in 2300



DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
		African-American - classic CF	1 in 61	1 in 6000
		Ashkenazi Jewish - classic CF	1 in 29	1 in 2800
CFTR-related conditions (AR)		Asian - classic CF	1 in 88	1 in 8700
NM_000492.3	CFTR	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
Charcot-Marie-Tooth disease type 4D (AR) NM_006096.3	NDRG1	Pan-ethnic Roma	≤1 in 500 1 in 22	Reduced 1 in 2100
Chorea-acanthocytosis (AR) NM_033305.2	VPS13A *	Pan-ethnic	≤1 in 500	Reduced
Chronic granulomatous disease (CYBA-related) (AR)		Pan-ethnic	≤1 in 500	Reduced
NM_000101.3	CYBA	Sephardic Jewish (Moroccan)	1 in 13	1 in 1200
		Chinese	1 in 65	1 in 6400
		Japanese	1 in 65	1 in 6400
Citrin deficiency (AR)	SLC25A13	Korean	1 in 112	1 in 11100
NM_014251.2		Pan-ethnic	1 in 313	1 in 31200
		Southern Chinese and Taiwanese	1 in 48	1 in 4700
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)		Ashkenazi Jewish	1 in 120	1 in 11900
NM_174878.2	CLRN1	Pan-ethnic	1 in 533	Reduced
Cobalamin C deficiency (AR) NM_015506.2	ММАСНС	Pan-ethnic	1 in 123	1 in 12200
Cobalamin D deficiency (AR) NM_015702.2	MMADHC *	Pan-ethnic	≤1 in 500	Reduced
Cockayne syndrome A (AR) NM_00082.3	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)	V/DC12D	Amish (Ohio)	1 in 12	1 in 1100
NM_017890.4	VPS13B	Pan-ethnic	≤1 in 500	Reduced
Combined malonic and methylmalonic aciduria (AR) NM_174917.4	ACSF3	Pan-ethnic	1 in 87	1 in 8600
Combined oxidative phosphorylation deficiency 1 (AR) NM_024996.5	GFM1	Pan-ethnic	≤1 in 500	Reduced
Combined oxidative phosphorylation deficiency 3 (AR)	тогм 🖈	Finnish	1 in 80	1 in 1129
NM_001172696.1	TSFM *	Pan-ethnic	≤1 in 500	Reduced
Combined pituitary hormone deficiency (LHX3-related) (AR) NM_014564.4	LHX3	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 3-beta- hydroxysteroid dehydrogenase deficiency (AR) NM_000198.3	HSD3B2	Pan-ethnic	≤1 in 500	Reduced
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 (SLC35A3-related)	CI 00774	Ashkenazi Jewish	1 in 469	1 in 46800
(AR) NM_012243.2	SLC35A3	Pan-ethnic	≤1 in 500	Reduced
		Ashkenazi Jewish	1 in 61	1 in 6000
Congenital disorder of glycosylation type Ia (AR)	PMM2	Caucasian	1 in 60	1 in 5900
NM_000303.2		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 insensitivity to pain with anhidrosis (AR) NM_001012331.1	NTRK1	Pan-ethnic	≤1 in 500	Reduced
Congenital myasthenic syndrome (CHRNE-related)		European Roma	1 in 25	1 in 2400
(AR) NM_000080.3	CHRNE	Pan-ethnic	1 in 200	1 in 19900
		Finnish	1 in 46	1 in 4500
Congenital nephrotic syndrome type 1 (AR)	NPHS1	Old Order Mennonite	1 in 12	1 in 1100
NM_004646.3		Pan-ethnic	≤1 in 500	Reduced
Congenital nephrotic syndrome type 2 (AR) NM_014625.3	NPHS2	Pan-ethnic	≤1 in 500	Reduced
Corneal dystrophy and perceptive deafness (AR) NM_032034.3	SLC4A11	Pan-ethnic	≤1 in 500	Reduced
CRB1-related conditions (AR) NM_201253.2	CRB1	Pan-ethnic	1 in 112	1 in 11100
CYP11B1-related conditions (AR)	CYP11B1	Pan-ethnic	1 in 194	1 in 19300
NM_000497.3	СТРПЫ	Sephardic Jewish (Moroccan)	1 in 40	1 in 3900
CYP17A1-related conditions (AR) NM_000102.3	CYP17A1	Pan-ethnic	≤1 in 500	Reduced
Cystinosis (AR)	CTNC	French Canadian (Saguenay-Lac-St- Jean)	1 in 39	1 in 3800
NM_004937.2	CTNS	Pan-ethnic	1 in 158	1 in 15700
		Sephardic Jewish (Moroccan)	1 in 100	1 in 9900
DHDDS-related conditions (AR)	DHDDS	Ashkenazi Jewish	1 in 117	1 in 11600
NM_024887.3	DHDD3	Pan-ethnic	≤1 in 500	Reduced
Dihydrolipoamide dehydrogenase deficiency (AR)	DLD	Ashkenazi Jewish	1 in 107	1 in 5300
NM_000108.4	DLD	Pan-ethnic	≤1 in 500	Reduced
Distal renal tubular acidosis with deafness		Pan-ethnic	≤1 in 500	Reduced
(ATP6V1B1-related) (AR) NM_001692.3	ATP6V1B1	Sephardic Jewish	1 in 140	1 in 13900
DYSF-related conditions (AR)	DYSF	Pan-ethnic	1 in 311	1 in 31000
NM_003494.3	DISF	Sephardic Jewish (Libyan)	1 in 10	1 in 900
Dyskeratosis congenita spectrum disorders		Ashkenazi Jewish	1 in 222	1 in 22100
(RTEL1-related) (AR) NM_001283009.1	RTEL1	Pan-ethnic	≤1 in 500	Reduced
Dystrophic epidermolysis bullosa (AR) NM_000094.3	COL7A1	Pan-ethnic	1 in 370	1 in 12300
Ehlers-Danlos syndrome, dermatosparaxis type (AR)	ADAMTS2	Ashkenazi Jewish	1 in 187	1 in 18600
NM_014244.4	ADAMT 32	Pan-ethnic	≤1 in 500	Reduced
Ellis-van Creveld syndrome (EVC-related) (AR)	EVC	Amish	1 in 8	1 in 700
NM_153717.2	LVC	Pan-ethnic	1 in 220	1 in 21900
Ethylmalonic encephalopathy (AR) NM_014297.3	ETHE1	Pan-ethnic	≤1 in 500	Reduced
EVC2-related conditions (AR) NM_147127.4	EVC2	Pan-ethnic	1 in 199	1 in 19800
Familial chylomicronemia syndrome (AR) NM 000237.2	LPL	French Canadian (Saguenay-Lac-St- Jean)	1 in 46	1 in 4500
<u>1111_000237.2</u>		Pan-ethnic	≤1 in 500	Reduced
Familial dysautonomia (AR)	ELP1	Ashkenazi Jewish	1 in 36	1 in 3500
NM_003640.3		Pan-ethnic	≤1 in 500	Reduced
		Afrikaner	1 in 72	1 in 7100
Familial hypercholesterolemia (LDLR-related) (AD)	LDLR	Ashkenazi Jewish	1 in 69	1 in 6800
NM_000527.4		French Canadian	1 in 270	1 in 26900
		Pan-ethnic	1 in 250	1 in 24900
Familial hypercholesterolemia (LDLRAP1-related) (AR)	LDLRAP1	Pan-ethnic	≤1 in 500	Reduced
NM_015627.2	2221011	Sardinian	1 in 143	1 in 14200
Fanconi anemia type A (AR)	FANCA	Afrikaner	1 in 83	1 in 8200
NM_000135.2		Pan-ethnic	1 in 345	1 in 34400



DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
		Sephardic Jewish	1 in 133	1 in 13200
		Spanish Roma	1 in 64	1 in 6300
Fanconi anemia type C (AR)	FANICO	Ashkenazi Jewish	1 in 89	1 in 8800
NM_000136.2	FANCC	Pan-ethnic	1 in 417	1 in 41600
Fanconi anemia type G (AR)	FANCG	African-American	1 in 100	1 in 9900
NM_004629.1	FANCG	Pan-ethnic	≤1 in 500	Reduced
FH-related conditions (AR) NM_000143.3	FH	Pan-ethnic	≤1 in 500	Reduced
Galactokinase deficiency galactosemia (AR)	GALK1	Pan-ethnic	1 in 122	1 in 12100
NM_000154.1	GALKI	Roma	1 in 47	1 in 4600
		African-American	1 in 87	1 in 8600
Galactosemia (GALT-related) (AR)	GALT	Ashkenazi Jewish	1 in 156	1 in 15500
NM_000155.3	GALI	Irish Traveller	1 in 11	1 in 1000
		Pan-ethnic	1 in 100	1 in 9900
GBA-related conditions including Gaucher disease (AR)	GBA *	Ashkenazi Jewish	1 in 15	1 in 234
NM_001005741.2	GBA ^	Pan-ethnic	1 in 158	1 in 561
GBE1-related conditions (AR)	CDEI	Ashkenazi Jewish	1 in 68	1 in 6700
NM_000158.3	GBE1	Pan-ethnic	1 in 387	1 in 38600
Gitelman syndrome (AR) NM_000339.2	SLC12A3	Pan-ethnic	1 in 100	1 in 9900
		Ashkenazi Jewish	1 in 13	1 in 1200
GJB2-related conditions (AR) NM_004004.5	GJB2	Pan-ethnic	1 in 50	1 in 4900
		Thai	1 in 9	1 in 800
		Pan-ethnic	1 in 158	1 in 15700
GLB1-related conditions (AR) NM_000404.2	GLB1	Roma	1 in 50	1 in 4900
	0101	South Brazilian	1 in 58	1 in 5700
GLE1-related conditions (AR)		Finnish	1 in 100	1 in 9900
VM_001003722.1	GLE1	Pan-ethnic	≤1 in 500	Reduced
		Amish	1 in 9	1 in 800
Glutaric acidemia type I (AR)	GCDH	Oji-Cree First Nations	1 in 9	1 in 800
NM_000159.3		Pan-ethnic	1 in 87	1 in 8600
Glutaric acidemia type IIA (AR) NM_000126.3	ETFA	Pan-ethnic	≤1 in 500	Reduced
Glutaric acidemia type IIC (AR)		Asian	1 in 87	1 in 8600
NM_004453.3	ETFDH	Pan-ethnic	1 in 250	1 in 24900
Glycine encephalopathy (AMT-related) (AR)		Finnish	1 in 142	1 in 14100
VM_000481.3	AMT	Pan-ethnic	1 in 325	1 in 32400
Glycine encephalopathy (GLDC-related) (AR)		Caucasian	1 in 141	1 in 14000
VM_000170.2	GLDC	Pan-ethnic	1 in 165	1 in 16400
Glycogen storage disease type Ia (AR)		Ashkenazi Jewish	1 in 71	1 in 1400
NM_000151.3	G6PC	Pan-ethnic	1 in 177	1 in 3520
		African-American	1 in 60	1 in 5900
Glycogen storage disease type II (Pompe disease) (AR)		Ashkenazi Jewish	1 in 58	1 in 5700
NM_000152.3	GAA	Asian	1 in 112	1 in 11100
	_	Pan-ethnic	1 in 100	1 in 9900
		Faroese	1 in 28	1 in 540
Glycogen storage disease type III (AR)	AGL	Pan-ethnic	1 in 159	1 in 3160
NM_000642.2	,.GL	Sephardic Jewish (Moroccan)	1 in 34	1 in 660
		Caucasian	1 in 158	1 in 15700
Glycogen storage disease type V (AR)	PYGM	Pan-ethnic	1 in 171	1 in 17000
NM_005609.3	FIGIVI	Sephardic Jewish (Kurdish)	1 in 84	1 in 8300
		Ashkenazi Jewish	1 in 250	1 in 24900
Glycogen storage disease type VII (AR) VM_000289.5	PFKM	,	≤1 in 500	
		Pan-ethnic		Reduced
GNE-related conditions (AR)	GNE	Pan-ethnic	1 in 179	1 in 17800
NM_001128227.2		Sephardic Jewish (Iranian)	1 in 10	1 in 900



DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
GNPTAB-related conditions (AR)	CHIPTAD	Irish Traveller	1 in 15	1 in 1400
NM_024312.4	GNPTAB	Pan-ethnic	1 in 200	1 in 19900
Guanidinoacetate methyltransferase deficiency (AR)	CANT	Pan-ethnic	≤1 in 500	Reduced
NM_000156.5	GAMT	Portuguese	1 in 125	1 in 12400
		Finnish	1 in 126	1 in 12500
Gyrate atrophy of the choroid and retina (AR) NM_000274.3	OAT *	Pan-ethnic	≤1 in 500	Reduced
100274.5		Sephardic Jewish	1 in 177	1 in 17600
		Caucasian	1 in 250	1 in 24900
HADHA-related conditions (AR) NM 000182.4	HADHA	Finnish	1 in 125	1 in 12400
		Pan-ethnic	1 in 350	1 in 34900
		African-American	1 in 8	1 in 700
		Asian	1 in 54	1 in 5300
HBB-related hemoglobinopathies (AR)	НВВ	Caucasian	1 in 373	1 in 37200
NM_000518.4	TIBB	Hispanic	1 in 17	1 in 1600
		Mediterranean	1 in 28	1 in 2700
		Pan-ethnic	1 in 49	1 in 4800
		African-American	1 in 226	1 in 22500
Hereditary fructose intolerance (AR) NM_000035.3	ALDOB	Middle Eastern	1 in 97	1 in 9600
101_000035.5	-	Pan-ethnic	1 in 122	1 in 12100
Hereditary hemochromatosis type 2 (HJV-related) (AR) NM_213653.3	HJV	Pan-ethnic	≤1 in 500	Reduced
Hereditary hemochromatosis type 3 (AR) NM_003227.3	TFR2	Pan-ethnic	≤1 in 500	Reduced
Hermansky-Pudlak syndrome type 1 (AR)	HPS1	Pan-ethnic	≤1 in 500	Reduced
NM_000195.4	пгэт	Puerto Rican (Northwestern)	1 in 21	1 in 2000
Hermansky-Pudlak syndrome type 3 (AR) NM_032383.4		Ashkenazi Jewish	1 in 235	1 in 23400
	HPS3	Pan-ethnic	≤1 in 500	Reduced
VIII_052505.4		Puerto Rican (Central)	1 in 63	1 in 6200
HGSNAT-related conditions (AR) NM_152419.2	HGSNAT	Pan-ethnic	≤1 in 500	Reduced
	HLCS	Faroese	1 in 20	1 in 1900
Holocarboxylase synthetase deficiency (AR) NM 000411.6		Japanese	1 in 158	1 in 15700
		Pan-ethnic	1 in 224	1 in 22300
Homocystinuria due to cobalamin E deficiency (AR) NM_002454.2	MTRR	Pan-ethnic	≤1 in 500	Reduced
Homocystinuria due to cystathionine beta-synthase		Norwegian	1 in 40	1 in 3900
deficiency (AR)	CBS	Pan-ethnic	1 in 224	1 in 22300
NM_000071.2	-	Qatari	1 in 21	1 in 2000
Homocystinuria due to MTHFR deficiency (AR)		Pan-ethnic	≤1 in 500	Reduced
NM_005957.4	MTHFR *	Sephardic Jewish (Bukharian)	1 in 39	1 in 3800
HSD17B4-related conditions (AR) NM_000414.3	HSD17B4	Pan-ethnic	1 in 158	1 in 15700
Hydrolethalus syndrome type 1 (AR)	HYLS1	Finnish	1 in 40	1 in 3900
NM_145014.2	HILSI	Pan-ethnic	≤1 in 500	Reduced
Hyperornithinemia-hyperammonemia-homocitrullinuria		Metis (Saskatchewan)	1 in 19	1 in 1800
syndrome (AR) NM_014252.3	SLC25A15	Pan-ethnic	≤1 in 500	Reduced
Hypophosphatasia (AR)	ALPL	Mennonite	1 in 25	1 in 480
NM_000478.5		Pan-ethnic	1 in 150	1 in 2980
sovaleric acidemia (AR) NM_002225.3	IVD	Pan-ethnic	1 in 250	1 in 24900
oubert syndrome and related disorders (MKS1-related)	N4WG3	Finnish	1 in 47	1 in 920
(AR) NM_017777.3	MKS1	Pan-ethnic	1 in 260	1 in 5180
Joubert syndrome and related disorders (RPGRIP1L- related) (AR) NM_015272.2	RPGRIP1L *	Pan-ethnic	1 in 259	1 in 5160



DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
Joubert syndrome and related disorders		Ashkenazi Jewish	1 in 92	1 in 9100
(TMEM216-related) (AR) NM_001173990.2	TMEM216	Pan-ethnic	≤1 in 500	Reduced
Junctional epidermolysis bullosa (LAMC2-related) (AR) NM_005562.2	LAMC2	Pan-ethnic	≤1 in 500	Reduced
KCNJ11-related conditions (AR) NM_000525.3	KCNJ11	Pan-ethnic	≤1 in 500	Reduced
Krabbe disease (AR)	GALC *	Druze	1 in 6	1 in 500
NM_000153.3	GALC	Pan-ethnic	1 in 158	1 in 15700
AMA2-related muscular dystrophy (AR) NM_000426.3	LAMA2	Pan-ethnic	1 in 87	1 in 8600
AMA3-related conditions (AR) NM_000227.4	LAMA3	Pan-ethnic	≤1 in 500	Reduced
_AMB3-related conditions (AR) NM_000228.2	LAMB3	Pan-ethnic	1 in 317	1 in 31600
_eber congenital amaurosis 5 (AR) NM_181714.3	LCA5	Pan-ethnic	1 in 645	Reduced
Leukoencephalopathy with vanishing white matter (EIF2B5-related) (AR) NM_003907.2	EIF2B5	Pan-ethnic	≤1 in 500	Reduced
_imb-girdle muscular dystrophy (CAPN3-related) (AR) NM_000070.2	CAPN3	Pan-ethnic	1 in 134	1 in 13300
		Caucasian	1 in 571	Reduced
imb girdle mussular dustrenky type 2C (AD)		Japanese	1 in 374	1 in 37300
.imb-girdle muscular dystrophy type 2C (AR) IM_000231.2	SGCG	Moroccan	1 in 250	1 in 24900
NM_000231.2		Pan-ethnic	≤1 in 500	Reduced
		Roma	1 in 59	1 in 5800
Limb-girdle muscular dystrophy type 2D (AR) NM_000023.2		Caucasian	1 in 286	1 in 28500
	SGCA	Finnish	1 in 150	1 in 14900
		Pan-ethnic	≤1 in 500	Reduced
imb-girdle muscular dystrophy type 2E (AR)	SGCB	Caucasian	1 in 404	1 in 5038
VM_000232.4	3000	Pan-ethnic	≤1 in 500	Reduced
ipoid congenital adrenal hyperplasia (AR)	STAR	Korean	1 in 170	1 in 16900
IM_000349.2	5774	Pan-ethnic	≤1 in 500	Reduced
usinuria protain intelerance (AD)		Finnish	1 in 120	1 in 2380
ysinuric protein intolerance (AR) IM_001126106.2	SLC7A7	Japanese	1 in 120	1 in 2380
		Pan-ethnic	≤1 in 500	Reduced
versemel seid linese deficienzy (AD)		Caucasian	1 in 112	1 in 1850
ysosomal acid lipase deficiency (AR) IM 000235.3	LIPA	Pan-ethnic	1 in 359	1 in 5967
		Sephardic Jewish (Iranian)	1 in 33	1 in 534
Major histocompatibility complex class II deficiency CIITA-related) (AR) NM_000246.3	CIITA	Pan-ethnic	≤1 in 500	Reduced
Maple syrup urine disease type 1A (AR)	BCKDHA	Mennonite	1 in 10	1 in 900
NM_000709.3	BCKDHA	Pan-ethnic	1 in 373	1 in 37200
Maple syrup urine disease type 1B (AR)	BCKDHB	Ashkenazi Jewish	1 in 97	1 in 9600
NM_183050.2 Maple syrup urine disease type 2 (AR)		Pan-ethnic	1 in 346	1 in 34500
NM_001918.3	DBT	Pan-ethnic	≤1 in 500	Reduced
/ledium-chain acyl-CoA dehydrogenase deficiency (AR) IM_000016.5	ACADM	Northern European	1 in 40	1 in 3900
		Pan-ethnic	1 in 66	1 in 6500
Aegalencephalic leukoencephalopathy with subcortical ysts 1 (AR)	MLC1	Pan-ethnic	≤1 in 500	Reduced
и́м_015166.3		Sephardic Jewish (Libyan)	1 in 40	1 in 3900
Aetachromatic leukodystrophy (ARSA-related) (AR)		Navajo	1 in 40	1 in 780
VM_000487.5	ARSA	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



DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
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
MFSD8-related conditions (AR) NM_152778.2	MFSD8	Pan-ethnic	≤1 in 500	Reduced
Microcephaly, postnatal progressive, with seizures and		Pan-ethnic	≤1 in 500	Reduced
brain atrophy (AR) NM_004268.4	MED17	Sephardic Jewish	1 in 20	1 in 1900
Mitochondrial complex I deficiency 9 (AR)		Ashkenazi Jewish	1 in 290	1 in 28900
NM_004553.4	NDUFS6	Caucasus Jewish	1 in 24	1 in 2300
		Pan-ethnic	≤1 in 500	Reduced
Mitochondrial complex I deficiency 16 (AR)	NDUFAF5	Ashkenazi Jewish	1 in 290	1 in 28900
NM_024120.4 Mitochondrial complex I deficiency 20/ACAD9 deficiency (AR) NM_014049.4	ACAD9	Pan-ethnic Pan-ethnic	≤1 in 500 ≤1 in 500	Reduced Reduced
Mitochondrial complex IV deficiency / Leigh syndrome, French Canadian type (AR)	LRPPRC	French Canadian (Saguenay-Lac-St- Jean)	1 in 23	1 in 2200
NM_133259.3		Pan-ethnic	≤1 in 500	Reduced
Mitochondrial neurogastrointestinal		Pan-ethnic	≤1 in 500	Reduced
encephalomyopathy (AR) NM_001953.4	ТҮМР	Sephardic Jewish	1 in 158	1 in 15700
MPL-related conditions (AR)	MPL	Ashkenazi Jewish	1 in 57	1 in 5600
NM_005373.2		Pan-ethnic	≤1 in 500	Reduced
MPV17-related conditions (AR) NM_002437.4	MPV17	Navajo	1 in 20	1 in 475
Mu_002437.4 Mucolipidosis type III gamma (AR) NM_032520.4	GNPTG	Pan-ethnic Pan-ethnic	≤1 in 500 ≤1 in 500	Reduced
Mucolipidosis type IV (AR)		Ashkenazi Jewish	1 in 100	1 in 9900
NM_020533.2	MCOLN1	Pan-ethnic	≤1 in 500	Reduced
Mucopolysaccharidosis type I (AR) NM_000203.4	IDUA	Pan-ethnic	1 in 148	1 in 4900
		Northern European	1 in 173	1 in 17200
Mucopolysaccharidosis type IIIA (AR) NM_000199.3	SGSH	Pan-ethnic	1 in 215	1 in 21400
NNI_000199.5		Taiwanese	≤1 in 500	Reduced
Mucopolysaccharidosis type IIIB (AR) NM_000263.3	NAGLU	Pan-ethnic	1 in 224	1 in 22300
Mucopolysaccharidosis type IIID (AR) NM_002076.3	GNS	Pan-ethnic	≤1 in 500	Reduced
Mucopolysaccharidosis type IX (AR) NM_153281.1	HYAL1	Pan-ethnic	≤1 in 500	Reduced
Mucopolysaccharidosis type VI (AR) NM_000046.3	ARSB	Pan-ethnic	1 in 250	1 in 24900
Multiple sulfatase deficiency (AR) NM_182760.3	SUMF1	Pan-ethnic	≤1 in 500	Reduced
Muscular dystrophy-dystroglycanopathy (FKRP-related)	EKDD	Norwegian	1 in 116	1 in 11500
(AR) NM_024301.4	FKRP	Pan-ethnic	1 in 158	1 in 15700
Muscular dystrophy-dystroglycanopathy (FKTN-related)		Ashkenazi Jewish	1 in 80	1 in 7900
(AR) NM_001079802.1	FKTN	Japanese	1 in 188	1 in 18700
MM_001079802.1 MYO7A-related conditions (AR)	MYOZA	Pan-ethnic	≤1 in 500	Reduced
NM_000260.3 Myopathy, lactic acidosis, and sideroblastic anemia 1	MYO7A	Pan-ethnic	1 in 200	1 in 3980
(AR) NM_025215.5	PUS1	Pan-ethnic	≤1 in 500	Reduced
N-acetylglutamate synthase deficiency (AR) NM_153006.2	NAGS	Pan-ethnic	≤1 in 500	Reduced
Nemaline myopathy 2 (AR)	NEB *	Ashkenazi Jewish	1 in 108	1 in 10700
NM_001271208.1		Pan-ethnic	1 in 158	1 in 3140



DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
Nephrogenic diabetes insipidus (AQP2-related) (AR) NM_000486.5	AQP2	Pan-ethnic	1 in 1118	Reduced
Neuronal ceroid lipofuscinosis type 1 (AR)	PPT1	Finnish	1 in 70	1 in 3450
NM_000310.3	FFII	Pan-ethnic	1 in 199	1 in 9900
Neuronal ceroid lipofuscinosis type 2 (AR)	TPP1	Newfoundland	1 in 53	1 in 1734
NM_000391.3	11771	Pan-ethnic	1 in 250	1 in 8300
Neuronal ceroid lipofuscinosis type 5 (AR)	CLN5	Finnish	1 in 115	1 in 11400
NM_006493.2	CENS	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)	SMPD1	Ashkenazi Jewish	1 in 90	1 in 1780
NM_000543.4	5	Pan-ethnic	1 in 250	1 in 4980
Nijmegen breakage syndrome (AR)	NBN *	Eastern European	1 in 155	1 in 15400
NM_002485.4		Pan-ethnic	≤1 in 500	Reduced
Nonsyndromic deafness (LOXHD1-related) (AR)	LOXHD1	Ashkenazi Jewish	1 in 180	1 in 17900
NM_144612.6	-	Pan-ethnic	≤1 in 500	Reduced
NR2E3-related conditions (AR) NM_014249.3	NR2E3	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
Osteopetrosis (TCIRG1-related) (AR) NM_006019.3		Ashkenazi Jewish	1 in 350	1 in 34900
	TCIRG1	Chuvash	1 in 30	1 in 2900
		Pan-ethnic	1 in 317	1 in 31600
PCDH15-related conditions (AR)	PCDH15	Ashkenazi Jewish	1 in 78	1 in 7700
NM_033056.3	rebins	Pan-ethnic	1 in 400	1 in 39900
PEX7-related conditions (AR) NM_000288.3	PEX7	Pan-ethnic	1 in 157	1 in 15600
	РАН	African-American	1 in 111	1 in 11000
		Ashkenazi Jewish	1 in 225	1 in 22400
		East Asian	1 in 50	1 in 1225
Phenylalanine hydroxylase deficiency (AR)		Finnish	1 in 225	1 in 22400
NM_000277.1		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
Phosphoglycerate dehydrogenase deficiency (AR)	PHGDH	Ashkenazi Jewish	1 in 400	1 in 39900
NM_006623.3	FIGDI	Pan-ethnic	≤1 in 500	Reduced
Polycystic kidney disease (PKHD1-related) (AR) NM_138694.3	PKHD1	Pan-ethnic	1 in 70	1 in 6900
Polymicrogyria (ADGRG1-related) (AR) NM_005682.6	ADGRG1	Pan-ethnic	≤1 in 500	Reduced
POMGNT1-related conditions (AR)	POMGNT1	Finnish	1 in 111	1 in 11000
NM_017739.3	FOINGINT	Pan-ethnic	≤1 in 500	Reduced
Pontocerebellar hypoplasia type 2D (AR)		Pan-ethnic	≤1 in 500	Reduced
NM_016955.3	SEPSECS	Sephardic Jewish (Moroccan and Iraqi)	1 in 43	1 in 4200
Pontocerebellar hypoplasia type 6 (AR) NM_020320.3	RARS2	Pan-ethnic	≤1 in 500	Reduced
		Faroese	1 in 9	1 in 800
Primary carnitine deficiency (AR)	SLC22A5	Japanese	1 in 100	1 in 9900
NM_003060.3		Pan-ethnic	1 in 71	1 in 7000



DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
Primary ciliary dyskinesia (DNAH5-related) (AR) NM_001369.2	DNAH5	Pan-ethnic	1 in 109	1 in 10800
Primary ciliary dyskinesia (DNAI1-related) (AR) NM_012144.3	DNAI1	Pan-ethnic	1 in 250	1 in 24900
Primary ciliary dyskinesia (DNAI2-related) (AR)	DNIAID	Ashkenazi Jewish	1 in 200	1 in 19900
NM_023036.4	DNAI2	Pan-ethnic	1 in 354	1 in 35300
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)	PCCA	Arab	1 in 100	1 in 2475
NM_000282.3	FCCA	Pan-ethnic	1 in 224	1 in 5575
Proping acidemia (PCCP related) (AP)		Arab	1 in 100	1 in 9900
Propionic acidemia (PCCB-related) (AR) NM_000532.4	PCCB	Greenlandic Inuit	1 in 20	1 in 1900
NW_000552.4		Pan-ethnic	1 in 224	1 in 22300
PSAP-related conditions (AR) NM_002778.3	PSAP	Pan-ethnic	≤1 in 500	Reduced
Pycnodysostosis (AR) NM_000396.3	СТЅК	Pan-ethnic	1 in 438	1 in 43700
Pyruvate carboxylase deficiency (AR)	PC	Algonquian Indian	1 in 10	1 in 180
NM_000920.3	PC	Pan-ethnic	1 in 250	1 in 4980
Pyruvate dehydrogenase complex deficiency (PDHB- related) (AR) NM_000925.3	PDHB	Pan-ethnic	≤1 in 500	Reduced
RAPSN-related conditions (AR) NM_005055.4	RAPSN	Pan-ethnic	1 in 283	1 in 28200
RDH12-related conditions (AR) NM_152443.2	RDH12	Pan-ethnic	1 in 460	1 in 45900
Retinitis pigmentosa 25 (AR)	EYS	Pan-ethnic	1 in 129	1 in 12800
NM_001142800.1	ETS	Sephardic Jewish	1 in 42	1 in 4100
		Ashkenazi Jewish	1 in 214	1 in 21300
Retinitis pigmentosa 28 (AR) NM_001201543.1	FAM161A	Pan-ethnic	1 in 289	1 in 28800
NW_001201343.1		Sephardic Jewish	1 in 41	1 in 4000
Rhizomelic chondrodysplasia punctata type 3 (AR) NM_003659.3	AGPS	Pan-ethnic	≤1 in 500	Reduced
Roberts syndrome (AR) NM_001017420.2	ESCO2	Pan-ethnic	≤1 in 500	Reduced
RPE65-related conditions (AR)	DDECE	Pan-ethnic	1 in 228	1 in 22700
NM_000329.2	RPE65	Sephardic Jewish	1 in 90	1 in 8900
Sandhoff disease (AR)		Metis (Saskatchewan)	1 in 15	1 in 1400
NM_000521.3	HEXB	Pan-ethnic	1 in 180	1 in 17900
Schimke immuno-osseous dysplasia (AR) NM_014140.3	SMARCAL1	Pan-ethnic	≤1 in 500	Reduced
Severe combined immunodeficiency due to DCLRE1C		Navajo and Apache	1 in 10	1 in 900
(Artemis) deficiency (AR) NM_001033855.2	DCLRE1C	Pan-ethnic	≤1 in 500	Reduced
Severe combined immunodeficiency due to RAG2 deficiency (AR) NM_000536.3	RAG2	Pan-ethnic	≤1 in 500	Reduced
Severe congenital neutropenia due to HAX1 deficiency (AR) NM_006118.3	HAX1	Pan-ethnic	≤1 in 500	Reduced
Severe congenital neutropenia due to VPS45 deficiency (AR) NM_007259.4	VPS45	Pan-ethnic	≤1 in 500	Reduced
Sialic acid storage diseases (AR)	CI C1745	Finnish	1 in 100	1 in 9900
NM_012434.4	SLC17A5	Pan-ethnic	≤1 in 500	Reduced
Sjögren-Larsson syndrome (AR)		Pan-ethnic	≤1 in 500	Reduced
NM_000382.2	ALDH3A2	Swedish	1 in 250	1 in 24900



DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
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
Spastic paraplegia type 49 (AR) NM_014844.3	TECPR2	Pan-ethnic	≤1 in 500	Reduced
	TECPRZ	Sephardic Jewish - Bukharian	1 in 38	1 in 3700
Spinal muscular atrophy (AR) NM_000344.3 SMN1: 2 copies		African-American	1 in 59	1 in 342
		Ashkenazi Jewish	1 in 62	1 in 1017
		Asian	1 in 50	1 in 701
c.*3+80T>G not detected Carrier residual risks listed are for 2 copy SMN1 results.	SMN1 *	Caucasian	1 in 45	1 in 880
Carrier residual risk for >2 copies are 5- to 10-fold		Hispanic	1 in 48	1 in 784
lower.		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
Steel syndrome (AR)		Pan-ethnic	≤1 in 500	Reduced
NM_032888.3	COL27A1 *	Puerto Rican	1 in 51	1 in 5000
Stüve-Wiedemann syndrome (AR) NM_002310.5	LIFR	Pan-ethnic	≤1 in 500	Reduced
	НЕХА	Ashkenazi Jewish	1 in 27	1 in 2600
		Asian	1 in 126	1 in 12500
		Caucasian	1 in 182	1 in 18100
Tay-Sachs disease (AR)		French Canadian	1 in 27	1 in 2600
NM_000520.4		Irish	1 in 41	1 in 4000
		Pan-ethnic	1 in 250	1 in 24900
		Sephardic Jewish	1 in 125	1 in 12400
Transient infantile liver failure (AR)	TDM	Pan-ethnic	≤1 in 500	Reduced
NM_018006.4	TRMU	Sephardic Jewish (Yemenite)	1 in 34	1 in 3300
Tyrosine hydroxylase deficiency (AR) NM_199292.2	тн	Caucasian	1 in 224	1 in 22300
		Pan-ethnic	≤1 in 500	Reduced
	FAH *	Ashkenazi Jewish	1 in 143	1 in 2840
Tyrosinemia type I (AR) NM_000137.2		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



DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
Very long-chain acyl-CoA dehydrogenase deficiency (AR) NM_00018.3	ACADVL	Pan-ethnic	1 in 100	1 in 9900
VRK1-related conditions (AR) NM_003384.2	VRK1	Ashkenazi Jewish	1 in 225	1 in 22400
		Pan-ethnic	≤1 in 500	Reduced
VSX2-related conditions (AR) NM_182894.2	VSX2	Pan-ethnic	≤1 in 500	Reduced
		Sephardic Jewish	1 in 145	1 in 14400
Wilson disease (AR) NM_000053.3	АТР7В	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
WNT10A-related conditions (AR) NM_025216.2	WNT10A	Pan-ethnic	1 in 305	1 in 30400
Xeroderma pigmentosum complementation group A (AR) NM_000380.3	ХРА	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 - α 3.7 subtypes, and all - α 3.7 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: ABCB11 (NM_003742.2), ABCC8 (NM_000352.4), ACAD9 (NM_014049.4), ACADM (NM_000016.5), ACADVL (NM_000018.3), ACAT1 (NM_000019.3), ACOX1 (NM_004035.6), ACSF3 (NM_174917.4), ADA (NM_000022.2), ADAMTS2 (NM_014244.4), ADGRG1 (NM_005682.6), AGA (NM_000027.3), AGL (NM_000642.2), AGPS (NM_003659.3), 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), AQP2 (NM_000486.5), ARG1 (NM_000045.3), ARSA (NM_000487.5), ARSB (NM_000046.3), ASL (NM_000048.3), ASNS (NM_133436.3), ASPA (NM_000049.2), ASS1 (NM_000050.4), ATM (NM_000051.3), ATP6V1B1 (NM_001692.3), 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), BSND (NM_057176.2), CAPN3 (NM_000070.2), CBS (NM_000071.2), CDH23 (NM_022124.5), CEP290 (NM_025114.3), CERKL (NM_001030311.2), CFTR (NM_000492.3), CHRNE (NM_000080.3), CIITA (NM_000246.3), CLN3 (NM_001042432.1), CLN5 (NM_006493.2), CLN6 (NM_017882.2), CLN8 (NM_018941.3), CLRN1 (NM_174878.2), CNGB3 (NM_019098.4), COL27A1 (NM_032888.3), COL4A3 (NM_000091.4), COL4A4 (NM_000092.4), COL7A1 (NM_000094.3), CPS1 (NM_001875.4), CPT1A (NM_001876.3), CPT2 (NM_000098.2), CRB1 (NM_201253.2), CTNS (NM_004937.2), CTSK (NM_000396.3), CYBA (NM_000101.3), CYP11B1 (NM_000497.3), CYP11B2 (NM_000498.3), CYP17A1 (NM_000102.3), CYP19A1 (NM_031226.2), CYP21A2 (NM_000500.7), CYP27A1 (NM_000784.3), DBT (NM_001918.3), DCLRE1C (NM_001033855.2), DHCR7 (NM_001360.2), DHDDS (NM_024887.3), DLD (NM_000108.4), DNAH5 (NM_001369.2), DNAI1 (NM_012144.3), DNAI2 (NM_023036.4), DYSF (NM_003494.3), EIF2B5 (NM_003907.2), ELP1 (NM_003640.3), ERCC6 (NM_000124.3), ERCC8 (NM_000082.3), ESCO2 (NM_001017420.2), ETFA (NM_000126.3), ETFDH (NM_004453.3), ETHE1 (NM_014297.3), EVC (NM_153717.2), EVC2 (NM_147127.4), EVS (NM_001142800.1), FAH (NM_000137.2), FAM161A (NM_001201543.1), FANCA (NM_000135.2), FANCC (NM_000136.2), FANCG (NM_004629.1), FH (NM_000143.3), FKRP (NM_024301.4), FKTN (NM_001079802.1), G6PC (NM_000151.3), GAA (NM_000152.3), GALC (NM_000153.3), GALK1 (NM_000154.1), GALT (NM_000155.3), GAMT (NM_000156.5), GBA (NM_001005741.2), GBE1 (NM_000158.3), GCDH (NM_000159.3), GFM1 (NM_024996.5), GJB2 (NM_004004.5), GLB1 (NM_000404.2), GLDC (NM_000170.2), GLE1 (NM_001003722.1), GNE (NM_001128227.2), GNPTAB (NM_024312.4), GNPTG (NM_032520.4), GNS (NM_002076.3), GRHPR (NM_012203.1), HADHA (NM_000182.4), HAX1 (NM_006118.3), HBA1 (NM_000558.4), HBA2 (NM_000517.4), HBB (NM_000518.4), HEXA (NM_000520.4), HEXB (NM_000521.3), HGSNAT (NM_152419.2), HJV (NM_213653.3), HLCS (NM_000411.6), HMGCL (NM_000191.2), HOGA1 (NM_138413.3), HPS1 (NM_000195.4), HPS3 (NM_032383.4), HSD17B4 (NM_000414.3), HSD3B2 (NM_000198.3), HYAL1 (NM_153281.1), HYLS1 (NM_145014.2), IDUA (NM_000203.4), IVD (NM_002225.3), KCNJ11 (NM_000525.3), LAMA2 (NM_000426.3), LAMA3 (NM_000227.4), LAMB3 (NM_000228.2), LAMC2 (NM_005562.2), LCA5 (NM_181714.3), LDLR (NM_000527.4), LDLRAP1 (NM_015627.2), LHX3 (NM_014564.4), LIFR (NM_002310.5), LIPA (NM_000235.3), LOXHD1 (NM_144612.6), LPL (NM_000237.2), LRPPRC (NM_133259.3), MAN2B1 (NM_000528.3), MCOLN1 (NM_020533.2), MED17 (NM_004268.4), MESP2 (NM_001039958.1), MFSD8 (NM_152778.2), MKS1 (NM_017777.3), MLC1 (NM_015166.3), MMAA (NM_172250.2), MMAB (NM_052845.3), MMACHC (NM_015506.2), MMADHC (NM_015702.2), MPI (NM_002435.2), MPL (NM_005373.2), MPV17 (NM_002437.4), MTHFR (NM_005957.4), MTRR (NM_002454.2), MTTP (NM_000253.3), MUT (NM_000255.3), MYO7A (NM_000260.3), NAGLU (NM_000263.3), NAGS (NM_153006.2), NBN (NM_002485.4), NDRG1 (NM_006096.3), NDUFAF5 (NM_024120.4), NDUFS6 (NM_004553.4), NEB (NM_001271208.1), NPC1 (NM_000271.4), NPC2 (NM_006432.3), NPHS1 (NM_004646.3), NPHS2 (NM_014625.3), NR2E3 (NM_014249.3), NTRK1 (NM_001012331.1), OAT (NM_000274.3), OPA3 (NM_025136.3), PAH (NM_000277.1), PC (NM_000920.3), PCCA (NM_000282.3), PCCB (NM_000532.4), PCDH15 (NM_033056.3), PDHB (NM_000925.3), PEX1 (NM_000466.2), PEX10 (NM_153818.1), PEX12 (NM_000286.2), PEX2 (NM_000318.2), PEX6 (NM_000287.3), PEX7 (NM_000288.3), PFKM (NM_000289.5), PHGDH (NM_006623.3), PKHD1 (NM_138694.3), PMM2 (NM_000303.2), POMGNT1 (NM_017739.3), PPT1 (NM_000310.3), PROP1 (NM_006261.4), PSAP (NM_002778.3), PTS (NM_000317.2), PUS1 (NM_025215.5), PYGM (NM_005609.3), RAB23 (NM_183227.2), RAG2 (NM_000536.3), RAPSN (NM_005055.4), RARS2 (NM_020320.3), RDH12 (NM_152443.2), RMRP (NR_003051.3), RPE65 (NM_000329.2), RPGRIP1L (NM_015272.2), RTEL1 (NM_001283009.1), SACS (NM_014363.5), SAMHD1 (NM_015474.3), SEPSECS (NM_016955.3), SGCA (NM_000023.2), SGCB (NM_000232.4), SGCG (NM_000231.2), SGSH (NM_000199.3), SLC12A3 (NM_000339.2), SLC12A6 (NM_133647.1), SLC17A5 (NM_012434.4), SLC22A5 (NM_003060.3), SLC25A13 (NM_014251.2), SLC25A15 (NM_014252.3), SLC26A2 (NM_000112.3), SLC26A4 (NM_000441.1), SLC35A3



(NM_012243.2), SLC37A4 (NM_001164277.1), SLC39A4 (NM_130849.3), SLC4A11 (NM_032034.3), SLC7A7 (NM_001126106.2), SMARCAL1 (NM_014140.3), SMN1 (NM_000344.3), SMPD1 (NM_000543.4), STAR (NM_000349.2), SUMF1 (NM_182760.3), TAT (NM_000353.2), TCIRG1 (NM_006019.3), TECPR2 (NM_014844.3), TFR2 (NM_003227.3), TGM1 (NM_000359.2), TH (NM_199292.2), TMEM216 (NM_001173990.2), TPP1 (NM_000391.3), TRMU (NM_018006.4), TSFM (NM_001172696.1), TTPA (NM_000370.3), TYMP (NM_001953.4), USH1C (NM_005709.3), USH2A (NM_206933.2), VPS13A (NM_033305.2), VPS13B (NM_017890.4), VPS45 (NM_007259.4), VRK1 (NM_003384.2), VSX2 (NM_182894.2), WNT10A (NM_025216.2), 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.</p>
- RPGRIP1L: Sequencing analysis is not offered for exon 23. 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". 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. 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. TSFM: Sequencing analysis is not offered for exon 5. OAT: Deletion/duplication analysis is not offered for exon 2. VPS13A: Deletion/duplication analysis is not offered for exons 2-3, 27-28. MMADHC: Deletion/duplication analysis is not offered for exons 5-6. ALG6: Deletion/duplication analysis is not offered for exons 11-12. COL27A1: Deletion/duplication analysis is not offered for exons 46-47. MTHFR: The NM_005957.4:c.665C>T (p.Ala222Val) (aka 677C>T) and c.1286A>C (p.Glu429Ala) (aka 1298A>C) variants are not reported in our primary report. SMN1 or SMN2: NM_000344.3:c.*3+80T>G variant only. 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.

This report has been reviewed and approved by:

Im behlm anz

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