INVITAE

INVITAE CARRIER SCREEN RESULTS

Patient name:	[redacted]	**Sample type:**	B ood	**Report date:**	11/26/2021
DOB:	[redacted]	**Sample collection date:**	11/05/2021	[redacted]	[redacted]
Sex assigned at birth:	Ma e	**Sample accession date:**	11/19/2021	**Clinical team:**	M th a Be ekar
Gender:		**MRN:**			

Reason for testing

Gamete donor

Test performed

Inv tae Carr er Screen

- Inv tae pr mary pane (CF, SMA)
- Add on genes

RESULT: POSITIVE

This ca ie test eva uated 283 gene(s) fo genetic changes (va iants) that a e associated with an inc eased isk of having a chi d with a genetic condition. Know edge of ca ie status fo one of these conditions may p ovide info mation that can be used to assist with fami y p anning and/o p epa ation.

This test shows the p esence of c inica y significant genetic change(s) in this individua in the gene(s) indicated be ow. No othe c inica y significant changes we e identified in the emaining genes eva uated with this test.

RESULTS	GENE	VARIANT(S)	INHERITANCE	PARTNER TESTING RECOMMENDED
Carrier: GNE- e a ed cond ons	GNE	c 2179G>A (p Va 727Me)	Au osoma ecess ve	Yes

Next steps

- See the tab e above fo ecommendations ega ding testing of this individua s ep oductive pa tne .
- Even fo genes that have a negative test esu t, the e is a ways a sma isk that an individua cou d sti be a ca ie . This is ca ed " esidua isk." See the tab e be ow fo esidua isks, which p esumes a negative fami y histo y of the conditions isted.
- Genetic counse ing is ecommended to fu the exp ain the imp ications of this test esu t and assess fami y hea th histo y, which may point to hea th info mation that me its additiona conside ation.
- A patients, ega d ess of esu t, may wish to conside additiona sc eening fo hemog obinopathies by comp ete b ood count (CBC) and hemog obin e ect opho esis, if this has not a eady been comp eted.
- Individua s can egiste thei tests at https://www.invitae.com/patients/ to access on ine esu ts, educationa esou ces, and next steps.

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Clinical summary

RESULT: CARRIER

GNE-related conditions

A s ng e Pathogen c var ant c 2179G>A (p Va 727Met) was dent f ed n GNE

What are GNE-related conditions?

The GNE gene s assoc ated w th mu t p e cond t ons that can have both d st nct and over app ng symptoms as we as d fferent nher tance patterns GNE re ated cond t ons nc ude autosoma recess ve myopathy and autosoma dom nant s a ur a To understand wh ch cond t on a genet c change s assoc ated w th a rev ew of the ent re repo t nc ud ng the var ant deta s sect on s recommended

P ease note that the GNE var ant dent f ed n th s nd v dua s expected to be assoc ated w th autosoma recess ve myopathy

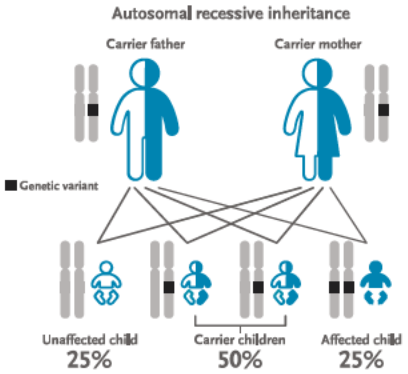
GNE re ated myopathy a so ca ed nc us on body myopathy 2 s a cond t on wh ch affects the neuromuscu ar system Symptoms typ ca y present n the ate teens to ear y adu thood w th s ow y progress ve musc e weakness (myopathy) n the musc es away from the center of the body (d sta musc es) espec a y n the ower egs and feet as we as foot drop nduced ga t d ff cu t es due to musc e weakness The myopathy progresses to nvo ve the upper mbs as we as the eg musc es c osest to the body (prox ma musc es) w th marked spar ng of the quadr ceps Affected nd v dua s often eventua y ose the ab ty to wa k Invo vement of the heart musc e s not a c ass c feature of GNE re ated myopathy a though t has been reported Fo ow up depends on each affected nd v dua 's spec f c s tuat on and d scuss on w th a hea thcare prov der shou d be cons dered

Next steps

Carr er test ng for the reproduct ve partner s recommended

If your partner tests positive:

In autosoma recess ve nher tance an nd v dua must have d sease caus ng genet c changes n each copy of the GNE gene to be affected Carr ers who have a d sease caus ng genet c change n on y one copy of the gene typ ca y do not have symptoms When both reproduct ve partners are carr ers of an autosoma recess ve cond t on there s a 25% chance for each ch d to have the cond t on



If your partner tests negative:

A negat ve carr er test resu t reduces but does not e m nate the chance that a person may be a carr er The r sk that a person cou d st be a carr er even after a negat ve test resu t s ca ed a res dua r sk See the tab e be ow for your partner's hypothet ca res dua r sk after test ng negat ve for GNE re ated cond t ons These va ues are prov ded on y as a gu de are based on the detect on rate for the cond t on as tested at Inv tae and assume a negat ve fam y h sto y the absence of symptoms and vary based on the ethn c background of an nd v dua For genes assoc ated w th both dom nant and recess ve nher tance the numbers prov ded app y to the recess ve cond t on(s) assoc ated w th the gene

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
GNE-re a ed cond ons (AR) NM 001128227 2	GNE	Pan-e hn c	1 n 179	1 n 17800
		Sephard c Jew sh (ran an)	1 n 10	1 n 900

Results to note

Pseudodeficiency allele

Ben gn change c 1685T>C (p I e562Thr) known to be a pseudodef c ency a e e dent f ed n the GALC gene Pseudodef c ency a e es are not known to be assoc ated w th d sease nc ud ng Krabbe d sease

The presence of a pseudodef c ency a e e does not mpact th s nd v dua s r sk to be a carr er Ind v dua s w th pseudodef c ency a e es may exh b t fa se pos t ve resu ts on re ated b ochem ca tests nc ud ng newborn screen ng however pseudodef c ency a e es are not known to cause d sease nc ud ng Krabbe d sease Carr er test ng for the reproduct ve partner s not nd cated

Variant details

GNE, Exon 12, c.2179G>A (p.Val727Met), eterozygous, PATHOGENIC

- Th s sequence change rep aces va ne wh ch s neutra and non po ar w th meth on ne wh ch s neutra and non po ar at codon 727 of the GNE prote n (p Va 727Met)
- Th s var ant s present n popu at on databases (rs121908627 gnomAD 1 4%) nc ud ng at east one homozygous and/or hem zygous nd v dua
- Th s m ssense change has been observed n nd v dua (s) w th GNE myopathy/d sta myopathy w th r mmed vacuo es (PMID 11528398 12497639 20175955 21708040 23437777 24005727 25182749 27829678 28320138 28717665) In at east one nd v dua the data s cons stent w th be ng n trans (on the oppos te chromosome) from a pathogen c var ant It has a so been observed to segregate w th d sease n re ated nd v dua s
- Th s var ant s a so known as p Va 696Met
- C nVar conta ns an entry for th s var ant (Var at on ID 6028)
- Advanced mode ng of prote n sequence and b ophys ca propert es (such as structura funct ona and spat a nformat on am no ac d conservat on phys cochem ca var at on res due mob ty and thermodynam c stab ty) pe formed at Inv tae nd cates that th s m ssense var ant s expected to d srupt GNE prote n funct on
- For these reasons th s var ant has been c ass f ed as Pathogen c

Residual risk

Th s tab e d sp ays res dua r sks after a negat ve resu t for each of the genes and correspond ng d sorders The va ues prov ded assume a negat ve fam y h story and the absence of symptoms for each d sorder For genes assoc ated w th both dom nant and recess ve nher tance the numbers n th s tab e app y to the recess ve cond t on(s) assoc ated w th the gene Res dua r sk va ues are prov ded for d sorders when carr er frequency s greater than 1 n 500 For d sorders w th carr er frequency equa to or ess than 1 n 500 res dua r sk s cons dered to be reduced substant a y When prov ded res dua r sk va ues are nferred from pub shed carr er frequenc es and est mated detect on rates are based on test ng techno og es used at Inv tae Res dua r sks are prov ded on y as a gu de for assess ng approx mate r sk g ven a negat ve resu t va ues w va y based on the ethn c background of an nd v dua For nd v dua s of m xed ethn c ty t s recommended to use the h ghest res dua r sk est mate For any genes marked w th an aster sk* refer to the L m tat ons sect on be ow for deta ed coverage nformat on In the case of a samp e spec f c m tat on "N/A" nd cates that a res dua r sk va ue cou d not be ca cu ated AR = autosoma recess ve XL = X nked AD = autosoma dom nant

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
3-hydroxy-3-me hy g u ary -CoA yase de c ency (AR) NM 000191 2	HMGCL	Pan-e hn c	≤1 n 500	Reduced
		Por uguese	1 n 160	1 n 15900
3-me hy cro ony -CoA carboxy ase (3-MCC) de c ency (MCCC1-re a ed) (AR) NM 020166 4	MCCC1	Pan-e hn c	1 n 134	1 n 13300
3-me hy cro ony -CoA carboxy ase (3-MCC) de c ency (MCCC2-re a ed) (AR) NM 022132 4	MCCC2	Pan-e hn c	1 n 134	1 n 13300
ABCB11-re a ed cond ons (AR) NM 003742 2	ABCB11	Pan-e hn c	1 n 100	1 n 9900
ABCC8-re a ed cond ons (AR) NM 000352 4 When he mo her s a noncarr er, bu he a her s a carr er, here s a res dua r sk or oca d sease (1 n 540 or he Ashkenaz Jew sh popu a on; unde erm ned n o her e hn c groups)	ABCC8	Ashkenaz Jew sh	1 n 52	1 n 5100
		F nn sh	1 n 100	1 n 9900
		Pan-e hn c	1 n 177	1 n 17600
Abe a popro e nem a (AR) NM 000253 3	MTTP	Ashkenaz Jew sh	1 n 131	1 n 13000
		Pan-e hn c	≤1 n 500	Reduced
Achroma ops a (CNGB3-re a ed) (AR) NM 019098 4	CNGB3	Pan-e hn c	1 n 93	1 n 9200
ACOX1-re a ed cond ons (AR) NM 004035 6	ACOX1	Pan-e hn c	≤1 n 500	Reduced
Acroderma s en eropa h ca (AR) NM 130849 3	SLC39A4	Pan-e hn c	1 n 354	1 n 35300
Adenos ne deam nase de c ency (AR) NM 000022 2	ADA	Pan-e hn c	1 n 224	1 n 2788
A card -Gou eres syndrome 5 (AR) NM 015474 3	SAMHD1	Pan-e hn c	≤1 n 500	Reduced
A dos erone syn hase de c ency (AR) NM 000498 3	CYP11B2	Pan-e hn c	≤1 n 500	Reduced
		Sephard c Jew sh (ran an)	1 n 30	1 n 2900
A pha-mannos dos s (AR) NM 000528 3	MAN2B1	Pan-e hn c	1 n 354	1 n 35300
A pha- ha assem a (AR) NM 000517 4, NM 000558 4	HBA2/ HBA1 *	A r can-Amer can	1 n 30	1 n 291
		As an	1 n 20	1 n 191
		Caucas an	≤1 n 500	Reduced
		Pan-e hn c	1 n 25	1 n 241
A pha- ha assem a X- nked n e ec ua d sab y syndrome (XL) NM 000489 4	ATRX	Pan-e hn c	≤1 n 500	Reduced
A por syndrome (COL4A3-re a ed) (AR) NM 000091 4	COL4A3	Ashkenaz Jew sh	1 n 192	1 n 19100
		Caucas an	1 n 284	1 n 28300
		Pan-e hn c	1 n 354	1 n 35300
A por syndrome (COL4A4-re a ed) (AR) NM 000092 4	COL4A4	Pan-e hn c	1 n 353	1 n 35200

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
A por syndrome (COL4A5-re a ed) (XL) NM 000495 4	COL4A5 *	Pan-e hn c	≤1 n 500	Reduced
A s röm syndrome (AR) NM 015120 4	ALMS1	Pan-e hn c	≤1 n 500	Reduced
Arg n nosucc na e yase de c ency (AR) NM 000048 3	ASL	Pan-e hn c	1 n 133	1 n 1321
Aroma ase de c ency (AR) NM 031226 2	CYP19A1	Pan-e hn c	≤1 n 500	Reduced
Asparag ne syn he ase de c ency (AR) NM 133436 3	ASNS	Pan-e hn c	≤1 n 500	Reduced
		Sephard c Jew sh (ran an)	1 n 80	1 n 7900
Aspar y g ucosam nur a (AR) NM 000027 3	AGA	F nn sh	1 n 69	1 n 6800
		Pan-e hn c	≤1 n 500	Reduced
A ax a w h v am n E de c ency (AR) NM 000370 3	TTPA	a an	1 n 274	1 n 2731
		Pan-e hn c	≤1 n 500	Reduced
ATM-re a ed cond ons (AR) NM 000051 3	ATM	Pan-e hn c	1 n 100	1 n 9900
		Sephard c Jew sh	1 n 69	1 n 6800
ATP7A-re a ed cond ons (XL) NM 000052 6	ATP7A	Pan-e hn c	≤1 n 500	Reduced
Au o mmune po yendocr nopa hy w h cand d as s and ec oderma dysp as a (AR) NM 000383 3	A RE	F nn sh	1 n 79	1 n 7800
		Pan-e hn c	1 n 150	1 n 14900
		Sard n an	1 n 60	1 n 5900
		Sephard c Jew sh (ran an)	1 n 48	1 n 4700
Au osoma recess ve congen a ch hyos s (TGM1-re a ed) (AR) NM 000359 2	TGM1	Norweg an	1 n 151	1 n 3000
		Pan-e hn c	1 n 224	1 n 4460
Au osoma recess ve spas c a ax a o Char evo x-Saguenay (AR) NM 014363 5	SACS	French Canad an (Saguenay-Lac-S - Jean)	1 n 21	1 n 2000
		Pan-e hn c	≤1 n 500	Reduced
Barde -B ed syndrome (BBS10-re a ed) (AR) NM 024685 3	BBS10	Pan-e hn c	1 n 354	1 n 35300
Barde -B ed syndrome (BBS12-re a ed) (AR) NM 152618 2	BBS12	Pan-e hn c	1 n 708	Reduced
BBS1-re a ed cond ons (AR) NM 024649 4	BBS1	Faroese	1 n 30	1 n 2900
		Pan-e hn c	1 n 330	1 n 32900
BBS2-re a ed cond ons (AR) NM 031885 3	BBS2	Ashkenaz Jew sh	1 n 140	1 n 13900
		Pan-e hn c	1 n 560	Reduced
BCS1L-re a ed cond ons (AR) NM 004328 4	BCS1L	Caucas an	1 n 407	1 n 40600
		F nn sh	1 n 108	1 n 10700
		Pan-e hn c	≤1 n 500	Reduced
Bernard-Sou er syndrome (GP9-re a ed) (AR) NM 000174 4	GP9	Pan-e hn c	≤1 n 500	Reduced
Be a-ke o h o ase de c ency (AR) NM 000019 3	ACAT1	Caucas an	1 n 354	1 n 35300
		Pan-e hn c	≤1 n 500	Reduced
B op er n-de c en hyperpheny a an nem a (PTS-re a ed) (AR) NM 000317 2	PTS	Ch nese	1 n 122	1 n 12100
		Pan-e hn c	1 n 433	1 n 43200
B o n dase de c ency (AR) NM 000060 3	BTD	Pan-e hn c	1 n 125	1 n 12400
B oom syndrome (AR) NM 000057 3	BLM	Ashkenaz Jew sh	1 n 100	1 n 9900
		Pan-e hn c	≤1 n 500	Reduced
BSND-re a ed cond ons (AR) NM 057176 2	BSND	Pan-e hn c	≤1 n 500	Reduced
Canavan d sease (AR) NM 000049 2	ASPA	Ashkenaz Jew sh	1 n 57	1 n 5600
		Pan-e hn c	1 n 159	1 n 15800
Carbamoy phospha e syn he ase de c ency (AR) NM 001875 4	CPS1	Pan-e hn c	≤1 n 500	Reduced
Carn ne pa m oy rans erase de c ency (AR) NM 001876 3	CPT1A	Hu er e	1 n 16	1 n 1500
		Pan-e hn c	≤1 n 500	Reduced

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
Carn ne pa m oy rans erase de c ency (AR) NM 000098 2	CPT2	Ashkenaz Jew sh	1 n 45	1 n 4400
		Pan-e hn c	1 n 182	1 n 18100
Carpen er syndrome (RAB23-re a ed) (AR) NM 183227 2	RAB23	Pan-e hn c	≤1 n 500	Reduced
Car age-ha r hypop as a-anauxe c dysp as a spec rum d sorders (AR) NR 003051 3	RMRP	Am sh	1 n 10	1 n 900
		F nn sh	1 n 76	1 n 7500
		Pan-e hn c	≤1 n 500	Reduced
CDH23-re a ed cond ons (AR) NM 022124 5	CDH23	Pan-e hn c	1 n 202	1 n 4020
CEP290-re a ed cond ons (AR) NM 025114 3	CEP290	Pan-e hn c	1 n 185	1 n 18400
Cerebro end nous xan homa os s (AR) NM 000784 3	CYP27A1	Pan-e hn c	1 n 112	1 n 5550
		Sephard c Jew sh	1 n 76	1 n 3750
CERKL-re a ed cond ons (AR) NM 001030311 2	CERKL	Pan-e hn c	1 n 137	1 n 13600
		Sephard c Jew sh	1 n 24	1 n 2300
CFTR-re a ed cond ons (AR) NM 000492 3	CFTR	A r can-Amer can - c ass c CF	1 n 61	1 n 6000
		Ashkenaz Jew sh - c ass c CF	1 n 29	1 n 2800
		As an - c ass c CF	1 n 88	1 n 8700
		Caucas an - c ass c CF	1 n 28	1 n 2700
		Pan-e hn c - c ass c CF	1 n 45	1 n 4400
		Pan-e hn c - c ass c CF and CFTR-re a ed d sorders	1 n 9	1 n 800
Charco -Mar e-Too h d sease ype 1X (XL) NM 000166 5	GJB1	Pan-e hn c	≤1 n 500	Reduced
Charco -Mar e-Too h d sease ype 4D (AR) NM 006096 3	NDRG1	Pan-e hn c	≤1 n 500	Reduced
		Roma	1 n 22	1 n 2100
Chorea-acan hocy os s (AR) NM 033305 2	VPS13A *	Pan-e hn c	≤1 n 500	Reduced
Choro derem a (XL) NM 000390 2	CHM	Pan-e hn c	≤1 n 500	Reduced
Chron c granu oma ous d sease (CYBA-re a ed) (AR) NM 000101 3	CYBA	Pan-e hn c	≤1 n 500	Reduced
		Sephard c Jew sh (Moroccan)	1 n 13	1 n 1200
Chron c granu oma ous d sease (CYBB-re a ed) (XL) NM 000397 3	CYBB	Pan-e hn c	≤1 n 500	Reduced
C r n de c ency (AR) NM 014251 2	SLC25A13	Ch nese	1 n 65	1 n 6400
		Japanese	1 n 65	1 n 6400
		Korean	1 n 112	1 n 11100
		Pan-e hn c	1 n 313	1 n 31200
		Sou hern Ch nese and Ta wanese	1 n 48	1 n 4700
C ru nem a ype 1 (AR) NM 000050 4	ASS1	Pan-e hn c	1 n 120	1 n 2975
CLN3-re a ed cond ons (AR) NM 001042432 1	CLN3	Pan-e hn c	1 n 230	1 n 22900
CLRN1-re a ed cond ons (AR) NM 174878 2	CLRN1	Ashkenaz Jew sh	1 n 120	1 n 11900
		Pan-e hn c	1 n 533	Reduced
Coba am n C de c ency (AR) NM 015506 2	MMACHC	Pan-e hn c	1 n 123	1 n 12200
Coba am n D de c ency (AR) NM 015702 2	MMADHC *	Pan-e hn c	≤1 n 500	Reduced
Cohen syndrome (AR) NM 017890 4	VPS13B	Am sh (Oh o)	1 n 12	1 n 1100
		Pan-e hn c	≤1 n 500	Reduced
Comb ned ma on c and me hy ma on c ac dur a (AR) NM 174917 4	ACSF3	Pan-e hn c	1 n 87	1 n 8600
Comb ned ox da ve phosphory a on de c ency 1 (AR) NM 024996 5	GFM1	Pan-e hn c	≤1 n 500	Reduced
Comb ned ox da ve phosphory a on de c ency 3 (AR) NM 001172696 1	TSFM *	F nn sh	1 n 80	1 n 1129
		Pan-e hn c	≤1 n 500	Reduced

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
Comb ned p u ary hormone de c ency (LHX3-re a ed) (AR) NM 014564 4	LHX3	Pan-e hn c	≤1 n 500	Reduced
Comb ned p u ary hormone de c ency (PROP1-re a ed) (AR) NM 006261 4	PROP1	Pan-e hn c	1 n 45	1 n 2200
Congen a adrena hyperp as a due o 3-be a-hydroxys ero d dehydrogenase de c ency (AR) NM 000198 3	HSD3B2	Pan-e hn c	≤1 n 500	Reduced
Congen a adrena hyperp as a due o 21-hydroxy ase de c ency (AR) NM 000500 7	CYP21A2 *	Pan-e hn c	1 n 61	1 n 751
Congen a d sorder o g ycosy a on (SLC35A3-re a ed) (AR) NM 012243 2	SLC35A3	Ashkenaz Jew sh	1 n 469	1 n 46800
		Pan-e hn c	≤1 n 500	Reduced
Congen a d sorder o g ycosy a on ype a (AR) NM 000303 2	PMM2	Ashkenaz Jew sh	1 n 61	1 n 6000
		Caucas an	1 n 60	1 n 5900
		Pan-e hn c	1 n 190	1 n 18900
Congen a d sorder o g ycosy a on ype b (AR) NM 002435 2	MP	Pan-e hn c	≤1 n 500	Reduced
Congen a d sorder o g ycosy a on ype c (AR) NM 013339 3	ALG6 *	Pan-e hn c	≤1 n 500	Reduced
Congen a nsens v y o pa n w h anh dros s (AR) NM 001012331 1	NTRK1	Pan-e hn c	≤1 n 500	Reduced
Congen a myas hen c syndrome (CHRNE-re a ed) (AR) NM 000080 3	CHRNE	European Roma	1 n 25	1 n 2400
		Pan-e hn c	1 n 200	1 n 19900
Congen a nephro c syndrome ype 1 (AR) NM 004646 3	NPHS1	F nn sh	1 n 46	1 n 4500
		O d Order Mennon e	1 n 12	1 n 1100
		Pan-e hn c	≤1 n 500	Reduced
Congen a nephro c syndrome ype 2 (AR) NM 014625 3	NPHS2	Pan-e hn c	≤1 n 500	Reduced
Cornea dys rophy and percep ve dea ness (AR) NM 032034 3	SLC4A11	Pan-e hn c	≤1 n 500	Reduced
CRB1-re a ed cond ons (AR) NM 201253 2	CRB1	Pan-e hn c	1 n 112	1 n 11100
CYP17A1-re a ed cond ons (AR) NM 000102 3	CYP17A1	Pan-e hn c	≤1 n 500	Reduced
Cys nos s (AR) NM 004937 2	CTNS	French Canad an (Saguenay-Lac-S - Jean)	1 n 39	1 n 3800
		Pan-e hn c	1 n 158	1 n 15700
		Sephard c Jew sh (Moroccan)	1 n 100	1 n 9900
DHDDS-re a ed cond ons (AR) NM 024887 3	DHDDS	Ashkenaz Jew sh	1 n 117	1 n 11600
		Pan-e hn c	≤1 n 500	Reduced
D hydro poam de dehydrogenase de c ency (AR) NM 000108 4	DLD	Ashkenaz Jew sh	1 n 107	1 n 5300
		Pan-e hn c	≤1 n 500	Reduced
D s a rena ubu ar ac dos s w h dea ness (ATP6V1B1-re a ed) (AR) NM 001692 3	ATP6V1B1	Pan-e hn c	≤1 n 500	Reduced
		Sephard c Jew sh	1 n 140	1 n 13900
DMD-re a ed cond ons (XL) NM 004006 2	DMD	Pan-e hn c	1 n 667	Reduced
DYSF-re a ed cond ons (AR) NM 003494 3	DYSF	Pan-e hn c	1 n 311	1 n 31000
		Sephard c Jew sh (L byan)	1 n 10	1 n 900
Dyskera os s congen a spec rum d sorders (RTEL1-re a ed) (AR) NM 001283009 1	RTEL1	Ashkenaz Jew sh	1 n 222	1 n 22100
		Pan-e hn c	≤1 n 500	Reduced
Dys roph c ep dermo ys s bu osa (AR) NM 000094 3	COL7A1	Pan-e hn c	1 n 370	1 n 12300
EDA-re a ed cond ons (XL) NM 001399 4	EDA	Pan-e hn c	≤1 n 500	Reduced
Eh ers-Dan os syndrome, derma osparax s ype (AR) NM 014244 4	ADAMTS2	Ashkenaz Jew sh	1 n 187	1 n 18600
		Pan-e hn c	≤1 n 500	Reduced

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
E s-van Creve d syndrome (EVC-re a ed) (AR) NM 153717 2	EVC	Am sh	1 n 8	1 n 700
		Pan-e hn c	1 n 220	1 n 21900
Emery-Dre uss muscu ar dys rophy (EMD-re a ed) (XL) NM 000117 2	EMD	Pan-e hn c	≤1 n 500	Reduced
E hy ma on c encepha opa hy (AR) NM 014297 3	ETHE1	Pan-e hn c	≤1 n 500	Reduced
Fabry d sease (XL) NM 000169 2	GLA	Pan-e hn c	≤1 n 500	Reduced
Fac or X de c ency (hemoph a B) (XL) NM 000133 3	F9	Pan-e hn c	≤1 n 500	Reduced
Fac or X de c ency (hemoph a C) (AR) NM 000128 3	F11	Ashkenaz Jew sh	1 n 11	1 n 1000
		Pan-e hn c	≤1 n 500	Reduced
Fam a chy om cronem a syndrome (AR) NM 000237 2	LPL	French Canad an (Saguenay-Lac-S - Jean)	1 n 46	1 n 4500
		Pan-e hn c	≤1 n 500	Reduced
Fam a dysau onom a (AR) NM 003640 3	ELP1	Ashkenaz Jew sh	1 n 36	1 n 3500
		Pan-e hn c	≤1 n 500	Reduced
Fam a hypercho es ero em a (LDLR-re a ed) (AD) NM 000527 4	LDLR	A r kaner	1 n 72	1 n 7100
		Ashkenaz Jew sh	1 n 69	1 n 6800
		French Canad an	1 n 270	1 n 26900
		Pan-e hn c	1 n 250	1 n 24900
Fam a hypercho es ero em a (LDLRAP1-re a ed) (AR) NM 015627 2	LDLRAP1	Pan-e hn c	≤1 n 500	Reduced
		Sard n an	1 n 143	1 n 14200
Fam a Med erranean ever (AR) NM 000243 2	MEFV	Armen an	1 n 8	1 n 71
		Ashkenaz Jew sh	1 n 13	1 n 121
		Pan-e hn c	1 n 64	1 n 631
		Sephard c Jew sh	1 n 14	1 n 131
		Turk sh	1 n 8	1 n 71
Fancon anem a ype A (AR) NM 000135 2	FANCA	A r kaner	1 n 83	1 n 8200
		Pan-e hn c	1 n 345	1 n 34400
		Sephard c Jew sh	1 n 133	1 n 13200
		Span sh Roma	1 n 64	1 n 6300
Fancon anem a ype C (AR) NM 000136 2	FANCC	Ashkenaz Jew sh	1 n 89	1 n 8800
		Pan-e hn c	1 n 417	1 n 41600
Fancon anem a ype G (AR) NM 004629 1	FANCG	A r can-Amer can	1 n 100	1 n 9900
		Pan-e hn c	≤1 n 500	Reduced
FH-re a ed cond ons (AR) NM 000143 3	FH	Pan-e hn c	≤1 n 500	Reduced
FMR1-re a ed cond ons nc ud ng rag e X syndrome (XL) NM 002024 5 CGG repea s observed 30	FMR1 *	Ashkenaz Jew sh	1 n 58	1 n 5700
		As an	≤1 n 500	Reduced
		Caucas an	1 n 187	1 n 18600
		H span c	≤1 n 500	Reduced
		Pan-e hn c	1 n 259	1 n 25800
Ga ac ok nase de c ency ga ac osem a (AR) NM 000154 1	GALK1	Pan-e hn c	1 n 122	1 n 12100
		Roma	1 n 47	1 n 4600
Ga ac osem a (GALT-re a ed) (AR) NM 000155 3	GALT	A r can-Amer can	1 n 87	1 n 8600
		Ashkenaz Jew sh	1 n 156	1 n 15500
		r sh Trave er	1 n 11	1 n 1000
		Pan-e hn c	1 n 100	1 n 9900
GBA-re a ed cond ons nc ud ng Gaucher d sease (AR) NM 001005741 2	GBA *	Ashkenaz Jew sh	1 n 15	1 n 234
		Pan-e hn c	1 n 158	1 n 561
GBE1-re a ed cond ons (AR) NM 000158 3	GBE1	Ashkenaz Jew sh	1 n 68	1 n 6700
		Pan-e hn c	1 n 387	1 n 38600
G e man syndrome (AR) NM 000339 2	SLC12A3	Pan-e hn c	1 n 100	1 n 9900
GJB2-re a ed cond ons (AR) NM 004004 5	GJB2	Ashkenaz Jew sh	1 n 13	1 n 1200
		Pan-e hn c	1 n 50	1 n 4900

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
		Tha	1 n 9	1 n 800
GLB1-re a ed cond ons (AR) NM 000404 2	GLB1	Pan-e hn c	1 n 158	1 n 15700
		Roma	1 n 50	1 n 4900
		Sou h Braz an	1 n 58	1 n 5700
GLE1-re a ed cond ons (AR) NM 001003722 1	GLE1	F nn sh	1 n 100	1 n 9900
		Pan-e hn c	≤1 n 500	Reduced
G u ar c ac dem a ype (AR) NM 000159 3	GCDH	Am sh	1 n 9	1 n 800
		Oj -Cree F rs Na ons	1 n 9	1 n 800
		Pan-e hn c	1 n 87	1 n 8600
G u ar c ac dem a ype A (AR) NM 000126 3	ETFA	Pan-e hn c	≤1 n 500	Reduced
G u ar c ac dem a ype C (AR) NM 004453 3	ETFDH	As an	1 n 87	1 n 8600
		Pan-e hn c	1 n 250	1 n 24900
G yc ne encepha opa hy (AMT-re a ed) (AR) NM 000481 3	AMT	F nn sh	1 n 142	1 n 14100
		Pan-e hn c	1 n 325	1 n 32400
G yc ne encepha opa hy (GLDC-re a ed) (AR) NM 000170 2	GLDC	Caucas an	1 n 141	1 n 14000
		Pan-e hn c	1 n 165	1 n 16400
G ycogen s orage d sease ype a (AR) NM 000151 3	G6PC	Ashkenaz Jew sh	1 n 71	1 n 1400
		Pan-e hn c	1 n 177	1 n 3520
G ycogen s orage d sease ype b (AR) NM 001164277 1	SLC37A4	Pan-e hn c	1 n 354	1 n 7060
G ycogen s orage d sease ype (Pompe d sease) (AR) NM 000152 3	GAA	A r can-Amer can	1 n 60	1 n 5900
		Ashkenaz Jew sh	1 n 58	1 n 5700
		As an	1 n 112	1 n 11100
		Pan-e hn c	1 n 100	1 n 9900
G ycogen s orage d sease ype (AR) NM 000642 2	AGL	Faroese	1 n 28	1 n 540
		Pan-e hn c	1 n 159	1 n 3160
		Sephard c Jew sh (Moroccan)	1 n 34	1 n 660
G ycogen s orage d sease ype V (AR) NM 005609 3	PYGM	Caucas an	1 n 158	1 n 15700
		Pan-e hn c	1 n 171	1 n 17000
		Sephard c Jew sh (Kurd sh)	1 n 84	1 n 8300
G ycogen s orage d sease ype V (AR) NM 000289 5	PFKM	Ashkenaz Jew sh	1 n 250	1 n 24900
		Pan-e hn c	≤1 n 500	Reduced
GNPTAB-re a ed cond ons (AR) NM 024312 4	GNPTAB	r sh Trave er	1 n 15	1 n 1400
		Pan-e hn c	1 n 200	1 n 19900
GP1BA-re a ed cond ons (AR) NM 000173 6	GP1BA *	Pan-e hn c	≤1 n 500	Reduced
Guan d noace a e me hy rans erase de c ency (AR) NM 000156 5	GAMT	Pan-e hn c	≤1 n 500	Reduced
		Por uguese	1 n 125	1 n 12400
Gyra e a rophy o he choro d and re na (AR) NM 000274 3	OAT *	F nn sh	1 n 126	1 n 12500
		Pan-e hn c	≤1 n 500	Reduced
		Sephard c Jew sh	1 n 177	1 n 17600
HADHA-re a ed cond ons (AR) NM 000182 4	HADHA	Caucas an	1 n 250	1 n 24900
		F nn sh	1 n 125	1 n 12400
		Pan-e hn c	1 n 350	1 n 34900
HBB-re a ed hemog ob nopa h es (AR) NM 000518 4	HBB	A r can-Amer can	1 n 8	1 n 700
		As an	1 n 54	1 n 5300
		Caucas an	1 n 373	1 n 37200
		H span c	1 n 17	1 n 1600
		Med erranean	1 n 28	1 n 2700
		Pan-e hn c	1 n 49	1 n 4800
Hered ary ruc ose n o erance (AR) NM 000035 3	ALDOB	A r can-Amer can	1 n 226	1 n 22500
		M dd e Eas ern	1 n 97	1 n 9600
		Pan-e hn c	1 n 122	1 n 12100
Hered ary hemochroma os s ype 2 (HJV-re a ed) (AR) NM 213653 3	HJV	Pan-e hn c	≤1 n 500	Reduced

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
Hered ary hemochroma os s ype 3 (AR) NM 003227 3	TFR2	Pan-e hn c	≤1 n 500	Reduced
Hermansky-Pud ak syndrome ype 1 (AR) NM 000195 4	HPS1	Pan-e hn c	≤1 n 500	Reduced
		Puer o R can (Nor hwes ern)	1 n 21	1 n 2000
Hermansky-Pud ak syndrome ype 3 (AR) NM 032383 4	HPS3	Ashkenaz Jew sh	1 n 235	1 n 23400
		Pan-e hn c	≤1 n 500	Reduced
		Puer o R can (Cen ra)	1 n 63	1 n 6200
HGSNAT-re a ed cond ons (AR) NM 152419 2	HGSNAT	Pan-e hn c	≤1 n 500	Reduced
Ho ocarboxy ase syn he ase de c ency (AR) NM 000411 6	HLCS	Faroese	1 n 20	1 n 1900
		Japanese	1 n 158	1 n 15700
		Pan-e hn c	1 n 224	1 n 22300
Homocys nur a due o coba am n E de c ency (AR) NM 002454 2	MTRR	Pan-e hn c	≤1 n 500	Reduced
Homocys nur a due o cys a h on ne be a-syn hase de c ency (AR) NM 000071 2	CBS	Norweg an	1 n 40	1 n 3900
		Pan-e hn c	1 n 224	1 n 22300
		Qa ar	1 n 21	1 n 2000
Homocys nur a due o MTHFR de c ency (AR) NM 005957 4	MTHFR *	Pan-e hn c	≤1 n 500	Reduced
		Sephard c Jew sh (Bukhar an)	1 n 39	1 n 3800
HSD17B4-re a ed cond ons (AR) NM 000414 3	HSD17B4	Pan-e hn c	1 n 158	1 n 15700
Hydro e ha us syndrome ype 1 (AR) NM 145014 2	HYLS1	F nn sh	1 n 40	1 n 3900
		Pan-e hn c	≤1 n 500	Reduced
Hyperorn h nem a-hyperammonem a-homoc ru nur a syndrome (AR) NM 014252 3	SLC25A15	Me s (Saska chewan)	1 n 19	1 n 1800
		Pan-e hn c	≤1 n 500	Reduced
Hypophospha as a (AR) NM 000478 5	ALPL	Mennon e	1 n 25	1 n 480
		Pan-e hn c	1 n 150	1 n 2980
sova er c ac dem a (AR) NM 002225 3	VD	Pan-e hn c	1 n 250	1 n 24900
Jouber syndrome and re a ed d sorders (MKS1-re a ed) (AR) NM 017777 3	MKS1	F nn sh	1 n 47	1 n 920
		Pan-e hn c	1 n 260	1 n 5180
Jouber syndrome and re a ed d sorders (RPGR P1L-re a ed) (AR) NM 015272 2	RPGR P1L *	Pan-e hn c	1 n 259	1 n 5160
Jouber syndrome and re a ed d sorders (TMEM216-re a ed) (AR) NM 001173990 2	TMEM216	Ashkenaz Jew sh	1 n 92	1 n 9100
		Pan-e hn c	≤1 n 500	Reduced
Junc ona ep dermo ys s bu osa (LAMC2-re a ed) (AR) NM 005562 2	LAMC2	Pan-e hn c	≤1 n 500	Reduced
KCNJ11-re a ed cond ons (AR) NM 000525 3	KCNJ11	Pan-e hn c	≤1 n 500	Reduced
Krabbe d sease (AR) NM 000153 3	GALC *	Druze	1 n 6	1 n 500
		Pan-e hn c	1 n 158	1 n 15700
LAMA3-re a ed cond ons (AR) NM 000227 4	LAMA3	Pan-e hn c	≤1 n 500	Reduced
LAMB3-re a ed cond ons (AR) NM 000228 2	LAMB3	Pan-e hn c	1 n 317	1 n 31600
Leber congen a amauros s 5 (AR) NM 181714 3	LCA5	Pan-e hn c	1 n 645	Reduced
Leukoencepha opa hy w h van sh ng wh e ma er (E F2B5-re a ed) (AR) NM 003907 2	E F2B5	Pan-e hn c	≤1 n 500	Reduced
L mb-g rd e muscu ar dys rophy (CAPN3-re a ed) (AR) NM 000070 2	CAPN3	Pan-e hn c	1 n 134	1 n 13300
L mb-g rd e muscu ar dys rophy ype 2C (AR) NM 000231 2	SGCG	Caucas an	1 n 571	Reduced
		Japanese	1 n 374	1 n 37300
		Moroccan	1 n 250	1 n 24900
		Pan-e hn c	≤1 n 500	Reduced

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
		Roma	1 n 59	1 n 5800
L mb-g rd e muscu ar dys rophy ype 2D (AR) NM 000023 2	SGCA	Caucas an	1 n 286	1 n 28500
		F nn sh	1 n 150	1 n 14900
		Pan-e hn c	≤1 n 500	Reduced
L mb-g rd e muscu ar dys rophy ype 2E (AR) NM 000232 4	SGCB	Caucas an	1 n 404	1 n 5038
		Pan-e hn c	≤1 n 500	Reduced
L po d congen a adrena hyperp as a (AR) NM 000349 2	STAR	Korean	1 n 170	1 n 16900
		Pan-e hn c	≤1 n 500	Reduced
Lys nur c pro e n n o erance (AR) NM 001126106 2	SLC7A7	F nn sh	1 n 120	1 n 2380
		Japanese	1 n 120	1 n 2380
		Pan-e hn c	≤1 n 500	Reduced
Lysosoma ac d pase de c ency (AR) NM 000235 3	L PA	Caucas an	1 n 112	1 n 1850
		Pan-e hn c	1 n 359	1 n 5967
		Sephard c Jew sh (ran an)	1 n 33	1 n 534
Major h s ocompa b y comp ex c ass de c ency (C TA-re a ed) (AR) NM 000246 3	C TA	Pan-e hn c	≤1 n 500	Reduced
Map e syrup ur ne d sease ype 1A (AR) NM 000709 3	BCKDHA	Mennon e	1 n 10	1 n 900
		Pan-e hn c	1 n 373	1 n 37200
Map e syrup ur ne d sease ype 1B (AR) NM 183050 2	BCKDHB	Ashkenaz Jew sh	1 n 97	1 n 9600
		Pan-e hn c	1 n 346	1 n 34500
Med um-cha n acy -CoA dehydrogenase de c ency (AR) NM 000016 5	ACADM	Nor hern European	1 n 40	1 n 3900
		Pan-e hn c	1 n 66	1 n 6500
Mega encepha c eukoencepha opa hy w h subcor ca cys s 1 (AR) NM 015166 3	MLC1	Pan-e hn c	≤1 n 500	Reduced
		Sephard c Jew sh (L byan)	1 n 40	1 n 3900
Me achroma c eukodys rophy (ARSA-re a ed) (AR) NM 000487 5	ARSA	Navajo	1 n 40	1 n 780
		Pan-e hn c	1 n 100	1 n 1980
		Sephard c Jew sh	1 n 46	1 n 900
Me hy ma on c ac dem a (MMAA-re a ed) (AR) NM 172250 2	MMAA	Pan-e hn c	1 n 316	1 n 10500
Me hy ma on c ac dem a (MMAB-re a ed) (AR) NM 052845 3	MMAB	Pan-e hn c	1 n 456	1 n 22750
Me hy ma on c ac dem a (MUT-re a ed) (AR) NM 000255 3	MUT	Pan-e hn c	1 n 204	1 n 5075
MFSD8-re a ed cond ons (AR) NM 152778 2	MFSD8	Pan-e hn c	≤1 n 500	Reduced
M crocepha y, pos na a progress ve, w h se zures and bra n a rophy (AR) NM 004268 4	MED17	Pan-e hn c	≤1 n 500	Reduced
		Sephard c Jew sh	1 n 20	1 n 1900
M ochondr a comp ex de c ency 9 (AR) NM 004553 4	NDUFS6	Ashkenaz Jew sh	1 n 290	1 n 28900
		Caucasus Jew sh	1 n 24	1 n 2300
		Pan-e hn c	≤1 n 500	Reduced
M ochondr a comp ex de c ency 16 (AR) NM 024120 4	NDUFAF5	Ashkenaz Jew sh	1 n 290	1 n 28900
		Pan-e hn c	≤1 n 500	Reduced
M ochondr a comp ex de c ency 20/ACAD9 de c ency (AR) NM 014049 4	ACAD9	Pan-e hn c	≤1 n 500	Reduced
M ochondr a comp ex V de c ency / Le gh syndrome, French Canad an ype (AR) NM 133259 3	LRPPRC	French Canad an (Saguenay-Lac-S - Jean)	1 n 23	1 n 2200
		Pan-e hn c	≤1 n 500	Reduced
M ochondr a DNA dep e on syndrome-6 (AR) NM 002437 4	MPV17	Navajo	1 n 20	1 n 475
		Pan-e hn c	≤1 n 500	Reduced
M ochondr a neurogas ro n es na encepha omyopa hy (AR) NM 001953 4	TYMP	Pan-e hn c	≤1 n 500	Reduced
		Sephard c Jew sh	1 n 158	1 n 15700
MPL-re a ed cond ons (AR) NM 005373 2	MPL	Ashkenaz Jew sh	1 n 57	1 n 5600
		Pan-e hn c	≤1 n 500	Reduced

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
Muco p dos s ype gamma (AR) NM 032520 4	GNPTG	Pan-e hn c	≤1 n 500	Reduced
Muco p dos s ype V (AR) NM 020533 2	MCOLN1	Ashkenaz Jew sh	1 n 100	1 n 9900
		Pan-e hn c	≤1 n 500	Reduced
Mucopo ysacchar dos s ype (AR) NM 000203 4	DUA	Pan-e hn c	1 n 148	1 n 4900
Mucopo ysacchar dos s ype (XL) NM 000202 6	DS *	Pan-e hn c	≤1 n 500	Reduced
Mucopo ysacchar dos s ype A (AR) NM 000199 3	SGSH	Nor hern European	1 n 173	1 n 17200
		Pan-e hn c	1 n 215	1 n 21400
		Ta wanese	≤1 n 500	Reduced
Mucopo ysacchar dos s ype B (AR) NM 000263 3	NAGLU	Pan-e hn c	1 n 224	1 n 22300
Mucopo ysacchar dos s ype D (AR) NM 002076 3	GNS	Pan-e hn c	≤1 n 500	Reduced
Mucopo ysacchar dos s ype X (AR) NM 153281 1	HYAL1	Pan-e hn c	≤1 n 500	Reduced
Mucopo ysacchar dos s ype V (AR) NM 000046 3	ARSB	Pan-e hn c	1 n 250	1 n 24900
Mu p e su a ase de c ency (AR) NM 182760 3	SUMF1	Pan-e hn c	≤1 n 500	Reduced
Muscu ar dys rophy-dys rog ycanopa hy (FKRP-re a ed) (AR) NM 024301 4	FKRP	Norweg an	1 n 116	1 n 11500
		Pan-e hn c	1 n 158	1 n 15700
Muscu ar dys rophy-dys rog ycanopa hy (FKTN-re a ed) (AR) NM 001079802 1	FKTN	Ashkenaz Jew sh	1 n 80	1 n 7900
		Japanese	1 n 188	1 n 18700
		Pan-e hn c	≤1 n 500	Reduced
MYO7A-re a ed cond ons (AR) NM 000260 3	MYO7A	Pan-e hn c	1 n 200	1 n 3980
Myopa hy, ac c ac dos s, and s derob as c anem a 1 (AR) NM 025215 5	PUS1	Pan-e hn c	≤1 n 500	Reduced
N-ace y g u ama e syn hase de c ency (AR) NM 153006 2	NAGS	Pan-e hn c	≤1 n 500	Reduced
Nema ne myopa hy 2 (AR) NM 001271208 1	NEB *	Ashkenaz Jew sh	1 n 108	1 n 10700
		Pan-e hn c	1 n 158	1 n 3140
Nephrogen c d abe es ns p dus (AQP2-re a ed) (AR) NM 000486 5	AQP2	Pan-e hn c	1 n 1118	Reduced
Neurona cero d po usc nos s ype 1 (AR) NM 000310 3	PPT1	F nn sh	1 n 70	1 n 3450
		Pan-e hn c	1 n 199	1 n 9900
Neurona cero d po usc nos s ype 2 (AR) NM 000391 3	TPP1	New ound and	1 n 53	1 n 1734
		Pan-e hn c	1 n 250	1 n 8300
Neurona cero d po usc nos s ype 5 (AR) NM 006493 2	CLN5	F nn sh	1 n 115	1 n 11400
		Pan-e hn c	≤1 n 500	Reduced
Neurona cero d po usc nos s ype 6 (AR) NM 017882 2	CLN6	Pan-e hn c	≤1 n 500	Reduced
Neurona cero d po usc nos s ype 8 (AR) NM 018941 3	CLN8	F nn sh	1 n 135	1 n 13400
		Pan-e hn c	≤1 n 500	Reduced
N emann-P ck d sease ype C (NPC1-re a ed) (AR) NM 000271 4	NPC1	Pan-e hn c	1 n 183	1 n 18200
N emann-P ck d sease ype C (NPC2-re a ed) (AR) NM 006432 3	NPC2	Pan-e hn c	1 n 871	Reduced
N emann-P ck d sease ypes A and B (AR) NM 000543 4	SMPD1	Ashkenaz Jew sh	1 n 90	1 n 1780
		Pan-e hn c	1 n 250	1 n 4980
N jmegen breakage syndrome (AR) NM 002485 4	NBN *	Eas ern European	1 n 155	1 n 15400
		Pan-e hn c	≤1 n 500	Reduced
Nonsyndrom c dea ness (LOXHD1-re a ed) (AR) NM 144612 6	LOXHD1	Ashkenaz Jew sh	1 n 180	1 n 17900
		Pan-e hn c	≤1 n 500	Reduced
NR2E3-re a ed cond ons (AR) NM 014249 3	NR2E3	Pan-e hn c	≤1 n 500	Reduced

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
OPA3-re a ed cond ons (AR) NM 025136 3	OPA3	Pan-e hn c	≤1 n 500	Reduced
		Sephard c Jew sh (raq)	1 n 10	1 n 900
Orn h ne ranscarbamy ase de c ency (XL) NM 000531 5	OTC	Pan-e hn c	≤1 n 500	Reduced
Os eope ros s (TC RG1-re a ed) (AR) NM 006019 3	TC RG1	Ashkenaz Jew sh	1 n 350	1 n 34900
		Chuvash	1 n 30	1 n 2900
		Pan-e hn c	1 n 317	1 n 31600
PCDH15-re a ed cond ons (AR) NM 033056 3	PCDH15	Ashkenaz Jew sh	1 n 78	1 n 7700
		Pan-e hn c	1 n 400	1 n 39900
PEX7-re a ed cond ons (AR) NM 000288 3	PEX7	Pan-e hn c	1 n 157	1 n 15600
Pheny a an ne hydroxy ase de c ency (AR) NM 000277 1	PAH	A r can-Amer can	1 n 111	1 n 11000
		Ashkenaz Jew sh	1 n 225	1 n 22400
		Eas As an	1 n 50	1 n 1225
		F nn sh	1 n 225	1 n 22400
		r sh	1 n 33	1 n 3200
		Japanese	1 n 200	1 n 19900
		Pan-e hn c	1 n 58	1 n 5700
		Turk sh	1 n 26	1 n 2500
Phosphog ycera e dehydrogenase de c ency (AR) NM 006623 3	PHGDH	Ashkenaz Jew sh	1 n 400	1 n 39900
		Pan-e hn c	≤1 n 500	Reduced
Po ycys c k dney d sease (PKHD1-re a ed) (AR) NM 138694 3	PKHD1	Pan-e hn c	1 n 70	1 n 6900
Po ym crogyr a (ADGRG1-re a ed) (AR) NM 005682 6	ADGRG1	Pan-e hn c	≤1 n 500	Reduced
POMGNT1-re a ed cond ons (AR) NM 017739 3	POMGNT1	F nn sh	1 n 111	1 n 11000
		Pan-e hn c	≤1 n 500	Reduced
Pon ocerebe ar hypop as a ype 2D (AR) NM 016955 3	SEPSECS	Pan-e hn c	≤1 n 500	Reduced
		Sephard c Jew sh (Moroccan and raq)	1 n 43	1 n 4200
Pon ocerebe ar hypop as a ype 6 (AR) NM 020320 3	RARS2	Pan-e hn c	≤1 n 500	Reduced
Pr mary carn ne de c ency (AR) NM 003060 3	SLC22A5	Faroese	1 n 9	1 n 800
		Japanese	1 n 100	1 n 9900
		Pan-e hn c	1 n 71	1 n 7000
Pr mary c ary dysk nes a (DNAH5-re a ed) (AR) NM 001369 2	DNAH5	Pan-e hn c	1 n 109	1 n 10800
Pr mary c ary dysk nes a (DNA 1-re a ed) (AR) NM 012144 3	DNA 1	Pan-e hn c	1 n 250	1 n 24900
Pr mary c ary dysk nes a (DNA 2-re a ed) (AR) NM 023036 4	DNA 2	Ashkenaz Jew sh	1 n 200	1 n 19900
		Pan-e hn c	1 n 354	1 n 35300
Pr mary hyperoxa ur a ype 1 (AR) NM 000030 2	AGXT	Pan-e hn c	1 n 135	1 n 13400
Pr mary hyperoxa ur a ype 2 (AR) NM 012203 1	GRHPR	Pan-e hn c	≤1 n 500	Reduced
Pr mary hyperoxa ur a ype 3 (AR) NM 138413 3	HOGA1	Pan-e hn c	1 n 354	1 n 35300
Prop on c ac dem a (PCCA-re a ed) (AR) NM 000282 3	PCCA	Arab	1 n 100	1 n 2475
		Pan-e hn c	1 n 224	1 n 5575
Prop on c ac dem a (PCCB-re a ed) (AR) NM 000532 4	PCCB	Arab	1 n 100	1 n 9900
		Green and c nu	1 n 20	1 n 1900
		Pan-e hn c	1 n 224	1 n 22300
PRPS1-re a ed cond ons (XL) NM 002764 3	PRPS1	Pan-e hn c	≤1 n 500	Reduced
PSAP-re a ed cond ons (AR) NM 002778 3	PSAP	Pan-e hn c	≤1 n 500	Reduced
Pycnodysos os s (AR) NM 000396 3	CTSK	Pan-e hn c	1 n 438	1 n 43700

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
Pyruva e dehydrogenase comp ex de c ency (PDHA1-re a ed) (XL) NM 000284 3	PDHA1	Pan-e hn c	≤1 n 500	Reduced
Pyruva e dehydrogenase comp ex de c ency (PDHB-re a ed) (AR) NM 000925 3	PDHB	Pan-e hn c	≤1 n 500	Reduced
RAPSN-re a ed cond ons (AR) NM 005055 4	RAPSN	Pan-e hn c	1 n 283	1 n 28200
RDH12-re a ed cond ons (AR) NM 152443 2	RDH12	Pan-e hn c	1 n 460	1 n 45900
Re n s p gmen osa 25 (AR) NM 001142800 1	EYS	Pan-e hn c	1 n 129	1 n 12800
		Sephard c Jew sh	1 n 42	1 n 4100
Re n s p gmen osa 28 (AR) NM 001201543 1	FAM161A	Ashkenaz Jew sh	1 n 214	1 n 21300
		Pan-e hn c	1 n 289	1 n 28800
		Sephard c Jew sh	1 n 41	1 n 4000
Rh zome c chondrodysp as a punc a a ype 3 (AR) NM 003659 3	AGPS	Pan-e hn c	≤1 n 500	Reduced
Rober s syndrome (AR) NM 001017420 2	ESCO2	Pan-e hn c	≤1 n 500	Reduced
RPE65-re a ed cond ons (AR) NM 000329 2	RPE65	Pan-e hn c	1 n 228	1 n 22700
		Sephard c Jew sh	1 n 90	1 n 8900
Sandho d sease (AR) NM 000521 3	HEXB	Me s (Saska chewan)	1 n 15	1 n 1400
		Pan-e hn c	1 n 180	1 n 17900
Sch mke mmuno-osseous dysp as a (AR) NM 014140 3	SMARCAL1	Pan-e hn c	≤1 n 500	Reduced
Severe comb ned mmunode c ency due o DCLRE1C (Ar em s) de c ency (AR) NM 001033855 2	DCLRE1C	Navajo and Apache	1 n 10	1 n 900
		Pan-e hn c	≤1 n 500	Reduced
Severe comb ned mmunode c ency due o RAG2 de c ency (AR) NM 000536 3	RAG2	Pan-e hn c	≤1 n 500	Reduced
Severe congen a neu ropen a due o HAX1 de c ency (AR) NM 006118 3	HAX1	Pan-e hn c	≤1 n 500	Reduced
Severe congen a neu ropen a due o VPS45 de c ency (AR) NM 007259 4	VPS45	Pan-e hn c	≤1 n 500	Reduced
S a c ac d s orage d seases (AR) NM 012434 4	SLC17A5	F nn sh	1 n 100	1 n 9900
		Pan-e hn c	≤1 n 500	Reduced
Sjögren-Larsson syndrome (AR) NM 000382 2	ALDH3A2	Pan-e hn c	≤1 n 500	Reduced
		Swed sh	1 n 250	1 n 24900
SLC12A6-re a ed cond ons (AR) NM 133647 1	SLC12A6	French Canad an (Saguenay-Lac-S - Jean)	1 n 23	1 n 2200
		Pan-e hn c	≤1 n 500	Reduced
SLC26A2-re a ed cond ons (AR) NM 000112 3	SLC26A2	F nn sh	1 n 75	1 n 1480
		Pan-e hn c	1 n 158	1 n 3140
SLC26A4-re a ed cond ons (AR) NM 000441 1	SLC26A4	As an	1 n 74	1 n 7300
		Pan-e hn c	1 n 80	1 n 7900
Sm h-Lem -Op z syndrome (AR) NM 001360 2	DHCR7	A r can-Amer can	1 n 339	1 n 33800
		Ashkenaz Jew sh	1 n 41	1 n 4000
		H span c	1 n 135	1 n 13400
		Nor hern European	1 n 50	1 n 4900
		Pan-e hn c	1 n 71	1 n 7000
		Sephard c Jew sh	1 n 68	1 n 6700
		Sou hern European	1 n 83	1 n 8200
Spas c parap eg a ype 49 (AR) NM 014844 3	TECPR2	Pan-e hn c	≤1 n 500	Reduced
		Sephard c Jew sh - Bukhar an	1 n 38	1 n 3700
Sp na muscu ar a rophy (AR) NM 000344 3 SMN1 2 cop es	SMN1 *	A r can-Amer can	1 n 59	1 n 342
		Ashkenaz Jew sh	1 n 62	1 n 1017
		As an	1 n 50	1 n 701

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
c *3+80T>G no de ec ed Carr er res dua r sks s ed are or 2 copy SMN1 resu s Carr er res dua r sk or >2 cop es are 5- o 10- o d ower		Caucas an	1 n 45	1 n 880
		H span c	1 n 48	1 n 784
		Pan-e hn c	1 n 49	1 n 800
Spondy ocos a dysos os s (AR) NM 001039958 1	MESP2	Pan-e hn c	1 n 224	1 n 22300
		Puer o R can	1 n 55	1 n 5400
S ee syndrome (AR) NM 032888 3	COL27A1 *	Pan-e hn c	≤1 n 500	Reduced
		Puer o R can	1 n 51	1 n 5000
S üve-W edemann syndrome (AR) NM 002310 5	L FR	Pan-e hn c	≤1 n 500	Reduced
Tay-Sachs d sease (AR) NM 000520 4	HEXA	Ashkenaz Jew sh	1 n 27	1 n 2600
		As an	1 n 126	1 n 12500
		Caucas an	1 n 182	1 n 18100
		French Canad an	1 n 27	1 n 2600
		r sh	1 n 41	1 n 4000
		Pan-e hn c	1 n 250	1 n 24900
		Sephard c Jew sh	1 n 125	1 n 12400
Trans en n an e ver a ure (AR) NM 018006 4	TRMU	Pan-e hn c	≤1 n 500	Reduced
		Sephard c Jew sh (Yemen e)	1 n 34	1 n 3300
Tyros ne hydroxy ase de c ency (AR) NM 199292 2	TH	Caucas an	1 n 224	1 n 22300
		Pan-e hn c	≤1 n 500	Reduced
Tyros nem a ype (AR) NM 000137 2	FAH *	Ashkenaz Jew sh	1 n 143	1 n 2840
		French Canad an	1 n 66	1 n 1300
		French Canad an (Saguenay-Lac-S - Jean)	1 n 16	1 n 300
		Pan-e hn c	1 n 125	1 n 2480
USH1C-re a ed cond ons (AR) NM 005709 3	USH1C *	French Canad an/Acad an	1 n 227	1 n 22600
		Pan-e hn c	1 n 353	1 n 3521
		Sephard c Jew sh	1 n 125	1 n 1241
USH2A-re a ed cond ons (AR) NM 206933 2	USH2A	Caucas an	1 n 70	1 n 6900
		Pan-e hn c	1 n 112	1 n 11100
		Sephard c Jew sh	1 n 36	1 n 3500
Very ong-cha n acy -CoA dehydrogenase de c ency (AR) NM 000018 3	ACADVL	Pan-e hn c	1 n 100	1 n 9900
VRK1-re a ed cond ons (AR) NM 003384 2	VRK1	Ashkenaz Jew sh	1 n 225	1 n 22400
		Pan-e hn c	≤1 n 500	Reduced
VSX2-re a ed cond ons (AR) NM 182894 2	VSX2	Pan-e hn c	≤1 n 500	Reduced
		Sephard c Jew sh	1 n 145	1 n 14400
W son d sease (AR) NM 000053 3	ATP7B	Ashkenaz Jew sh	1 n 67	1 n 3300
		Canary s ander	1 n 25	1 n 1200
		Pan-e hn c	1 n 90	1 n 4450
		Sard n an	1 n 50	1 n 2450
		Sephard c Jew sh	1 n 65	1 n 3200
WNT10A-re a ed cond ons (AR) NM 025216 2	WNT10A	Pan-e hn c	1 n 305	1 n 30400
X- nked adreno eukodys rophy (XL) NM 000033 3	ABCD1	Pan-e hn c	1 n 16800	Reduced
		Sephard c Jew sh	≤1 n 500	Reduced
X- nked crea ne ranspor er de c ency (XL) NM 005629 3	SLC6A8	Pan-e hn c	≤1 n 500	Reduced
X- nked juven e re nosch s s (XL) NM 000330 3	RS1	Pan-e hn c	≤1 n 500	Reduced
X- nked myo ubu ar myopa hy (XL) NM 000252 2	MTM1	Pan-e hn c	≤1 n 500	Reduced
X- nked severe comb ned mmunode c ency (XL) NM 000206 2	L2RG	Pan-e hn c	≤1 n 500	Reduced
Ze weger spec rum d sorder (PEX1-re a ed) (AR) NM 000466 2	PEX1	Pan-e hn c	1 n 144	1 n 14300

DISORDER (INHERITANCE)	GENE	ETHNICITY	CARRIER FREQUENCY BEFORE SCREENING	CARRIER RESIDUAL RISK AFTER NEGATIVE RESULT
Ze weger spec rum d sorder (PEX2-re a ed) (AR) NM 000318 2	PEX2	Ashkenaz Jew sh	1 n 227	1 n 22600
		Pan-e hn c	≤1 n 500	Reduced
Ze weger spec rum d sorder (PEX6-re a ed) (AR) NM 000287 3	PEX6	French Canad an	1 n 55	1 n 5400
		Pan-e hn c	1 n 294	1 n 29300
		Sephard c Jew sh	1 n 18	1 n 1700
Ze weger spec rum d sorder (PEX10-re a ed) (AR) NM 153818 1	PEX10	Pan-e hn c	1 n 606	Reduced

Methods

- Genom c DNA obta ned from the subm tted samp e s enr ched for targeted reg ons us ng a hybr d zat on based protoco and sequenced us ng I um na techno ogy Un ess otherw se nd cated a targeted reg ons are sequenced w th ≥50x depth or are supp emented w th add t ona ana ys s Reads are a gned to a reference sequence (GRCh37) and sequence changes are dent f ed and nterpreted n the context of a s ng e c n ca y re evant transcr pt nd cated be ow Enr chment and ana ys s focus on the cod ng sequence of the nd cated transcr pts 10bp of f ank ng ntron c sequence and other spec f c genom c reg ons demonstrated to be causat ve of d sease at the t me of assay des gn Promoters untrans ated reg ons and other non cod ng reg ons are not otherw se nterrogated Exon c de et ons and dup cat ons are ca ed us ng an n house a gor thm that determ nes copy number at each target by compar ng the read depth for each target n the proband sequence w th both mean read depth and read depth d str but on obta ned from a set of c n ca samp es Markers across the X and Y chromosomes are ana yzed for qua ty contro purposes and may detect dev at ons from the expected sex chromosome comp ement Such dev at ons may be nc uded n the report n accordance w th nterna gu de nes Inv tae ut zes a c ass f cat on methodo ogy to dent fy next generat on sequenc ng (NGS) detected var ants that requ re orthogona conf rmat on (L nco n et a J Mo D agn 2019 Mar 21(2) 318 329) Pathogen c and L ke y Pathogen c var ants that do not meet the va dated qua ty thresho ds are conf rmed Conf rmat on techno og es may nc ude any of the fo ow ng Sanger sequenc ng Pac f c B osc ences SMRT sequenc ng MLPA MLPA seq Array CGH Array CGH conf rmat on of NGS CNV ca ng performed by Inv tae Corporat on (1400 16th Street San Franc sco CA 94103 #05D2040778) The fo ow ng ana yses are performed f re evant to the requ s t on For GBA and CYP21A2 the reference genome has been mod f ed to mask the s tes of po ymorph c para og sequence var ants (PSVs) n both the gene and pseudogene If one or more repo tab e var ants s dent f ed (see L m tat ons) the gene s amp f ed by ong range PCR PacB o sequenc ng of the ong range amp cons s used to conf rm the var ant Gene convers on and fus on events are f agged by our NGS p pe ne and reportab e pseudogene der ved var ants are dent f ed by ong range PCR fo owed by PacB o sequenc ng of the ong range amp cons In some cases t may not be poss b e to d samb guate between the gene and pseudogene For HBA1/2 the reference genome has been mod f ed to force some sequenc ng reads der ved from HBA1 to a gn to HBA2 and var ant ca ng a gor thms are mod f ed to support an expectat on of 4 a e es n these reg ons HBA1/2 copy number ca ng s pe formed by a custom hypothes s test ng a gor thm wh ch generates d p otype ca s If sequence data for a samp e does not support a un que h gh conf dence match from among hypotheses tested that samp e s f agged for manua rev ew Copy number var at on s on y reported for cod ng sequence of HBA1 and HBA2 and the HS 40 reg on Th s assay does not d st ngu sh among the α3 7 subtypes and a α3 7 var ants are ca ed as HBA1 de et ons Th s assay may not detect over app ng copy ga n and copy oss events when the breakpo nts of those events are s m ar For FMR1 tr p et repeats are detected by PCR w th f uorescent y abe ed pr mers fo owed by cap a y e ectrophores s Reference ranges Norma <45 CGG repeats ntermed ate 45 54 CGG repeats premutat on 55 200 CGG repeats fu mutat on >200 CGG repeats For a e es w th 55 90 tr p et repeats the reg on surround ng the FMR1 repeat s amp f ed by PCR The PCR amp cons are then processed through PacB o SMRTBe bra y prep and sequenced us ng PacB o ong read techno ogy The number of AGG nterrupt ons w th n the 55 90 tr p et repeat s read d rect y from the resu t ng DNA sequences Techn ca component of conf rmatory sequenc ng s performed by Inv tae Corporat on (1400 16th Street San Franc sco CA 94103 #05D2040778)
- The fo ow ng transcr pts were used n th s ana ys s If more than one transcr pt s sted for a s ng e gene var ants were reported us ng the f rst transcr pt sted un ess othe w se nd cated n the report ABCB11 (NM 003742 2) ABCC8 (NM 000352 4) ABCD1 (NM 000033 3) 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) 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) ATP7A (NM 000052 6) ATP7B (NM 000053 3) ATRX (NM 000489 4) 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)

BTD (NM 000060 3) CAPN3 (NM 000070 2) CBS (NM 000071 2) CDH23 (NM 022124 5) CEP290 (NM 025114 3) CERKL (NM 001030311 2) CFTR (NM 000492 3) CHM (NM 000390 2) 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) COL4A5 (NM 000495 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) CYBB (NM 000397 3) CYP11B2 (NM 000498 3) CYP17A1 (NM 000102 3) CYP19A1 (NM 031226 2) CYP21A2 (NM 000500 7) CYP27A1 (NM 000784 3) DCLRE1C (NM 001033855 2) DHCR7 (NM 001360 2) DHDDS (NM 024887 3) DLD (NM 000108 4) DMD (NM 004006 2) DNAH5 (NM 001369 2) DNAI1 (NM 012144 3) DNAI2 (NM 023036 4) DYSF (NM 003494 3) EDA (NM 001399 4) EIF2B5 (NM 003907 2) ELP1 (NM 003640 3) EMD (NM 000117 2) ESCO2 (NM 001017420 2) ETFA (NM 000126 3) ETFDH (NM 004453 3) ETHE1 (NM 014297 3) EVC (NM 153717 2) EYS (NM 001142800 1) F11 (NM 000128 3) F9 (NM 000133 3) 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) FMR1 (NM 002024 5) 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) GJB1 (NM 000166 5) GJB2 (NM 004004 5) GLA (NM 000169 2) 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) GP1BA (NM 000173 6) GP9 (NM 000174 4) 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) IDS (NM 000202 6) IDUA (NM 000203 4) IL2RG (NM 000206 2) IVD (NM 002225 3) KCNJ11 (NM 000525 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) MCCC1 (NM 020166 4) MCCC2 (NM 022132 4) MCOLN1 (NM 020533 2) MED17 (NM 004268 4) MEFV (NM 000243 2) 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) MTM1 (NM 000252 2) 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) OTC (NM 000531 5) PAH (NM 000277 1) PCCA (NM 000282 3) PCCB (NM 000532 4) PCDH15 (NM 033056 3) PDHA1 (NM 000284 3) PDHB (NM 000925 3) PEX1 (NM 000466 2) PEX10 (NM 153818 1) 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) PRPS1 (NM 002764 3) 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) RS1 (NM 000330 3) 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) SLC6A8 (NM 005629 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) 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)

- Var ants of uncerta n s gn f cance are not nc uded n th s repo t however f add t ona ev dence becomes ava ab e to nd cate that a prev ous y uncerta n var ant s c n ca y s gn f cant Inv tae w update th s report and prov de not f cat on
- A PMID s a un que dent f er referr ng to a pub shed sc ent f c paper Search by PMID at http://www.ncbi.nlm.nih.gov/pubmed
- An rsID s a un que dent f er referr ng to a s ng e genom c pos t on and s used to assoc ate popu at on frequency nformat on w th sequence changes at that pos t on Reported popu at on frequenc es are der ved from a number of pub c s tes that aggregate data from arge sca e popu at on sequenc ng projects nc ud ng ExAC (http://exac.broadinstitute.org) and dbSNP (http://ncbi.nlm.nih.gov/SNP)

Disclaimer

DNA stud es do not const tute a def n t ve test for the se ected cond t on(s) n a nd v dua s It shou d be rea zed that there are poss b e sources of error Errors can resu t from trace contam nat on rare techn ca errors rare genet c var ants that nterfere w th ana ys s recent sc ent f c deve opments and a ternat ve c ass f cat on systems Th s test shou d be one of many aspects used by the hea thcare prov der to he p w th a d agnos s and treatment p an but t s not a d agnos s tse f Th s test was deve oped and ts performance character st cs determ ned by Inv tae It has not been c eared or approved by the FDA The aborato y s regu ated under the C n ca Laborato y Improvement Act (CLIA) as qua f ed to perform h gh comp ex ty c n ca tests (CLIA ID 05D2040778) Th s test s used for c n ca purposes It shou d not be regarded as nvest gat ona or for research

Limitations

- Based on va dat on study resu ts th s assay ach eves >99% ana yt ca sens t v ty and spec f c ty for s ng e nuc eot de var ants nsert ons and de et ons <15bp n ength and exon eve de et ons and dup cat ons Inv tae s methods a so detect nse t ons and de et ons arger than 15bp but sma er than a fu exon but sens t v ty for these may be marg na y reduced Inv tae's de et on/dup cat on ana ys s determ nes copy number at a s ng e exon reso ut on at v rtua y a targeted exons However n rare s tuat ons s ng e exon copy number events may not be ana yzed due to nherent sequence propert es or so ated reduct on n data qua ty Certa n types of var ants such as structura rearrangements (e g nvers ons gene convers on events trans ocat ons etc) or var ants embedded n sequence w th comp ex arch tecture (e g short tandem repeats or segmenta dup cat ons) may not be detected Add t ona y t may not be poss b e to fu y reso ve certa n deta s about var ants such as mosa c sm phas ng or mapp ng amb gu ty Un ess exp c t y guaranteed sequence changes n the promoter non cod ng exons and other non cod ng reg ons are not covered by th s assay P ease consu t the test def n t on on our webs te for deta s regard ng reg ons or types of var ants that are covered or exc uded for th s test Th s report ref ects the ana ys s of an extracted genom c DNA samp e Wh e th s test s ntended to ref ect the ana ys s of extracted genom c DNA from a referred pat ent n very rare cases the ana yzed DNA may not represent that nd v dua 's const tut ona genome such as n the case of a c rcu at ng hemato ympho d neop asm bone marrow transp ant b ood transfus on ch mer sm cu ture art fact or materna ce contam nat on
- FMR1 S z ng accuracy s expected to be / 1 for CGG repeat a e es ess than or equa to 90 repeat un ts and / 3 for CGG repeat a e es greater than 90 repeat un ts If the two CGG repeats sted are the same th s may nd cate that both a e es are the same s ze or that one a e e s too sma to be detected by th s ana ys s The number of AGG nterrupt ons s on y determ ned for fema es w th tr p et repeat s zes of 55 90 GBA c 84dupG (p Leu29A afs*18) c 115 1G>A (Sp ce donor) c 222 224de TAC (p Thr75de) c 475C>T (p Arg159Trp) c 595 596de CT (p Leu199Aspfs*62) c 680A>G (p Asn227Ser) c 721G>A (p G y241Arg) c 754T>A (p Phe252I e) c 1226A>G (p Asn409Ser) c 1246G>A (p G y416Ser) c 1263 1317de (p Leu422Profs*4) c 1297G>T (p Va 433Leu) c 1342G>C (p Asp448H s) c 1343A>T (p Asp448Va) c 1448T>C (p Leu483Pro) c 1504C>T (p Arg502Cys) c 1505G>A (p Arg502H s) c 1603C>T (p Arg535Cys) c 1604G>A (p Arg535H s) var ants on y Rare y sens t v ty to detect these var ants may be reduced When sens t v ty s reduced zygos ty may be reported as "unknown" IDS Detect on of comp ex rearrangements not offered (PMID 7633410 20301451) RPGRIP1L Sequenc ng ana ys s s not offered for exon 23 NBN De et on/dup cat on ana ys s s not offered for exons 15 16 USH1C De et on/dup cat on ana ys s s not offered for exons 5 6 CYP21A2 Ana ys s nc udes the most common var ants (c 92C>T(p Pro31Leu) c 293 13C>G (ntron c) c 332 339de GAGACTAC (p G y111Va fs*21) c 518T>A (p I e173Asn) c 710T>A (p I e237Asn) c 713T>A (p Va 238G u) c 719T>A (p Met240Lys) c 844G>T (p Va 282Leu) c 923dupT (p Leu308Phefs*6) c 955C>T (p G n319*) c 1069C>T(p Arg357Trp) c 1360C>T (p Pro454Ser) and the 30Kb de et on) as we as se ect rare HGMD var ants on y (st ava ab e upon request) Fu gene dup cat ons are reported on y n the presence of a pathogen c var ant(s) When a dup cat on and a pathogen c var ant(s) s dent f ed phase (c s/trans) cannot be determ ned Fu gene de et on ana ys s s not offered Sens t v ty to detect these var ants f they resu t from comp ex gene convers on/fus on events may be reduced COL4A5 De et on/dup cat on ana ys s s not offered for exons 11 12 HBA1/2 Th s assay s des gned to detect de et ons and dup cat ons of HBA1 and/or HBA2 resu t ng from the a pha20 5 MED SEA FIL/ THAI a pha3 7 a pha4 2 ant 3 7 and ant 4 2 Sens t v ty to detect other copy number var ants may be reduced Detect on of over app ng de et on and dup cat on events w be m ted to comb nat ons of events w th s gn f cant y d ffer ng boundar es In add t on de et on of the enhancer e ement HS 40 and the sequence var ant Constant Spr ng (NM 000517 4 c 427T>C) can be dent f ed by th s assay HBA2 Sequenc ng ana ys s s not offered for exons 1 2 NEB De et on/dup cat on ana ys s s not offered for exons 82 105 NEB var ants n th s reg on w th no ev dence towards pathogen c ty are not nc uded n th s report but are ava ab e upon request TSFM Sequenc ng ana ys s s not offered for exon 5 FAH De et on/dup cat on ana ys s s not offered for exon 14 GALC De et on/dup cat on ana ys s s not offered for exon 6 MMADHC De et on/dup cat on ana ys s s not offered for exons 5 6 OAT De et on/dup cat on ana ys s s not offered for exon 2 VPS13A De et on/dup cat on ana ys s s not offered for exons 2 3 27 28 ALG6 De et on/dup cat on ana ys s s not offered for exons 11 12 COL27A1 De et on/dup cat on ana ys s s not offered for exons 46 47 GP1BA c 104de A (p Lys35Argfs*4) c 165 168de TGAG (p Ser55Argfs*12) c 376A>G (p Asn126Asp) c 434T>C (p Leu145Pro) c 515C>T

(p A a172Va) c 584 586de TCC (p Leu195de) c 673T>A (p Cys225Ser) c 1454dupT (p Ser486I efs*12) c 1480de A (p Thr494Profs*59) c 1601 1602de AT (p Tyr534Cysfs*82) c 1620G>A (p Trp540*) var ants on y MTHFR The NM 005957 4 c 665C>T (p A a222Va) (aka 677C>T) and c 1286A>C (p G u429A a) (aka 1298A>C) var ants are not reported n our pr mary report SMN1 or SMN2 NM 000344 3 c *3 80T>G var ant on y SMN1 Systemat c exon number ng s used for a genes nc ud ng SMN1 and for th s reason the exon typ ca y referred to as exon 7 n the terature (PMID 8838816) s referred to as exon 8 n th s repo t Th s assay unamb guous y detects SMN1 exon 8 copy number The presence of the g 27134T>G var ant (a so known as c *3 80T>G) s reported f SMN1 copy number = 2

This report has been reviewed and approved by:

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