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Genetic Testing Summary

Enclosed are the genetic testing results for

CB 953-B

No amount of genetic testing can guarantee that a child will not be affected with a genetic condition. Genetic testing can inform you of the likelihood of passing on the genetic conditions that are tested for, but it cannot eliminate the risk of passing on any genetic condition.

The genetic conditions Cryobio tests for are inherited in an autosomal recessive manner. This means that the child would have to inherit a genetic mutation from both the sperm source and the egg source to be affected with the condition. When both the sperm source and the egg source have undergone genetic carrier screening and the test results are negative, the risk of a child being affected with the conditions tested for is significantly reduced, but it cannot be completely eliminated.

All recipients should discuss both their own risk for passing on genetic conditions and whether they would benefit from genetic counseling and testing with their health care provider. Before using a donor that is a carrier for a specific recessive genetic condition or conditions, we strongly recommend that the recipient (or egg source, if different) consider genetic counseling and testing to determine if they are a carrier for the same genetic condition or conditions as the donor.

Screening and testing have changed dramatically over the years, and so the screening and testing done on each donor may vary depending on the testing that was in place when he was actively in Cryobio's donor program. Earlier donors may not have had as extensive testing as later donors. Screening and testing may change again in the future, so please review the results each time before ordering as both the testing done and the results may change.



Patient Information

Name: Cb 953-B
 Date of Birth: [REDACTED]
 Sema4 ID: [REDACTED]
 Client ID: [REDACTED]
 Indication: Carrier Testing

Specimen Information

Specimen Type: Blood
 Date Collected: [REDACTED]
 Date Received: [REDACTED]
 Final Report: [REDACTED]

Referring Provider

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Expanded Carrier Screen (283)

Number of genes tested: 283

SUMMARY OF RESULTS AND RECOMMENDATIONS

⊕ Positive	⊖ Negative
<p>Carrier of Glycogen Storage Disease, Type V (AR) Associated gene(s): <i>PYGM</i> Variant(s) Detected: c.679_686dupTACGATAC, p.P230TfsX68, Likely Pathogenic, Heterozygous (one copy)</p>	<p>Negative for all other genes tested To view a full list of genes and diseases tested please see Table 1 in this report</p>

AR=Autosomal recessive; XL=X-linked

Recommendations

- Testing the partner for the above positive disorder(s) and genetic counseling are recommended.
- Please note that for female carriers of X-linked diseases, follow-up testing of a male partner is not indicated.
- CGG repeat analysis of *FMR1* for fragile X syndrome is not performed on males as repeat expansion of premutation alleles is not expected in the male germline.
- Individuals of Asian, African, Hispanic and Mediterranean ancestry should also be screened for hemoglobinopathies by CBC and hemoglobin electrophoresis.
- Consideration of residual risk by ethnicity after a negative carrier screen is recommended for the other diseases on the panel, especially in the case of a positive family history for a specific disorder.



Interpretation of positive results

Glycogen Storage Disease, Type V (AR)

Results and Interpretation

A heterozygous (one copy) likely pathogenic frameshift variant, c.679_686dupTACGATAC, p.P230TfsX68, was detected in the *PYGM* gene (NM_005609.2). When this variant is present in trans with a pathogenic variant, it is considered to be causative for glycogen storage disease, type V. Therefore, this individual is expected to be at least a carrier for glycogen storage disease, type V. Heterozygous carriers are not expected to exhibit symptoms of this disease.

What is Glycogen Storage Disease, Type V?

Glycogen storage disease, type V (GSD5) is an autosomal recessive muscle disease caused by pathogenic variants in the gene *PYGM*. The clinical presentation is variable, although symptoms commonly begin in the first decade of life. Symptoms include exercise intolerance (pain when exercising) and muscle weakness, which may worsen in the patient's 40s or 50s. Most individuals are able to tolerate mild exercise and stay physically fit. Life expectancy is not affected. It is not currently possible to predict how severe the disease will be based on the inherited variants. GSD5 may affect people of any ethnicity, but it is more common among Sephardic Jewish individuals from Iran, Iraq and Syria.

Test description

This patient was tested for a panel of diseases using a combination of sequencing, targeted genotyping and copy number analysis. Please note that negative results reduce but do not eliminate the possibility that this individual is a carrier for one or more of the disorders tested. Please see Table 1 for a list of genes and diseases tested, and go.sema4.com/residualrisk for specific detection rates and residual risk by ethnicity. With individuals of mixed ethnicity, it is recommended to use the highest residual risk estimate. Only variants determined to be pathogenic or likely pathogenic are reported in this carrier screening test.

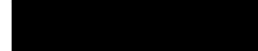
Fatimah Nahhas-Alwan, Ph.D., DABMGG, Laboratory Director
 Laboratory Medical Consultant: George A. Diaz, M.D., Ph.D.

Genes and diseases tested

For specific detection rates and residual risk by ethnicity, please visit go.sema4.com/residualrisk

Table 1: List of genes and diseases tested with detailed results

Disease	Gene	Inheritance Pattern	Status	Detailed Summary
⊕ Positive				
Glycogen Storage Disease, Type V	<i>PYGM</i>	AR	Carrier	c.679_686dupTACGATAC, p.P230TfsX68. Likely Pathogenic, Heterozygous (one copy)
⊖ Negative				
3-Beta-Hydroxysteroid Dehydrogenase Type II Deficiency	<i>HSD3B2</i>	AR	Reduced Risk	
3-Methylcrotonyl-CoA Carboxylase Deficiency (MCCC1-Related)	<i>MCCC1</i>	AR	Reduced Risk	



3-Methylcrotonyl-CoA Carboxylase Deficiency (MCCC2-Related)	MCCC2	AR	Reduced Risk
3-Methylglutaconic Aciduria, Type III	OPA3	AR	Reduced Risk
3-Phosphoglycerate Dehydrogenase Deficiency	PHGDH	AR	Reduced Risk
6-Pyruvoyl-Tetrahydropterin Synthase Deficiency	PIS	AR	Reduced Risk
Abetalipoproteinemia	MTTP	AR	Reduced Risk
Achromatopsia (CNGB3-related)	CNGB3	AR	Reduced Risk
Acrodermatitis Enteropathica	SLC39A4	AR	Reduced Risk
Acute Infantile Liver Failure	TRMU	AR	Reduced Risk
Acyl-CoA Oxidase I Deficiency	ACOX1	AR	Reduced Risk
Adenosine Deaminase Deficiency	ADA	AR	Reduced Risk
Adrenoleukodystrophy, X-Linked	ABCD1	XL	Reduced Risk
Aicardi-Goutieres Syndrome (SAMHD1-Related)	SAMHD1	AR	Reduced Risk
Alpha-Mannosidosis	MAN2B1	AR	Reduced Risk
Alpha-Thalassemia	HBA1/HBA2	AR	Reduced Risk
HBA1 Copy Number: 2 HBA2 Copy Number: 2 No pathogenic copy number variants detected HBA1/HBA2 Sequencing: Negative			
Alpha-Thalassemia Mental Retardation Syndrome	ATRX	XL	Reduced Risk
Alport Syndrome (COL4A3-Related)	COL4A3	AR	Reduced Risk
Alport Syndrome (COL4A4-Related)	COL4A4	AR	Reduced Risk
Alport Syndrome (COL4A5-Related)	COL4A5	XL	Reduced Risk
Alstrom Syndrome	ALMS1	AR	Reduced Risk
Andermann Syndrome	SLC12A6	AR	Reduced Risk
Argininosuccinic Aciduria	ASL	AR	Reduced Risk
Aromatase Deficiency	CYP19A1	AR	Reduced Risk
Arthrogryposis, Mental Retardation, and Seizures	SLC35A3	AR	Reduced Risk
Asparagine Synthetase Deficiency	ASNS	AR	Reduced Risk
Aspartylglycosaminuria	AGA	AR	Reduced Risk
Ataxia With Isolated Vitamin E Deficiency	TTPA	AR	Reduced Risk
Ataxia-Telangiectasia	ATM	AR	Reduced Risk
Autosomal Recessive Spastic Ataxia of Charlevoix-Saguenay	SACS	AR	Reduced Risk
Bardet-Biedl Syndrome (BBS10-Related)	BBS10	AR	Reduced Risk
Bardet-Biedl Syndrome (BBS12-Related)	BBS12	AR	Reduced Risk
Bardet-Biedl Syndrome (BBS1-Related)	BBS1	AR	Reduced Risk
Bardet-Biedl Syndrome (BBS2-Related)	BBS2	AR	Reduced Risk
Bare Lymphocyte Syndrome, Type II	CIITA	AR	Reduced Risk
Bartter Syndrome, Type 4A	BSND	AR	Reduced Risk
Bernard-Soulier Syndrome, Type A1	GP1BA	AR	Reduced Risk
Bernard-Soulier Syndrome, Type C	GP9	AR	Reduced Risk
Beta-Globin-Related Hemoglobinopathies	HBB	AR	Reduced Risk
Beta-Ketothiolase Deficiency	ACAT1	AR	Reduced Risk
Bilateral Frontoparietal Polymicrogyria	GPR56	AR	Reduced Risk
Biotinidase Deficiency	BTD	AR	Reduced Risk
Bloom Syndrome	BLM	AR	Reduced Risk
Canavan Disease	ASPA	AR	Reduced Risk
Carbamoylphosphate Synthetase I Deficiency	CPS1	AR	Reduced Risk
Carnitine Palmitoyltransferase IA Deficiency	CPT1A	AR	Reduced Risk
Carnitine Palmitoyltransferase II Deficiency	CPT2	AR	Reduced Risk
Carpenter Syndrome	RAB23	AR	Reduced Risk
Cartilage-Hair Hypoplasia	RMRP	AR	Reduced Risk
Cerebral Creatine Deficiency Syndrome 1	SLC6A8	XL	Reduced Risk
Cerebral Creatine Deficiency Syndrome 2	GAMT	AR	Reduced Risk
Cerebrotendinous Xanthomatosis	CYP27A1	AR	Reduced Risk
Charcot-Marie-Tooth Disease, Type 4D	NUMG1	AR	Reduced Risk
Charcot-Marie-Tooth Disease, Type 5 / Arts Syndrome	PRPS1	XL	Reduced Risk
Charcot-Marie-Tooth Disease, X-Linked	GJB1	XL	Reduced Risk
Choreoacanthocytosis	VPS13A	AR	Reduced Risk
Choroideremia	CHM	XL	Reduced Risk



Chronic Granulomatous Disease (CYBA-Related)	CYBA	AR	Reduced Risk	
Chronic Granulomatous Disease (CYBB-Related)	CYBB	XL	Reduced Risk	
Citrin Deficiency	SLC25A13	AR	Reduced Risk	
Citrullinemia, Type 1	ASS1	AR	Reduced Risk	
Cohen Syndrome	VPS13B	AR	Reduced Risk	
Combined Malonic and Methylmalonic Aciduria	ACSF3	AR	Reduced Risk	
Combined Oxidative Phosphorylation Deficiency 1	GFM1	AR	Reduced Risk	
Combined Oxidative Phosphorylation Deficiency 3	TSFM	AR	Reduced Risk	
Combined Pituitary Hormone Deficiency 2	PROP1	AR	Reduced Risk	
Combined Pituitary Hormone Deficiency 3	LHX3	AR	Reduced Risk	
Combined SAP Deficiency	PSAP	AR	Reduced Risk	
Congenital Adrenal Hyperplasia due to 17-Alpha-Hydroxylase Deficiency	CYP17A1	AR	Reduced Risk	
Congenital Adrenal Hyperplasia due to 21-Hydroxylase Deficiency	CYP21A2	AR	Reduced Risk	CYP21A2 copy number: 2 CYP21A2 sequencing: Negative
Congenital Amegakaryocytic Thrombocytopenia	MPL	AR	Reduced Risk	
Congenital Disorder of Glycosylation, Type Ia	PMM2	AR	Reduced Risk	
Congenital Disorder of Glycosylation, Type Ib	MPI	AR	Reduced Risk	
Congenital Disorder of Glycosylation, Type Ic	ALG6	AR	Reduced Risk	
Congenital Insensitivity to Pain with Anhidrosis	NTRK1	AR	Reduced Risk	
Congenital Myasthenic Syndrome (CHRNE-Related)	CHRNE	AR	Reduced Risk	
Congenital Myasthenic Syndrome (RAPSIN-Related)	RAPSIN	AR	Reduced Risk	
Congenital Neutropenia (HAX1-Related)	HAX1	AR	Reduced Risk	
Congenital Neutropenia (VPS45-Related)	VPS45	AR	Reduced Risk	
Corneal Dystrophy and Perceptive Deafness	SLC4A11	AR	Reduced Risk	
Corticosterone Methyloxidase Deficiency	CYP11B2	AR	Reduced Risk	
Cystic Fibrosis	CFTR	AR	Reduced Risk	
Cystinosis	CTNS	AR	Reduced Risk	
D-Bifunctional Protein Deficiency	HSD17B4	AR	Reduced Risk	
Deafness, Autosomal Recessive 77	LOXHD1	AR	Reduced Risk	
Duchenne Muscular Dystrophy / Becker Muscular Dystrophy	DMD	XL	Reduced Risk	
Dyskeratosis Congenita (RTEL1-Related)	RTEL1	AR	Reduced Risk	
Dystrophic Epidermolysis Bullosa	COL7A1	AR	Reduced Risk	
Ehlers-Danlos Syndrome, Type VIIC	ADAMTS2	AR	Reduced Risk	
Ellis-van Creveld Syndrome (EVC-Related)	EVC	AR	Reduced Risk	
Emery-Dreifuss Myopathy 1	EMD	XL	Reduced Risk	
Enhanced S-Cone Syndrome	NR2E3	AR	Reduced Risk	
Ethylmalonic Encephalopathy	E1HE1	AR	Reduced Risk	
Fabry Disease	GLA	XL	Reduced Risk	
Factor IX Deficiency	F9	XL	Reduced Risk	
Factor XI Deficiency	F11	AR	Reduced Risk	
Familial Autosomal Recessive Hypercholesterolemia	LDLRAP1	AR	Reduced Risk	
Familial Dysautonomia	IKBKAP	AR	Reduced Risk	
Familial Hypercholesterolemia	LDLR	AR	Reduced Risk	
Familial Hyperinsulinism (ABCC8-Related)	ABCC8	AR	Reduced Risk	
Familial Hyperinsulinism (KCNJ11-Related)	KCNJ11	AR	Reduced Risk	
Familial Mediterranean Fever	MEFV	AR	Reduced Risk	
Fanconi Anemia, Group A	FANCA	AR	Reduced Risk	
Fanconi Anemia, Group C	FANCC	AR	Reduced Risk	
Fanconi Anemia, Group G	FANCG	AR	Reduced Risk	
Fragile X Syndrome	FMR1	XL	Reduced Risk	FMR1CGG repeat sizes: Not Performed FMR1 Sequencing: Negative Fragile X CGG triplet repeat expansion testing was not performed at this time, as the patient has either been previously tested or is a male.
Fumarase Deficiency	FH	AR	Reduced Risk	
GRACILE Syndrome and Other BCS1L-Related Disorders	BCS1L	AR	Reduced Risk	
Galactokinase Deficiency	GALK1	AR	Reduced Risk	
Galactosemia	GALT	AR	Reduced Risk	



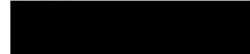
Gaucher Disease	GBA	AR	Reduced Risk
Gitelman Syndrome	SLC12A3	AR	Reduced Risk
Glutaric Acidemia, Type I	GCDH	AR	Reduced Risk
Glutaric Acidemia, Type IIa	ETFA	AR	Reduced Risk
Glutaric Acidemia, Type IIc	ETFDH	AR	Reduced Risk
Glycine Encephalopathy (AMT-Related)	AM1	AR	Reduced Risk
Glycine Encephalopathy (GLDC-Related)	GLDC	AR	Reduced Risk
Glycogen Storage Disease, Type II	GAA	AR	Reduced Risk
Glycogen Storage Disease, Type III	AGL	AR	Reduced Risk
Glycogen Storage Disease, Type IV / Adult Polyglucosan Body Disease	GBE1	AR	Reduced Risk
Glycogen Storage Disease, Type Ia	G6PC	AR	Reduced Risk
Glycogen Storage Disease, Type Ib	SLC37A4	AR	Reduced Risk
Glycogen Storage Disease, Type VII	PFKM	AR	Reduced Risk
HMG-CoA Lyase Deficiency	HMGCL	AR	Reduced Risk
Hemochromatosis, Type 2A	HFE2	AR	Reduced Risk
Hemochromatosis, Type 3	TFR2	AR	Reduced Risk
Hereditary Fructose Intolerance	ALDOB	AR	Reduced Risk
Hereditary Spastic Paraparesis 4g	LECPH2	AR	Reduced Risk
Hermansky-Pudlak Syndrome, Type 1	HPS1	AR	Reduced Risk
Hermansky-Pudlak Syndrome, Type 3	HPS3	AR	Reduced Risk
Holocarbonylase Synthetase Deficiency	HLCS	AR	Reduced Risk
Homocystinuria (CBS-Related)	CBS	AR	Reduced Risk
Homocystinuria due to MTHFR Deficiency	MTHFR	AR	Reduced Risk
Homocystinuria, cblE Type	MTRR	AR	Reduced Risk
Hydrolethalus Syndrome	HYLS1	AR	Reduced Risk
Hyperomithinemia-Hyperammonemia- Homocitrullinuria Syndrome	SLC25A15	AR	Reduced Risk
Hypohidrotic Ectodermal Dysplasia 1	EVA	XL	Reduced Risk
Hypophosphatasia	ALPL	AR	Reduced Risk
Inclusion Body Myopathy 2	GNE	AR	Reduced Risk
Infantile Cerebral and Cerebellar Atrophy	MED17	AR	Reduced Risk
Isovaleric Acidemia	IVD	AR	Reduced Risk
Joubert Syndrome 2	TMEM216	AR	Reduced Risk
Joubert Syndrome 7 / Meckel Syndrome 5 / COACH Syndrome	RPGRIPI1	AR	Reduced Risk
Junctional Epidermolysis Bullosa (LAMA3-Related)	LAMA3	AR	Reduced Risk
Junctional Epidermolysis Bullosa (LAMB3-Related)	LAMB3	AR	Reduced Risk
Junctional Epidermolysis Bullosa (LAMC2-Related)	LAMC2	AR	Reduced Risk
Krabbe Disease	GALC	AR	Reduced Risk
Lamellar Ichthyosis, Type 1	TGM1	AR	Reduced Risk
Leber Congenital Amaurosis 10 and Other CEP290- Related Olopathies	CEP290	AR	Reduced Risk
Leber Congenital Amaurosis 13	RDH12	AR	Reduced Risk
Leber Congenital Amaurosis 2 / Retinitis Pigmentosa 20	RPE65	AR	Reduced Risk
Leber Congenital Amaurosis 5	LCA5	AR	Reduced Risk
Leber Congenital Amaurosis 8 / Retinitis Pigmentosa 12 / Pigmented Paravenous Chorioretinal Atrophy	CRB1	AR	Reduced Risk
Leigh Syndrome, French-Canadian Type	LRPPRC	AR	Reduced Risk
Lethal Congenital Contracture Syndrome 1 / Lethal Arthrogyposis with Anterior Horn Cell Disease	GLE1	AR	Reduced Risk
Leukoencephalopathy with Vanishing White Matter	EIF2B5	AR	Reduced Risk
Limb-Girdle Muscular Dystrophy, Type 2A	CAPN3	AR	Reduced Risk
Limb-Girdle Muscular Dystrophy, Type 2B	DYSF	AR	Reduced Risk
Limb-Girdle Muscular Dystrophy, Type 2C	SGCG	AR	Reduced Risk
Limb-Girdle Muscular Dystrophy, Type 2D	SGCA	AR	Reduced Risk
Limb-Girdle Muscular Dystrophy, Type 2E	SGCB	AR	Reduced Risk
Limb-Girdle Muscular Dystrophy, Type 2I	FKRP	AR	Reduced Risk
Lipoamide Dehydrogenase Deficiency	DLD	AR	Reduced Risk
Lipoid Adrenal Hyperplasia	S1A1	AR	Reduced Risk



Lipoprotein Lipase Deficiency	LPL	AR	Reduced Risk
Long-Chain 3-Hydroxyacyl-CoA Dehydrogenase Deficiency	HADHA	AR	Reduced Risk
Lysinuric Protein Intolerance	SLC7A7	AR	Reduced Risk
Maple Syrup Urine Disease, Type 1a	BCKDHA	AR	Reduced Risk
Maple Syrup Urine Disease, Type 1b	BCKDHB	AR	Reduced Risk
Meckel 1 / Bardet-Biedl Syndrome 13	MKS1	AR	Reduced Risk
Medium Chain Acyl-CoA Dehydrogenase Deficiency	ACADM	AR	Reduced Risk
Megalencephalic Leukoencephalopathy with Subcortical Cysts	MLC1	AR	Reduced Risk
Menkes Disease	ATP7A	XL	Reduced Risk
Metachromatic Leukodystrophy	AHSA	AR	Reduced Risk
Methylmalonic Acidemia (MMAA-Related)	MMAA	AR	Reduced Risk
Methylmalonic Acidemia (MMAB-Related)	MMAB	AR	Reduced Risk
Methylmalonic Acidemia (MUT-Related)	MU1	AR	Reduced Risk
Methylmalonic Aciduria and Homocystinuria, Cobalamin C Type	MMACHC	AR	Reduced Risk
Methylmalonic Aciduria and Homocystinuria, Cobalamin D Type	MMADHC	AR	Reduced Risk
Microphthalmia / Anophthalmia	VSX2	AR	Reduced Risk
Mitochondrial Complex I Deficiency (ACAD9-Related)	ACAD9	AR	Reduced Risk
Mitochondrial Complex I Deficiency (NDUFAF5-Related)	NDUFAF5	AR	Reduced Risk
Mitochondrial Complex I Deficiency (NDUFS6-Related)	NDUFS6	AR	Reduced Risk
Mitochondrial DNA Depletion Syndrome 6 / Navajo Neurohepatopathy	MPV17	AR	Reduced Risk
Mitochondrial Myopathy and Sideroblastic Anemia 1	PUS1	AR	Reduced Risk
Mucopolidosis II / IIIA	GNPTAB	AR	Reduced Risk
Mucopolidosis III Gamma	GNP1G	AR	Reduced Risk
Mucopolidosis IV	MCOLN1	AR	Reduced Risk
Mucopolysaccharidosis Type I	IDUA	AR	Reduced Risk
Mucopolysaccharidosis Type II	IDS	XL	Reduced Risk
Mucopolysaccharidosis Type IIIA	SGSH	AR	Reduced Risk
Mucopolysaccharidosis Type IIIB	NAGLU	AR	Reduced Risk
Mucopolysaccharidosis Type IIIC	HGSNAT	AR	Reduced Risk
Mucopolysaccharidosis Type IIID	GNS	AR	Reduced Risk
Mucopolysaccharidosis Type IVb / GM1 Gangliosidosis	GLB1	AR	Reduced Risk
Mucopolysaccharidosis type IX	HYAL1	AR	Reduced Risk
Mucopolysaccharidosis type VI	ARSB	AR	Reduced Risk
Multiple Sulfatase Deficiency	SUMF1	AR	Reduced Risk
Muscle-Eye-Brain Disease and Other POMGNT1-Related Congenital Muscular Dystrophy-Dystroglycanopathies	POMGNT1	AR	Reduced Risk
Myoneurogastrointestinal Encephalopathy	TYMP	AR	Reduced Risk
Myotubular Myopathy 1	MTM1	XL	Reduced Risk
N-Acetylglutamate Synthase Deficiency	NAGS	AR	Reduced Risk
Nemaline Myopathy 2	NEB	AR	Reduced Risk
Nephrogenic Diabetes Insipidus, Type II	AQP2	AR	Reduced Risk
Nephrotic Syndrome (NPHS1-Related) / Congenital Finnish Nephrosis	NPHS1	AR	Reduced Risk
Nephrotic Syndrome (NPHS2-Related) / Steroid-Resistant Nephrotic Syndrome	NPHS2	AR	Reduced Risk
Neuronal Ceroid-Lipofuscinosis (CLN3-Related)	CLN3	AR	Reduced Risk
Neuronal Ceroid-Lipofuscinosis (CLN5-Related)	CLN5	AR	Reduced Risk
Neuronal Ceroid-Lipofuscinosis (CLN6-Related)	CLN6	AR	Reduced Risk
Neuronal Ceroid-Lipofuscinosis (CLN8-Related)	CLN8	AR	Reduced Risk
Neuronal Ceroid-Lipofuscinosis (MFSD8-Related)	MFSD8	AR	Reduced Risk
Neuronal Ceroid-Lipofuscinosis (PPT1-Related)	PPT1	AR	Reduced Risk
Neuronal Ceroid-Lipofuscinosis (TPP1-Related)	TPP1	AR	Reduced Risk
Niemann-Pick Disease (SMPD1-Related)	SMPD1	AR	Reduced Risk
Niemann-Pick Disease, Type C (NPC1-Related)	NPC1	AR	Reduced Risk
Niemann-Pick Disease, Type C (NPC2-Related)	NPC2	AR	Reduced Risk



Nijmegen Breakage Syndrome	<i>NBN</i>	AR	Reduced Risk	
Non-Syndromic Hearing Loss (GJB2-Related)	<i>GJB2</i>	AR	Reduced Risk	
Oclon-to-Onycho-Dermal Dysplasia / Schopf-Schultz-Passarge Syndrome	<i>WNT10A</i>	AR	Reduced Risk	
Omnenn Syndrome (RAG2-Related)	<i>HAG2</i>	AR	Reduced Risk	
Omnenn Syndrome / Severe Combined Immunodeficiency, Athabaskan-Type	<i>DCLRE1C</i>	AR	Reduced Risk	
Ornithine Aminotransferase Deficiency	<i>OAT</i>	AR	Reduced Risk	
Ornithine Transcarbamylase Deficiency	<i>OTC</i>	XL	Reduced Risk	
Osteopetrosis 1	<i>TCRG1</i>	AR	Reduced Risk	
Pendred Syndrome	<i>SLC26A4</i>	AR	Reduced Risk	
Phenylalanine Hydroxylase Deficiency	<i>PAH</i>	AR	Reduced Risk	
Polycystic Kidney Disease, Autosomal Recessive	<i>PKHD1</i>	AR	Reduced Risk	
Polyglandular Autoimmune Syndrome, Type 1	<i>AIRE</i>	AR	Reduced Risk	
Pontocerebellar Hypoplasia, Type 1A	<i>VHK1</i>	AR	Reduced Risk	
Pontocerebellar Hypoplasia, Type 6	<i>RARS2</i>	AR	Reduced Risk	
Primary Carnitine Deficiency	<i>SLC22A5</i>	AR	Reduced Risk	
Primary Ciliary Dyskinesia (DNAH5-Related)	<i>DNAH5</i>	AR	Reduced Risk	
Primary Ciliary Dyskinesia (DNAI1-Related)	<i>DNAI1</i>	AR	Reduced Risk	
Primary Ciliary Dyskinesia (DNAI2-Related)	<i>DNAI2</i>	AR	Reduced Risk	
Primary Hyperoxaluria, Type 1	<i>AGXT</i>	AR	Reduced Risk	
Primary Hyperoxaluria, Type 2	<i>GRHPR</i>	AR	Reduced Risk	
Primary Hyperoxaluria, Type 3	<i>HOGA1</i>	AR	Reduced Risk	
Progressive Cerebello-Cerebral Atrophy	<i>SEPSECS</i>	AR	Reduced Risk	
Progressive Familial Intrahepatic Cholestasis, Type 2	<i>ABCB11</i>	AR	Reduced Risk	
Propionic Acidemia (PCCA-Related)	<i>PCCA</i>	AR	Reduced Risk	
Propionic Acidemia (PCCB-Related)	<i>PCCB</i>	AR	Reduced Risk	
Pycnodysostosis	<i>CTSK</i>	AR	Reduced Risk	
Pyruvate Dehydrogenase E1-Alpha Deficiency	<i>PDHA1</i>	XL	Reduced Risk	
Pyruvate Dehydrogenase E1-Beta Deficiency	<i>PDHB</i>	AR	Reduced Risk	
Renal Tubular Acidosis and Deafness	<i>ATP6V1B1</i>	AR	Reduced Risk	
Retinitis Pigmentosa 25	<i>EYS</i>	AR	Reduced Risk	
Retinitis Pigmentosa 26	<i>CERKL</i>	AR	Reduced Risk	
Retinitis Pigmentosa 28	<i>FAM161A</i>	AR	Reduced Risk	
Retinitis Pigmentosa 59	<i>DHDDS</i>	AR	Reduced Risk	
Rhizomelic Chondrodysplasia Punctata, Type 1	<i>PEX7</i>	AR	Reduced Risk	
Rhizomelic Chondrodysplasia Punctata, Type 3	<i>AGPS</i>	AR	Reduced Risk	
Roberts Syndrome	<i>ESCO2</i>	AR	Reduced Risk	
Salla Disease	<i>SLC17A5</i>	AR	Reduced Risk	
Sandhoff Disease	<i>HEXB</i>	AR	Reduced Risk	
Schimke Immunosseous Dysplasia	<i>SMARCAL1</i>	AR	Reduced Risk	
Segawa Syndrome	<i>TH</i>	AR	Reduced Risk	
Sjogren-Larsson Syndrome	<i>ALDH3A2</i>	AR	Reduced Risk	
Smith-Lemli-Opitz Syndrome	<i>DHCR7</i>	AR	Reduced Risk	
Spinal Muscular Atrophy	<i>SMN1</i>	AR	Reduced Risk	SMN1 copy number: >=3 SMN2 copy number: 1 c.3+80T>G Detected
Spondylothoracic Dysostosis	<i>MESP2</i>	AR	Reduced Risk	
Steal Syndrome	<i>COL27A1</i>	AR	Reduced Risk	
Stuve-Wiedemann Syndrome	<i>LIFR</i>	AR	Reduced Risk	
Sulfate Transporter-Related Osteochondrodysplasia	<i>SLC26A2</i>	AR	Reduced Risk	



Tay-Sachs Disease	HEXA	AR	Reduced Risk	<p>Tay-Sachs disease enzyme: Non-carrier</p> <p>White blood cells: Non-carrier</p> <ul style="list-style-type: none"> Hex A% 68.6% (Non-carrier : 55.0 - 72.0% Carrier: <50%) Total hexosaminidase activity: 1462 nmol/hr/mg <p>Plasma: Non carrier</p> <ul style="list-style-type: none"> Hex A% 66.0 (Non-carrier : 58.0 - 72.0% Carrier: <54%) Total hexosaminidase activity: 607 nmol/hr/ml <p>HEXA Sequencing: Negative</p>
Tyrosinemia, Type I	FAH	AR	Reduced Risk	
Usher Syndrome, Type IB	MYO7A	AR	Reduced Risk	
Usher Syndrome, Type IC	USH1C	AR	Reduced Risk	
Usher Syndrome, Type ID	CDH23	AR	Reduced Risk	
Usher Syndrome, Type IF	PCDH15	AR	Reduced Risk	
Usher Syndrome, Type IIA	USH2A	AR	Reduced Risk	
Usher Syndrome, Type III	CLRN1	AR	Reduced Risk	
Very Long Chain Acyl-CoA Dehydrogenase Deficiency	ACADVL	AR	Reduced Risk	
Walker-Warburg Syndrome and Other FKTN-Related Dystrophies	FKTN	AR	Reduced Risk	
Wilson Disease	ATP7B	AR	Reduced Risk	
Wolman Disease / Cholesteryl Ester Storage Disease	LIPA	AR	Reduced Risk	
X-Linked Juvenile Retinoschisis	RS1	XL	Reduced Risk	
X-Linked Severe Combined Immunodeficiency	IL2RG	XL	Reduced Risk	
Zellweger Syndrome Spectrum (PEX10-Related)	PEX10	AR	Reduced Risk	
Zellweger Syndrome Spectrum (PEX1-Related)	PEX1	AR	Reduced Risk	
Zellweger Syndrome Spectrum (PEX2-Related)	PEX2	AR	Reduced Risk	
Zellweger Syndrome Spectrum (PEX6-Related)	PEX6	AR	Reduced Risk	

AR=Autosomal recessive; XL=X-linked

Test methods and comments

Genomic DNA isolated from this patient was analyzed by one or more of the following methodologies, as applicable:

Fragile X CGG Repeat Analysis (Analytical Detection Rate >99%)

PCR amplification using Asuragen, Inc. AmpliDeX® *FMR1* PCR reagents followed by capillary electrophoresis for allele sizing was performed. Samples positive for *FMR1* CGG repeats in the premutation and full mutation size range were further analyzed by Southern blot analysis to assess the size and methylation status of the *FMR1* CGG repeat.

Genotyping (Analytical Detection Rate >99%)

Multiplex PCR amplification and allele specific primer extension analyses using the MassARRAY® System were used to identify variants that are complex in nature or are present in low copy repeats. Rare sequence variants may interfere with assay performance.

Multiplex Ligation-Dependent Probe Amplification (MLPA) (Analytical Detection Rate >99%)

MLPA® probe sets and reagents from MRC-Holland were used for copy number analysis of specific targets versus known control samples. False positive or negative results may occur due to rare sequence variants in target regions detected by MLPA probes. Analytical sensitivity and specificity of the MLPA method are both 99%.

For alpha thalassemia, the copy numbers of the *HBA1* and *HBA2* genes were analyzed. Alpha-globin gene deletions, triplications, and the Constant Spring (CS) mutation are assessed. This test is expected to detect approximately 90% of all alpha-thalassemia mutations, varying by ethnicity. Carriers of alpha-thalassemia with three or more *HBA* copies on one chromosome, and one or no copies on the other chromosome, may not be detected. With the exception of triplications, other benign alpha-globin gene polymorphisms will not be reported. Analyses of *HBA1* and *HBA2* are performed in association with long-range PCR of the coding regions followed by short-read sequencing.

For Duchenne muscular dystrophy, the copy numbers of all *DMD* exons were analyzed. Potentially pathogenic single exon deletions and duplications are confirmed by a second method. Analysis of *DMD* is performed in association with sequencing of the coding regions.

For congenital adrenal hyperplasia, the copy number of the *CYP21A2* gene was analyzed. This analysis can detect large deletions due to unequal meiotic crossing-over between *CYP21A2* and the pseudogene *CYP21A1P*. These 30-kb deletions make up approximately 20% of *CYP21A2* pathogenic alleles. This test may also identify certain point mutations in *CYP21A2* caused by gene conversion events between *CYP21A2* and *CYP21A1P*. Some carriers may not be identified by dosage sensitive methods as this testing cannot detect individuals with two copies (duplication) of the *CYP21A2* gene on one chromosome and loss of *CYP21A2* (deletion) on the other chromosome. Analysis of *CYP21A2* is performed in association with long-range PCR of the coding regions followed by short-read sequencing.

For spinal muscular atrophy (SMA), the copy numbers of the *SMN1* and *SMN2* genes were analyzed. The individual dosage of exons 7 and 8 as well as the combined dosage of exons 1, 4, 6 and 8 of *SMN1* and *SMN2* were assessed. Copy number gains and losses can be detected with this assay. Depending on ethnicity, 6 - 29% of carriers will not be identified by dosage sensitive methods as this testing cannot detect individuals with two copies (duplication) of the *SMN1* gene on one chromosome and loss of *SMN1* (deletion) on the other chromosome (silent 20 carrier) or individuals that carry an intragenic mutation in *SMN1*. Please also note that 2% of individuals with SMA have an *SMN1* mutation that occurred *de novo*. Typically in these cases, only one parent is an SMA carrier.

The presence of the c.*380T>G (chr5:70,247,901T>G) variant allele in an individual with Ashkenazi Jewish or Asian ancestry is typically indicative of a duplication of *SMN1*. When present in an Ashkenazi Jewish or Asian individual with two copies of *SMN1*, c.*380T>G is likely indicative of a silent (20) carrier. In individuals with two copies of *SMN1* with African American, Hispanic or Caucasian ancestry, the presence or absence of c.*380T>G significantly increases or decreases, respectively, the likelihood of being a silent 20 carrier.

Pathogenic or likely pathogenic sequence variants in exon 7 may be detected during testing for the c.*380T>G variant allele; these will be reported if confirmed to be located in *SMN1* using locus-specific Sanger primers

MLPA for Gaucher disease (*GBA*), cystic fibrosis (*CFTR*), and non-syndromic hearing loss (*GJB2/GJB6*) will only be performed if indicated for confirmation of detected CNVs. If *GBA* analysis was performed, the copy numbers of exons 1, 3, 4, and 6 - 10 of the *GBA* gene (of 11 exons total) were analyzed. If *CFTR* analysis was performed, the copy numbers of all 27 *CFTR* exons were analyzed. If *GJB2/GJB6* analysis was performed, the copy number of the two *GJB2* exons were analyzed, as well as the presence or absence of the two upstream deletions of the *GJB2* regulatory region, del(*GJB6*-D13S1830) and del(*GJB6*-D13S1854).

Next Generation Sequencing (NGS) (Analytical Detection Rate >95%)

NGS was performed on a panel of genes for the purpose of identifying pathogenic or likely pathogenic variants.

Agilent SureSelect^{IM}QXT technology was used with a custom capture library to target the exonic regions and intron/exon splice junctions of the relevant genes, as well as a number of UTR, intronic or promoter regions that contain previously reported mutations. Samples were pooled and sequenced on the Illumina HiSeq 2500 platform in the Rapid Run mode or the Illumina NovaSeq platform in the Xp workflow, using 100 bp paired-end reads. This sequencing data was analyzed using a custom bioinformatics algorithm designed and validated in house.

The coding exons and splice junctions of the known protein-coding RefSeq genes were assessed for the average depth of coverage (minimum of 20X) and data quality threshold values. Most exons not meeting a minimum of >20X read depth across the exon are further analyzed by Sanger sequencing. Please note that several genomic regions present difficulties in mapping or obtaining read depth >20X. The exons contained within these regions are noted within Table 1 (as "Exceptions") and will not be reflexed to Sanger sequencing if the mapping quality or coverage is poor. Any variants identified during testing in these regions are confirmed by a second method and reported if determined to be pathogenic or likely pathogenic. However, as there is a possibility of false negative results within these regions, detection rates and residual risks for these genes have been calculated with the presumption that variants in these exons will not be detected, unless included in the MassARRAY[®] genotyping platform.

This test will detect variants within the exons and the intron-exon boundaries of the target regions. Variants outside these regions may not be detected, including, but not limited to, UTRs, promoters, and deep intronic areas, or regions that fall into the Exceptions mentioned above. This technology may not detect all small insertion/deletions and is not diagnostic for repeat expansions and structural genomic variation. In addition, a mutation(s) in a gene not included on the panel could be present in this patient.

Variant interpretation and classification was performed based on the American College of Medical Genetics Standards and Guidelines for the Interpretation of Sequence Variants (Richards et al. 2015). All potentially pathogenic variants may be confirmed by either a specific genotyping assay or Sanger sequencing, if indicated. Any benign variants, likely benign variants or variants of uncertain significance identified during this analysis will not be reported.

Copy Number Variant Analysis (Analytical Detection Rate >95%)

Large duplications and deletions were called from the relative read depths on an exon-by-exon basis using a custom exome hidden Markov model (XHMM) algorithm. Deletions or duplications determined to be pathogenic or likely pathogenic were confirmed by either a custom array CGH platform, quantitative PCR, or MLPA (depending on CNV size and gene content). While this algorithm is designed to pick up deletions and duplications of 2 or more exons in length, potentially pathogenic single-exon CNVs will be confirmed and reported, if detected.

Exon Array (Confirmation method) (Accuracy >99%)

The customized oligonucleotide microarray (Oxford Gene Technology) is a highly-targeted exon-focused array capable of detecting medically relevant microdeletions and microduplications at a much higher resolution than traditional aCGH methods. Each array matrix has approximately 180,000 60-mer oligonucleotide probes that cover the entire genome. This platform is designed based on human genome NCBI Build 37 (hg19) and the CGH probes are enriched to target the exonic regions of the genes in this panel.

Quantitative PCR (Confirmation method) (Accuracy >99%)

The relative quantification PCR is utilized on a Roche Universal Library Probe (UPL) system, which relates the PCR signal of the target region in one group to another. To test for genomic imbalances, both sample DNA and reference DNA is amplified with primer/probesets that specific to the target region and a control region with known genomic copy number. Relative genomic copy numbers are calculated based on the standard $\Delta\Delta Ct$ formula.

Long-Range PCR (Analytical Detection Rate >99%)

Long-range PCR was performed to generate locus-specific amplicons for *CYP21A2*, *HBA1* and *HBA2* and *GBA*. The PCR products were then prepared for short-read NGS sequencing and sequenced. Sequenced reads were mapped back to the original genomic locus and run through the bioinformatics pipeline. If indicated, copy number from MLPA was correlated with this sequencing output to analyze the results. For *CYP21A2*, a certain percentage of healthy individuals carry a duplication of the *CYP21A2* gene, which has no clinical consequences. In cases where two copies of a gene are located on the same chromosome in tandem, only the second copy will be amplified and assessed for potentially pathogenic variants, due to size limitations of the PCR reaction. However, because these alleles contain at least two copies of the *CYP21A2* gene in tandem, it is expected that this patient has at least one functional gene in the tandem allele and this patient is therefore less likely to be a carrier. When an individual carries both a duplication allele and a pathogenic variant, or multiple pathogenic variants, the current analysis may not be able to determine the phase (cis/trans configuration) of the *CYP21A2* alleles identified. Family studies may be required in certain scenarios where phasing is required to determine the carrier status.

Residual Risk Calculations

Carrier frequencies and detection rates for each ethnicity were calculated through the combination of internal curations of >28,000 variants and genomic frequency data from >138,000 individuals across seven ethnic groups in the gnomAD database. Additional variants in HGMD and novel deleterious variants were also incorporated into the calculation. Residual risk values are calculated using a Bayesian analysis combining the *a priori* risk of being a pathogenic mutation carrier (carrier frequency) and the detection rate. They are provided only as a guide for assessing approximate risk given a negative result, and values will vary based on the exact ethnic background of an individual. This report does not represent medical advice but should be interpreted by a genetic counselor, medical geneticist or physician skilled in genetic result interpretation and the relevant medical literature.

Sanger Sequencing (Confirmation method) (Accuracy >99%)

Sanger sequencing, as indicated, was performed using BigDye Terminator chemistry with the ABI 3730 DNA analyzer with target specific amplicons. It also may be used to supplement specific guaranteed target regions that fail NGS sequencing due to poor quality or low depth of coverage (<20 reads) or as a confirmatory method for NGS positive results. False negative results may occur if rare variants interfere with amplification or annealing.

Tay-Sachs Disease (TSD) Enzyme Analysis (Analytical Detection Rate \geq 98%)

Hexosaminidase activity and Hex A% activity were measured by a standard heat-inactivation, fluorometric method using artificial 4-MU- β -N-acetyl glucosaminide (4-MUG) substrate. This assay is highly sensitive and accurate in detecting Tay-Sachs carriers and individuals affected with TSD. Normal ranges of Hex A% activity are 55.0-72.0 for white blood cells and 58.0-72.0 for plasma. It is estimated that less than 0.5% of Tay-Sachs carriers have non-carrier levels of percent Hex A activity, and therefore may not be identified by this assay. In addition, this assay may detect individuals that are carriers of or are affected with Sandhoff disease. False positive results may occur if benign variants, such as pseudodeficiency alleles, interfere with the enzymatic assay. False negative results may occur if both *HEXA* and *HEXB* pathogenic or pseudodeficiency variants are present in the same individual.

Please note these tests were developed and their performance characteristics were determined by Mount Sinai Genomics, Inc. They have not been cleared or approved by the FDA. These analyses generally provide highly accurate information regarding the patient's carrier or affected status. Despite this high level of accuracy, it should be kept in mind that there are many potential sources of diagnostic error, including misidentification of samples, polymorphisms, or other rare genetic variants that interfere with analysis. Families should understand that rare diagnostic errors may occur for these reasons.

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Chen L et al. An information-rich CGG repeat primed PCR that detects the full range of Fragile X expanded alleles and minimizes the need for Southern blot analysis. *J Mol Diag* 2010 12:589-600.

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Ashkenazi Jewish Disorders:

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Duchenne Muscular Dystrophy:

Flanigan KM et al. Mutational spectrum of DMD mutations in dystrophinopathy patients: application of modern diagnostic techniques to a large cohort. *Hum Mutat* . 2009 30:1657-66.

Variant Classification:

Richards S et al. Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. *Genet Med*. 2015 May;17(5):405-24

Additional disease-specific references available upon request.

Patient	Sample	Referring Doctor
Patient Name: Cb 953-B Date of Birth: [REDACTED] Reference #: [REDACTED] Indication: CARR Test Type: Chromosome Analysis, Blood	Specimen Type: Peripheral Blood Lab #: [REDACTED] Date Collected: [REDACTED] Date Received: [REDACTED] Final Report: [REDACTED]	David Prescott, M.D. Cryobiology, Inc. 4845 Knightsbridge Blvd. Suite 200 Columbus, OH 43214 Fax: 614-451-5284

CYTOGENETIC ANALYSIS

Results

Staining: **G-bands by trypsin using Giemsa (GTG)** Chromosome count: **46** Cells captured: **5**
 Band level: **550** Cells analyzed: **20** Cells karyotyped: **3**

Karyotype: **46,XY**

Interpretation

Cytogenetic analysis revealed the presence of a **normal male** karyotype in peripheral blood lymphocytes. This analysis does not show any evidence of a clinically significant numerical or structural chromosome abnormality.

The standard procedures used in this analysis do not routinely detect microdeletions, small rearrangements or low level mosaicism.

This case has been reviewed and electronically signed by Ram Singh, PhD, Associate Laboratory Director
 Laboratory Medical Consultant: Bryn Webb, M.D.

If the ordering provider has questions about this report, please contact Sema4 at 800-298-6470, option 2 to speak with a genetic counselor or email gc@sema4.com

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