Baylor Miraca Genetics Laboratories

BAYLOR MIRACA GENETICS LABORATORIES

2450 Holcombe Blvd - Houston, TX 77021 - 1-800-411-4363
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Patient Name:	DONOR 4622			Fairfax Cryobank Sendouts-Fairfax	
Date of birth:	[redacted]	Lab Number:	[redacted]	3015 Williams Dr #110	
Gender:	M	Family #:		Tel No.: 703-876-3869	
Hospital/MR #:		Date Collected:	08/10/2015	Fax No: 703-698-3933	
Accession #:		Date Received:	08/11/2015	CC: Suzanne Seitz	Fax # 703-698-3933
Sample Type:	EXT DNA	Date Reported:	8/27/2015	CC: Harvey Stern	Fax # 703-698-3933
Test Code:	3356				
Indication:	Asymptomatic/Positive Family History				

VLCAD Deficiency
ACADVL Sequence Analysis
Familial Mutation/Variant Analysis

62817-1390128

RESULTS:

A heterozygous c.553G>A (p.G185S) familial pathogenic variant was detected.

Pathogenic Variant(s)/ Mutation(s)

Nucleotide Change	Amino Acid Change	Location	Zygosity	Reference(s) / Comment(s)
c.553G>A	p.G185S	exon 7	heterozygous	PMID: 9973285

INTERPRETATION:

Test results should be interpreted in the context of the patient's clinical presentation and family history. Previous sequence analysis performed in this laboratory detected a heterozygous c.553G>A (p.G185S) pathogenic variant in this individual's child who had abnormal newborn screening results suggestive of VLCAD deficiency (Lab# 56744). This variant has been reported in patients with VLCAD deficiency (PMID: 9973285). We were requested to investigate this individual for the c.553G>A (p.G185S) pathogenic variant.

We received extracted DNA and the DNA sample was PCR amplified for the relevant region and then sequenced in the forward and reverse directions. Other regions of the ACADVL gene were not examined. This analysis indicates that this individual is heterozygous for the c.553G>A (p.G185S) pathogenic variant. Thus, this individual is a carrier of the familial c.553G>A (p.G185S) pathogenic variant.

Clinical correlation and genetic counseling are recommended. Targeted sequence analysis (test code 3356) is available for that this individual's relatives.

METHOD:

The region(s) containing the previously identified familial mutations/variants in the ACADVL (NM_000018.2) gene were PCR amplified and then sequenced in the forward and reverse directions using automated fluorescent dideoxy sequencing methods. Nucleotide 1 corresponds to the A of the start codon ATG.

William J. Craigen, M.D., Ph.D., FACMG
ABMG Certified Clinical Geneticist and Biochemical Geneticist
Medical Director

Lee-Jun C. Wong, Ph.D., FACMG
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Senior Laboratory Director

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Recombine

CarrierMap™

Ordering Practice:

Practice Code: 926
Fairfax Cryobank
3015 Williams Drive, #110, Fairfax, VA, 22031, US
Physician: Suzanne Seitz
Report Generated: 2015-09-08
Report Updated: 2015-09-08

Donor 4622

DOB: 1[redacted]
Gender: Male
Ethnicity: Other
Procedure ID: 29150
Kit Barcode: [redacted]
Method: Genotyping
Specimen: Sperm, #30392
Specimen Collection: 2015-08-25
Specimen Received: 2015-08-28
Specimen Analyzed: 2015-09-08

Partner Not Tested

SUMMARY OF RESULTS

NO MUTATIONS IDENTIFIED

Donor 4622 was not identified to carry any of the mutations tested.

All mutations analyzed were not detected, reducing but not eliminating your chance to be a carrier for the associated genetic diseases. A list of all the diseases and mutations you were screened for is included later in this report. The test does not screen for every possible genetic disease.

For disease information, please visit www.recombine.com/diseases. To speak with a Genetic Counselor, call 855.OUR.GENES.

♂ Male

Panel: Fairfax Cryobank Panel , Diseases Tested: 21, Mutations Tested: 382, Genes Tested: 22, Null Calls: 0

Assay performed by Reprogenetics
CLIA ID: 31D1054821
Lab Technician Bo Chu

Reviewed by Pere Colls, PhD, HCLD, Lab Director

Methods and Limitations

Genotyping: Genotyping is performed using the Illumina Infinium Custom HD Genotyping assay to identify mutations in >200 genes. The assay is not validated for homozygous mutations, and it is possible that individuals affected with disease may not be accurately genotyped.

Spinal Muscular Atrophy: Spinal Muscular Atrophy is tested for via an Identity-by-State shared haplotype comparison algorithm. Detection is limited to haplotypes within our library of known carriers of the most common mutation (deletion of Exon 7).

Limitations: In some cases, genetic variations other than that which is being assayed may interfere with mutation detection, resulting in false-negative or false-positive results. Additional sources of error include, but are not limited to: sample contamination, sample mix-up, bone marrow transplantation, blood transfusions, and technical errors.

The test does not test for all forms of genetic disease, birth defects, and intellectual disability. All results should be interpreted in the context of family history; additional evaluation may be indicated based on a history of these conditions. Additional testing may be necessary to determine mutation phase in individuals identified to carry more than one mutation in the same gene. All mutations included within the genes assayed may not be detected, and additional testing may be appropriate for some individuals.

Diseases & Mutations Assayed

High Impact | Treatment Benefits | X-Linked | Moderate Impact

H	T	X	M	Disease	#	Mutations
●	○	○	○	Alpha Thalassemia	10	♂ Genotyping | SEA deletion, 11.1kb deletion, c.207C>A (p.N69K), c.223G>C (p.D75G), c.2T>C (p.M1T), c.207C>G (p.N69K), c.340_351delCTCCCCGCCGAG (p.L114_ E117del), c.377T>C (p.L126P), c.427T>C (p.X143Qext32), c.*+94A>G
●	●	○	○	Beta Thalassemia	83	♂ Genotyping | c.17_18delCT, c.20delA (p.E7Gfs), c.217insA (p.S73Kfs), c.223+702_444+342del620insAAGTAGA, c.230delC, c.25_26delAA, c.315+1G>A, c.315+2T>C, c.316-197C>T, c.316-146T>G, c.315+745C>G, c.316-1G>A, c.316-1G>C, c.316-2A>G, c.316-3C>A, c.316-3C>G, c.4delG (p.V2Cfs), c.51delC (p.K18Rfs), c.93-21G>A, c.92+1G>A, c.92+5G>A, c.92+5G>C, c.92+5G>T, c.92+6T>C, c.93-1G>A, c.93-1G>T, c.-50A>C, c.a-78g, c.a-79g, c.a-81g, c.A52T (p.K18X), c.c-137g, c.c-138t, c.c-151t, c.C118T (p.Q40X), c.G169C (p.G57R), c.G295A (p.V99M), c.G34A (p.V12I), c.G415C (p.A139P), c.G47A (p.W16X), c.G48A (p.W16X), c.t-80a, c.T2C (p.M1T), c.T75A (p.G25G), c.444+111A>G, c.g-29a, c.68_74delAAGTTGG, c.G92C (p.R31T), c.27_28insG, c.92+1G>T, c.92+1G>C, c.93-15T>G, c.93-1G>C, c.112delT, c.G113A (p.W38X), c.G114A (p.W38X), c.126delC, c.444+113A>G, c.250delG, c.225delC, c.383_385delAGG (p.Q128_A129delQAinsP), c.321_322insG (p.N109fs), c.316-1G>T, c.316-2A>C, c.316-106C>T, c.287_288insA (p.L97fs), c.271G>T (p.E91X), c.203_204delTG (p.V68Afs), c.154delC (p.P52fs), c.135delC (p.F46fs), c.92+2T>A, c.92+2T>C, c.90C>T (p.G30G), c.59A>G (p.N20S), c.46delT (p.W16Gfs), c.45_46insG (p.L16fs), c.36delT (p.T13fs), c.2T>G (p.M1R), c.1A>G (p.M1V), c.c-137t, c.c-136g, c.c-142t, c.c-140t
●	○	○	○	Bloom Syndrome	24	♂ Genotyping | c.2207_2212delATCTGAinsTAGATTC (p.Y736Lfs), c.2407insT, c.557_559delCAA (p.S186X), c.1284G>A (p.W428X), c.1701G>A (p.W567X), c.1933C>T (p.Q645X), c.C2528T (p.T843I), c.C2695T (p.R899X), c.G3107T (p.C1036F), c.2923delC (p.Q975K), c.3558+1G>T, c.3875-2A>G, c.2074+2T>A, c.2343_2344dupGA (p.781EfsX), c.380delC (p.127Tfs), c.3564delC (p.1188Dfs), c.4008delG (p.1336Rfs), c.C947G (p.S316X), c.2193+1_2193+9del9, c.C1642T (p.Q548X), c.3143delA (p.1048NfsX), c.356_357delTA (p.Cys120Hisfs), c.4076+1delG, c.C3281A (p.S1094X)
●	○	○	○	Canavan Disease	8	♂ Genotyping | c.433-2A>G, c.A854C (p.E285A), c.C693A (p.Y231X), c.C914A (p.A305E), c.A71G (p.E24G), c.C654A (p.C218X), c.T2C (p.M1T), c.G79A (p.G27R)

H	T	X	M	Disease	#	Mutations
●	●	○	○	Cystic Fibrosis	130	♂ Genotyping | c.1029delC, 1153_1154insAT, c.1519_1521delATC (p.507delI), c.1521_1523delCTT (p.508delF), c.1545_1546delTA (p.Y515Xfs), c.1585-1G>A, c.164+12T>C, c.1680-886A>G, c.1680-1G>A, c.1766+1G>A, c.1766+1G>T, c.1766+5G>T, c.1818del84, c.1911delG, c.1923delCTCAAAACTinsA, c.1973delGAAATTCAATCCTinsAGAAA, c.2052delA (p.K684fs), c.2052insA (p.Q685fs), c.2051_2052delAAinsG (p.K684SfsX38), c.2174insA, c.261delTT, c.2657+5G>A, c.273+1G>A, c.273+3A>C, c.274-1G>A, c.2988+1G>A, c.3039delC, c.3140-26A>G, c.325delTATinsG, c.3527delC, c.3535delACCA, c.3691delT, c.3717+12191C>T, c.3744delA, c.3773_3774insT (p.L1258fs), c.442delA, c.489+1G>T, c.531delT, c.579+1G>T, c.579+5G>A (IVS4+5G>A), c.803delA (p.N268fs), c.805_806delAT (p.I269fs), c.933_935delCTT (p.311delF), c.A1645C (p.S549R), c.A2128T (p.K710X), c.C1000T (p.R334W), c.C1013T (p.T338I), c.C1364A (p.A455E), c.C1477T (p.Q493X), c.C1572A (p.C524X), c.C1654T (p.Q552X), c.C1657T (p.R553X), c.C1721A (p.P574H), c.C2125T (p.R709X), c.C223T (p.R75X), c.C2668T (p.Q890X), c.C3196T (p.R1066C), c.C3276G (p.Y1092X), c.C3472T (p.R1158X), c.C3484T (p.R1162X), c.C349T (p.R117C), c.C3587G (p.S1196X), c.C3712T (p.Q1238X), c.C3764A (p.S1255X), c.C3909G (p.N1303K), c.G1040A (p.R347H), c.G1040C (p.R347P), c.G1438T (p.G480C), c.G1624T (p.G542X), c.G1646A (p.S549N), c.G1646T (p.S549I), c.G1652A (p.G551D), c.G1675A (p.A559T), c.G1679C (p.R560T), c.G178T (p.E60X), c.G1865A (p.G622D), c.G254A (p.G85E), c.G271A (p.G91R), c.G274T (p.E92X), c.G3209A (p.R1070Q), c.G3266A (p.W1089X), c.G3454C (p.D1152H), c.G350A (p.R117H), c.G3611A (p.W1204X), c.G3752A (p.S1251N), c.G3846A (p.W1282X), c.G3848T (p.R1283M), c.G532A (p.G178R), c.G988T (p.G330X), c.T1090C (p.S364P), c.T3302A (p.M1101K), c.T617G (p.L206W), c.C14T (p.P5L), c.G19T (p.E7X), c.G171A (p.W57X), c.313delA (p.I105fs), c.G328C (p.D110H), c.580-1G>T, c.G1055A (p.R352Q), c.C1075A (p.Q359K), c.C1079A (p.T360K), c.T1647G (p.S549R), c.1976delA (p.N659fs), c.C2290T (p.R764X), c.2737_2738insG (p.Y913X), c.3067_3072delATAGTG (p.I1023_V1024delT), c.3536_3539delCCAA (p.T1179fs), c.3659delC (p.T1220fs), c.G3808A (p.D1270N), c.G4056C (p.Q1352H), c.C4364G (p.S1455X), c.C4003T (p.L1335F), c.G2538A (p.W846X), c.C200T (p.P67L), c.C4426T (p.Q1476X), c.1116+1G>A, c.1986_1989delAACT (p.T663R), c.2089_2090insA (p.R697Kfs), c.2215delG (p.V739Y), c.T263G (p.L196X), c.3022delG (p.V1008S), c.3908dupA (p.N1303Kfs), c.C658T (p.Q220X), c.C868T (p.Q290X), c.1526delG (p.G509fs), c.2908+1085-3367+260del7201, c.C11A (p.S4X), c.A3700G (p.I1234V), c.A416T (p.H139L), c.T366A (p.Y122X)
●	○	○	○	Familial Dysautonomia	4	♂ Genotyping | c.2204+6T>C, c.C2741T (p.P914L), c.G2087C (p.R696P), c.C2128T (p.Q710X)
●	○	○	○	Familial Hyperinsulinism: Type 1: ABCC8 Related	10	♂ Genotyping | c.3989-9G>A, c.4159_4161delTTC (p.1387delF), c.C4258T (p.R1420C), c.C4477T (p.R1493W), c.G2147T (p.G716V), c.G4055C (p.R1352P), c.T560A (p.V187D), c.4516G>A (p.E1506K), c.C2506T (p.Q836X), c.579+2T>A
●	●	○	○	Fanconi Anemia: Type C	8	♂ Genotyping | c.456+4A>T, c.67delG, c.C37T (p.Q13X), c.C553T (p.R185X), c.T1661C (p.L554P), c.C1642T (p.R548X), c.G66A (p.W22X), c.G65A (p.W22X)
●	●	○	○	Gaucher Disease	6	♂ Genotyping | c.84_85insG, c.A1226G (p.N409S), c.A1343T (p.D448V), c.C1504T (p.R502C), c.G1297T (p.V433L), c.G1604A (p.R535H)
●	●	○	○	Glycogen Storage Disease: Type IA	13	♂ Genotyping | c.376_377insTA, c.79delC, c.979_981delTTC (p.327delF), c.C1039T (p.Q347X), c.C247T (p.R83C), c.C724T (p.Q242X), c.G248A (p.R83H), c.G562C (p.G188R), c.G648T, c.G809T (p.G270V), c.A113T (p.D38V), c.975delG (p.L326fs), c.724delC
●	○	○	○	Joubert Syndrome	1	♂ Genotyping | c.G35T (p.R12L)
●	●	○	○	Maple Syrup Urine Disease: Type 1B	6	♂ Genotyping | c.G1114T (p.E372X), c.G548C (p.R183P), c.G832A (p.G278S), c.C970T (p.R324X), c.G487T (p.E163X), c.C853T (p.R285X)

H	T	X	M	Disease	#	Mutations
●	●	○	○	Maple Syrup Urine Disease: Type 3	8	♂ Genotyping | c.104_105insA, c.G685T (p.G229C), c.A214G (p.K72E), c.A1081G (p.M361V), c.G1123A (p.E375K), c.T1178C (p.I393T), c.C1463T (p.P488L), c.A1483G (p.R495G)
●	○	○	○	Mucolipidosis: Type IV	4	♂ Genotyping | c.406-2A>G, c.G1084T (p.D362Y), c.C304T (p.R102X), c.244delC (p.L82fsX)
●	○	○	○	Nemaline Myopathy: NEB Related	1	♂ Genotyping | c.7434_7536del2502bp
●	○	○	○	Niemann-Pick Disease: Type A	6	♂ Genotyping | c.996delC, c.G1493T (p.R498L), c.T911C (p.L304P), c.C1267T (p.H423Y), c.G1734C (p.K578N), c.1493G>A (p.R498H)
●	○	○	○	Spinal Muscular Atrophy: SMN1 Linked	19	♂ Genotyping | DEL EXON 7, c.22_23insA, c.43C>T (p.Q15X), c.91_92insT, c.305G>A (p.W102X), c.400G>A (p.E134K), c.439_443delGAAGT, c.558delA, c.585_586insT, c.683T>A (p.L228X), c.734C>T (p.P245L), c.768_778dupTGCTGATGCTT, c.815A>G (p.Y272C), c.821C>T (p.T274I), c.823G>A (p.G275S), c.834+2T>G, c.835-18_835-12delCCTTTAT, c.835G>T, c.836G>T
●	○	○	○	Tay-Sachs Disease	30	♂ Genotyping | c.1073+1G>A, c.1277_1278insTATC, c.1421+1G>C, c.805+1G>A, c.C532T (p.R178C), c.G533A (p.R178H), c.G805A (p.G269S), c.C1510T (p.R504C), c.G1496A (p.R499H), c.G509A (p.R170Q), c.A1003T (p.I335F), c.910_912delTTC (p.305delF), c.G749A (p.G250D), c.T632C (p.F211S), c.C629T (p.S210F), c.613delC, c.A611G (p.H204R), c.G598A (p.V200M), c.A590C (p.K197T), c.571-1G>T, c.C540G (p.Y180X), c.T538C (p.Y180H), c.G533T (p.R178L), c.C508T (p.R170W), c.C409T (p.R137X), c.T380G (p.L127R), c.346+1G>C, c.T116G (p.L39R), c.G78A (p.W26X), c.A1G (p.M1V)
●	○	○	○	Usher Syndrome: Type 1F	6	♂ Genotyping | c.C733T (p.R245X), c.2067C>A (p.Y684X), c.C7T (p.R3X), c.C1942T (p.R648X), c.2800C>T (p.R934X), c.4272delA (p.L1425fs)
●	○	○	○	Usher Syndrome: Type 3	4	♂ Genotyping | c.T144G (p.N48K), c.T359A (p.M120K), c.300T>G (p.Y176X), c.C634T (p.Q212X)
●	○	○	○	Walker-Warburg Syndrome	1	♂ Genotyping | c.1167insA (p.F390fs)

LABORATORY REPORT 2006 IKONMAIL

12738 FAIRFAX CRYOBANK-[redacted]

[redacted]

Sonora Quest Laboratories
A Subsidiary of Laboratory Sciences of Arizona

Collected Date	Received Date	Collection Time
10/01/2012	10/01/2012 1847	1330

Reported Date	Other I.D.	Fasting
10/05/2012		U

REQUISITION NO.	PHYSICIAN
127380000000	086

PATIENT	DOB	AGE	SEX	PATIENT ID	ACCESSION NO.
ID,4622 DONOR	[redacted]	[redacted]	M		[redacted]

* Previously Reported on: 10/04/2012 @ 8:13PM *

REQUESTS	RESULTS	OUT OF RANGE RESULTS	REFERENCE RANGE	UNITS	FN
CBC W/DIFF,W/PLT					
WBC	6.2		4.0-11.0	k/mm3	
RBC	5.04		4.30-6.00	m/mm3	
HEMOGLOBIN	15.4		13.0-18.0	g/dL	
HEMATOCRIT	45.1		40.0-53.0	%	
MCV	90		78-100	fL	
MCH	30.6		27.0-34.0	pg	
MCHC	34.1		31.0-37.0	g/dL	
RDW(cv)	12.9		12.1-18.2	%	
RDW(sd)	41.9		36.0-55.0	fL	
PLATELET COUNT	225		130-450	k/mm3	
MPV	10.8		7.5-14.0	fL	
SEGMENTED NEUTROPHILS	60		40-85	%	
LYMPHOCYTES	27		10-45	%	
MONOCYTES	6		3-15	%	
EOSINOPHILS	7		0-7	%	
BASOPHILS	1		0-2	%	
ABSOLUTE NEUTROPHIL	3.7		1.6-9.3	k/uL	
ABSOLUTE LYMPHOCYTE	1.7		0.6-5.5	k/uL	
ABSOLUTE MONOCYTE	0.3		0.1-1.6	k/uL	
ABSOLUTE EOSINOPHIL	0.4		0.0-0.7	k/uL	
ABSOLUTE BASOPHIL	0.0		0.0-0.2	k/uL	
DIFFERENTIAL TYPE	Automated				
AST	22		10-50	IU/L	
CHOLESTEROL	191		<200	mg/dL	
ALT	19		2-60	IU/L	
BLOOD GROUP AND RH TYPE	O Negative				

ENTERED lv 2.7.13

Sonora Quest Laboratories no longer performs "weak D" or "Du" testing routinely. It is no longer a regulatory requirement, nor is it recommended by the American Association of Blood Banks (AABB), except in testing of donor units.
Supplemental testing for weak D/Du Testing, may be performed for an additional charge by request. Please call the Client Services Department at 602-685-5050 and request test number 102317.

HEMOGLOBINOPATHY EVALUATION					
RED BLOOD CELL COUNT	5.10		4.30-6.00	M/MM3	G
HEMOGLOBIN	15.4		13.5-17.0	g/dL	G
MCV	90		78-100	fL	G
RDW	13.2		11.0-16.0	%	G

CONTINUED ON PAGE 2

LABORATORY REPORT 2006 IKONMAIL

12738 FAIRFAX CRYOBANK [redacted]

Sonora Quest Laboratories
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Collected Date	Received Date	Collection Time
10/01/2012	10/01/2012 1847	1330

Reported Date	Other I.D.	Fasting
10/05/2012		U

REQUISITION NO.	PHYSICIAN
127380000000	086

PATIENT	DOB	AGE	SEX	PATIENT ID	ACCESSION NO.
ID,4622 DONOR	[redacted]	[redacted]	M		[redacted]

REQUESTS	RESULTS	OUT OF RANGE RESULTS	REFERENCE RANGE	UNITS	FN
HEMOGLOBIN A	97.3		94.5-98.5	%	G
HEMOGLOBIN A2	2.7		1.8-3.5	%	G
PATHOLOGIST INTERPRETATION					G

Normal phenotype. Reviewed by Dr. Louis Novoa-Takara

Evaluation performed by High Performance Liquid Chromatography (HPLC). Gel electrophoresis performed only when indicated.

Hemoglobinopathy Evaluation examines specimens for common variant hemoglobins such as S, C, and E as well as most other less common variant hemoglobins. Many, but not all, thalassemic disorders may be detected.

If, in spite of normal findings, a clinical suspicion of a hemoglobin abnormality persists please contact the laboratory.

RDWSD	43.4		36.0-55.0	%	G

TESTS ORDERED: AST;CHOLESTEROL;ALT;BLOOD GROUP AND RH TYPE
CBC W/DIFF,W/PLT;HEMOGLOBINOPATHY EVALUATION

Unless otherwise noted, all testing performed at:
Sonora Quest Laboratories
1255 West Washington Street
Tempe, AZ 85281
602.685.5000 or 800.766.6721

G = Test performed at:
Banner Good Samaritan Medical Center
1111 E. McDowell Road
Phoenix, AZ 85006
602.239.2000

ENTERED 12-7-13

END OF REPORT. PRINTED 10/05/2012 @ 08:31:24 AM
ID,4622 DONOR - E90278930 - REPRINT REPORT

GENETICS & IVF
Institute

ENTERED
AUG 1 13

Cytogenetic Report

Client Fairfax Cryobank - [redacted]

Address [redacted]

Reporting Phone # [redacted] Fax # [redacted] Email [redacted]

Patient name/Donor Alias Donor # 4622

Donor # 4622-121001

Collection Date 10/01/12012

Date Received 10/02/2012

Patient DOB N/A

Specimen type Peripheral Blood

Accession # [redacted]

RESULTS

CYTOGENETIC ANALYSIS

Cells counted	20	Type of banding	GTG
Cells analyzed	5	Band resolution	550
Cells karyotyped	2		
Modal chromosome #	46		

FISH

Probe(s) N/A

Nuclei scored N/A

KARYOTYPE 46,XY

INTERPRETATION

Normal male karyotype

No clonal numerical or structural abnormalities were identified. This normal cytogenetic result does not exclude the possibility of the presence of subtle rearrangements beyond the technical limits of detection with this test.

Comments

Wayne S. Stanley, Ph.D., FACMG
Clinical Cytogeneticist

10/16/12
Date

3015 Williams Drive | Fairfax, Virginia 22031 | 703-698-7355 | 800-552-4363 | givf@givf.com | www.givf.com

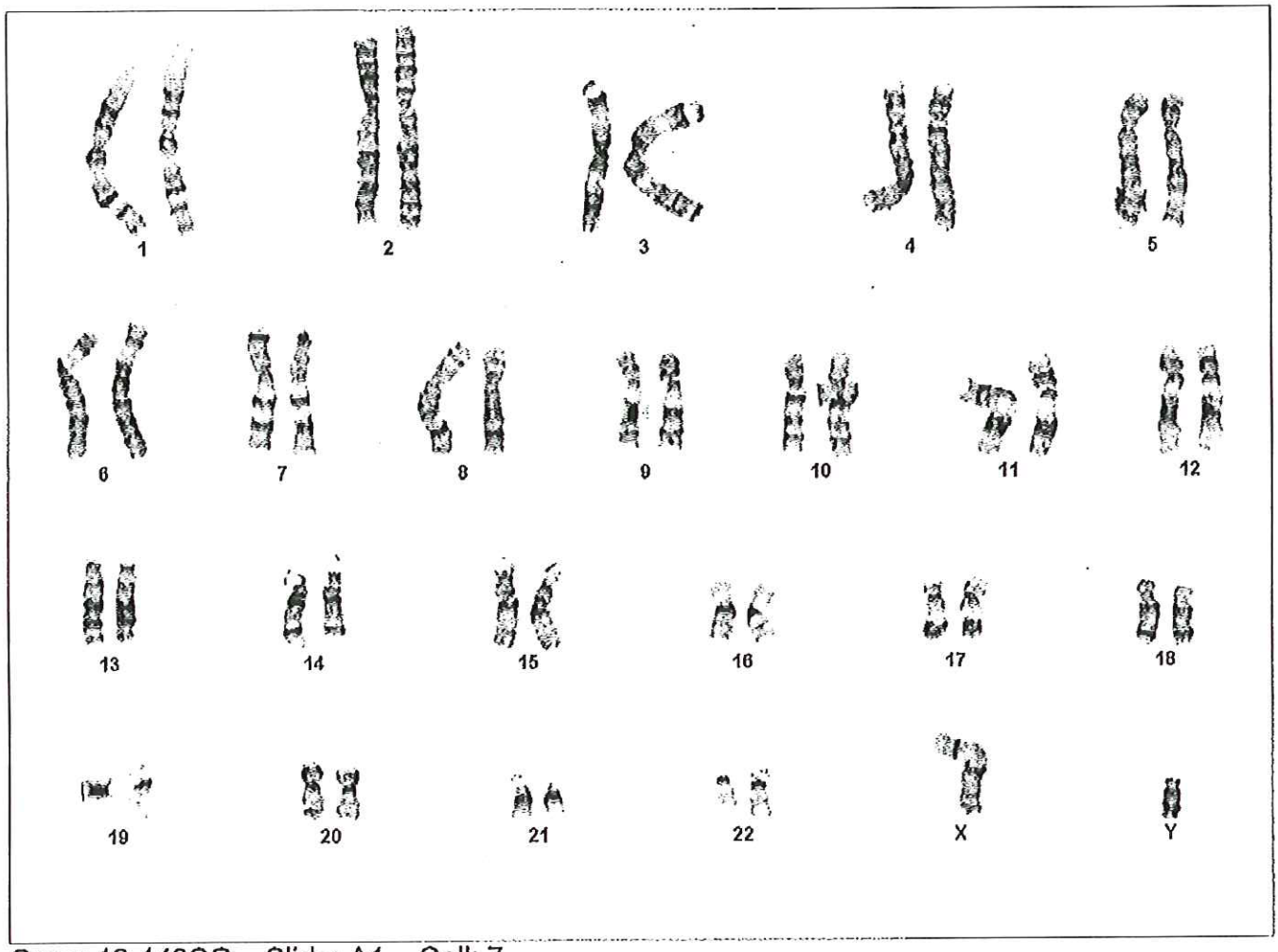
Genetics and IVF Preimplantation Genetics Laboratory

Patient name: DONOR # 4622

Case name: [redacted]

ENTERED 12.7.19

46,XY



Case: 12-143CG Slide: A1 Cell: 7