
Ordering Practice:

Practice Code: 926
Fairfax Cryobank
3015 Williams Drive, #110, Fairfax, VA,
22031, US
Physician: [REDACTED]
Report Generated: 2015-12-09

Donor 5043

DOB:
Gender: Male
Ethnicity: African, European, and Native
American
Procedure ID: 35843
Kit Barcode: [REDACTED]
Method: Genotyping
Specimen: Blood, #37258
Specimen Collection: 2015-11-13
Specimen Received: 2015-11-16
Specimen Analyzed: 2015-12-09

Partner Not Tested

SUMMARY OF RESULTS**NO MUTATIONS IDENTIFIED**

Donor 5043 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 V2 , Diseases Tested: 22, Mutations Tested: 451, 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

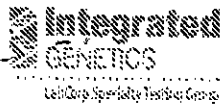
H	T	X	M	Disease	#	Mutations
●	○	○	○	Alpha Thalassemia	11	♂ Genotyping SEA deletion, 11.1kb deletion, c.207C>A (p.N69K), c.223G>C (p.D75G), c.2T>C (p.M1T), c.95+2_95+6delTGAGG, c.207C>G (p.N69K), c.340_351delCTCCCGCCGAG (p.L114_E117del), c.377T>C (p.L126P), c.427T>C (p.X143Qext32), c.*+94A>G
●	●	○	○	Beta Thalassemia	84	♂ Genotyping c.124_127delTTCT (p.F42Lfs), 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	147	<p>♂ 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.1818delB4, c.1911delG, c.1923delCTCAAACTinsA, c.1973delGAAATTCATCTinsAGAAA, 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.54-5940_273+10250del21080bp (p.S18fs), 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), c.3767_3768insC (p.A1256fs), c.613C>T (p.P205S), c.293A>G (p.Q98R), c.3731G>A (p.G1244E), c.535C>A (p.Q179K), c.3368-2A>G, c.4557>G (p.M152R), c.1610_1611delAC (p.D537fs), c.3254A>G (p.H1085R), c.496A>G (p.K166E), c.1408_1417delGTGATTATGG (p.V470fs), c.1585-8G>A, c.2909G>A (p.G970D), c.653T>A (p.L218X), c.1175T>G (p.V392G), c.3139_3139+1delGG</p>
				Familial Dysautonomia	4	<p>♂ Genotyping c.2204+6T>C, c.C2741T (p.P914L), c.G2087C (p.R696P), c.C2128T (p.Q710X)</p>
				Familial Hyperinsulinism: Type 1: ABCC8 Related	10	<p>♂ 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</p>
				Fanconi Anemia: Type C	8	<p>♂ 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)</p>
				Gaucher Disease	6	<p>♂ Genotyping c.84_85insG, c.A1226G (p.N409S), c.A1343T (p.D448V), c.C1504T (p.R502C), c.G1297T (p.V433L), c.G1604A (p.R535H)</p>
				Glycogen Storage Disease: Type IA	13	<p>♂ 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</p>

H	T	X	M	Disease	#	Mutations
●	○	○	○	Joubert Syndrome	2	♂ Genotyping c.G35T (p.R12L), c.218G>A (p.R73H)
●	●	○	○	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)
●	●	○	○	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)
●	○	○	○	Mucopolipidosis: 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)
●	●	○	○	Sickle-Cell Anemia	1	♂ Genotyping c.A20T (p.E7V)
●	○	○	○	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	76	♂ 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), c.1495C>T (p.R499C), c.459+5G>A, c.1422-2A>G, c.535C>T (p.H179Y), c.1141delG (p.V381fs), c.796T>G (p.W266G), c.155C>A (p.S52X), c.426delT (p.F142fs), c.413-2A>G, c.570+3A>G, c.536A>G (p.H179R), c.1146+1G>A, c.736G>A (p.A246T), c.1302C>G (p.F434L), c.778C>T (p.P260S), c.1008G>T (p.Q336H), c.1385A>T (p.E462V), c.964G>A (p.D322N), c.340G>A (p.E114K), c.1432G>A (p.G478R), c.1178G>C (p.R393P), c.805+1G>C, c.1426A>T (p.R476X), c.623A>T (p.D208V), c.1537C>T (p.Q513X), c.1511G>T (p.R504L), c.1307_1308delTA (p.I436fs), c.571-8A>G, c.624_627delTCCT (p.D208fs), c.1211_1212delTG (p.L404fs), c.621T>G (p.D207E), c.1511G>A (p.R504H), c.1177C>T (p.R393X), c.2T>C (p.M1T), c.1292G>A (p.W431X), c.947_948insA (p.Y316fs), c.607T>G (p.W203G), c.1061_1063delTCT (p.F354_Y355delinsX), c.615delG (p.L205fs), c.805+2T>C, c.1123delG (p.E375fs), c.1121A>G (p.Q374R), c.1043_1046delITCAA (p.F348fs), c.1510delC (p.R504fs), c.1451T>C (p.L484P), c.964G>T (p.D322Y)
●	○	○	○	Usher Syndrome: Type 1F	7	♂ Genotyping c.C733T (p.R245X), c.2067C>A (p.Y684X), c.C7T (p.R3X), c.C1942T (p.R648X), c.1101delT (p.A367fsX), c.2800C>T (p.R934X), c.4272delA (p.L1425fs)
●	○	○	○	Usher Syndrome: Type 3	5	♂ Genotyping c.T144G (p.N48K), c.T359A (p.M120K), c.300T>G (p.Y176X), c.C634T (p.Q212X), c.221T>C (p.L74P)
●	○	○	○	Walker-Warburg Syndrome	1	♂ Genotyping c.1167insA (p.F390fs)

TO: Fairfax Cryobank / Genet

ATTN: Fairfax Cryobank / Genetics and IVF Inst

**Tay-Sachs Enzyme Analysis**

Patient Name: Donor 5043, .
Referring Physician: Harvey Stern, MD
Specimen #: [REDACTED]
Patient ID: [REDACTED]

Client #: [REDACTED]Fairfax Cryobank / Genetics and IVF
Institute
[REDACTED]

DOB: [REDACTED]
SSN: ***-**-****

Date Collected: 07/22/2016
Date Received: 07/23/2016
Lab ID:
Hospital ID:
Specimen Type: White Blood Cells

RESULTS: **Hexosaminidase Activity :** 1251 nmol/mg protein
 Hexosaminidase Percent A: 65.4

		Plasma/Serum	WBC
Expected Non-Carrier Range:	Hex A	≥54%	≥54%
Expected Carrier Range:	Hex A	20 - 49%	20 - 49%

INTERPRETATION: NON CARRIER

This result is within the non-carrier range for Tay-Sachs disease. Less than 0.1% of patients having non-carrier levels of Hexosaminidase-A activity are Tay-Sachs carriers.

NOTE: Maximum sensitivity and specificity for Tay-Sachs disease carrier testing are achieved by using enzymology and DNA mutation analysis together.

Integrated Genetics is a business unit of Esoterix Genetic Laboratories, LLC, a wholly-owned subsidiary of Laboratory Corporation of America Holdings.

Under the direction of:

Philip R. Wyatt M.D., Ph.D

Date: 07/29/2016

Page 1 of 1



Testing Performed At Esoterix Genetic Laboratories, LLC 2000 Vivigen Way Santa Fe, NM 87505 Philip R. Wyatt M.D., Ph.D, Laboratory Director 1-800-848-4436

PATIENT INFORMATION

5043, DONOR

REPORT STATUS **Final**

Nichols Institute, Chantilly

DOB: [REDACTED]

Age: [REDACTED]

ORDERING PHYSICIAN

SEX: M

CLIENT INFORMATION

ID: [REDACTED]

9595

SPECIMEN INFORMATION

SPECIMEN: [REDACTED]

REQUISITION: [REDACTED]

LAB REF NO: [REDACTED]

COLLECTED: 11/13/2015 00:00

RECEIVED: 11/16/2015 10:36

REPORTED: 11/25/2015 11:44

Test Name	In Range	Out of Range	Reference Range	Lab
Hemoglobinopathy Evaluation				AMD
ERYTHROCYTE COUNT	5.06		4.20-5.80 Mill/uL	
HEMOGLOBIN	15.3		13.2-17.1 g/dL	
HEMATOCRIT	47.5		38.5-50.0 %	
MCV	93.7		80.0-100.0 FL	
MCH	30.2		27.0-33.0 pg	
RDW	14.5		11.0-15.0 %	
Hemoglobin A	97.9		>96.0 %	
Hemoglobin F	0.0		<2.0 %	
Hemoglobin A2	2.1		1.8-3.5 %	
Interpretation				

NORMAL PATTERN

By high-performance liquid chromatography (HPLC), there is a normal pattern of hemoglobins and normal levels of HbA2 and HbF are present.

No variant hemoglobins are observed. This is consistent with A/A phenotype.

If iron deficiency coexists with beta thalassemia trait HbA2 may be in the normal range.

Rare variant hemoglobins have been known to co-elute with hemoglobin A by high-performance liquid chromatography. If clinically indicated, Thalassemia and Hemoglobinopathy comprehensive is available (Test code 17365X[12658]).

ENTERED
11/25/15

PATIENT INFORMATION

5043, DONOR

REPORT STATUS **Final**

Nichols Institute, Chantilly

ORDERING PHYSICIAN

DOB: [REDACTED] Age: [REDACTED]

SEX: M

ID: [REDACTED]

COLLECTED: 11/13/2015 00:00

REPORTED: 11/25/2015 11:44

Test Name	In Range	Out of Range	Reference Range	Lab
Chromosome Analysis, Blood				AMD
Chromosome Analysis, Blood				

CYTOGENETIC RESULTS

Cytogenetic Reference #: CB-15-020288

Test Setup Date: 11/16/2015

Test Completion Date: 11/25/2015

Specimen Source: Peripheral Blood

Clinical History: Screening

Metaphases Counted: 20 Analyzed: 5 Karyotyped: 2

Banding Level (G-bands): >=550

KARYOTYPE:

46,XY

INTERPRETATION and COMMENTS:

NORMAL MALE karyotype

Within the limits of standard cytogenetic methodologies, the chromosomes had normal G-banding patterns without apparent structural abnormality or rearrangement.

This test does not address genetic disorders that cannot be detected by standard cytogenetic methods, or rare events such as low level mosaicism or very subtle rearrangements.

Electronic Signature on File

Nicole C. Christacos, Ph.D., FACMG

Technical Director, Cytogenetics, 703-802-7156

Results Received

11/25/15

Reference lab accession: CB15020288EC

For more information on this test, go to
<http://education.questdiagnostics.com/faq/chromsblood>

Performing Laboratory Information:

AMD QUEST DIAGNOSTICS INCORPORATED NICHOLS INSTITUTE 14225 NEWBROOK DR CHANTILLY VA 20151

Laboratory Director: PATRICK W. MASON, MD, PHD

Patient Information	Specimen Information	Client Information
5043, DONOR DOB: [REDACTED] AGE: [REDACTED] Gender: M Phone: NG Patient ID: NG	Specimen: [REDACTED] Requisition: Lab Ref #: [REDACTED] Collected: 11/13/2015 / 00:00 EST Received: 11/16/2015 / 10:36 EST Reported: 11/25/2015 / 11:51 EST	Client #: 9595 Not Provided [REDACTED]

Cytogenetics Report**Chromosome Analysis, Blood - 14596****Lab:AMD**

Case Number	CB-15-020288
Specimen Source	Peripheral Blood
Clinical History	Screening
Metaphases Counted	20
Metaphases Analyzed	5
Metaphases Karyotyped	2
Banding Level	>=550
Karyotype	46,XY

Interpretation and Comments

NORMAL MALE karyotype

Within the limits of standard cytogenetic methodologies, the chromosomes had normal G-banding patterns without apparent structural abnormality or rearrangement.

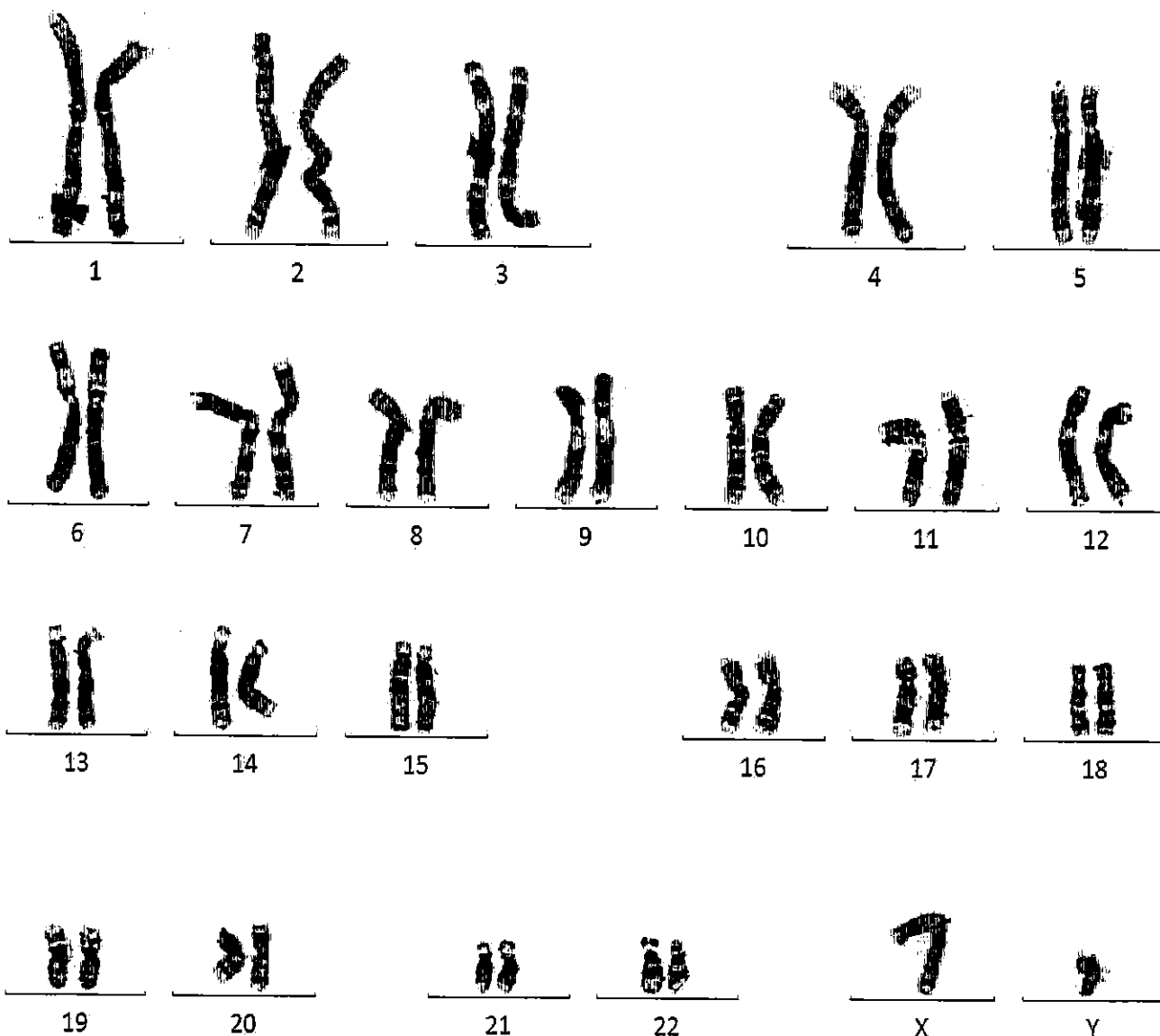
This test does not address genetic disorders that cannot be detected by standard cytogenetic methods, or rare events such as low level mosaicism or very subtle rearrangements.

Signature

Electronic Signature on File

Nicole C. Christacos, Ph.D., FACMG
Technical Director, Cytogenetics, 703-802-7156

Patient Information	Specimen Information	Client Information
5043, DONOR DOB: [REDACTED] AGE: [REDACTED] Gender: M Patient ID: NG	Specimen: CH313884G Collected: 11/13/2015 / 00:00 EST Received: 11/16/2015 / 10:36 EST Reported: 11/25/2015 / 11:51 EST	Client #: 9595 Not Provided



PERFORMING SITE:

AMD QUEST DIAGNOSTICS/NICHOLS CHANTILLY, 14225 NEWBROOK DRIVE, CHANTILLY, VA 20151-0841 Laboratory Director: Patrick W Mason, MD., Ph.D., CLIA: 49D0221801

This is supplemental to your standard report.