CGT Bank v3.3.10

Patient Information		Sample Information		Clinic Information	
Unique pat id.:	0245865	**Sample type:**	Blood	**Clinic:**	WeFIV
Patient name:		**Date of draw:**	06/03/2024	**Doctor:**	CAROLINA BOUTEILLER
Patient DOB:		**Date of receipt:**	13/03/2024		
Ethnic group:	Caucasian	**Report date/time:**	05/03/2026		
Indication:	No family history				

TEST RESULTS

NEGATIVE

INTERPRETATION OF TEST RESULTS

For a negative test result, the risk of having children affected by the investigated conditions decreases significantly compared to the general population. This is also the case for a negative personal result when a partner or gamete donor is a carrier for one or more of these analyzed genes. However, due to test limitations associated with any genetic test, this low risk is not zero (see limitations section and informed consent)

LOW COVERAGE VARIANTS

There are no low coverage variants.

TEST DESCRIPTION

The Carrier Genetic Test (CGT) is a preconception DNA screening test that aims to identify individuals and couples at increased risk of conceiving children affected by a monogenic disease. Knowledge of this risk may influence a couple's decision to conceive or encourage the couple to adopt preventive measures, including preimplantation genetic testing for the at risk disease (PGT-M) prenatal genetic testing, or to use donated gametes. The multigene CGT interrogates thousands of DNA variants using a high-throughput technology (Next Generation Sequencing, NGS).

COMMENTS

Language change at the clinic's request.

TEST METHODOLOGY

1.DNA extraction from the biological sample. 2. Next Generation Sequencing of gene regions where known pathogenic variants are located (list available at https://cgt.igenomix.com/diseases-list/). 3. Raw data analysis using bioinformatics (bioinformatic pipeline v1.1). QC parameters require that more than 99.7% of the tested variants have coverage greater than the minimum read depth (7x). 4. Complementary testing by other techniques for: a) the SMN1 gene: exon 7 deletion; b) HBA1/HBA2 genes: frequent deletions; c) the FMR1 gene: CGG repeat (females only); d) the DMD gene: frequent deletions/duplications; e) the F8 gene: intron 22 inversion (females only).

TEST LIMITATIONS

The CGT test only includes analysis of the specific variants included in the list (list of variants analysed are available by request), and no others. Therefore, the CGT test does not cover all monogenic diseases nor 100% of disease-causing variants for each tested gene. The test does not include the analysis of conditions associated with mitochondrial DNA, multifactorial, digenic or dominant inheritance. The test does not detect large rearrangements (inversions, deletions and duplications more than 15 nucleotides), pathogenic variants located in regulatory regions or intronic regions outside the +/-3bp cut off or in low sequence coverage areas. DNA changes caused by trinucleotide repeat expansions are not detected, except those indicated in the methodology section. For copy number variation analysis, when a normal result is obtained (2 copies detected), it is not possible to be certain that the two copies are each in one of the two alleles (non-carrier) or if both are in the same allele (cis) and no copies in the other (silent carrier). Finally, if our assessment of a variant fails to meet our QC parameters due to low coverage, a result for the variant(s) will not be issued.
The analytical detection rate is higher than 99%. The clinical sensitivity varies among conditions (e.g.: for the HEXB gene, 30% of affected patients are carriers of a 16 kb deletion that is not included in the test). The sensitivity for SMN1 is approximately 96% because point mutations or small insertions/deletions are not analyzed and, for a normal result (2 copies detected), it is not possible to be certain that the two copies are each in one of the two alleles (non-carrier) or if both are in the same allele (cis) and no copies in the other (carrier).
A negative result for the variants included in the CGT test does not exclude the possibility of being a carrier. The presence of pseudogenes and/or rare polymorphisms and/or homopolymers may lead to false negative or false positive results. A negative result for the CGT variants does not exclude the possibility of a de novo pathogenic variant being present in the offspring. In the general population there is a 3-5% risk for birth defects caused by genetic and/or non-genetic factors not detected by this type of test. Germline mosaicism or low-level somatic mosaicism cannot be detected. As with any laboratory test, there is a small chance that this result may be inaccurate for a procedural reason such as an error during sample collection, labelling, processing, data collection or interpretation. Please note that the classification of variants can change over time. To check whether there have been any changes to the classification of reported variants, please contact IGENOMIX.

LEGAL/QUALITY

IGENOMIX ARGENTINA S.A will only release the report once a completed test requisition form is received. The clinic/clinician/certified health professional requesting the test is responsible for obtaining and taking custody of "Informed Consent" from the patient as depicted by national guidelines and/or legislation. This test was developed, and its performance characteristics determined by IGENOMIX SPAIN LAB, SLU. It has not been cleared or approved by the US Food and Drug Administration. The test is used as a laboratory developed test for clinical purposes.

Part of this test has been outsourced to a reference laboratory whose Quality Management System is based on high Quality Standards, periodically monitored by Igenomix SPAIN* and audited by independent external groups.

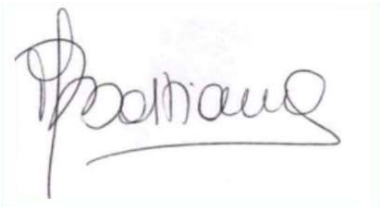
*IGENOMIX SPAIN holds CLIA Certificate of Compliance: #99D2146167.

EXEMPTION CLAUSE OF DIAGNOSTIC LIABILITY

The genetic diagnosis services carried out by IGENOMIX ARGENTINA S.A are exclusively intended to be interpreted by qualified/certified health professionals.

The result obtained by this test and the information that could be derived from it, cannot be considered in any case as substitute of genetic counselling or medical treatment by a trained professional neither represent itself a medical enquiry. We recommend that you consult your physician for genetic testing & counselling upon reception of your results.

Any result should be interpreted in the context of all available clinical findings, within the general context of a medical investigation, which must be conducted by clinically trained professionals. IGENOMIX ARGENTINA S.A is not responsible for any decisions made or actions undertaken by the contracting party based on the results provided by IGENOMIX ARGENTINA S.A or otherwise., nor the harmful temporary consequences diverted by its use, making specific discretion of taking appropriate legal measures assuming an improper use of those mentioned studies and analysis.

SIGNED	COUNTERSIGNED
	
Martina Di Bastiano Laboratory Leader	**Arantxa Hervas PhD** 3025-CV Biotechnologist

This test or part of this test has been outsourced to a referral Laboratory. Lab CLIA No.: 99D2146167

LIST OF ANALYZED GENES

Gene mean coverage >100x GJB2, HBA1, HBA1, HBB, ATP7A, ATRX, DKC1, ARSL, IL1RAPL1, HSD17B10, UPF3B, BTK, CUL4B, DMD, EMD, CD40LG, WAS, THOC2, MTM1, OTC, PQBP1, CYBB, SH2D1A, PDHA1, OCRL, FGD1, BRWD3, PHF8, GLA, F9, RP2, GPR143, F8, COL4A5, G6PD, HPRT1, IL2RG, L1CAM, FMR1, PRPS1, RPGR, SYN1, KDM5C, ZNF711, CFTR, CYP21A2

Gene mean coverage 50x-100x HCFC1, SLC6A8, SLC16A2, OPHN1, DLG3, ABCD1, ARX, CHM, PLP1, NR0B1, FTSJ1, MID1, ZDHHC9, NDP, RS1, GJB1, PGK1

Gene mean coverage < 50x MECP2, POU3F4, DCX, PAK3, EDA, AP1S2, IDS, AR, SMN1

GLOSSARY

TYPES OF INHERITANCE:

- AR: Autosomal recessive

  Inherited conditions that require two pathogenic variants (one from each parent) in a given gene to display symptoms.
- XR: X-linked recessive

  The gene is located on the X chromosome. Men with a pathogenic variant have the disease. Women with a pathogenic variant are carriers and generally asymptomatic or may mild symptoms.
- Digenic inheritance

  In some diseases, the symptoms could be explained by the coexistence of pathogenic variants in two different genes related with the disease instead of two pathogenic variants in the same gene.

ALLELES:

Pathogenic variants present in the two copies of a gene.

- Homozygous pathogenic variant (Hom.):

  Each copy of the gene has the same pathogenic variant. Generally, this is associated with clinical symptoms.
- Compound heterozygous (Het.):

  Each copy of the gene has a different pathogenic variant. Generally, this is associated with clinical symptoms. This situation is referred as having variants "in trans".

Pathogenic variant present in one copy of a gene.

- Heterozygous pathogenic variant (Het.):
  Only one copy of a gene has a pathogenic variant. There is another normal gene copy.

Note: Sometimes an individual has two pathogenic variants in the same gene copy. This situation is referred as having variants in cis and it is considered as a single pathogenic variant.

CNV:

Refers to copy number variation (deletion or duplication), i.e., the number of copies of a particular gene (or gene region) is different from the usual two copies.

LARGE GENE CONVERSION:

Refers to pathogenic variants caused by gene sequence exchange or replacement between a normal functional gene and a quasi-identical non-functional gene (pseudogene).

X-linked conditions				
Chrom	**Gene**	**Disease/Condition**	**Carrier Rate**	**Residual Risk**
X	ABCD1	Adrenoleukodystrophy	1 in 14,000	1 in 28,579
X	AP1S2	Mental retardation, X-linked, syndromic, type 5 (Pettigrew syndrome)	1 in 500,000	1 in 1,000,000
X	AR	Androgen insensitivity syndrome, complete	1 in 16,639	1 in 37,670
X	ARSL	Chondrodysplasia punctata, brachytelephalangic	1 in 250,000	1 in 477,528
X	ARX	Epileptic encephalopathy, early infantile, type 1; ARX-related developmental disorders	1 in 37,038	1 in 64,815
X	ATP7A	Menkes disease; Occipital horn syndrome	1 in 150,000	1 in 501,722
X	ATRX	Mental retardation-hypotonic facies syndrome, X-linked; Alpha-thalassemia/mental retardation syndrome	1 in 500,000	1 in 919,360
X	BRWD3	Mental retardation, X-linked, type 93	1 in 45,000	1 in 65,000
X	BTK	Agammaglobulinemia X-linked, type 1	1 in 126,556	1 in 275,310
X	CD40LG	Hyper-IgM syndrome, type 1 (immunodeficiency, X-linked, with hyper-IgM, type 1)	1 in 250,000	1 in 532,258
X	CHM	Choroideremia	1 in 33,334	1 in 64,000
X	COL4A5	Alport syndrome, X-linked	1 in 34,622	1 in 72,761
X	CUL4B	Mental retardation, X-linked, syndromic, type 15 (Cabezas type)	1 in 500,000	1 in 636,300
X	CYBB	Chronic granulomatous disease, X-linked	1 in 100,000	1 in 250,000
X	DCX	Lissencephaly, X-linked, type 1	1 in 50,000	1 in 158,748
X	DKC1	Dyskeratosis congenita, X-linked	1 in 250,000	1 in 459,999
X	DLG3	Mental retardation, X-linked, type 90	1 in 45,000	1 in 100,000
X	DMD	Duchenne/Becker muscular dystrophy	1 in 2,942	1 in 58,819
X	EDA	Ectodermal dysplasia, type 1, hypohidrotic, X-linked	1 in 5,715	1 in 10,610
X	EMD	Emery-Dreifuss muscular dystrophy, type 1, X-linked	1 in 88,496	<1 in 1,000,000
X	F8	Hemophilia A	1 in 4,635	<1 in 16,550
X	F9	Hemophilia B	1 in 15,000	<1 in 29,000
X	FGD1	Aarskog-Scott syndrome; Mental retardation, X-linked syndromic, type 16	1 in 500000	1 in 937,499
X	FMR1	Fragile X syndrome	< 1 in 368	<1 in 37,000
X	FTSJ1	Mental retardation, X-linked 44	1 in 45,000	N/A
X	G6PD	Hemolytic anemia, G6PD deficient (favism)	1 in 25	<1 in 241
X	GJB1	Charcot-Marie-Tooth neuropathy, X-linked dominant, type 1	1 in 15,161	1 in 44,254
X	GLA	Fabry disease	1 in 35,031	<1 in 217,000
X	GPR143	Ocular albinism, type 1 (Nettleship-Falls type)	1 in 42,858	<1 in 48,000
X	HCFC1	Mental retardation, X-linked 3 (methylmalonic acidemia and homocysteinemia, cblX type)	1 in 500,000	N/A
X	HPRT1	Lesch-Nyhan syndrome	1 in 145,204	1 in 382,808
X	HSD17B10	HSD10 mitochondrial disease	1 in 500,000	1 in 1,000,000
X	IDS	Mucopolysaccharidosis, type 2	1 in 38,000	1 in 90,827
X	IL1RAPL1	Mental retardation, X-linked, type 21/34	1 in 45,000	1 in 90,000
X	IL2RG	Severe combined immunodeficiency, X-linked	1 in 33,334	<1 in 84,000
X	KDM5C	Mental retardation, X-linked, syndromic, Claes-Jensen type	1 in 500,000	1 in 1,000,000
X	L1CAM	L1 Syndrome	1 in 15,000	<1 in 49,000
X	MECP2	Encephalopathy, neonatal severe; Rett syndrome	1 in 500,000	1 in 1,000,000
X	MID1	Opitz GBBB syndrome, type 1	1 in 137	1 in 913
X	MTM1	Myotubular myopathy, X-linked	1 in 29,412	<1 in 140,000
X	NDP	Norrie disease	1 in 50,000	<1 in 1,000,000
X	NR0B1	Adrenal hypoplasia, congenital	1 in 35,000	<1 in 66,000
X	OCRL	Lowe Syndrome; Dent disease type 2	1 in 357,144	<1 in 1,000,000
X	OPHN1	Mental retardation, X-linked, with cerebellar hypoplasia and distinctive facial appearance	1 in 500,000	1 in 1,000,000
X	OTC	Ornithine transcarbamylase deficiency	1 in 37,667	<1 in 96,000
X	PAK3	Mental retardation, X-linked, type 30	1 in 45,000	1 in 90,000
X	PDHA1	Pyruvate dehydrogenase E1-alpha deficiency	N/A	N/A
X	PGK1	Phosphoglycerate kinase 1 deficiency	1 in 500,000	1 in 1,000,000
X	PHF8	Mental retardation syndrome, X-linked, Siderius type	1 in 500,000	1 in 916,000
X	PLP1	Pelizaeus-Merzbacher disease	1 in 91,838	1 in 113,109
X	POU3F4	Deafness, X-linked, type 2	1 in 556,112	<1 in 1,000,000
X	PQBP1	Renpenning syndrome	1 in 50,000	1 in 107,142
X	PRPS1	PRPS1-related disoders	<1 in 50,000	<1 in 221,000
X	RP2	Retinitis pigmentosa, type 2, X-linked	1 in 177,778	1 in 249,736
X	RPGR	Retinitis pigmentosa, type 3, X-linked; Cone-rod dystrophy, X-linked, 1	1 in 31,373	1 in 35,705
X	RS1	Retinoschisis	1 in 25,000	1 in 44,241
X	SH2D1A	Lymphoproliferative syndrome, X-linked, type 1	<1 in 500,000	<1 in 829,000
X	SLC16A2	Allan-Herndon-Dudley syndrome	1 in 50,000	1 in 67,647
X	SLC6A8	Cerebral creatine deficiency syndrome, type 1	N/A	N/A
X	SYN1	Epilepsy, X-linked, with variable learning disabilities and behavior disorders	1 in 45,000	1 in 55,588
X	THOC2	Mental retardation, X-linked 12	1 in 500,000	N/A
X	UPF3B	Mental retardation, X-linked, syndromic, type 14	1 in 45,000	1 in 49,500
X	WAS	Wiskott-Aldrich syndrome; Thrombocytopenia, X-linked	1 in 500,000	<1 in 1,000,000
X	ZDHHC9	Mental retardation, X-linked syndromic, Raymond type	1 in 45,000	1 in 60,000
X	ZNF711	Mental retardation, X-linked, type 97	1 in 45,000	1 in 54,000

Autosomal recessive conditions				
Chrom	**Gene**	**Disease/Condition**	**Carrier Rate**	**Residual Risk**
7	CFTR	Cystic fibrosis	1 in 25	1 in 833
6	CYP21A2	Congenital adrenal hyperplasia due to 21-hydroxylase deficiency	1 in 62	1 in 1,228
13	GJB2	Deafness, autosomal recessive, type 1A; Deafness, digenic, GJB2/GJB6	1 in 40	1 in 489
16	HBA1	Thalassemia, alpha-	1 in 30	1 in 194
16	HBA2	Thalassemia, alpha-	1 in 30	1 in 194
11	HBB	Beta-thalassemia, Sickle cell anemia and other HBB-related hemoglobinopathies	1 in 67	1 in 411
5	SMN1	Spinal muscular atrophy	1 in 36	1 in 869

N/A: no data prevalence unknown