CGT Exome v3.2.3

Patient Information		Sample Information			Clinic Information	
Unique pat id.:	0078732 - 15429095	**Sample type:**	Blood		**Clinic:**	WeFIV
Patient name:		**Date of draw:**	28/04/2022		**Doctor:**	FERNANDO NEUSPILLER
Patient DOB:		**Date of receipt:**	05/05/2022			
Ethnic group:	Caucasian	**Report date/time:**	23/07/2024	17:28		
Indication:	No family history					

TEST RESULTS

POSITIVE

The individual is carrier of:

Amyotrophic lateral sclerosis, type 5, juvenile

Gene :	SPG11	**Allele:**	Het
DNA Change:	NM_025137.3:c.6100C>T	**Inheritance:**	AR
Protein change:	p.Arg2034*	**OMIM phenotype:**	602099
Variant classification:	Pathogenic		

Congenital adrenal hyperplasia due to 21-hydroxylase deficiency

Gene :	CYP21A2	**Allele:**	Het
DNA Change:	NM_000500.9:c.955C>T + CYP21A2 gene duplication	**Inheritance:**	AR
Protein change:		**OMIM phenotype:**	201910
Variant classification:	Pathogenic		

Deafness, autosomal recessive, type 84B

Gene :	OTOGL	**Allele:**	Het
DNA Change:	NM_173591.3:c.5422C>T	**Inheritance:**	AR
Protein change:	p.Arg1808*	**OMIM phenotype:**	614944
Variant classification:	Pathogenic		

Myeloperoxidase deficiency

Gene :	MPO	**Allele:**	Het
DNA Change:	NM_000250.1:c.1555_1568delATGGAACCCAACCC	**Inheritance:**	AR
Protein change:	p.Met519fs	**OMIM phenotype:**	254600
Variant classification:	Pathogenic		

Primary coenzyme Q10 deficiency, type 1

Gene :	COQ2	**Allele:**	Het
DNA Change:	NM_015697.7:c.854C>G	**Inheritance:**	AR
Protein change:	p.Pro285Arg	**OMIM phenotype:**	607426
Variant classification:	Pathogenic		

INTERPRETATION OF TEST RESULTS

Typically, a positive result does not have direct clinical consequences for the carrier individual. There is another normal gene copy for all positive autosomal recessive (AR) genes indicated in the table which provides normal biological information. The likelihood of transmission of the variant(s) to offspring is 50%, independent for each variant. If the partner, or gamete donor, screens negative for the pathogenic or likely pathogenic variants in the gene(s) included in the table for this patient, the reproductive risk would be reduced. Please note that family members may also carry the variant(s) reported here, and this information may be significant for them and their offspring.
If a patient and partner, or gamete donor, are both carriers of variants in the same gene associated with AR inheritance, there is a 25% chance that any child they have together would be affected. If a female patient is a carrier for an X-linked condition, there is a 50% chance that each of the reproductive couple's children would also be a carrier. Males would typically express symptoms of the condition, and females are typically unaffected or may display milder symptoms.
For genes with a negative test result, the risk of having children affected by the associated disorders decreases significantly compared to the general population. This also the case for a negative personal result when a reproductive partner or a gamete donor is a carrier for a pathogenic or likely pathogenic variant in one or more of the tested genes. However, due to test limitations associated with any genetic test, this low risk is not zero (see limitations section and informed consent form)

In this individual, we detected two variants in the CYP21A2 gene, located in chromosome 6: (i) three CYP21A2 gene copies are detected during CNV analysis, i.e., presence of gene duplication in one allele; (ii) during sequence analysis, the variant c.955C>T (p.Q318*) is detected. Nevertheless, according to the literature (Pajares et al., 2008), risk of being CAH carrier is low since in about 85% of the cases both variants (c.955C>T and gene duplication) are in cis configuration (in the same chromosome) and then there is still one functional CYP21A2 gene copy in that chromosome 6. Remarkably, having both DNA changes in different chromosomes (trans configuration) will represent a true CAH carrier. Conclusion: most probably this individual is not carrier of CAH. In order to determine if the individual is a true positive (carrier), a separate family analysis must be performed to study both variant's segregation. If the p.Q318X variant and the duplicated gene were inherited from different parent (less than 15% of the times), the c.955C>T (p.Q318*) will represent a true CAH-allele, ie., the individual will be CAH carrier.

LOW COVERAGE VARIANTS

SGCB:NM_000232.4:c.29_33delAACAG;SGCB:NM_000232.4:c.33+1G>A;SGCB:NM_000232.4:c.33+1G>C;NAGLU:NM_000263.3:c.245G>A;GP1BB:NM_000407.4:c.505_516dupGTGCTGCTGCTG;MESP2:NM_001039958.1:c.500_503dupACCG;NEK1:NM_001199397.1:c.3616G>T;TYMP:NM_001257989.1:c.1316-1G>A;TYMP:NM_001257989.1:c.1323dupC;TYMP:NM_001257989.1:c.1326delG;TYMP:NM_001257989.1:c.1326G>A;RECQL4:NM_004260.3:c.50_51dupCG;GCSH:NM_004483.4:c.1A>G;FOXE3:NM_012186.2:c.720C>A;GLDN:NM_181789.2:c.59T>C;BLOC1S3:NM_212550.4:c.448delC.These variants have a coverage lower than 7X and it is not possible to determine if they are present or not in the sample (non-informative 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 chang

TEST METHODOLOGY

1.DNA extraction from the biological sample. 2. Next Generation Sequencing of gene regions where known mutations are located (list available at https://cgt.igenomix.com/diseases-list/). 3. Raw data analysis using bioinformatics (bioinformatic pipeline v1.0). 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) SMN1 gene: exon 7 deletion; b) CYP21A2 gene: frequent mutations; c) HBA1/HBA2 genes: frequent deletions; d) FMR1 gene: CGG repeat sizing (females only); e) DMD gene: frequent deletions/duplications; f) F8 gene: intron 22 inversion (females only); g) FXN gene: GAA repeat sizing.

TEST LIMITATIONS

The CGT test only includes analysis of the specific variants included into the list (list of variants analyzed are available by request), and no others. Therefore, the CGT test does not cover all monogenic diseases nor 100% of disease-causing mutations 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), mutations 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 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 ins/del 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 CGT 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 mutation being present in the offspring. In the general population there is a 3-5% risk for bith 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

This test was developed, and its performance characteristics determined by Igenomix Group. 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. *IGENOMIX SPAIN holds CLIA Certificate of Compliance: #99D2146167. Part of this test has been outsourced to a referral laboratory whose QMS is based on high Quality Standards, periodically monitored by Igenomix SPAIN and audited by independent external parties.

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
	
Camila Ayala Lira da Cruz CRBIO 113163 Bióloga	**Lic. Daniela Lorenzi** Manager de Laboratorio

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

Amyotrophic lateral sclerosis, type 5, juvenile

What is Amyotrophic lateral sclerosis, type 5, juvenile?

Amyotrophic lateral sclerosis, type 5, juvenile follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SPG11 gene located on chromosomal region 15q21.1. The age of onset is infancy/childhood. This disease is characterized by progressive upper and lower motor neuron degeneration causing facial spasticity, dysarthria, and gait disorders with onset before 25 years of age. The prevalence is <1/1,000,000.

What is the next step if I am a carrier of Amyotrophic lateral sclerosis, type 5, juvenile?

If you are a carrier of Amyotrophic lateral sclerosis, type 5, juvenile it is important that your partner (or gamete donor) is tested to determine if she/he is also a carrier of this condition.

What if my partner isn't a carrier?

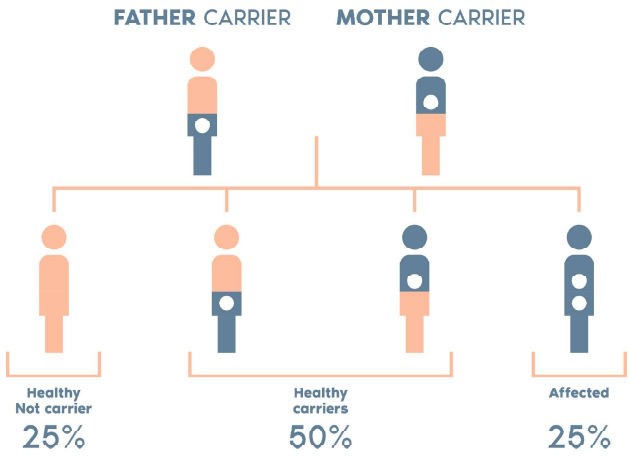
If your partner tests negative for Amyotrophic lateral sclerosis, type 5, juvenile, the possibility of having an affected child is very low, significantly lower than the incidence of disease in the general population. However, there is not a test capable of detecting all existing pathogenic variants. Therefore, a residual risk remains of having unknown or undetectable pathogenic variants using current technology.

What if both parents are carriers of Amyotrophic lateral sclerosis, type 5, juvenile?

When both parents are carriers of Amyotrophic lateral sclerosis, type 5, juvenile, the probability of having a child with the disease is 25% in each pregnancy. (See graph)

What if I am going to use gamete donation?

In this case it is advisable to use the same assay (CGT) to test candidate donors and choose one that is negative for the same condition.



If both are carriers of the disease contact your doctor or genetic counselor for information on genetic options for family planning.

Congenital adrenal hyperplasia due to 21-hydroxylase deficiency

What is Congenital adrenal hyperplasia due to 21-hydroxylase deficiency?

Classic congenital adrenal hyperplasia due to 21-hydroxylase deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CYP21A2 gene located on chromosomal region 6p21.3. The age of onset is neonatal/infantile. This disease is characterized by simple virilizing or salt wasting forms that can manifest with genital ambiguity in females, and in both sexes with adrenal insufficiency with dehydration during the neonatal period, life threatening hypoglycemia and hyperandrogenia. The prevalence is 1/100,000 to 9/100,000. There is a common milder form of congenital adrenal hyperplasia (Nonclassic) characterized by a later onset of androgen excess symptoms seen in females and precocious pseudopuberty in both sexes. Cortisol and aldosterone levels are normal but there is an increased amount of androgens. Nonclassic form onset occurs in adolescence with variable degrees of postnatal androgen excess (precocious pubarche, hirsutism, acne, alopecia, anovulation and menstrual irregularities and in the post-pubertal period it can mimic polycystic ovary syndrome. It is also sometimes asymptomatic. The prevalence ranges from 1/1,000-1/500 in the general Caucasian population, but up to 1-2% among inbred populations, such as Eastern European (Ashkenazi) Jews.

What is the next step if I am a carrier of Congenital adrenal hyperplasia due to 21-hydroxylase deficiency?

If you are a carrier of Congenital adrenal hyperplasia due to 21-hydroxylase deficiency it is important that your partner (or gamete donor) is tested to determine if she/he is also a carrier of this condition.

What if my partner isn't a carrier?

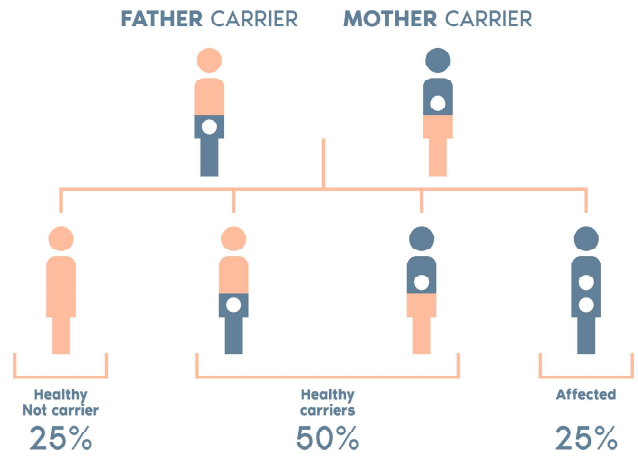
If your partner tests negative for Congenital adrenal hyperplasia due to 21 -hydroxylase deficiency, the possibility of having an affected child is very low, significantly lower than the incidence of disease in the general population. However, there is not a test capable of detecting all existing pathogenic variants. Therefore, a residual risk remains of having unknown or undetectable pathogenic variants using current technology.

What if both parents are carriers of Congenital adrenal hyperplasia due to 21-hydroxylase deficiency?

When both parents are carriers of Congenital adrenal hyperplasia due to 21-hydroxylase deficiency, the probability of having a child with the disease is 25% in each pregnancy. (See graph)

What if I am going to use gamete donation?

In this case it is advisable to use the same assay (CGT) to test candidate donors and choose one that is negative for the same condition.



If both are carriers of the disease contact your doctor or genetic counselor for information on genetic options for family planning.

Deafness, autosomal recessive, type 84B

What is Deafness, autosomal recessive, type 84B?

Nonsyndromic hearing loss is a partial or total loss of hearing that is not associated with other signs and symptoms. Nonsyndromic hearing loss can be classified by the condition's pattern of inheritance: autosomal dominant (DFNA), autosomal recessive (DFNB), X-linked (DFNX), or mitochondrial (which does not have a special designation). DFNA, DFNB, and DFNX subtypes are numbered in the order in which they were first described. The characteristics vary among the different types. Hearing loss can affect one ear (unilateral) or both ears (bilateral). Degrees of hearing loss range from mild (difficulty understanding soft speech) to profound (inability to hear even very loud noises). The term "deafness" is often used to describe severe-to-profound hearing loss. Hearing loss can be stable, or it may be progressive, becoming more severe as a person gets older. Particular types of nonsyndromic hearing loss show distinctive patterns of hearing loss. Most forms of nonsyndromic hearing loss are described as sensorineural, which means they are associated with a permanent loss of hearing caused by damage to structures in the inner ear.

What is the next step if I am a carrier of Deafness, autosomal recessive, type 84B?

If you are a carrier of Deafness, autosomal recessive, type 84B it is important that your partner (or gamete donor) is tested to determine if she/he is also a carrier of this condition.

What if my partner isn't a carrier?

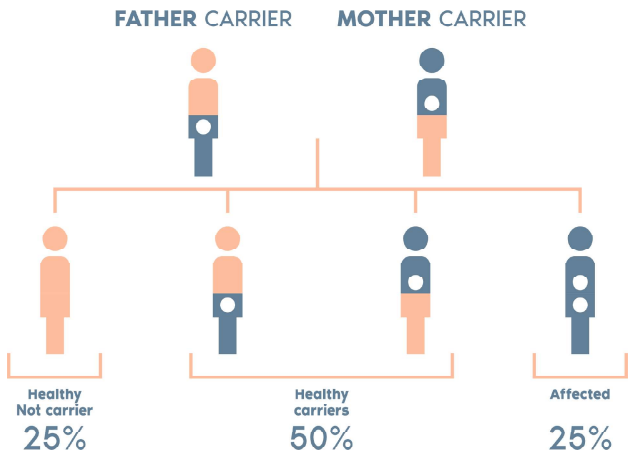
If your partner tests negative for Deafness, autosomal recessive, type 84B, the possibility of having an affected child is very low, significantly lower than the incidence of disease in the general population. However, there is not a test capable of detecting all existing pathogenic variants. Therefore, a residual risk remains of having unknown or undetectable pathogenic variants using current technology.

What if both parents are carriers of Deafness, autosomal recessive, type 84B?

When both parents are carriers of Deafness, autosomal recessive, type 84B, the probability of having a child with the disease is 25% in each pregnancy. (See graph)

What if I am going to use gamete donation?

In this case it is advisable to use the same assay (CGT) to test candidate donors and choose one that is negative for the same condition.



If both are carriers of the disease contact your doctor or genetic counselor for information on genetic options for family planning.

Myeloperoxidase deficiency

What is Myeloperoxidase deficiency?

Myeloperoxidase deficiency is a disorder characterized by decreased myeloperoxidase activity in neutrophils and monocytes that results in disseminated candidiasis.

What is the next step if I am a carrier of Myeloperoxidase deficiency?

If you are a carrier of Myeloperoxidase deficiency it is important that your partner (or gamete donor) is tested to determine if she/he is also a carrier of this condition.

What if my partner isn't a carrier?

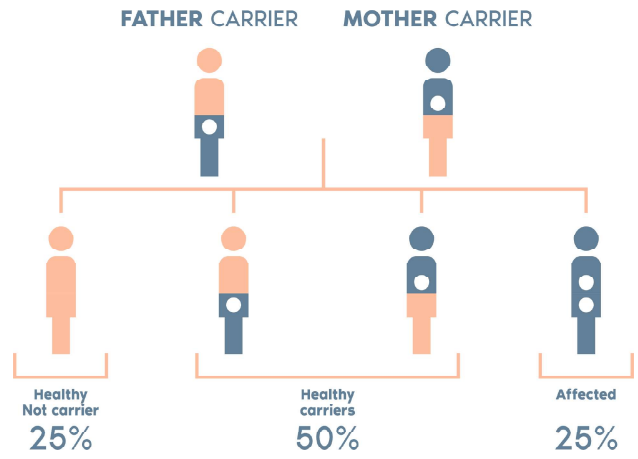
If your partner tests negative for Myeloperoxidase deficiency, the possibility of having an affected child is very low, significantly lower than the incidence of disease in the general population. However, there is not a test capable of detecting all existing pathogenic variants. Therefore, a residual risk remains of having unknown or undetectable pathogenic variants using current technology.

What if both parents are carriers of Myeloperoxidase deficiency?

When both parents are carriers of Myeloperoxidase deficiency, the probability of having a child with the disease is 25% in each pregnancy. (See graph)

What if I am going to use gamete donation?

In this case it is advisable to use the same assay (CGT) to test candidate donors and choose one that is negative for the same condition.



If both are carriers of the disease contact your doctor or genetic counselor for information on genetic options for family planning.

Primary coenzyme Q10 deficiency, type 1

What is Primary coenzyme Q10 deficiency, type 1?

Primary coenzyme Q10 deficiency type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the COQ2 gene located on chromosomal region 4q21.23. The age of onset is neonatal/infantile. The phenotypes include an encephalomyopathic form with seizures and ataxia; a multisystem infantile form with encephalopathy, cardiomyopathy and renal failure; a predominantly cerebellar form with ataxia and cerebellar atrophy; Leigh syndrome with growth retardation; and an isolated myopathic form.

What is the next step if I am a carrier of Primary coenzyme Q10 deficiency, type 1?

If you are a carrier of Primary coenzyme Q10 deficiency, type 1 it is important that your partner (or gamete donor) is tested to determine if she/he is also a carrier of this condition.

What if my partner isn't a carrier?

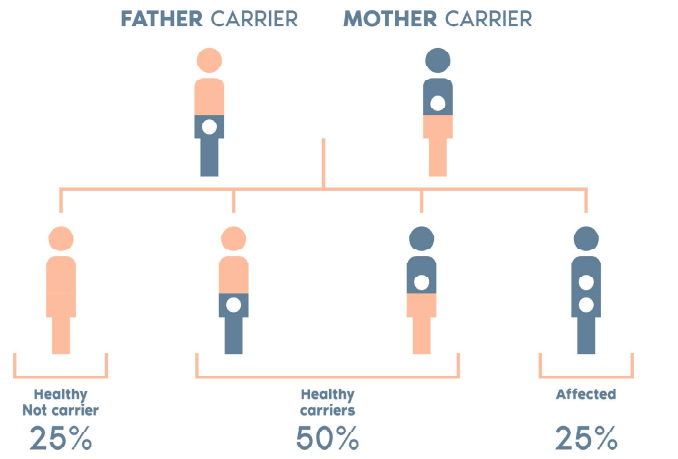
If your partner tests negative for Primary coenzyme Q10 deficiency, type 1, the possibility of having an affected child is very low, significantly lower than the incidence of disease in the general population. However, there is not a test capable of detecting all existing pathogenic variants. Therefore, a residual risk remains of having unknown or undetectable pathogenic variants using current technology.

What if both parents are carriers of Primary coenzyme Q10 deficiency, type 1?

When both parents are carriers of Primary coenzyme Q10 deficiency, type 1, the probability of having a child with the disease is 25% in each pregnancy. (See graph)

What if I am going to use gamete donation?

In this case it is advisable to use the same assay (CGT) to test candidate donors and choose one that is negative for the same condition.



If both are carriers of the disease contact your doctor or genetic counselor for information on genetic options for family planning.

LIST OF ANALYZED GENES

Gene mean coverage >100x CHRNA1, CHRNB1, CHRND, CHRNE, CHRNG, ACO2, APRT, ACTA1, ADK, AMPD1, AMPD2, SLC25A4, FDXR, AGRN, ALB, ALDOA, AFP, NAGA, SLC3A1, ACY1, AGT, AGTR1, ACE, CD19, SERPINC1, ALDH7A1, SERPINA1, IFNGR1, AQP2, RARS1, CYP19A1, DDC, ASNS, ATP2A1, ATP6V1E1, NPR2, SLC4A1, CD40, B2M, BLVRA, CD79A, BMP1, DST, COL17A1, CAD, CDH3, CAST, CACNA1D, CAPN1, CAPN3, CASQ2, CA5A, CAT, TYRP1, CTSD, CP, HSPD1, CLCN1, CYP11A1, COL4A3, COL7A1, COL4A4, COL1A2, COL9A1, COL6A1, COL6A2, COL6A3, COL9A2, COL11A1, COL11A2, COL18A1, COL13A1, MMP2, DCC, C1S, CR2, C3, C5, C8B, GJB2, GJA1, CRYAA, CRYAB, CRYBB3, CNGA1, PPIB, CTPS1, IL10RB, CYC1, POR, CYP11B2, COX6B1, CD55, ALAD, DSP, DES, DSG1, CYP24A1, PCBD1, ERCC2, SLC26A3, EGR2, NT5E, ETFB, TYMP, EDN3, EDNRB, ENO3, ERCC3, ERCC4, ERCC5, SLC1A1, CFH, F13A1, F13B, FTL, FGA, FGB, FGG, FLG, FMO3, FOLR1, FSHR, FSHB, FH, ABAT, GGCX, TACSTD2, MPV17, GCK, SLC2A1, GOT2, SLC2A2, GRIK2, GRIN1, ALDH18A1, GFPT1, EPRS1, GPX4, GLRA1, GLRB, GYS1, GYS2, GNRHR, GRN, CSF3R, GHRHR, GH1, GNAT1, GNAT2, HBB, HGF, HSPG2, HK1, HARS1, HOXA1, VSX2, HADHB, IL7R, IGLL1, ADAR, CD79B, ITPR1, IGF1R, IGF1, SOD1, ITGA6, ITGB4, ITGB6, ISG15, INSR, IL1RN, IL2RA, KRT5, KRT14, KRT10, LDHA, LAMB1, LAMC2, LAMB3, LAMA1, LAMB2, LMNA, LARS1, LIFR, PTPRC, LIPE, LHB, LHCGR, LCK, PLOD1, LIM2, MAK, MGP, LAMA2, MARS1, MTR, MITF, MAPT, MTTP, MPZ, MAG, MPL, MYH2, MYO5A, MYBPC1, NDUFV1, IL12B, NEB, NGF, PCSK1, NEFL, TAC3, PNP, LEP, SPINK1, PTH, PTH1R, TAP1, PRF1, PEX2, ABCB4, ALPL, PGM1, GPI, MTHFD1, PHKG2, PSPH, PHKB, SERPINF1, POU1F1, JUP, ENPP1, PLG, SERPINE1, ITGB3, POLE, POLG, KCNE1, INS, PRDX1, PSAP, PROS1, F2, TYK2, ZAP70, PRKCD, PSMB8, EPB42, BCHE, PYCR1, PDHB, RDX, PRPH2, RAG1, RAG2, REN, RD3, RPE65, PDE6A, PDE6B, RLBP1, RARB, RBP4, RBP3, RHO, ROM1, RYR1, AHCY, SAG, STIL, SPR, SLC34A1, SLC5A1, SLC5A2, SPTA1, CSTA, EPCAM, SURF1, CD27, CD3D, CD3E, ITK, TERT, TK2, TG, TSHB, TTN, TFRC, ERBB3, THRB, TGM1, SLC25A1, TNNT1, TH, NTRK1, UQCRC2, UCHL1, DPAGT1, UNG, UGT1A1, ATP6V1B1, VARS1, XRCC4, ZP1, BBS1, CFI, C6, C7, KLKB1, ETFDH, PCCA, PCCB, GLDC, AMT, GCSH, DLD, INVS, DBT, BCKDHB, MVK, IDUA, F11, TBXAS1, PRSS1, MYO7A, 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, LBR, ABCA1, CNGA3, ITGB2, LRP2, MMP13, SGCA, JAK3, GUCY2D, GCH1, SCNN1A, HMGCS2, CENPF, PEX19, PI4KA, ACADSB, KCNJ1, BBS4, PEX5, TTPA, NT5C2, GCNT2, IGHMBP2, ABCC8, RELN, AUH, NDUFV2, ITGA7, HSPA9, STAT1, STAT2, NRXN1, CLCN2, LZTR1, PTPRO, STAR, CPT2, CHUK, SLC16A1, IARS1, PPT1, CNGB1, SCNN1B, SCNN1G, TAF13, LAMA3, PLCB4, DDB2, MRE11, PDE6C, INPPL1, SLC12A1, SDHA, AIMP2, MSH3, HADHA, SGCB, CRYBB1, IL11RA, SERPINH1, DHPS, GHR, AMHR2, SLC12A3, MYO6, DMP1, GSS, NPC2, AARS1, PMP22, CTSK, ABCC2, CSTB, GDF6, DDX11, PDE6H, ATR, BIN1, KIF1A, AMBN, C1QBP, PLEC, HINT1, GUCY2C, MOGS, TUSC3, 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Gene mean coverage 50x-100x AK1, AK2, APOE, BCAT2, CALCRL, CHAT, MME, C1QA, C1QB, C1QC, DHFR, DHODH, ERCC1, SLC6A3, DAG1, EPB41, EDN1, EGFR, CFD, B4GALT1, GPT2, GLUL, GPD1, GSC, CSF2RB, HMOX1, HPCA, IL10RA, ITPA, IFNGR2, MDH2, MPI, NDUFS1, RMRP, TACR3, CHMP1A, FGF3, TAP2, ACP5, PGM3, CD36, GP9, POMC, SFTPB, PDE6G, GRK1, SPARC, SLC9A3, CD3G, CD247, CD81, TRHR, TPI1, TPM3, DDR2, VLDLR, FLI1, HCFC1, SLC6A8, SLC16A2, OPHN1, DLG3, ABCD1, ARX, CHM, PLP1, NR0B1, FTSJ1, MID1, ZDHHC9, NDP, AFF2, RS1, GJB1, PGK1, CDH11, SLC1A4, SLC18A3, SLC25A3, AKR1C2, ALDH1A3, P2RY12, MASP1, SLC11A2, CPT1A, LHX3, ASPH, NECTIN1, IHH, CEBPE, FOXN1, NDST1, LSS, KCNJ11, AMH, TNXB, LEPR, SLC6A9, CLPP, GDF5, CASR, GAMT, TOP3A, SLC10A2, MUSK, SLCO2A1, MYO1E, IRF8, UBE3A, SERPINB8, HESX1, NDUFS7, B4GALNT1, RAX, WNT10B, ARHGDIA, TAPBP, IMPA1, ESRRB, MYD88, ECM1, SCARB2, LAT, WIPF1, CTSC, FUT8, CDSN, PEX10, ORC4, KIF1C, CAVIN1, TRDN, CRADD, TNFRSF11A, BCL10, DPH1, AP1S1, CTSF, DPM2, AIMP1, COX15, CYP7B1, SGPL1, MED17, NDUFA10, PEX11B, GOSR2, GRM6, TBX15, DNAJB2, SLC6A5, KISS1R, STAT5B, AGXT, BLOC1S6, B4GALT7, LAMC3, ST3GAL5, PLPBP, SP110, GRM1, ZNHIT3, BLNK, ZNF423, WARS2, MALT1, MKKS, DGAT1, BRF1, STK4, SPTBN2, CORO1A, STX11, SPINT2, GAS8, MESP2, CHST6, IL21R, ALX4, ABCG8, B4GAT1, CDT1, ATF6, CIB2, CLDN14, PCDH12, PRX, SOST, DCDC2, NUP62, TMC6, TMC8, SLC35C1, ALG1, STIM1, DPM3, DCLRE1C, MBOAT7, PIP5K1C, SLC19A3, IRX5, SLC45A2, SIX6, ESPN, ANTXR1, STRC, EIF2B2, NHP2, CD320, LZTFL1, SFRP4, OPA3, SP7, UPB1, HEXA, JAM3, COG8, ATP6V1A, LIAS, CLN3, HYAL1, MTHFR, MCPH1, ALG12, FYCO1, PTF1A, TMIE, SRD5A2, AIRE, LIPH, DYM, HPS6, EPM2A, ARSA, ADA2, COLEC10, CCNO, HSD3B7, MCFD2, GNPTG, RCBTB1, SLC52A2, ASPA, NHLRC1, CLN5, PUS1, XYLT2, TTC8, EXT1, CHSY1, ADSL, NEU1, LGI4, CHST14, SMOC1, NCF1, GTPBP3, GLIS2, GRHL2, GLDN, PTRH2, PSMC3IP, SLC39A8, SLC39A13, SLC39A14, TSEN15, SLC5A7, GJC2, ARL6, LRIG2, SLC6A19, ARL13B, CABP4, MRPS16, WDR45B, LPAR6, SLC25A22, TTC7A, REEP6, ERCC8, ERCC6, MAP3K20, NECTIN4, NAGLU, CRB2, MARS2, NEK9, MMACHC, RNF216, COL25A1, CLDN19, DNAL1, PRMT7, MCM9, B3GALNT2, MED25, PIGV, PIGW, ORAI1, DOK7, SLC6A17, LINS1, TRAPPC6B, GLYCTK, UBA5, UFM1, PDSS2, MARVELD2, FLAD1, PRCD, GINS1, PDE10A, PIGY, CYP2U1, HYLS1, CNPY3, HYDIN, SLC25A46, RBCK1, FTO, OBSL1, TRMT5, SLC25A26, RUSC2, FAM20C, FAM20A, SLC30A10, FARS2, ERLIN1, ARV1, PGAP1, TBC1D20, LMF1, MTFMT, NKX2-6, PGAP3, ISCU, B9D2, TRAPPC9, MRPS34, OTUD6B, IYD, ZNF469, PNPLA1, ADAMTSL2, CILK1, NDUFAF5, FECH, RSPH9, TBC1D7, DSTYK, RNF168, GPIHBP1, SDHAF1, COQ4, TRNT1, NDUFAF3, SERPINF2, SMG9, CYB5R3, PPP1R15B, MOCOS, USB1, ZC3H14, FEZF1, KIAA1549, SLC52A3, TPRN, HPSE2, SCARF2, ALG11, SOBP, GZF1, BPGM, SPATA5, ZBTB24, MCIDAS, TRIM2, CCDC8, WDR81, HSD11B2, ACSF3, C19orf12, NUP93, ATAD1, BRAT1, LRMDA, KANK2, UVSSA, MPC1, COA6, SNX10, POMGNT2, DHTKD1, TECPR2, DDHD2, POMK, METTL23, CERS3, ADAT3, ANKS6, ARL2BP, TIMMDC1, COQ8B, CEP19, CDIN1, ERCC6L2, NADK2, VPS53, JAGN1, TRMT10A, ELP2, SPRTN, FAR1, LMOD3, TMEM107, LEMD2, PYCR2, ARHGEF18, PRDM12, TMEM199, TANGO2, TBCK, DNAJC21, PYROXD1, TECRL, PRUNE1, CLDN10, ALPK3, ARMC9, MSTO1, IQCE, TRIT1

Gene mean coverage < 50x LRPAP1, CD59, CA8, PCYT1A, ESR1, KDSR, H6PD, GP1BB, HOXB1, HOXC13, HMX1, NRL, WNT1, WNT3, PAX7, PRRX1, ZBTB16, PDXK, CD8A, TF, UQCRB, MECP2, POU3F4, DCX, PAK3, EDA, AP1S2, IDS, AR, CIITA, MEOX1, SCN1B, SMN1, PDX1, GFER, FOXE3, GPR68, DGKE, WNT7A, SOX18, ENTPD1, NKX3-2, EMP2, FADD, FOXE1, PHOX2A, OCLN, CA12, SCO1, SLC33A1, CLDN1, NDUFA9, GYG1, RNASEH1, GNB5, FRRS1L, CRIPT, NEUROG3, CPLX1, S1PR2, KYNU, CYP26B1, RBM8A, GAN, DHH, SLC35A3, FBXL4, KY, EXTL3, NKX6-2, ALX3, PANK2, STAMBP, BSND, MPIG6B, FKRP, MLYCD, FXN, AP4S1, TIMM50, TWIST2, CLCF1, SAR1B, CNNM2, CLN8, HES7, XYLT1, CYP26C1, PEX26, TP53RK, NMNAT1, GTF2H5, BTD, MPLKIP, IER3IP1, L2HGDH, GLRX5, BLOC1S3, SLC24A4, ATOH7, KREMEN1, VPS37A, PIGM, DCPS, RSPO4, SLC35D1, SYT14, ISCA1, PPM1K, NHEJ1, CISD2, TXNL4A, ERLIN2, CLMP, NDUFAF6, NDUFA11, RNASET2, CYB5A, POLR1D, MSRB3, CCDC115, TMCO1, B9D1, FKBP14, DDHD1, MTO1, COX20, TMEM231, B3GALT6, IBA57, ISCA2, BHLHA9, OTULIN, SLC7A14, LYRM7, RSPH3, WDR73, CLPB, CEP78, LIPT2

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).