



Patient Information:

10958, Donor

DOB: [REDACTED]

Sex: M

MR#:

Patient#: FT-PT8907340

Partner Information:

Not Tested

Physician:

Kuan, James

Phoenix Sperm Bank

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Laboratory:

Fulgent Therapeutics LLC

CAP#: 8042697

CLIA#: 05D2043189

Laboratory Director:

Dr. Amar Jariwala

Report Date: Dec 07, 2024

Accession:

FT-7414252

Test#: FT-TS15014264

Specimen Type: Blood (EDTA)

Collected: Nov 20, 2024

Accession:

N/A

FINAL RESULTS



Carrier for genetic conditions in **multiple** genes.
Genetic counseling is recommended.

TEST PERFORMED

Beacon Preconception Carrier Screening - 515 Genes (without X-linked Disorders)

(515 Gene Panel; gene sequencing with deletion and duplication analysis)

| Condition and Gene | Inheritance | 10958, Donor | Partner |
|--|-------------|-------------------------------------|---------|
| WNT10A-related ectodermal dysplasias <i>WNT10A</i> | AR | ⊕ Carrier c.682T>A (p.Phe228Ile) | N/A |
| Nonsyndromic hearing loss 1A <i>GJB2</i> | AR | ⊕ Carrier c.101T>C (p.Met34Thr) | N/A |

INTERPRETATION:

Notes and Recommendations:

- **PLEASE NOTE:** Heterozygous carriers of a WNT10A variant may be at risk of autosomal dominant selective tooth agenesis-4 (STHAG4) (PubMed: [29772684](#); OMIM: [606268](#)). Autosomal dominant phenotypes have also been described to include dry skin, abnormal sweating, nail abnormalities and sparse hair in some patients (PubMed: [20301291](#), [34184264](#); OMIM: [150400](#)). As such, correlation with clinical and family history is recommended. Consultation with a medical geneticist and/or other specialist is recommended.
- **PLEASE NOTE:** While some heterozygous variants in the GJB2 gene have been associated with autosomal dominant deafness-3A (DFNA3A), Bart-Pumphrey syndrome, Hystrix-like ichthyosis with deafness (HID syndrome), Keratitis-ichthyosis-deafness (KID) syndrome, palmoplantar keratoderma with deafness, and Vohwinkel syndrome, the reported variant has not been associated with those findings. Please also note that about 1% of individuals with nonsyndromic hearing loss 1A are compound heterozygous for a pathogenic variant in GJB2 and a GJB6/CRYL1 gene deletion spanning the upstream cis-regulatory regions of GJB2 (PubMed: [20301449](#)).
- Based on these results, this individual is positive for carrier mutations in 2 genes. Carrier screening for the reproductive partner is recommended to accurately assess the risk for any autosomal recessive conditions. A negative result reduces, but does not eliminate, the chance to be a carrier for any condition included in this screen. Please see the supplemental table for details.
- Testing for copy number changes in the SMN1 gene was performed to screen for the carrier status of Spinal Muscular Atrophy. The results for this individual are within the normal range for non-carriers. See Limitations section for more information.
- This carrier screening test does not screen for all possible genetic conditions, nor for all possible mutations in every gene tested. This report does not include variants of uncertain significance; only variants classified as pathogenic or likely pathogenic at the time of testing, and considered relevant for reproductive carrier screening, are reported. Please see the gene specific notes for details. Please note that the classification of variants can change over time.
- Patients may wish to discuss any carrier results with blood relatives, as there is an increased chance that they are also carriers. These results should be interpreted in the context of this individual's clinical findings, biochemical profile, and family history.
- X-linked genes are not routinely analyzed for male carrier screening tests. Gene specific notes and limitations may be

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present. See below.

- Genetic counseling is recommended. Available genetic counselors and additional resources can be found at the National Society of Genetic Counselors (NSGC; <https://www.nsgc.org>)



WNT10A-RELATED ECTODERMAL DYSPLASIAS

| Patient | 10958, Donor | Partner |
|-----------------|---|---------|
| Result |  Carrier | N/A |
| Variant Details | WNT10A (NM_025216.3) c.682T>A (p.Phe228Ile) | N/A |

What is WNT10A-related ectodermal dysplasias?

The WNT10A gene produces proteins that aid in the formation of several types of tissues that arise from an embryonic cell layer called the ectoderm. There are several conditions associated with this gene including Schopf-Schulz-Passarge syndrome and Odonto-onycho-dermal dysplasia.

- Schopf-Schulz-Passarge syndrome (SSPS) and Odonto-onycho-dermal dysplasia (OODD) are rare ectodermal dysplasias characterized by hypodontia, keratoderma, nail dystrophy, and hair abnormalities. Individuals with SPSS also have multiple eyelid cysts, and hypotrichosis. Dry hair, smooth tongue with marked reduction of fungiform and filiform papillae, hyperhidrosis of palms and soles, and hyperkeratosis of the skin are additional features seen in individuals with OODD. For both conditions, some features may not be present until adulthood, causing diagnoses to be delayed in some cases.

What is my risk of having an affected child?

Schopf-Schulz-Passarge syndrome and Odontoonychodermal dysplasia are inherited in an autosomal recessive manner. If the patient and the partner are both carriers, the risk for an affected child is 1 in 4 (25%).

What kind of medical management is available?


Each condition is managed differently based on its symptoms. The treatment of SSPS and OODD is symptomatic. Standard dental care is indicated in most cases. Eyelid cysts seen in those with SSPS may be improved by electrocautery. If necessary, counseling and psychological support and dermatological examination to detect non-melanoma skin cancer should be offered.

What mutation was detected?

The detected heterozygous variant was NM_025216.3:c.682T>A (p.Phe228Ile). This variant, p.Phe228Ile, has been reported in many individuals with isolated oligodontia (PubMed: [22581971](#), [24449199](#), [24311251](#)). This variant has been reported in affected individuals in the homozygous, compound heterozygous, and heterozygous state, but also has been identified in unaffected individuals (PubMed: [36294409](#), [32618450](#), [34593752](#)). This variant is prevalent and is known to be associated with reduced penetrance (PubMed: [28976000](#), [24700731](#)), suggesting all carriers may not show symptoms of the disease. This variant is classified as "Pathogenic" or "Likely Pathogenic" by multiple clinical laboratories in ClinVar (Variation ID: 4462). The laboratory classifies this variant as likely pathogenic.



NONSYNDROMIC HEARING LOSS 1A

| Patient | 10958, Donor | Partner |
|-----------------|---|---------|
| Result |  Carrier | N/A |
| Variant Details | GJB2 (NM_004004.6) c.101T>C (p.Met34Thr) | N/A |

What is Nonsyndromic hearing loss 1A?

This condition is characterized by congenital, generally non-progressive sensorineural hearing loss. Vestibular function is normal and affected infants do not experience balance problems. Except for hearing loss, affected individuals are healthy and their life span is normal.

What is my risk of having an affected child?

Nonsyndromic hearing loss 1A is inherited in an autosomal recessive manner. If the patient and the partner are both carriers, the risk for an affected child is 1 in 4 (25%). Additionally, if the patient is a carrier for a pathogenic variant in GJB2 and the partner is a carrier for a GJB6/CRYL1 gene deletion spanning the upstream cis-regulatory regions of GJB2, there is also a 1 in 4 risk for an affected child.

What kind of medical management is available?

Other than hearing loss, affected individuals are healthy and their lifespan is normal. Hearing aids are commonly used and individuals with this type of hearing loss may benefit from cochlear implantation. Speech therapy and additional education tools may also aid in daily activities.

What mutation was detected?

The detected heterozygous variant was NM_004004.6:c.101T>C (p.Met34Thr). This variant, p.Met34Thr, is a controversial alteration found in individuals with hearing loss with a carrier frequency of up to 2.8% in certain populations (PubMed: [27224056](#), [14694360](#), [15070423](#), [22668073](#)). This variant has been identified in the homozygous and compound heterozygous states in both unaffected and affected individuals with mild to severe hearing loss (PubMed: [11134236](#), [14694360](#), [17935238](#), [17041943](#), [22668073](#), [26482070](#), [26896187](#), [9139825](#), [10556284](#), [16849369](#), [16380907](#), [20708129](#)). Clinical presentation for this variant can range from asymptomatic to severe hearing loss, suggesting reduced penetrance. This alteration has been shown to segregate with disease in a three-generation family study (PubMed: [22668073](#)). Additionally, missense variants at the same codon have been reported in the Human Gene Mutation Database in association with hearing loss (PubMed: [17666888](#), [25388846](#), [11698809](#), [19941053](#), [9139825](#)). Functional and biophysical studies suggest this variant inhibits wild-type connexin 26 channel activity (PubMed: [12176036](#), [16849369](#)). However, a separate study did not observe the same results (PubMed: [12384501](#)). Moreover, some studies have shown that this variant alone is insufficient to cause hearing loss suggesting a second mutation in the GJB2 gene and/or digenic inheritance of other mutations may contribute to the phenotypic presentation (PubMed: [9139825](#), [11134236](#), [23141803](#)). The heterogeneity of the disorder and frequency of the variant in control populations suggest the involvement of other factors (e.g. environmental or modifier genes) in influencing the penetrance and severity of the p.Met34Thr GJB2 mutation. The Deafness Variation Database, which re-categorizes previously reported variants based on ethnic-specific differences in minor allele frequencies, classified this variant as "Pathogenic" (PubMed: [25262649](#); <https://deafnessvariationdatabase.org/hg19s?terms=13%3A20763620%3AA%3EG>). This variant is classified as "Pathogenic" with expert panel review (ClinVar: 17000). The laboratory classifies this variant as pathogenic.



GENES TESTED:

Beacon Preconception Carrier Screening - 515 Genes (without X-linked Disorders) - 515 Genes

This analysis was run using the Beacon Preconception Carrier Screening - 515 Genes (without X-linked Disorders) gene list. 515 genes were tested with 99.5% of targets sequenced at >20x coverage. For more gene-specific information and assistance with residual risk calculation, see the SUPPLEMENTAL TABLE.

AAAS, ABCA12, ABCA3, ABCA4, ABCB11, ABCB4, ABCC2, ABCC8, ACAD9, ACADM, ACADVL, ACAT1, ACOX1, ACSF3, ADA, ADAMTS2, ADAMTSL4, ADGRG1, ADGRV1, AGA, AGL, AGPS, AGXT, AHI1, AIPL1, AIRE, ALDH3A2, ALDH7A1, ALDOB, ALG1, ALG6, ALMS1, ALPL, AMN, AMT, ANO10, AP1S1, AQP2, ARG1, ARL6, ARSA, ARSB, ASL, ASNS, ASPA, ASS1, ATM, ATP6V1B1, ATP7B, ATP8B1, BBS1, BBS10, BBS12, BBS2, BBS4, BBS5, BBS7, BBS9, BCKDHA, BCKDHB, BCS1L, BLM, BLOC1S3, BLOC1S6, BMP1, BRIP1, BSND, CAD, CANT1, CAPN3, CASQ2, CBS, CC2D1A, CC2D2A, CCDC103, CCDC39, CCDC88C, CD3D, CD3E, CD40, CD59, CDH23, CEP152, CEP290, CERKL, CFTR, CHAT, CHRNE, CHRNA, CIITA, CLCN1, CLN3, CLN5, CLN6, CLN8, CLRN1, CNGB3, COL11A2, COL17A1, COL27A1, COL4A3, COL4A4, COL7A1, COX15, CPS1, CPT1A, CPT2, CRB1, CRTAP, CRYL1, CTNS, CTSA, CTSC, CTSD, CTSK, CYBA, CYP11A1, CYP11B1, CYP11B2, CYP17A1, CYP19A1, CYP1B1, CYP21A2, CYP27A1, CYP27B1, CYP7B1, DBT, DCAF17, DCLRE1C, DDX11, DGAT1, DGUOK, DHCR7, DHDDS, DLD, DLL3, DNAH11, DNAH5, DNAI1, DNAI2, DNMT3B, DOK7, DUOX2, DYNC2H1, DYSF, EIF2AK3, EIF2B1, EIF2B2, EIF2B3, EIF2B4, EIF2B5, ELP1, EPG5, ERCC2, ERCC6, ERCC8, ESCO2, ETFA, ETFB, ETFDH, ETHE1, EVC, EVC2, EXOSC3, EYS, FAH, FAM161A, FANCA, FANCC, FANCD2, FANCE, FANCG, FANCI, FANCL, FBP1, FBXO7, FH, FKBP10, FKBP, FKTN, FMO3, FOXN1, FOXRED1, FRAS1, FREM2, FUCA1, G6PC, G6PC3, GAA, GALT, GALE, GALK1, GALNS, GALNT3, GALT, GAMT, GATM, GBA, GBE1, GCDH, GCH1, GDF5, GFM1, GHR, GJB2, GJB6, GJB1, GLDC, GLE1, GNE, GNPAT, GNPTAB, GNPTG, GNS, GORAB, GRHRP, GRIP1, GSS, GUCY2D, GUSB, HADH, HADHA, HADHB, HAMP, HAX1, HBA1, HBA2, HBB, HEXA, HEXB, HGSNAT, HJV, HLCS, HMGCL, HMOX1, HOGA1, HPD, HPS1, HPS3, HPS4, HPS5, HPS6, HSD17B3, HSD17B4, HSD3B2, HYAL1, HYLS1, IDUA, IGHMBP2, IKBK, IL7R, INVS, ITGA6, ITGB3, ITGB4, IVD, JAK3, KCNJ1, KCNJ11, LAMA2, LAMA3, LAMB3, LAMC2, LARGE1, LCA5, LDLR, LDLRAP1, LHX3, LIFR, LIG4, LIPA, LMBRD1, LOXHD1, LPL, LRAT, LRP2, LRPPRC, LYST, MAK, MAN2B1, MANBA, MCEE, MCOLN1, MCPH1, MECP, MED17, MESF2, MFSDB, MKK5, MKS1, MLC1, MLYCD, MMAA, MMAB, MMACHC, MMADHC, MOCS1, MOCS2, MPI, MPL, MPV17, MRE11, MTHFR, MTR, MTRR, MTPP, MUSK, MUT, MVK, MYO15A, MYO7A, NAGA, NAGLU, NAGS, NBN, NCF2, NDRG1, NDUFAF2, NDUFAF5, NDUFS4, NDUFS6, NDUFS7, NDUFV1, NEB, NEU1, NGLY1, NPC1, NPC2, NPHP1, NPHS1, NPHS2, NR2E3, NSMCE3, NTRK1, OAT, OCA2, OPA3, OSTM1, OTOA, OTOF, P3H1, PAH, PANK2, PC, PCBD1, PCCA, PCCB, PCDH15, PCNT, PDHB, PEPD, PET100, PEX1, PEX10, PEX12, PEX13, PEX16, PEX2, PEX26, PEX5, PEX6, PEX7, PFKM, PGM3, PHGDH, PHKB, PHKG2, PHYH, PIGN, PUVK, PKHD1, PLA2G6, PLEKHG5, PLOD1, PMM2, PNPO, POLG, POLH, POMGNT1, POMT1, POMT2, POR, POU1F1, PPT1, PRCD, PRDM5, PRF1, PROP1, PSAP, PTPRC, PTS, PUS1, PYGM, QDPR, RAB23, RAG1, RAG2, RAPSN, RARS2, RDH12, RLBP1, RMRP, RNASEH2A, RNASEH2B, RNASEH2C, RPE65, RPGRIP1L, RTEL1, RXYLT1, RYR1, SACS, SAMD9, SAMHD1, SCO2, SEC23B, SEPSecs, SGCA, SGCB, SGCD, SGCG, SGSH, SKIV2L, SLC12A1, SLC12A3, SLC12A6, SLC17A5, SLC19A2, SLC19A3, SLC1A4, SLC22A5, SLC25A13, SLC25A15, SLC25A20, SLC26A2, SLC26A3, SLC26A4, SLC27A4, SLC35A3, SLC37A4, SLC38A8, SLC39A4, SLC45A2, SLC4A11, SLC5A5, SLC7A7, SMARCA1, SMN1, SMPD1, SNAP29, SPG11, SPR, SRD5A2, ST3GAL5, STAR, STX11, STXBP2, SUMF1, SUOX, SURF1, SYNE4, TANGO2, TAT, TBCD, TBCE, TCIRG1, TCN2, TECPR2, TERT, TF, TFR2, TG, TGM1, TH, TK2, TMC1, TMEM216, TMEM67, TMPPRS3, TPO, TPP1, TREX1, TRIM32, TRIM37, TRMU, TSEN54, TSFM, TSHB, TSHR, TTC37, TTPA, TULP1, TYMP, TYR, TYRP1, UBR1, UNC13D, USH1C, USH2A, VDR, VLDLR, VPS11, VPS13A, VPS13B, VPS45, VPS53, VRK1, VSX2, WISP3, WNT10A, WRN, XPA, XPC, ZBTB24, ZFYVE26, ZNF469

METHODS:

Genomic DNA was isolated from the submitted specimen indicated above (if cellular material was submitted). DNA was barcoded, and enriched for the coding exons of targeted genes using hybrid capture technology. Prepared DNA libraries were then sequenced using a Next Generation Sequencing technology. Following alignment to the human genome reference sequence (assembly GRCh37), variants were detected in regions of at least 10x coverage. For this specimen, 99.53% and 99.50% of coding regions and splicing junctions of genes listed had been sequenced with coverage of at least 10x and 20x, respectively, by NGS or by Sanger sequencing. The remaining regions did not have 10x coverage, and were not evaluated. Variants were interpreted manually using locus specific databases, literature searches, and other molecular biological principles. To minimize false positive results, any variants that do not meet internal quality standards are confirmed by Sanger sequencing. Variants classified as pathogenic, likely pathogenic, or risk allele which are located in the coding regions and nearby intronic regions (+/- 20bp) of the genes listed above are reported. Variants outside these intervals may be reported but are typically not guaranteed. When a single pathogenic or likely pathogenic variant is identified in a clinically relevant gene with autosomal recessive inheritance, the laboratory will attempt to ensure 100% coverage of coding sequences either through NGS or Sanger sequencing technologies ("fill-in"). All genes listed were evaluated for large deletions and/or duplications. However, single exon deletions or duplications will not be detected in this assay, nor will copy number alterations in regions of genes with significant pseudogenes. Putative deletions or duplications are analyzed using Fulgent Germline proprietary pipeline for this specimen. Bioinformatics: The Fulgent Germline v2019.2 pipeline was used to analyze this specimen.

LIMITATIONS:

General Limitations

These test results and variant interpretation are based on the proper identification of the submitted specimen, accuracy of any stated familial relationships, and use of the correct human reference sequences at the queried loci. In very rare instances, errors may result due to mix-up or co-mingling of specimens. Positive results do not imply that there are no other contributors, genetic or



otherwise, to future pregnancies, and negative results do not rule out the genetic risk to a pregnancy. Official gene names change over time. Fulgent uses the most up to date gene names based on HUGO Gene Nomenclature Committee (<https://www.genenames.org>) recommendations. If the gene name on report does not match that of ordered gene, please contact the laboratory and details can be provided. Result interpretation is based on the available clinical and family history information for this individual, collected published information, and Alamut annotation available at the time of reporting. This assay is not designed or validated for the detection of low-level mosaicism or somatic mutations. This assay will not detect certain types of genomic aberrations such as translocations, inversions, or repeat expansions other than specified genes. DNA alterations in regulatory regions or deep intronic regions (greater than 20bp from an exon) may not be detected by this test. Unless otherwise indicated, no additional assays have been performed to evaluate genetic changes in this specimen. There are technical limitations on the ability of DNA sequencing to detect small insertions and deletions. Our laboratory uses a sensitive detection algorithm, however these types of alterations are not detected as reliably as single nucleotide variants. Rarely, due to systematic chemical, computational, or human error, DNA variants may be missed. Although next generation sequencing technologies and our bioinformatics analysis significantly reduce the confounding contribution of pseudogene sequences or other highly-homologous sequences, sometimes these may still interfere with the technical ability of the assay to identify pathogenic alterations in both sequencing and deletion/duplication analyses. Deletion/duplication analysis can identify alterations of genomic regions which include one whole gene (buccal swab specimens and whole blood specimens) and are two or more contiguous exons in size (whole blood specimens only); single exon deletions or duplications may occasionally be identified, but are not routinely detected by this test. When novel DNA duplications are identified, it is not possible to discern the genomic location or orientation of the duplicated segment, hence the effect of the duplication cannot be predicted. Where deletions are detected, it is not always possible to determine whether the predicted product will remain in-frame or not. Unless otherwise indicated, deletion/duplication analysis has not been performed in regions that have been sequenced by Sanger.

Gene Specific Notes and Limitations

ALG1: Due to the interference by highly homologous regions, our current testing method has less sensitivity to detect variants in exons 6-13 of the ALG1 gene (NM_019109.4). **CEP290:** Copy number analysis for exons 8-13 and exons 39-42 may have reduced sensitivity in the CEP290 gene. Confirmation of these exons are limited to individuals with a positive personal history of CEP290-related conditions and/or individuals carrying a pathogenic/likely pathogenic sequence variant. **CFTR:** Analysis of the intron 8 polymorphic region (e.g. IVS8-5T allele) is only performed if the p.Arg117His (R117H) mutation is detected. Single exon deletion/duplication analysis is limited to deletions of previously reported exons: 1, 2, 3, 11, 19, 20, 21. Analysis of the intron 8 polymorphic region (e.g. IVS8-5T allele) is only performed if the p.Arg117His (R117H) mutation is detected. Single exon deletion/duplication analysis is limited to deletions of previously reported exons: 1, 2, 3, 11, 19, 20, 21. CFTR variants primarily associated with CFTR-related isolated congenital bilateral absence of the vas deferens and CFTR-related pancreatitis are not included in this analysis. CFTR variants with insufficient evidence of being cystic fibrosis mutations will not be reported either. **CRYL1:** As mutations in the CRYL1 gene are not known to be associated with any clinical condition, sequence variants in this gene are not analyzed. However, to increase copy number detection sensitivity for large deletions including this gene and a neighboring gene on the panel (GJB6, also known as connexin 30), this gene was evaluated for copy number variation. **CYP11B1:** The current testing method is not able to reliably detect certain pathogenic variants in this gene due to the interference by highly homologous regions. This analysis is not designed to detect or rule-out copy-neutral chimeric CYP11B1/CYP11B2 gene. **CYP11B2:** The current testing method is not able to reliably detect certain pathogenic variants in this gene due to the interference by highly homologous regions. This analysis is not designed to detect or rule-out copy-neutral chimeric CYP11B1/CYP11B2 gene. **CYP21A2:** Significant pseudogene interference and/or reciprocal exchanges between the CYP21A2 gene and its pseudogene, CYP21A1P, have been known to occur and may impact results. As such, the relevance of variants reported in this gene must be interpreted clinically in the context of the clinical findings, biochemical profile, and family history of each patient. LR-PCR is not routinely ordered for NM_000500.9:c.955C>T (p.Gln319Ter). Individuals with c.955C>T (p.Gln319Ter) will be reported as a Possible Carrier indicating that the precise nature of the variant has not been determined by LR-PCR and that the variant may occur in the CYP21A2 wild-type gene or in the CYP21A1P pseudogene. The confirmation test is recommended if the second reproductive partner is tested positive for variants associated with classic CAH. **DDX11:** Due to the interference by highly homologous regions, our current testing method has less sensitivity to detect variants in the DDX11 gene. **DUOX2:** The current testing method is not able to reliably detect variants in exons 6-8 of the DUOX2 gene (NM_014080.5) due to significant interference by the highly homologous gene, DUOX1. **FANCD2:** Due to pseudogene interference, copy-number-variants within exon 14-17 of the FANCD2 gene (NM_033084.4) are not evaluated and detection of single-nucleotide variants and small insertions/deletions in this region is not guaranteed. **GALT:** In general, the D2 "Duarte" allele is not reported if detected, but can be reported upon request. While this allele can cause positive newborn screening results, it is not known to cause clinical symptoms in any state. See GeneReviews for more information: <https://www.ncbi.nlm.nih.gov/books/NBK1518/> **GBA:** Significant pseudogene interference and/or reciprocal exchanges between the GBA gene and its pseudogene, GBAP1, have been known to occur and may impact results. As such, the relevance of variants reported in this gene must be interpreted clinically in the context of this individual's clinical findings, biochemical profile, and family history. The current testing method cannot detect copy-neutral rearrangements between the pseudogene and the functional gene, which have been reported in very rare cases of Gaucher disease (PubMed: 21704274). **HBA1:** Significant interference



from highly homologous regions in exons 1-2 of the HBA1 gene has been recognized to occur, potentially impeding the assay's technical capability to detect pathogenic alterations during sequencing analyses. HBA2: Significant interference from highly homologous regions in exons 1-2 of the HBA2 gene has been recognized to occur, potentially impeding the assay's technical capability to detect pathogenic alterations during sequencing analyses. HSD17B4: Copy number analysis for exons 4-6 may have reduced sensitivity in the HSD17B4 gene. Confirmation of these exons are limited to individuals with a positive personal history of D-bifunctional protein deficiency and Perrault syndrome and/or individuals carrying a pathogenic/likely pathogenic sequence variant. LMBRD1: Copy number analysis for exons 9-12 may have reduced sensitivity in the LMBRD1 gene. Confirmation of these exons are limited to individuals with a positive personal history of combined methylmalonic aciduria and homocystinuria and/or individuals carrying a pathogenic/likely pathogenic sequence variant. MTHFR: As recommended by ACMG, the two common polymorphisms in the MTHFR gene - c.1286A>C (p.Glu429Ala, also known as c.1298A>C) and c.665C>T (p.Ala222Val, also known as c.677C>T) - are not reported in this test due to lack of sufficient clinical utility to merit testing (PubMed: [23288205](#)). NEB: This gene contains a 32-kb triplicate region (exons 82-105) which is not amenable to sequencing and deletion/duplication analysis. NPHS2: If detected, the variant NM_014625.3:c.686G>A (p.Arg229Gln) will not be reported as this variant is not significantly associated with disease when homozygous or in the compound heterozygous state with variants in exons 1-6 of NPHS2. OTOA: Due to pseudogene interference, our current testing method is not able to reliably detect variants in exons 20-28 (NM_144672.3) in the OTOA gene. SMN1: The current testing method detects sequencing variants in exon 7 and copy number variations in exons 7-8 of the SMN1 gene (NM_022874.2). Sequencing and deletion/duplication analysis are not performed on any other region in this gene. About 5%-8% of the population have two copies of SMN1 on a single chromosome and a deletion on the other chromosome, known as a [2+0] configuration (PubMed: [20301526](#)). The current testing method cannot directly detect carriers with a [2+0] SMN1 configuration but can detect linkage between the silent carrier allele and certain population-specific single nucleotide changes. As a result, a negative result for carrier testing greatly reduces but does not eliminate the chance that a person is a carrier. Only abnormal results will be reported. TERT: The TERT promoter region is analyzed for both sequencing and copy number variants. TYR: Due to the interference by highly homologous regions, our current testing method has less sensitivity to detect variants in exons 4-5 of the TYR gene (NM_000372.5). VPS45: LoF is not a known disease mechanism. WRN: Due to the interference by highly homologous regions within the WRN gene, our current testing method has less sensitivity to detect variants in exons 10-11 of WRN (NM_000553.6).

SIGNATURE:



Zhenbin Chen, Ph.D., CGMB, FACMG on 12/7/2024
Laboratory Director, Fulgent

DISCLAIMER:

This test was developed and its performance characteristics determined by Fulgent Therapeutics LLC CAP #8042697 CLIA #05D2043189; 4399 Santa Anita Ave., El Monte, CA, 91731. It has not been cleared or approved by the FDA. The laboratory is regulated under CLIA as qualified to perform high-complexity testing. This test is used for clinical purposes. It should not be regarded as investigational or for research. Since genetic variation, as well as systematic and technical factors, can affect the accuracy of testing, the results of testing should always be interpreted in the context of clinical and familial data. For assistance with interpretation of these results, healthcare professionals may contact us directly at [626-350-0537](tel:626-350-0537) or by email at info@fulgentgenetics.com. It is recommended that patients receive appropriate genetic counseling to explain the implications of the test result, including its residual risks, uncertainties and reproductive or medical options.

To view the supplemental table describing the carrier frequencies, detection rates, and residual risks associated with the genes tested on any Beacon panel, please visit the following link:

[Beacon Expanded Carrier Screening Supplemental Table](#)



Report Status FINAL
Route 2017 Ordered by:
Phoenix Sperm Bank
1492 S Mill Ave
Suite 306
Tempe, AZ 85281

James Kuan, MD

Patient Information:

10958, DONOR

Account: 18131
ID/MR#: 10958
Patient Lab ID: 673f659068493062c7e9f457

Collected: 11/20/2024 10:46 AM
Received: 11/21/2024 09:18 AM
Reported: 11/29/2024 04:08 PM

Order #: 181
DOB:
Sex: M
Patient Phone: 602-888-7255

9 / NL
Age:
64

PL

GENETICS

Accession #:
CG240012463
Cell Type/Source:
Blood

Clinician Provided Information:
DONOR TESTING

Chromosome Analysis: Routine Blood

Analysis Details:

Metaphases/Cells Counted : 20
Metaphases/Cells Analyzed : 5
Metaphases Karyotyped : 3

PV

Results:

NORMAL MALE KARYOTYPE

PV

46,XY

PV

Interpretation:

Normal

PV

Normal karyotype at the band level 550 or above as determined by the trypsin-Giemsa method. There was no evidence for a chromosome abnormality within the limits of the band level and technology utilized in this study.

PHA-stimulated lymphocyte chromosome analysis is an accurate technique to detect many constitutional chromosome abnormalities. More extensive investigation may be required to detect mosaicism or subtle structural rearrangement. It also should be noted that this type of testing does not rule out the possibility of mendelian, mitochondrial, multifactorial or environmental etiologies.

Cytogenetics Director:

PV



Electronically signed by Guang Liu MD, ABMGG, FACMG, Genetics/Genomics
Director
Verified 11/29/24

Tests Ordered: Chromosome Analysis: Routine Blood

Unless otherwise noted, testing performed by: Sonora Quest Laboratories, 424 S 56th St, Phoenix, AZ 85034 800.766.6721
Testing noted as PV performed by: Genetics/Genomics Div., Sonora Quest Laboratories, 424 S. 56th St, Phoenix, AZ 85034 602.685.5700

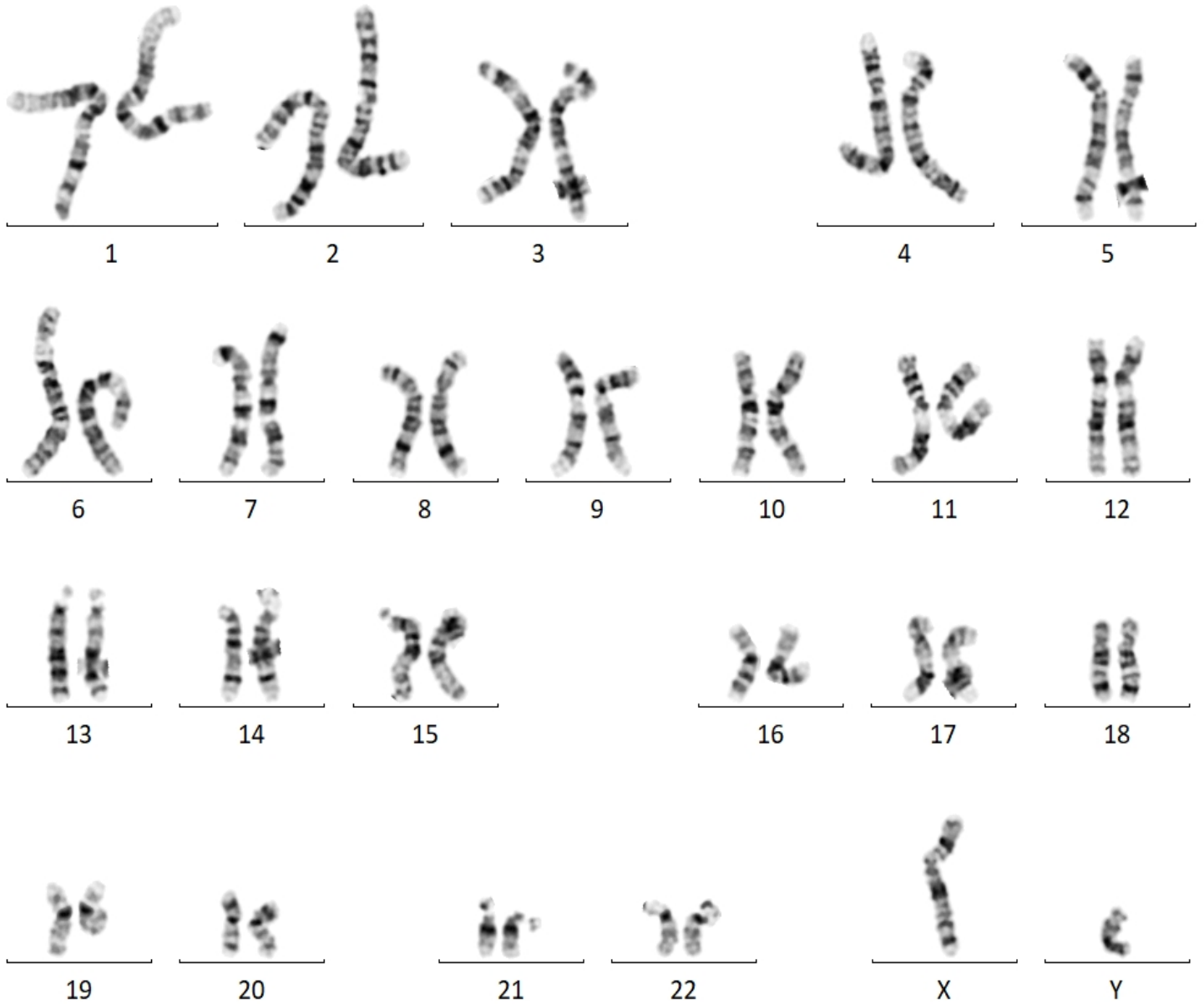
End of Report

10958, DONOR Order #: 181310000159 / NL107054964 - FINAL Report

L=Low, H=High, C=Critical Abnormal, CL=Critical Low, CH=Critical High, *=Comment

Distribution #: 759291118-41674661





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Result Report

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