Fairfax Cryobank
The Trusted Choice for Donor Sperm

# Donor 5037

# Genetic Testing Summary

Fairfax Cryobank recommends reviewing this genetic testing summary with your healthcare provider to determine suitability.

Last Updated 09/08/23

Donor Reported Ancestry: Irish, English, German, Italian, French  Jewish Ancestry: No

| Genetic Test* | Result | Comments/Donor's Residual Risk** |
|---|---|---|
| Chromosome analysis (karyotype) | Normal male karyotype | No evidence of clinically significant chromosome abnormalities |
| Hemoglobin evaluation | Normal hemoglobin fractionation and MCV/MCH results | Reduced risk to be a carrier for sickle cell anemia, beta thalassemia, alpha thalassemia trait (aa/-- and a-/a-) and other hemoglobinopathies |
| Cystic Fibrosis (CF) carrier screening | Negative by genotyping of 130 mutations in the CFTR gene | 1/476 |
| Spinal Muscular Atrophy (SMA) carrier screening | Negative for deletions of exon 7 in the SMN1 gene | 1/632 |
| Tay Sachs enzyme analysis | Non-carrier by Hexosaminidase A activity | |
| Standard testing attached-<br>22 diseases by genotyping | Negative for mutations tested | |
| Special Testing | | |
| Primary Hyperoxaluria Type 1 (AGXT) | Carrier: Primary Hyperoxaluria Type 1 (AGXT) | Partner testing is recommended before using this donor. |
| Gene: ALDOB, TMC1 | Negative by gene sequencing | |

*No single test can screen for all genetic disorders. A negative screening result significantly reduces, but cannot eliminate, the risk for these conditions in a pregnancy.**Donor residual risk is the chance the donor is still a carrier after testing negative.

Recombine

CarrierMap™

**Ordering Practice:**

**Practice Code:** [redacted]
Fairfax Cryobank
[redacted]
**Physician:** [redacted]
**Report Generated:** 2015-10-26

**Donor # 5037**

**DOB:** [redacted]
**Gender:** Male
**Ethnicity:** European
**Procedure ID:** 33245
**Kit Barcode:** [redacted]
**Method:** Genotyping
**Specimen:** Blood, #34795
**Specimen Collection:** 2015-10-17
**Specimen Received:** 2015-10-20
**Specimen Analyzed:** 2015-10-26

**Partner Not Tested**

## SUMMARY OF RESULTS

**NO MUTATIONS IDENTIFIED**

Donor # 5037 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: 383, Genes Tested: 22, Null Calls: 0

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

Reviewed by Pere Colls, PhD, HCLD, Lab Director

## Methods and Limitations

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

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

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

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

## Diseases & Mutations Assayed

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

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

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

| H | T | X | M | Disease | # | Mutations |
|---|---|---|---|---|---|---|
| ● | ● | ○ | ○ | Maple Syrup Urine Disease: Type 3 | 8 | ♂ Genotyping \| c.104_105insA, c.G685T (p.G229C), c.A214G (p.K72E), c.A1081G (p.M361V), c.G1123A (p.E375K), c.T1178C (p.I393T), c.C1463T (p.P488L), c.A1483G (p.R495G) |
| ● | ○ | ○ | ○ | Mucolipidosis: Type IV | 4 | ♂ Genotyping \| c.406-2A>G, c.G1084T (p.D362Y), c.C304T (p.R102X), c.244delC (p.L82fsX) |
| ● | ○ | ○ | ○ | Nemaline Myopathy: NEB Related | 1 | ♂ Genotyping \| c.7434_7536del2502bp |
| ● | ○ | ○ | ○ | Niemann-Pick Disease: Type A | 6 | ♂ Genotyping \| c.996delC, c.G1493T (p.R498L), c.T911C (p.L304P), c.C1267T (p.H423Y), c.G1734C (p.K578N), c.1493G>A (p.R498H) |
| ● | ● | ○ | ○ | 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 | 30 | ♂ Genotyping \| c.1073+1G>A, c.1277_1278insTATC, c.1421+1G>C, c.805+1G>A, c.C532T (p.R178C), c.G533A (p.R178H), c.G805A (p.G269S), c.C1510T (p.R504C), c.G1496A (p.R499H), c.G509A (p.R170Q), c.A1003T (p.I335F), c.910_912delTTC (p.305delF), c.G749A (p.G250D), c.T632C (p.F211S), c.C629T (p.S210F), c.613delC, c.A611G (p.H204R), c.G598A (p.V200M), c.A590C (p.K197T), c.571-1G>T, c.C540G (p.Y180X), c.T538C (p.Y180H), c.G533T (p.R178L), c.C508T (p.R170W), c.C409T (p.R137X), c.T380G (p.L127R), c.346+1G>C, c.T116G (p.L39R), c.G78A (p.W26X), c.A1G (p.M1V) |
| ● | ○ | ○ | ○ | Usher Syndrome: Type 1F | 6 | ♂ Genotyping \| c.C733T (p.R245X), c.2067C>A (p.Y684X), c.C7T (p.R3X), c.C1942T (p.R648X), c.2800C>T (p.R934X), c.4272delA (p.L1425fs) |
| ● | ○ | ○ | ○ | Usher Syndrome: Type 3 | 4 | ♂ Genotyping \| c.T144G (p.N48K), c.T359A (p.M120K), c.300T>G (p.Y176X), c.C634T (p.Q212X) |
| ● | ○ | ○ | ○ | Walker-Warburg Syndrome | 1 | ♂ Genotyping \| c.1167insA (p.F390fs) |

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fulgent

[redacted]

Patient Information:
**5037, Donor**
**DOB:** [redacted]
Sex: M
MR#: 5037
Patient#: [redacted]

Partner Information:
**Not Tested**

Physician:
**Seitz, Suzanne**
ATTN: Seitz, Suzanne
Fairfax Cryobank
3015 Williams Drive
Fairfax, VA 22031

Laboratory:
**Fulgent Genetics**
CAP#: 8042697
CLIA#: 05D2043189
Laboratory Director:
Dr. Hanlin (Harry) Gao
Report Date: **Jul 18,2023**

Accession:
[redacted]
Test#: [redacted]
Specimen Type: DNA
Collected: Jun 23,2023

Accession:
**N/A**

## FINAL RESULTS

Carrier for **ONE** genetic condition
Genetic counseling is recommended.

## TEST PERFORMED

**Custom Beacon Carrier Screening Panel**
(2 Gene Panel: *AGXT and ALDOB*; gene sequencing with deletion and duplication analysis)

| Condition and Gene | Inheritance | 5037, Donor | Partner |
|---|---|---|---|
| **Primary hyperoxaluria type 1**<br>*AGXT* | AR | ⊕ Carrier<br>c.33dup (p.Lys12Glnfs*156) | N/A |

## INTERPRETATION:

**Notes and Recommendations:**

- Based on these results, this individual is positive for a carrier mutation in 1 gene. The risk estimates below are quantified based on general population carrier frequencies. Carrier screening for the reproductive partner is recommended to accurately assess the risk for any autosomal recessive conditions:
  - There is a 1/480 chance of having a child affected with Primary hyperoxaluria type 1, a *AGXT*-related condition.
- This carrier screening test does not screen for all possible genetic conditions, nor for all possible mutations in every gene tested. Individuals with negative test results may still have up to a 3-4% risk to have a child with a birth defect due to genetic and/or environmental factors.
- 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 present. See below.
- This report does not include variants of uncertain significance.
- 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)

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[redacted]

# PRIMARY HYPEROXALURIA TYPE 1

| Patient | 5037, Donor | Partner |
|---|---|---|
| **Result** | ⊕ Carrier | N/A |
| **Variant Details** | ***AGXT*** (NM_000030.3)<br>c.33dup (p.Lys12Glnfs*156) | N/A |

## *What is Primary hyperoxaluria type 1?*

Primary hyperoxaluria type 1 is caused by a deficiency of a liver enzyme named alanine glyoxylate aminotransferase (AGT), which leads to chronic and recurrent kidney and bladder stones. The condition often results in end-stage renal disease. Kidney stones typically begin to appear anytime from childhood to early adulthood. End-stage renal disease can develop at any age.

## *What is my risk of having an affected child?*

Primary hyperoxaluria type 1 is inherited in an autosomal recessive manner. The risk for being a carrier for AGXT-related primary hyperoxaluria type 1 is very low (carrier frequency less than 1/500). 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?*

The prognosis for a person with primary hyperoxaluria type 1 is variable and depends on how early the disease is detected and treated. High doses of vitamin B6 helps to reduce oxalate levels in some people. However, many people develop end stage renal disease and require a kidney transplant.

## *What mutation was detected?*

The detected heterozygous variant was NM_000030.3:c.33dup (p.Lys12Glnfs*156). This frameshift variant introduces a premature stop codon upstream of the last 50 base pairs of the canonical donor splice site of the penultimate exon consistent with a resultant transcript being targeted by nonsense-mediated decay (PubMed: 27618451, 11532962, 18066079) and thus predicted to result in loss of function of AGXT gene. There's sufficient evidence that loss of function in this gene is a known disease mechanism for hyperoxaluria (PubMed: 11708860, 27915025, 32102150). This variant has been reported in both homozygous and compound heterozygous states in multiple patients with primary hyperoxaluria type 1 (PH1) (PubMed: 15327387, 19479957, 28619084, 27135212, 20549407). Functional analysis has demonstrated that this variant leads to absent protein expression and thus absent normal protein activity (PubMed: 30341509).This variant is classified as "Pathogenic" or "Likely Pathogenic" in ClinVar, with multiple submitters in agreement (Variation ID: 140583). The laboratory classifies this variant as pathogenic.

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[redacted]

## GENES TESTED:

**Custom Beacon Carrier Screening Panel - 2 Genes**

This analysis was run using the Custom Beacon Carrier Screening Panel gene list. 2 genes were tested with 100.0% of targets sequenced at >20x coverage. For more gene specific information and assistance with residual risk calculation, see the SUPPLEMENTAL TABLE.

*AGXT, ALDOB*

## 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, 100.00% and 100.00% 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.

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[redacted]

**Gene Specific Notes and Limitations**

No gene specific limitations apply to the genes on the tested panel.

## SIGNATURE:

**Dr. Harry Gao, DABMG, FACMG** on **7/18/2023 10:16 PM PDT**
Electronically signed

## DISCLAIMER:

This test was developed and its performance characteristics determined by **Fulgent Genetics**. 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** or **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.

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Supplemental Table

| Gene | Condition | Inheritance | Ethnicity | Carrier Rate | Detection Rate | Post-test Carrier Probability* | Residual Risk* |
|---|---|---|---|---|---|---|---|
| *AGXT* | Primary hyperoxaluria type 1 | AR | General Population | 1 in 120 | 99% | 1 in 11,901 | 1 in 5,712,480 |
| | | | Caucasian / European Population | 1 in 173 | 99% | 1 in 17,201 | <1 in 10 million |
| *ALDOB* | Hereditary fructose intolerance | AR | General Population | 1 in 122 | 99% | 1 in 12,101 | 1 in 5,905,288 |
| | | | African/African American Population | 1 in 250 | 99% | 1 in 24,901 | <1 in 10 million |
| | | | Caucasian / European Population | 1 in 67 | 99% | 1 in 6,601 | 1 in 1,769,068 |
| | | | Middle-Eastern Population | 1 in 97 | 99% | 1 in 9,601 | 1 in 3,725,188 |

* For genes that have tested negative
Abbreviations: AR, autosomal recessive; XL, X-linked

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[redacted]

Patient Information:
**5037, Donor**
**DOB:** [redacted]
Sex: M
MR#: 5037
Patient#: [redacted]

Accession:
[redacted]
Test#: [redacted]
Order#: [redacted]
Ext Test#: [redacted]
Ext Order#: [redacted]
Specimen Type: DNA
Collected: Jun 23,2023
Received Date: Jul 05,2023
Authorized Date: Sep 01,2023

Physician:
**Seitz, Suzanne**
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3015 Williams Drive
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Phone:
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Laboratory:
**Fulgent Genetics**
CAP#: 8042697
CLIA#: 05D2043189
Laboratory Director:
Dr. Hanlin (Harry) Gao
Report Date: **Sep 07,2023**

Final Report

## TEST PERFORMED

**TMC1 Single Gene**
(1 Gene Panel: *TMC1*; gene sequencing with deletion and duplication analysis)

## RESULTS:

**No clinically significant sequence or copy-number variants were identified in the submitted specimen.**

**A negative result does not rule out the possibility of a genetic predisposition nor does it rule out any pathogenic mutations of the sort not queried by this test or in areas not reliably assessed by this test.**

## INTERPRETATION:

**Notes and Recommendations:**

- As requested, this report only includes variants classified as Pathogenic, Likely Pathogenic, or Risk Allele at the time of analysis. If detected, this report does not include variants classified as of uncertain significance.
- Gene specific notes and limitations may be present. See below.
- These results should be interpreted in the context of this individual's clinical findings, biochemical profile, and family history.
- 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)
- Guide to Interpreting Genomic Reports: A Genomics Toolkit (CSER Consortium; February 2017) (https://www.genome.gov/For-Health-Professionals/Provider-Genomics-Education-Resources#hep)

## GENES TESTED:

**TMC1 Single Gene**
1 genes tested (100.00% at >20x).

*TMC1*

**Gene Specific Notes and Limitations**

No gene specific limitations apply to the genes on the tested panel.

## METHODS:

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## LIMITATIONS:

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## SIGNATURE:

**Yan Meng, Ph.D., CGMB, FACMG** on **9/7/2023 07:18 PM PDT**
Electronically signed

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