fulgent

PATIENT

Patient First, Patient Last
DOB: Jan 01, 2000
Gender: Female
MRN#: 12345
Gestational Age: 11w2d
Pregnancy Type: Singleton
Ovum Donor Age: N/A

ACCESSION

Accession ID: FT-9997979
Specimen Type: Blood
Date Ordered: Dec 9, 2021
Date Collected: Dec 13, 2021
Date Received: Dec 16, 2021

PHYSICIAN

Provider Name
Clinic Name
Address
City, State, Zip
Phone: 555-555-5555
Fax: 555-555-5555
Report Date: 01/01/2020

KNOVA Prenatal Screen - Full Panel

About the Test

The Fulgent KNOVA Prenatal Cell-Free DNA Screen is a non-invasive prenatal screening test (NIPT/NIPS)that detects whether a pregnancy is at increased risk for aneuploidies, microdeletions, and/or monogenic conditions. See report for full target list. This is not a diagnostic test.

Results Summary

Result	Fetal Sex	Fetal Fraction
High Risk	**Male**	**8.3%**

Result Details: Aneuploidy

Chromosome/Condition	Result
Trisomy 21 (Down Syndrome)	High Risk. Results consistent with trisomy of chromosome 21.

Result Details: Monogenic Condition

Condition	Inheritance	Gene / Variant	Pathogenicity	Result
Cleidocranial dysplasia or other RUNX2 associated conditions	Autosomal dominant	RUNX2 (NM_001024630.4): c.577C>T, p.Arg193Ter	Pathogenic	High Risk
Macrocephaly or other GENE2 associated conditions	Autosomal dominant	GENE2 (NM_001024630.4): c.577C>T, p.Arg193Ter	Pathogenic	High Risk

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Notes & Recommendations

- It is our understanding that the patient has no relevant clinical or family history related to conditions screened by this test.
- Genetic counseling is recommended.
- [Fetal Sex: Result is based on the absence of the Y Chromosome]
- [Copy generic for positive test]
- [Copy specific to specific abnormality]
- [Generic copy: See testing methodology and appendix for details]
- [Generic copy: See appendix X for PPV/NPV...]

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KNOVA Prenatal Screen

- Aneuploidies: trisomy 13, trisomy 15, trisomy 16, trisomy 18, trisomy 21, triosomy 22, 45X, 47XXX, 47XXY, 47XYY
- Microdeletions: 1p36 del, 2q33 del, 4p16 del, 5p15 del, 8q23q24 del, 9p del, 11q23q25 del, 15q11.2-q13 del, 17p11.2 del, 18p del, 18q22q23 del, 22q11.2 del
- Monogenic conditions associated with the following genes: *SXL1, BRAF, CBL, CD96, CDKL5, CHD7, COL10A1, COL11A1, COL1A1, COL1A2, COL2A1, EBP, EFNB1, ERF, FGFR1, FGFR2, FGFR3, FLNB, FREM1, GLI3, HDAC8, HNRNPK, HRAS, KAT6B, KMT2D, KRAS, LMNA, MAP2K1, MAP2K2, MECP2, NIPBL, NRAS, NSD1, NSDHL, PTPN11, RAD21, RAF1, RIT1, RUNX2, SHOC2, SKI, SLC25A24, SMC1A, SMC3, SNRPB, SOS1, SOS2, SOX9, SPECC1L, STAT3, TCF12, TRAF7, TSC1, TSC2, TWIST1, ZIC1*. (Coverage: 98.1% @ 20x)

Methods & Limitations

Methodology

Fulgent employs a proprietary technique for the comprehensive prenatal analysis of cell-free DNA (cfDNA). This method involves extracting cfDNA from maternal plasma, followed by target enrichment, and next-generation sequencing (NGS). Bioinformatic analyses employ multivariate techniques to quantitatively evaluate the sequencing read depth and the distribution patterns of maternal and fetal cfDNA fragments of distinct characteristics.. These processes are designed to facilitate targeted detection of specific genomic regions within the fetal genome, aiding in the identification of select chromosomal aneuploidies, microdeletions, and SNVs. Refer to the target list for more details.

Screening for Aneuploidies

The screening is designed to report on whole chromosome abnormalities for [list of targets] specifically at predetermined chromosomal locations and it may not detect all partial chromosomal aberrations in those chromosomes. The test does not detect certain abnormalities including, but not limited to, uniparental disomy, triploidy, tetraploidy, translocations, inversions, and rings.

Screening for Microdeletions

The screening is intended to identify targeted microdeletions covering the entirety of the specified region. Any duplications or partial deletions within these regions may not be detected or reported.

Screening for Monogenic Conditions

This test detects single nucleotide variants in the coding exons and 10 bp into the intronic regions flanking the exon/intron junctions of the targeted genes in the Appendix (the RefGene transcripts used in the Human Gene Mutation Database). This test does not detect variants outside target regions. In addition, this test does not detect large deletions, insertions, indels, dynamic variants, structural variants, whole gene/exonic/sub-exonic copy number variations (e.g., those in NF1, TSC1, TSC2 etc.), and other complex variants. This test does not fully cover target regions which are confounded by highly repetitive sequences, highly GC-rich regions, homologous sequences, and pseudogenes. This test only reports pathogenic or likely pathogenic variants classified by the American College of Medical genetics and Genomics standards and guidelines for the interpretation of sequence variants associated with possibly serious consequences (lethal or severely disabling conditions with infantile or child-hood onset). Variants exhibiting reduced penetrance, significant variability in expressivity, and those primarily associated with adult-onset conditions may not be reported. Variants of uncertain significance, likely benign and benign variants are not reported.

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Limitations

This screening test is intended for evaluation of fetal risks of certain genetic conditions. This screening test may yield false negative and false positive results. Consequently, any irreversible clinical and pregnancy management decisions should be based on the results of definitive diagnostic tests and/or comprehensive clinical assessments, rather than being solely dependent on this screening test.

The conditions screened by this test are limited to those resulting from certain aberrations in specific chromosomal regions and genes ("target regions"). A negative result does not eliminate the risk of genetic conditions caused by alterations within, partially, or completely beyond the targeted regions of this test. This test does not assess the risk for conditions beyond those targeted conditions, even if there are abnormalities, such as duplications, within the targeted regions.

This test may produce false results caused by various factors including, but not limited to, maternal genetic background, maternal mosaicism, confined placental mosaicism, fetal mosaicism, maternal malignancy, maternal medical procedures, multiple gestations, fetal demise, fetal reduction, low fetal fraction, gestational age, and the physical condition of the pregnant individual.

The interpretation of the test results is based on the information provided to the laboratory. Please contact Fulgent for clarification and potential amendment if the patient or the patient's clinical providers find any discrepancy regarding the information on the report within 7 days of receiving this report. The interpretation of the results on this report are based on the information available to the laboratory at the time when this report is issued. After the report is issued, updates to relevant scientific literature and databases may affect the interpretation of the test results.

The predicted fetal sex in singleton pregnancies via this test is determined by detecting a specific threshold of Y chromosome genetic material. Nonetheless, the fetal sex identified by prenatal ultrasound or postnatal examination may diverge from this prediction, as it is influenced by factors extending beyond the mere presence or absence of Y chromosome material. This test will only report the presence or absence of Y chromosome for twin pregnancies and no fetal sex will be predicted for twins.

Disclaimer

This test was developed, and its performance characteristics was determined by Fulgent, a laboratory certified under the Clinical Laboratory Improvement Amendments (CLIA). This test has not been cleared or approved by the U.S. Food and Drug Administration. 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.

Example Signature

Example Director, Ph.D., CGMBS, FACMG on 11/17/2023 06:46 PM PST
Electronically signed

PATIENT RESOURCE

Trisomy 21 (Down Syndrome)

What is Down Syndrome?

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How common is Down Syndrome?

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How is trisomy 21 (Down Syndrome) treated?

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PATIENT RESOURCE

RUNX2 Associated Conditions

Gene Description

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What conditions are associated with pathogenic variants in RUNX2?

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How are these conditions treated?

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Variant Details

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PATIENT RESOURCE

GENE2 Associated Conditions

Gene Description

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What conditions are associated with pathogenic variants in GENE2?

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How are these conditions treated?

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Variant Details

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APPENDIX

Target Conditions Screened + Analytical Performance for NOVA

Test Specifications

Pre-test risk is the estimated probability of a genetic condition in the fetus, determined prior to testing and grounded on the estimated population prevalence, excluding patient-specific factors such as the patient's age, clinical and family history.

Post-test risk is the estimated probability of a genetic condition in the fetus after the test, calculated using the test's sensitivity/specificity, the test result, and pre-test risk, excluding patient-specific factors such as the patient's age, clinical and family history.

Sensitivity is the ability to correctly identify a truly high risk case as high risk. For example, in a group of Trisomy 21 cases, NOVA will correctly identify more than 99% of those cases.

Specificity is the ability to correctly identify an unaffected case as low risk.

Positive Predictive Value is the likelihood the result says high risk and the fetus is actually affected.

Negative Predictive Value is the likelihood the result says low risk and the fetus is truly not affected.

Condition or Gene Screened	Pre-test Risk	Post-test Risk	Sensitivity (95% CI)	Specificity (95% CI)	Positive Predictive Value (95% CI)	Negative Predictive Value (95% CI)
Trisomy 21	1:800	1:36,000	97.8% (91.5%-99.6%)	99.4% (98.6%-99.8%)	93.7% (86.2%-97.4%)	99.8% (99.2%-100%)
Trisomy 18	1:5,000	1:220,000	97.8% (91.5%-99.6%)	99.4% (98.6%-99.8%)	93.7% (86.2%-97.4%)	99.8% (99.2%-100%)
Trisomy 13	1:25,000	1:1,100,000	97.8% (91.5%-99.6%)	99.4% (98.6%-99.8%)	93.7% (86.2%-97.4%)	99.8% (99.2%-100%)
Trisomy 15	<1:1,000,000	1:45,000,000	97.8% (91.5%-99.6%)	99.4% (98.6%-99.8%)	93.7% (86.2%-97.4%)	99.8% (99.2%-100%)
Trisomy 16	N/A	N/A	97.8% (91.5%-99.6%)	99.4% (98.6%-99.8%)	93.7% (86.2%-97.4%)	99.8% (99.2%-100%)
Trisomy 22	N/A	N/A	97.8% (91.5%-99.6%)	99.4% (98.6%-99.8%)	93.7% (86.2%-97.4%)	99.8% (99.2%-100%)
45X	1:2,000	1:90,000	97.8% (91.5%-99.6%)	99.4% (98.6%-99.8%)	93.7% (86.2%-97.4%)	99.8% (99.2%-100%)
47XXX	1:1,000	1:45,000	97.8% (91.5%-99.6%)	99.4% (98.6%-99.8%)	93.7% (86.2%-97.4%)	99.8% (99.2%-100%)
47XXY	1:800	1:36,000	97.8% (91.5%-99.6%)	99.4% (98.6%-99.8%)	93.7% (86.2%-97.4%)	99.8% (99.2%-100%)
47XYY	1:1,000	1:45,000	97.8% (91.5%-99.6%)	99.4% (98.6%-99.8%)	93.7% (86.2%-97.4%)	99.8% (99.2%-100%)
DiGeorge syndrome	1:4,000	<1:4,000,000	>99.9% (62.9%-100%)	>99.9% (99.6%-100%)	>99.9% (62.9%-100%)	>99.9%(99.6%-100%)
1p36 Deletion Syndrome	1:5,000	<1:5,000,000	>99.9% (62.9%-100%)	>99.9% (99.6%-100%)	>99.9% (62.9%-100%)	>99.9%(99.6%-100%)
2q33.1 deletion syndrome	N/A	N/A	>99.9% (62.9%-100%)	>99.9% (99.6%-100%)	>99.9% (62.9%-100%)	>99.9%(99.6%-100%)
Wolf-Hirschhorn Syndrome	1:35,000	<1:35,000,000	>99.9% (62.9%-100%)	>99.9% (99.6%-100%)	>99.9% (62.9%-100%)	>99.9%(99.6%-100%)
Cri du Chat Syndrome	1:30,000	<1:30,000,000	>99.9% (62.9%-100%)	>99.9% (99.6%-100%)	>99.9% (62.9%-100%)	>99.9%(99.6%-100%)
Langer-Giedion Syndrome	<1:1,000,000	<1:1,000,000,000	>99.9% (62.9%-100%)	>99.9% (99.6%-100%)	>99.9% (62.9%-100%)	>99.9%(99.6%-100%)
9p Deletion Syndrome	<1:1,000,000	<1:1,000,000,000	>99.9% (62.9%-100%)	>99.9% (99.6%-100%)	>99.9% (62.9%-100%)	>99.9%(99.6%-100%)
Jacobsen Syndrome	1:75,000	<1:75,000,000	>99.9% (62.9%-100%)	>99.9% (99.6%-100%)	>99.9% (62.9%-100%)	>99.9%(99.6%-100%)

Note: The NPVs and PPVs in this table reflect estimated risks for given low-risk or high-risk results, derived from general population disease prevalence and test performance data available at the time of this test's development. These calculations do not incorporate the patient's individual factors such as age, clinical history, and family history, which may significantly alter the actual risk levels in the fetus. This table is subject to periodic updates as new information on disease prevalence and test performance becomes available in the future.

Condition or Gene Screened	Pre-test Risk	Post-test Risk	Sensitivity (95% CI)	Specificity (95% CI)	Positive Predictive Value (95% CI)	Negative Predictive Value (95% CI)
Angelman Syndrome	1:15,000	<1:15,000,000	>99.9% (62.9%-100%)	>99.9% (99.6%-100%)	>99.9% (62.9%-100%)	>99.9%(99.6%-100%)
Prader-Willi Syndrome	1:22,500	<1:22,500,000	>99.9% (62.9%-100%)	>99.9% (99.6%-100%)	>99.9% (62.9%-100%)	>99.9%(99.6%-100%)
Smith-Magenis Syndrome	1:15,000	<1:15,000,000	>99.9% (62.9%-100%)	>99.9% (99.6%-100%)	>99.9% (62.9%-100%)	>99.9%(99.6%-100%)
18p Deletion Syndrome	N/A	N/A	>99.9% (62.9%-100%)	>99.9% (99.6%-100%)	>99.9% (62.9%-100%)	>99.9%(99.6%-100%)
18q22q23 Deletion Syndrome	N/A	N/A	>99.9% (62.9%-100%)	>99.9% (99.6%-100%)	>99.9% (62.9%-100%)	>99.9%(99.6%-100%)
BRAF	4-10:10,000	<1:2,700,000	>98.2% (87.6%-99.2%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
CBL		<1:1,200,000	92% (82.1%-92.9%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
HRAS		<1;10,000,000	>99% (88.3%-100%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
KRAS		<1:1,800,000	>98.9% (88.2%-99.9%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
MAP2K1		<1:5,000,000	>99% (88.3%-100%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
MAP2K2		<1:6,600,000	>98.5% (87.9%-99.5%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
NRAS		<1:10,000,000	>99% (88.3%-100%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
PTPN11		<1:130,000	>98.5% (87.9%-99.5%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
RAF1		<1:2,000,000	>99% (88.3%-100%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
RIT1		<1:2,000,000	>99% (88.3%-100%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
SHOC2		<1:3,000,000	67% (59.8%-67.7%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
SOS1		<1:690,000	>98.9% (88.2%-99.9%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
SOS2		<1:1,900,000	>98.7% (88%-99.7%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
NIPBL	1-10:100,000	1:380,000	96.7% (86.2%-97.7%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
SMC1A		<1:20,000,000	>99% (88.3%-100%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
SMC3		1:16,000,000	>96.9% (86.4%-97.9%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
RAD21		1:11,000,000	91% (81.2%-91.9%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
HDAC8		1:2,500,000	90% (80.3%-90.9%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
COL1A1	5-7:100,000	1:400,000	95% (84.7%-96%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
COL1A2		1:900,000	94.8% (84.6%-95.8%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
COL11A1	1:10,000	1:5,000,000	99% (88.3%-100%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
COL2A1		1:1,200,000	99% (88.3%-100%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
CDKL5	1:50,000	1:200,000	79% (70.5%-79.8%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
CHD7	6-12:100,000	1:410,000	98% (87.4%-99%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
FGFR2	1-9:100,000	1:1,100,000	99% (88.3%-100%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
FGFR3	1-2:10,000	1:200,000	98.2% (87.6%-99.2%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
KMT2D	2-3:100,000	1:1,900,000	98.3% (87.7%-99.3%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
MECP2	4-10:100,000	1:95,000	89.5% (79.8%-90.4%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
NSD1	7-8:100,000	1:22,000	43.7% (39%-44.1%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
RUNX2	1-2:100,000	1:200,000	75.5% (67.3%-76.3%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)

Condition or Gene Screened	Pre-test Risk	Post-test Risk	Sensitivity (95% CI)	Specificity (95% CI)	Positive Predictive Value (95% CI)	Negative Predictive Value (95% CI)
SOX9	1-3:100,000	1:260,000	87.5% (78%-88.4%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
TSC1	1-2:10,000	1:83,000	94% (83.8%-94.9%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
TSC2	<1:1,000,000	1:8,300,000	94% (83.8%-94.9%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
TWIST1	2-4:100,000	1:50,000	50.3% (44.9%-50.8%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
FREM1	1-5:10,000	1:20,000	90% (80.3%-90.9%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
LMNA	<1:1,000,000	<1:100,000,000	99% (88.3%-100%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
ASXL1	<1:1,000,000	<1:5,000,000	82% (73.1%-82.8%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
CD96	<1-9:1,000,000	<1:11,000,000	>99% (88.3%-100%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
COL10A1	3-6:1,000,000	<1:16,000,000	>99% (88.3%-100%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
EBP	5-10:1,000,000	<1:20,000,000	>99% (88.3%-100%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
FGFR1	<1:1,000,000	<1:100,000,000	>99% (88.3%-100%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
FLNB	1-9:1,000,000	<1:100,000,000	>99% (88.3%-100%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
GLI3	<1:1,000,000	<1:20,000,000	95% (84.7%-96%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
HNRNPK	<1:1,000,000	<1:16,000,000	94% (83.8%-94.9%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
KAT6B	<1:1,000,000	<1:50,000,000	98% (87.4%-99%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
NSDHL	<1:1,000,000	<1:8,000,000	88% (78.5%-88.9%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
SKI	<1:1,000,000	<1:18,000,000	>94.7% (84.5%-95.7%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
SLC25A24	<1:1,000,000	<1:90,000,000	>98.9% (88.2%-99.9%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
SNRPB	<1:1,000,000	<1:5,800,000	83% (74%-83.8%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
SPECC1L	<1:1,000,000	<1:100,000,000	>99% (88.3%-100%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
STAT3	<1:1,000,000	<1:100,000,000	99% (88.3%-100%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
TRAF7	<1:1,000,000	<1:100,000,000	>99% (88.3%-100%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
EFNB1	NA	NA	94% (83.8%-94.9%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
ERF	NA	NA	93.6% (83.5%-94.5%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
TCF12	NA	NA	93% (82.9%-93.9%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)
ZIC1	NA	NA	>99% (88.3%-100%)	>99.9% (99.5%-100%)	>99.9% (88.3%-100%)	>99.9% (99.5%-100%)