

Sequenom Laboratories

3595 John Hopkins Court Sequenom Laboratories CLIA#: 05D2015356 CAP#: 7527138 Lab Director: Phillip Cacheris, MD, PhD

Final Report

MaterniT® 21 PLUS (Core) + ESS Twin Gestation

877.821.7266

| Ordering Provider: | TEST, CCF-DR | Patient: | TEST |
|--------------------|----------------|-----------------------|------------------------|
| Provider Location: | Sequenom - LCA | DOB: | TEST |
| Provider Phone: | | Specimen: | TEST |
| Date Ordered: | 06/16/2013 | Fetal Fraction: | 11% |
| Date Collected: | 06/11/2013 | Gestational Age ≥ 9w: | Yes |
| Date Received: | 06/16/2013 | External Accession: | |
| Order ID: | ORD_TEST | Referral Clinician: | |
| Patient ID: | | Date Reported: | 06/01/2021 05:33 PM PT |

Test Result

Positive

Trisomy 18

Lab Director Comments

This is a reported twin gestation. This specimen showed an increased representation of chromosome 18, suggestive of trisomy 18. In the context of a twin gestation, data from this sample suggests aneuploidy affecting both fetuses, though the possibility of only one affected fetus cannot be ruled out. (Rafalko et al, PLOS ONE 2021) Results should be interpreted in the context of chorionicity and other clinical information. Genetic counseling and confirmatory diagnostic testing are recommended.

Additionally, Y chromosome material was detected. Based on the amount of Y material present, the probability of male/male twins is 91.3% and male/female twins is 8.7%. (Rafalko et al, PLOS ONE 2021) Results should be interpreted in the context of chorionicity and other clinical information.



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Date Reported:

Result Table

Patient ID:

| Content | Result | | | | | |
|---|------------------------|--|--|--|--|--|
| FETAL SEX | Consistent with Male | | | | | |
| AUTOSOMAL ANEUPLOIDIES | | | | | | |
| Trisomy 21 (Down syndrome) | Negative | | | | | |
| Trisomy 18 (Edwards syndrome) | Positive T18 PPV*: 80% | | | | | |
| Trisomy 13 (Patau syndrome) | Negative | | | | | |
| SEX CHROMOSOME ANEUPLOIDIES | | | | | | |
| Monosomy X (Turner syndrome) | Not Validated | | | | | |
| XYY (Jacob's syndrome) | Not Validated | | | | | |
| XXY (Klinefelter syndrome) | Not Validated | | | | | |
| XXX (Triple X syndrome) | Not Validated | | | | | |
| SELECT WHOLE CHROMOSOMES | | | | | | |
| Trisomy 16 | Not Detected | | | | | |
| Trisomy 22 | Not Detected | | | | | |
| SELECT MICRODELETIONS | | | | | | |
| 22q11 deletion (associated with DiGeorge syndrome) | Not Detected | | | | | |
| 15q11 deletion (associated with Prader-Willi / Angelman syndrome) | Not Detected | | | | | |
| 11q23 deletion (associated with Jacobsen syndrome) | Not Detected | | | | | |
| 8q24 deletion (associated with Langer-Giedion syndrome) | Not Detected | | | | | |
| 5p15 deletion (associated with Cri-du-chat syndrome) | Not Detected | | | | | |
| 4p16 deletion (associated with Wolf-Hirschhorn syndrome) | Not Detected | | | | | |
| 1p36 deletion syndrome | Not Detected | | | | | |

Positive Predictive Value

For a more accurate and individualized PPV calculation, include additional clinical information from the patient's clinical history (which may include serum screen results, personal/family history, ultrasound findings, etc.), and refer to the table below.

| A Priori Risk (1:X) | 10 | 20 | 30 | 40 | 50 | 100 | 200 | 300 | 400 | 500 | 1000 | 1500 | 2000 | 2500 | 3000 | 5000 |
|------------------------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| PPV (%) TRISOMY 18 | 96.5 | 92.9 | 89.6 | 86.5 | 83.6 | 71.6 | 55.7 | 45.5 | 38.5 | 33.4 | 20.0 | 14.3 | 11.1 | 9.1 | 7.7 | 4.8 |

Negative Predictive Value

The Negative Predictive Value (NPV) for trisomy 21, 18, and 13 is greater than 99%. The NPV for SCA and ESS cannot be calculated as SCA and ESS are only reported when an abnormality is detected.

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^{*} Positive Predictive Value (PPV) estimates the probability that a pregnancy with a positive test result is in fact an affected pregnancy. The PPV for this patient was calculated only using maternal age and gestational age[1], test performance[2] and the standard PPV formula.



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About the Test

Final Report

The MaterniT® 21 PLUS laboratory-developed test (LDT) analyzes circulating cell-free DNA from a maternal blood sample. The test is indicated for use in pregnant women with increased risk for fetal chromosomal aneuploidy. Validation data on twin pregnancies is limited and the ability of this test to detect aneuploidy in a triplet pregnancy has not yet been validated.

Test Method

Circulating cell-free DNA was purified from the plasma component of maternal blood. The extracted DNA was then converted into a genomic DNA library for aneuploidy analysis of chromosomes 21, 18, and 13 via next generation sequencing. [3] Optional findings based on the test order include sex chromosome aneuploidy (SCA)[2], and enhanced sequencing series (ESS)[4], which will only be reported on as an additional finding when an abnormality is detected. SCA testing includes information on X and Y representation, while ESS testing includes deletions in selected regions (22q, 15q, 11q, 8q, 5p, 4p, 1p) and trisomy of chromosomes 16 and 22.

Performance

The performance characteristics of the MaterniT* 21 PLUS laboratory-developed test (LDT) have been determined in a clinical validation study with pregnant women at increased risk for fetal chromosomal aneuploidy.[2],[3],[4],[5]

| Y-Chromosome (Fetal Sex) | Accuracy: 99.4% | | | | |
|--|-------------------------|-----------------------|--|--|--|
| Region (associated syndrome) | Estimated Sensitivity** | Estimated Specificity | | | |
| Trisomy 21 (Down Syndrome) | 99.1% | 99.9% | | | |
| Trisomy 18 (Edwards Syndrome) | >99.9% | 99.6% | | | |
| Trisomy 13 (Patau Syndrome) | 91.7% | 99.7% | | | |
| Sex Chromosome Aneuploidies (singleton gestation only) | 96.2% | 99.7% | | | |

^{*} As reported in ISCA database nstd37 [http://dbsearch.clinicalgenome.org/search/]

Limitations of the Test

While the results of these tests are highly accurate, discordant results, including inaccurate fetal sex prediction, may occur due to placental, maternal, or fetal mosaicism or neoplasm; vanishing twin; prior maternal organ transplant, or other causes. Sex chromosomal aneuploidies are not reportable for known multiple gestations. These tests are screening tests and not diagnostic; they do not replace the accuracy and precision of prenatal diagnosis with CVS or amniocentesis. A patient with a positive test result should be referred for genetic counseling and offered invasive prenatal diagnosis for confirmation of test results [6] A negative result does not ensure an unaffected pregnancy nor does it exclude the possibility of other chromosomal abnormalities or birth defects which are not a part of these tests. An uninformative result may be reported, the causes of which may include, but are not limited to, insufficient sequencing coverage, noise or artifacts in the region, amplification or sequencing bias, or insufficient fetal fraction. These tests are not intended to identify pregnancies at risk for neural tube defects or ventral wall defects. Testing for whole chromosome abnormalities (including sex chromosomes) and for subchromosomal abnormalities could lead to the potential discovery of both fetal and maternal genomic abnormalities that could have major, minor, or no, clinical significance. Evaluating the significance of a positive or a non-reportable result may involve both invasive testing and additional studies on the mother. Such investigations may lead to a diagnosis of maternal chromosomal or subchromosomal abnormalities, which on occasion may be associated with benign or malignant maternal neoplasms. These tests may not accurately identify fetal triploidy, balanced rearrangements, or the precise location of subchromosomal duplications or deletions; these may be detected by prenatal diagnosis with CVS or amniocentesis. The ability to report results may be impacted by maternal BMI, maternal leysift, mat

Note

This test was developed and its performance characteristics determined by LabCorp. It has not been cleared or approved by the Food and Drug Administration. This laboratory is certified under the Clinical Laboratory Improvement Amendments (CLIA) as qualified to perform high complexity clinical laboratory testing and accredited by the College of American Pathologists (CAP).

References

- 1. Snijders RJ, et al. Fetal Diag. 1995;10(6):356-367.
- Mazloom AR, et al. Prenat Diag. 2013;33(6):591-597.
 Palomaki GE, et al. Genet Med. 2012;14(3):296-305.
- 4. Zhao C, et al. *Clin Chem.* 2015 Apr;61(4):608-616.
- 5. Palomaki GE, et al. Genet Med. 2011;13(11):913-920
- 6. ACOG/SMFM Joint Committee Opinion No. 545, Dec 2012.

Asritha Challa, MD, PhD Director, LabCorp RTP 06/01/2021

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^{**} Sensitivity estimated across the observed size distribution of each syndrome [per ISCA database nstd37] and across the range of fetal fractions observed in routine clinical NIPT. Actual sensitivity can also be influenced by other factors such as the size of the event, total sequence counts, amplification bias, or sequence bias.



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Asritha Challa, MD, PhD Director, Sequenom Laboratories 04/23/2021

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