Patient Information
Patient Name:
Date of Birth:
Maternal Age at EDD:
Gestational Age:
Maternal Weight:
Collection Kit:
Case File ID:

Test Information
Ordering Physician:
Clinic Information: Prom-Test LLC
Additional Reports:
Report Date:
Samples Collected:
Samples Received:
Mother Blood

panorama® natera prenatal screen

ABOUT THIS SCREEN: Panorama™ is a screening test, not diagnostic. It evaluates genetic information in the maternal blood, which is a mixture of maternal and placental DNA, to determine the chance for specific chromosome abnormalities. The test does NOT tell with certainty if a fetus is affected, and only tests for the conditions ordered by the healthcare provider. A low risk result does not guarantee an unaffected fetus.

FINAL RESULTS SUMMARY: TWINS

Result	*Zygosity*	*Fetal Sex*	*Fetal Fraction(s)*
Atypical finding	**Dizygotic** *FRATERNAL TWINS*	**N/A**	**N/A**

Suspected finding outside the scope of the test, which could include, but is not limited to, fetal mosaicism, fetal chromosome abnormality, or normal variation. The atypical finding is not suspected to be of maternal origin. The finding, which involves chromosome 18, may be of placental and/or fetal origin. Repeat cell-free DNA testing is not recommended. Therefore, genetic counseling with the option of comprehensive ultrasound evaluation and diagnostic testing should be considered (ACOG Practice Bulletin 226, 2020). For questions contact us at niptgc@natera.com or call 650-646-9058.

RESULT DETAILS: ANEUPLOIDIES

Condition tested[1]	*Result*	*Risk Before Test*[2]	*Risk After Test*
Trisomy 21	No Result	1/166	N/A
Trisomy 18	No Result	1/387	N/A
Trisomy 13	No Result	1/1,217	N/A

1. mosaicism. 2. Based on maternal age, gestational age, and/or general population, as applicable. References available upon request.

Testing Methodology: DNA isolated from the maternal blood, which contains placental DNA, is amplified at specific loci using a targeted PCR assay and is sequenced using a high-throughput sequencer. Fetal fraction is determined using a proprietary algorithm incorporating data from single nucleotide polymorphism-based (SNP-based) next-generation sequencing [Pergament E et al. Obstet Gynecol. 2014 Aug;124(2 Pt 1):210-8]. If the estimated fetal fraction is ≥2.8%, sequencing data is analyzed using a proprietary SNP-based algorithm to determine the fetal copy number for chromosomes 13, 18, 21, X and Y [Ryan A et al. Am J Obstet Gynecol. 2014 Nov;211(5):527.e1-527.e17]. If ordered, specific microdeletions will be evaluated using similar methodology [Wapner RJ et al. Am J Obstet Gynecol. 2015 Mar;212(3):332.e1-9]. If a sample fails to meet the quality threshold, or the fetal fraction is insufficient, an additional algorithm is utilized to determine whether there is an increased risk for triploidy, trisomy 18 and trisomy 13 [McKanna et al. The European Human Genetics Conference. Copenhagen, Denmark. May 27-30, 2017]. However, some samples will not produce a result due to failure to meet the necessary quality thresholds.

This test has been validated on women with a singleton, twin or egg donor pregnancy of at least nine weeks gestation. A result will not be available for higher order multiples and multiple gestation pregnancies with an egg donor or surrogate, or bone marrow transplant recipients. Complete test panel is not available for twin gestations and pregnancies achieved with an egg donor or surrogate. For twin pregnancies with a fetal fraction value below the threshold for analysis, a sum of the fetal fractions for both twins will be reported. Findings of unknown significance will not be reported. As this assay is a screening test and not diagnostic, false positives and false negatives can occur. High risk test results need diagnostic confirmation by alternative testing methods. Low risk results do not fully exclude the diagnosis of any of the syndromes nor do they exclude the possibility of other chromosomal abnormalities or birth defects, which are not a part of this test. Potential sources of inaccurate results include, but are not limited to, mosaicism, low fetal fraction, limitations of current diagnostic techniques, or misidentification of samples. This test will not identify all deletions associated with each microdeletion syndrome. This test has been validated on full region deletions only and may be unable to detect smaller deletions. Microdeletion risk score is dependent upon fetal fraction, as deletions on the maternally inherited copy are difficult to identify at lower fetal fractions. Test results should always be interpreted by a clinician in the context of clinical and familial data with the availability of genetic counseling when appropriate.

Reviewed By: Wenbo Xu, M.D., Ph.D., FACMG, Senior Laboratory Director

CLIA Laboratory Director: J. Dianne Keen-Kim, Ph.D., FACMG

IF THE ORDERING PROVIDER HAS QUESTIONS OR WISHES TO DISCUSS THE RESULTS, PLEASE CONTACT US AT 650-249-9090 #3. Ask for the NIPT genetic counselor on call.