Overview

Useful For

First-tier, postnatal testing for individuals with multiple anomalies that are not specific to well-delineated genetic syndromes, apparently nonsyndromic developmental delay or intellectual disability, or autism spectrum disorders as recommended by the American College of Medical Genetics (ACMG)

Follow-up testing for individuals with unexplained developmental delay or intellectual disability, autism spectrum disorders, or congenital anomalies with a previously normal conventional chromosome study

Determining the size, precise breakpoints, gene content, and any unappreciated complexity of abnormalities detected by other methods such as conventional chromosome and FISH studies

Determining if apparently balanced abnormalities identified by previous conventional chromosome studies have cryptic imbalances, since a proportion of such rearrangements that appear balanced at the resolution of a chromosome study are actually unbalanced when analyzed by higher-resolution chromosomal microarray

Assessing regions of homozygosity related to uniparental disomy or identity by descent

Testing Algorithm

This test is not appropriate for detecting acquired copy number changes and excessive homozygosity. If this test is ordered with a reason for referral indicating a hematological disorder, the test will be cancelled and CMAH / Chromosomal Microarray, Hematologic Disorders will be performed as the appropriate test.

The following algorithms are available in Special Instructions:

- Epilepsy: Unexplained Refractory and/or Familial Testing Algorithm
- Prader-Willi and Angelman Syndromes: Laboratory Approach to Diagnosis

Special Instructions

- Informed Consent for Genetic Testing
- Prader-Willi and Angelman Syndromes: Laboratory Approach to Diagnosis
- Chromosomal Microarray Patient Information
- GenomeConnect Patient Portal
- Family Member Phenotype Information for Genomic Testing
- Epilepsy: Unexplained Refractory and/or Familial Testing Algorithm
- Informed Consent for Genetic Testing (Spanish)

Method Name

Chromosomal Microarray (CMA) Using Applied Biosystems (Affymetrix) Cytoscan HD

NY State Available

Yes

Specimen

Specimen Type

Whole blood
Necessary Information
The reason for referral is required.

Specimen Required
This test requires 2 blood specimens: 1 sodium heparin and 1 EDTA.

Specimen Type: Whole blood

Container/Tube: Green top (sodium heparin) and lavender top (EDTA)

Specimen Volume: 3 mL EDTA tube and 4 mL sodium heparin tube

Collection Instructions:
1. Invert several times to mix blood.
2. Send specimens in original tubes.

Forms
1. New York Clients-Informed consent is required. Document on the request form or electronic order that a copy is on file. The following documents are available in Special Instructions:
   - Informed Consent for Genetic Testing (T576)
   - Informed Consent for Genetic Testing-Spanish (T826)
2. Chromosomal Microarray Patient Information (T665) in Special Instructions
3. Family Member Phenotype Information for Genomic Testing in Special Instructions
4. If not ordering electronically, complete, print, and send a Neurology Specialty Testing Client Test Request (T732) with the specimen.

Specimen Minimum Volume
2 mL

Reject Due To
All specimens will be evaluated at Mayo Clinic Laboratories for test suitability.

Specimen Stability Information

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Clinical and Interpretive
Clinical Information

Aneuploidy or unbalanced chromosome rearrangements are often found in patients with intellectual disability, developmental delay, autism, dysmorphic features, or congenital anomalies. Some chromosomal abnormalities are large enough to be detected with conventional chromosome analysis. However, many pathogenic rearrangements are below the resolution limits of chromosome analysis (approximately 5 megabases). Chromosomal microarray (CMA) is a high-resolution method for detecting copy number changes (gains or losses) across the entire genome in a single assay and is sometimes called a molecular karyotype.

This CMA test utilizes greater than 1.9 million copy number probes and approximately 750,000 single nucleotide polymorphism probes for the detection of copy number changes and regions of excessive homozygosity. Identification of regions of excessive homozygosity on a single chromosome could suggest uniparental disomy (UPD), which may warrant further clinical investigation when observed on chromosomes with known imprinting disorders associated with UPD. In addition, the detection of excessive homozygosity on multiple chromosomes may suggest consanguinity and, therefore, could be useful in determining candidate genes for further testing for autosomal recessive disorders.

An online research opportunity called GenomeConnect (genomeconnect.org) is available for the recipients of genetic test results. This patient registry collects deidentified genetic and health information to advance knowledge of genetic variants. See GenomeConnect Patient Portal in Special Instructions for more information.

Reference Values

An interpretive report will be provided.

Interpretation

When interpreting results, the following factors need to be considered:

Copy number variation is found in all individuals, including patients with abnormal phenotypes and normal populations. Therefore, determining the clinical significance of a rare or novel copy number change can be challenging. Parental testing may be necessary to further assess the potential pathogenicity of a copy number change.

While most copy number changes observed by chromosomal microarray testing can readily be characterized as pathogenic or benign, there are limited data available to support definitive classification of a subset into either of these categories. In these situations, a number of considerations are taken into account to help interpret results including the size and gene content of the imbalance, whether the change is a deletion or duplication, the inheritance pattern, and the clinical and/or developmental history of a transmitting parent.

The continual discovery of novel copy number variation and published clinical reports means that the interpretation of any given copy number change may evolve with increased scientific understanding.

The detection of excessive homozygosity may suggest the need for additional clinical testing to confirm uniparental disomy or to test for mutations in genes associated with autosomal recessive disorders consistent with the patient's clinical presentation that are present in regions of homozygosity.

Families benefit from hearing genetic information multiple times and in multiple ways. A referral to a clinical genetics professional is appropriate for individuals and families to discuss the results of chromosomal microarray testing.

Cautions

This test is not approved by the US Food and Drug Administration and it is best used as an adjunct to existing clinical and pathologic information.
Chromosomal microarray data alone does not provide information about the structural nature of an imbalance.

This test does not detect balanced chromosome rearrangements such as Robertsonian or other reciprocal translocations, inversions, or balanced insertions.

This test does not detect all types and instances of uniparental disomy.

This test is not designed to detect mosaicism, although it can be detected in some cases.

This test does not detect point mutations, small deletions or insertions below the resolution of this assay, or other types of mutations such as epigenetic changes.

The results of this test may reveal incidental findings not related to the original reason for referral. In such cases, studies of additional family members may be required to help interpret the results.

Families benefit from hearing genetic information multiple times and in multiple ways. A referral to a clinical genetics professional is appropriate for individuals and families to discuss the results of chromosomal microarray testing.

Interfering factors:

- Use of an improper anticoagulant (sodium heparin is best) or improperly mixing the blood with the anticoagulant
- Excessive transport time
- Inadequate amount of blood
- Improper packaging may result in broken, leaky, and contaminated specimen during transport

Supportive Data

The array was validated by testing 113 specimens previously tested using another array platform, chromosome analysis, FISH analysis, or a PCR-based assay. The study set included specimens from phenotypically normal individuals, and patients identified with a gain or loss of an autosome or sex chromosome or identified with uniparental disomy. All abnormalities were confirmed.

Clinical Reference


Performance
Method Description
DNA extracted from the patient's peripheral blood is labeled and hybridized to the microarray. Following hybridization, the microarray is scanned and the intensity of signals is measured and compared to a reference data set. These data are used to determine copy number changes and regions of excess homozygosity. Chromosomal microarray data alone does not provide information about the structural nature of an imbalance and some abnormal results may be characterized by FISH, limited chromosome analysis or additional techniques. (Unpublished Mayo method)

PDF Report
No

Day(s) and Time(s) Test Performed
Specimens are processed Monday through Sunday.

Results reported Monday through Friday; 8 a.m.-5 p.m.

Analytic Time
8 days

Maximum Laboratory Time
21 days

Specimen Retention Time
Four weeks

Performing Laboratory Location
Rochester

Fees and Codes

Fees
- Authorized users can sign in to Test Prices for detailed fee information.
- Clients without access to Test Prices can contact Customer Service 24 hours a day, seven days a week.
- Prospective clients should contact their Regional Manager. For assistance, contact Customer Service.

Test Classification
This test was developed and its performance characteristics determined by Mayo Clinic in a manner consistent with CLIA requirements. This test has not been cleared or approved by the U.S. Food and Drug Administration.

CPT Code Information
81229

LOINC® Information

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