TEST ID: CMAP

CHROMOSOMAL MICROARRAY, PRENATAL, AMNIOTIC FLUID/CHORIONIC VILLUS SAMPLING

USEFUL FOR

- Prenatal diagnosis of copy number changes (gains or losses) across the entire genome
- 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

CLINICAL INFORMATION

Chromosomal abnormalities cause a wide range of disorders associated with birth defects and intellectual disability. Many of these disorders can be diagnosed prenatally by analysis of chorionic villi or amniocytes.

The most common reasons for performing cytogenetic studies for prenatal diagnosis include advanced maternal age, abnormal prenatal screen, a previous child with a chromosome abnormality, abnormal fetal ultrasound, or a family history of a chromosome abnormality. 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. The American College of Obstetricians and Gynecologists and the Society for Maternal-Fetal Medicine recommend the chromosomal microarray as a replacement for the fetal karyotype in patients with a pregnancy demonstrating 1 or more major structural abnormalities on ultrasound when undergoing invasive prenatal diagnosis.¹

This CMA test utilizes >1.9 million copy number probes and approximately 750,000 single nucleotide polymorphism probes for the detection of copy number changes and regions with absence of heterozygosity. Identification of regions of excessive homozygosity on a single chromosome could suggest uniparental disomy, which may warrant further clinical investigation when observed on chromosomes with known imprinting disorders. In addition, the detection of excessive homozygosity on multiple chromosomes may suggest consanguinity.

REFERENCE VALUES

An interpretive report will be provided.

ANALYTIC TIME

10 days

MOBILE APPS FROM MAYO MEDICAL LABORATORIES

Lab Catalog for iPad and Lab Reference for iPhone and iPod Touch

Requires iOS 5.1+

CONTENT AND VALUES SUBJECT TO CHANGE. SEE THE MAYO MEDICAL LABORATORIES TEST CATALOG FOR CURRENT INFORMATION.
INTERPRETATION

Copy number variants are classified based on known, predicted, or possible pathogenicity and reported with interpretive comments detailing their potential or known significance.

When interpreting results it is important to realize that 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 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.

Copy number changes with unknown significance will be reported when at least 1 gene is involved in a deletion >1 megabases (Mb) or a duplication >2 Mb.

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. Regions with absence of heterozygosity (AOH) with unknown significance will be reported when >10 Mb. Whole genome AOH will be reported when >10% of the genome.

CLINICAL REFERENCE