**Pediatric/Adult Chromosomal Microarray**

Chromosomal microarray (CMA) is a technology that analyzes patient DNA to detect gains and losses of genomic material at a much more detailed resolution than traditional chromosome analysis. CGL’s Infinium® CytoSNP-850K BeadChip array provides excellent coverage, improved accuracy of breakpoint estimation for both CNVs and regions of homozygosity (ROH), and more sensitive detection of low-level mosaicism.

**Indications for Testing**

CMA is the first tier test for individuals with:
- Unexplained intellectual disabilities
- Autism spectrum disorders
- Multiple congenital anomalies

CMA testing is also indicated for individuals with:
- Dysmorphic features
- Seizures
- Developmental problems suspected of having a chromosomal basis
- Normal chromosome analysis (karyotype)
- A known chromosome abnormality to better characterize the genetic content involved
- Normal array testing on an older CMA platform

**Advantages**

- Identifies microdeletion and microduplication syndromes in one single test
- Detects gains/losses involving thousands of known disease genes
- Provides identification of ROH utilized in analysis of uniparental isodisomy and recessive disorders

**Limitations**

Although CMA has the ability to detect abnormalities in a significant number of patients, it does have limitations. CMA will not detect:
- Balanced chromosome rearrangements
- Very low-level mosaicism
- Single gene mutations or single nucleotide mutations/polymorphisms
- Abnormalities that are smaller than the resolution of the array

**Pre-test Counseling**

It is important to discuss what information CMA testing provides, as well as its advantages and limitations, with the patient prior to ordering the test. Patients should also be informed of the potential testing outcomes as listed below.

**Copy Number Variant (CNV)**

A copy number variant (CNV) is a segment of DNA that differs in copy number, seen as a gain (duplication) or a loss (deletion), compared to the general population. The term CNV does not describe the clinical significance of the finding. The terms "benign", "pathogenic" or "uncertain" are often used to describe the clinical significance of a CNV. Every individual carries benign CNVs that are not reported. Pathogenic and uncertain CNVs are reported.

**Region of Homozygosity (ROH)**

A run or region of homozygosity (ROH) is a term used to describe a continuous area of the genome that appears to be the same (homozygous) on both chromosomes. Large and/or multiple ROH may suggest uniparental disomy (UPD) or shared ancestry (consanguinity), with possible implications for recessive disorders.

**Full CMA Interpretations**

CMA test results can be complicated, so the Colorado Genetics Laboratory provides a full interpretation of an abnormality. Our Directors and Genetic Counselors are on hand to aid clients in understanding the interpretation of an array result, and how to discuss results with patients and their families. This includes providing clinicians with current articles, images of test results, and other helpful materials.

**CNV Interpretation**

<table>
<thead>
<tr>
<th>Benign (Normal)</th>
<th>Pathogenic (Abnormal)</th>
<th>Uncertain Significance</th>
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<tbody>
<tr>
<td>- No clinically significant gains or losses of genomic material detected.</td>
<td>- CNV is likely to have caused the patient’s clinical features.</td>
<td>- CNV may or may not have caused clinical features.</td>
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<tr>
<td>- This result does not rule out the possibility of a single gene disorder or an abnormality not detected by CMA.</td>
<td>- Diagnosis of a defined genetic condition is made.</td>
<td>- Familial studies may help clarify the clinical significance.</td>
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<td>- More information on this finding may become available in the future.</td>
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