Constitutional Chromosomal Microarray Analysis – Peripheral Blood

CPT Code(s): 81229

Service Code (IU Health): 53024030

Ordering Recommendation: Detection of submicroscopic chromosomal genetic imbalances and identification of cryptic deletions and/or duplications beyond the resolution of conventional karyotyping. Utilized as a first tier test for unexplained developmental delay and autism spectrum disorder as well as multiple congenital anomalies that do not fall into a syndromic category.

Synonyms: CMA, Constitutional, CGH, SNP, Microarray

Methodology: Cytogenomic SNP microarray. Fluorescence in-situ hybridization (FISH) analysis may be utilized to confirm abnormalities.

Performed: Monday through Friday

Reported: 10-14 days

Specimen Requirements

Patient Preparation: None

Collect: Whole blood, (1) Green (Sodium Heparin) and (1) Lavender (EDTA).

Specimen Volume: 3-5 mL (Green) and 3-5 mL (Lavender).

Storage/Transport: Room temperature. Do not freeze or expose to extreme temperatures.


Stability: Ambient: 48 hours; Refrigerated: 48 hours; Frozen: Unacceptable.
Interpretive Data

**Characteristics:** Chromosomal microarray (CMA) analysis is a molecular cytogenetic technique that essentially scans the entire genome for gains and losses of genetic material. The microarray used is a SNP-based platform with millions of SNP and copy number probes. Each probe is designed to provide copy number information on a specific segment of the genome. The aggregate of information supplied by each individual probe on the array enables genome-wide evaluation of changes in copy number for thousands of genes simultaneously in just one test. The presence of SNP probes enables detection of long contiguous stretches of copy-neutral absence-of-heterozygosity (CN-AOH) that may indicate uniparental isodisomy (UPD) or regions of the genome identical by descent. Accurate identification, assessment, and correlation of copy number variants (CNVs) with clinical phenotypes and disease requires significant expertise in a clinical genetics setting.

**Clinical sensitivity:** CMA testing has been shown to detect genetic aberrations in 10-15% of individuals with unexplained intellectual disability, multiple congenital anomalies, or autism spectrum disorder.

**Limitations:** Does not detect balanced rearrangements such as translocations, insertions or inversions, single base pair mutations, very small deletions/duplications, or rearrangements of the mitochondrial genome. Low-level mosaicism may not be detected. Although detection of a large contiguous stretch of CN-AOH by this assay suggests UPD, further molecular analysis is necessary for UPD confirmation and determination of parent of origin. Failure to detect CN-AOH by this assay does not exclude the possibility of UPD. The observation of large contiguous regions of CN-AOH across multiple chromosomes encompassing more than 10% of the genome suggests a potential consanguineous relationship between the proband’s parents. This assay is not designed to be a paternity test, and should not be used definitively to assign a specific relationship between the parents of the proband.

**References:**