

CMA PARENTAL STUDIES POLICY

Philosophy: Our policy for Chromosomal Microarray Analysis (CMA) is to provide free parental analysis for genomic imbalances where parental studies may clarify the clinical significance.

CMA reports with a copy number change interval will have one of the following three recommendations.

1. Parental follow-up studies are recommended at no charge.
2. No parental follow-up studies are recommended at this time.
3. Parental studies are recommended to determine the inheritance of the clinical finding (at charge).

If further discussion regarding a specific case is desired, please call the Medical Genetics Laboratories at 800-411-GENE.

Instructions for submission of free parental studies are included on the reports. Normal results will not include any parental recommendations.

FREE PARENTAL STUDIES RECOMMENDED

1. Any CNV where it is the opinion of the sign out team that parental studies will aid in the clinical interpretation of the proband's findings.
 - a. Examples:
 - i. Deletions of uncertain clinical significance.
 - ii. Copy number gains within genes where mutations/deletions have a documented clinical significance.
 - iii. Copy number gains >500 kb in size with uncertain clinical significance; note that duplications of <500kb are usually NOT included here because our experience shows that they are inherited 90-95% of the time. Therefore, parental studies do not help clarify the clinical significance of the finding.

FREE PARENTAL STUDIES WILL NOT BE PERFORMED

1. Any abnormal finding where there is a general consensus that parental studies are indicated for genetic counseling.
 - a. Examples:
 - i. Unbalanced translocations
 - ii. Terminal deletions (to rule out possible balanced translocation in parent)
 - iii. CNVs where the CNV may be present in a parent but not be clinically obvious. These include DiGeorge syndrome region (22q11.21) deletion/duplication, and 16p11.2 autism region deletion/duplication, and many others.
 - iv. Other CNVs with questionable clinical relevance and/or incomplete penetrance. Some examples include 15q11.2 deletion of BP1-BP2, deletion or duplication involving 15q13 BP4-BP5/CHRNA7, and the 16p13.11 region duplication involving the ABCC1 and ABCC6 genes.
 - v. Many of the reciprocal duplications of known deletion syndrome regions that do not cause a severe abnormal phenotype.
2. Any abnormal finding where parental studies are generally felt to be nonessential because the genomic imbalance causes severe phenotypic abnormalities with complete penetrance and no or negligible likelihood of a predisposing parental balanced abnormality.

- a. Examples:
 - i. Prader-Willi or Angelman syndrome deletion with translocation excluded by confirmation studies Terminal deletions (to rule out possible balanced translocation in parent)
 - ii. Smith Magenis syndrome deletion
 - iii. Most interstitial deletions > 5 Mb in size
 - iv. Aneuploidy. All cases will be resolved to be free standing extra chromosome or translocation by the lab using standard confirmation methods. In cases where a translocation is present free parental studies will be offered
3. Copy number gains < 500 kb in size where there is no known clinical relevance.
 - a. Our experience shows that these types of findings are inherited 90-95% of the time. Therefore, parental studies do not help clarify the clinical significance of the finding.
4. CNV interval with no annotated RefSeq genes.
5. Genomic imbalances involving genes that when mutated result in syndromes/disorders that are inherited in an autosomal recessive manner.
 - a. If the patient has a clinical diagnosis of the autosomal recessive disorder in question (by clinical data or other lab findings), additional tests to study the parents for carrier status of the CNV can be performed. Please call the lab to discuss this option with a genetic counselor 800-411-GENE and to receive information regarding test codes and fees for these tests.