

Leaders in Laboratory Medicine

Laboratory Bulletin

| DATE: | 20 January 2025 |
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| TO: | All Zones |
| FROM: | Cytogenetics North and South, Genetics and Genomics, APL |
| RE: | Targeted Chromosomal Microarray for Copy Number Variant Analysis |

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Key Message

Familial segregation analysis of copy number variants (CNV) identified by chromosome microarray (CMA) will transition from a qPCR-based analysis to CMA limited to the chromosomal region(s) of interest.

Background

- Copy number variation analysis is used for parental follow-up of a CMA result. Based on the characteristics
 of the CNV, follow-up testing may be by FISH and/or by molecular analysis. Molecular testing was
 previously limited to qPCR and MLPA techniques.
- Targeted CMA testing, which will be limited to the chromosomal region(s) of interest, is now the preferred
 methodology for CNV follow-up familial testing. Alternate methods including FISH will be recommended in
 the proband's report when appropriate. This methodology change will streamline workflow and reduce
 follow-up costs.
- Parents will be tested sequentially. If testing of the first parent identifies the same CNV identified in the child, testing for the second parent is not required and will be cancelled if a specimen is received. If testing of the first parent is negative, testing will proceed on the second parent. An amended proband report will be issued when all appropriate parental testing is complete.

How this will impact you

 CNV analysis will continue to be ordered using the copy number variant analysis order (LAB4149) in Connect Care or utilizing a Molecular Genetics Laboratory General Requisition. While targeted CMA analysis will be the preferred testing methodology, qPCR and/or MLPA may be utilized under certain and rare circumstances. Refer to the methodology section of the patient's Copy Number Variation Analysis report to determine which methodology was used.

Action Required

No change in practice required.

Effective Immediately

Questions/Concerns

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