

ExonArrayDx Exon-focused array CGH analysis for detecting partial or full gene deletions or duplications

BACKGROUND

ExonArrayDx are GeneDx-designed oligonucleotide microarrays constructed for identification of exonic deletions or duplications within or encompassing a targeted gene. Using comparative genomic hybridization (array CGH), these arrays target clinically significant genes that are available on the GeneDx test menu, which can be ordered individually or as part of a clinically defined panel.

Deletion/duplication analysis can be ordered for a single gene or as part of a custom panel for 2-20 genes.

GeneDx offers sequence analysis for a large number of metabolic and other recessive disorders. If single gene sequencing is done at GeneDx and only one mutation has been identified in a patient, and if clinically indicated, GeneDx will perform ExonArrayDx analysis to exclude a deletion of the second allele at no extra cost.

ExonArrayDx is useful as a diagnostic test in many different situations. Some common examples include:

- Testing for an autosomal dominant disorder that results from haploinsufficiency for a clinically significant gene
- Testing for an autosomal recessive disorder when sequencing or another test identifies only a single pathogenic variant
- Testing clinically significant X-linked genes

TEST METHODS

Location of ExonArrayDx probes is based on human genome build hg19(GRCh37). Analysis of array data is performed using Genomic Workbench software (Agilent Technologies). The array design is optimized based on its performance and on newly published gene information. Results are compared to internal databases, as well as HGMD and other publicly available databases, and may be confirmed by qPCR, MLPA, or another array design. In cases where interpretation of results depends on whether the deletion or duplication is inherited or de novo, analysis of parental samples can be performed.

TEST SENSITIVITY

ExonArrayDx detects deletions or duplications as small as 250-500 bp. The sensitivity of ExonArrayDx is substantially higher than that of conventional testing by quantitative PCR (qPCR) or by multiplex ligation-dependent probe assay (MLPA) because it utilizes many more probes strategically positioned in or flanking most exons of a given target gene. The utility of high-resolution array CGH for single gene analysis has been demonstrated in multiple studies.¹⁻⁶

The clinical sensitivity of ExonArrayDx analysis depends on the specific gene that is being tested. Normal findings at a specific gene locus do not rule out the diagnosis of a genetic disorder associated with this gene, as a genetic abnormality may be present that is undetectable by ExonArrayDx. Specifically, Mendelian disorders that are predominantly caused by missense, nonsense, or splice site variants or by intragenic deletions or insertions that are <200bp are not detectable by ExonArrayDx. ExonArrayDx also cannot identify variants in genomic regions that are not represented on the microarray, deletions or duplications in genes that have pseudogene copies in the genome, or large unbalanced chromosomal rearrangements.

REFERENCES:

1. del Gaudio D et al. Hum Mutat 29:1100-1107, 2008
2. Saillour Y et al. Hum Mutat 29:1083-1090, 2008,
3. Staaf J et al. Hum Mutat 29:555-564, 2008
4. Hegde MR et al. Hum Mutat 29:1091-1099, 2008
5. Wong LJ et al. Clin Chem 54:1141-1148, 2008
6. Dhani P et al. Am J Hum Genet 76:750-762, 2005