



CentoArray[®]
Opening the door to early and
accurate diagnosis

PRODUCT SHEET

CentoArray[®] – Our Extensive Genome-Wide Cytogenetic Analysis

Cytogenic variations are known to cause a broad range of developmental disorders, primarily neurodevelopmental and congenital anomalies. Chromosomal microarray analysis (CMA) is recommended for analyzing cytogenic variations in patients suffering from unexplained developmental delays, intellectual disabilities, autism spectrum disorders, and/or multiple congenital malformations.

CENTOGENE's microarray-based solution – CentoArray[®] – enables genome-wide detection of known novel structural aberrations, copy number variations (CNVs), chromosomal imbalances, regions exhibiting loss/absence of heterozygosity (LOH), uniparental isodisomy (UPD), and mosaicism.

The CENTOGENE Advantage



High resolution and broad coverage, focusing on exonic regions to provide the best cytogenetic disease variant coverage



Disease-focused content covering more than 4,800 relevant genes with an up-to-date design



Dedicated team of medical experts
to provide the best clinical interpretation

When to Recommend This Panel?

- For cases of unexplained developmental delay/intellectual disability, autism spectrum disorders, and/or multiple congenital malformations
- For deletion/duplication analysis of extremely large genes where gross deletions involving large segments of genes, flanking intergenic regions, or neighboring genes are frequently reported
- To diagnose uniparental disomy (UPD) and regions exhibiting loss/absence of heterozygosity (LOH)
- In conjunction with Whole Exome Sequencing (WES) to complement large CNVs. CentoArray can be ordered either as a step-wise analysis after CentoXome® or together as a single-step approach
- For prenatal testing to help determine a cause of ultrasound-detected abnormalities via our CentoArray Prenatal product

Key Features and Performance

CHARACTERISTICS	Genome-wide cytogenetic analysis to detect structural aberrations, such as CNVs, chromosomal imbalances, LOH, UPD, and mosaicism
TOTAL MARKERS (POLYMORPHIC)	1.8 Million SNP markers
RESOLUTION OF CNVS DETECTION	>25kb for copy number loss >200kb for copy number gain
DETECTION OF AOH/LOH	>3 Mb
MOSAICISM DETECTION	Down to 30%
EXON LEVEL RESOLUTION FOR	~ 4,800 cytogenic relevant genes
SAMPLE REQUIREMENTS	CentoCard, EDTA-blood, ready to use DNA, buccal swab, amniotic fluid and chorionic villi
TAT	15 business days