CENTOGENE
THE RARE DISEASE COMPANY

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 analyisis to detect structural aberrations, such as CNVs, chromosomal imbalances, LOH, UPD, and mosaicism	
TOTAL MARKERS (POLYMORPHIC)	1.8 Million SNP markers	3.1 Polimorfinių žymenų kiekis: 1 800 000 VNP žymenų (angl. SNP markers).
RESOLUTION OF CNVS DETECTION	>25kb for copy number loss >200kb for copy number gain	3.4 Nustatomi kopijų skaičiaus pokyčiai: >25 kb delecijos; >200 kb dublikacijos.
DETECTION OF AOH / LOH	>3 Mb	3.2 Heterozigotiškumo praradimo nustatymas (angl. AOL/LOH): >3 Mb.
MOSAICISM DETECTION	Down to 30 %	3.3 Mozaicizmo nustatymas nustatymas: iki 30%.
EXON LEVEL RESOLUTION FOR	~ 4,800 cytogenic relevant genes	3.5 Skiriamoji geba egzomo lygmenyje: ~4800 genai
SAMPLE REQUIREMENTS	CentoCard, EDTA-blood, ready to use DNA, buccal swab, amniotic fluid and chorionic villi	4.1 Reikalvimai mėginiui: sauso kraujo lašas (CentoCard), kraujas EDTA megintuvėlyje, paruošta (išskirta) DNR, burnos gleivinės nuogramdos, amniono skystis, choriono gaureliai
TAT	15 business days	4.5 Rezultatų pateikimo laikas: iki 15 darbo dienų.