strand

CNSeq

Advanced Chromosomal Analysis with Low-pass whole genome sequencing

CAP ACCREDITED
COLLEGE of AMERICAN PATHOLOGISTS
#875094101

MC-2434

CNSeq: Low-pass Whole Genome Sequencing

CNSeq revolutionizes chromosomal analysis. Leveraging NGS technology, it detects Copy Number Variants (CNVs) with unmatched accuracy compared to traditional cytogenetic methods.

The key to CNSeq's power lies in its strategic use of low-pass whole genome sequencing, reading each base a few times. This focuses on identifying large-scale CNVs uniformly across the genome for faster analysis and potentially deeper insights into chromosomal abnormalities.

It empowers clinicians with the ability to explore insights in detail, enabling a comprehensive grasp of structural variations in the genome with unbiased CNV calling across the genome.

500Kb Resolution — **CNSeq**

50Kb Resolution — **CNSeqHD**

Key Features

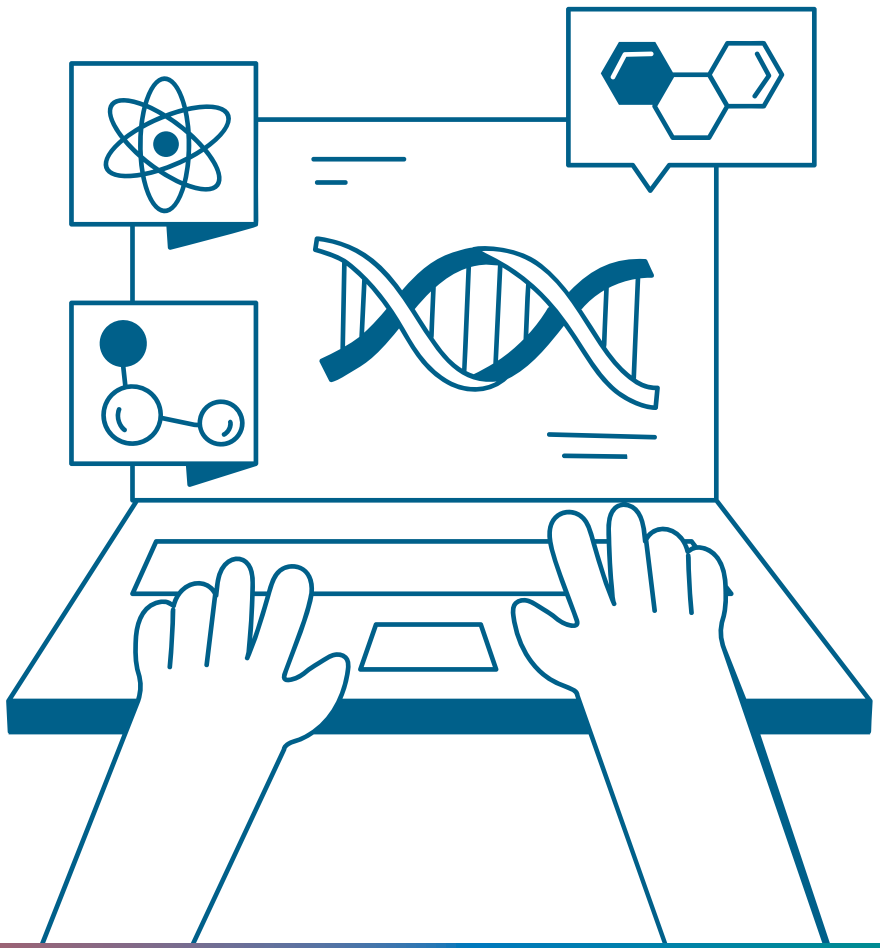
- Increased CNV callers for improved detection reliability
- Validated for both prenatal & pediatric settings
- Advanced pipeline adjusts for maternal cell contamination in calculating mosaicism and aneuploidies

Turnaround Time
21 Days

Sample Requirement
Amniotic Fluid, CVS, POC, PVB & gDNA

Going beyond traditional array with CNSeq

Technique	Karyotype	Prenatal CMA	750K	CNSeq	CNSeqHD
Coverage	>5Mb	Probe-based	Probe-based	Complete genome coverage	Complete genome coverage
Resolution	>5Mb	>500Kb	>100Kb	500Kb	>50Kb
DNA quantity requirement	Cell Based	250 ng	250 ng	50 ng	50 ng
Low-level Moscaism sensitivity	10%	>20%	>20%	>20%	>20%
Abnormalities detected	Aneuploidies, larger CNVs, Structural Abnormalities, Balanced Translocation	Aneuploidies, CNVs, UPDs, Polyploidy, AOH/LOH	Aneuploidies, CNVs, UPDs, Polyploidy, AOH	All Aneuploidies, CNVs & Structural Variants	All Aneuploidies, CNVs & Structural Variants



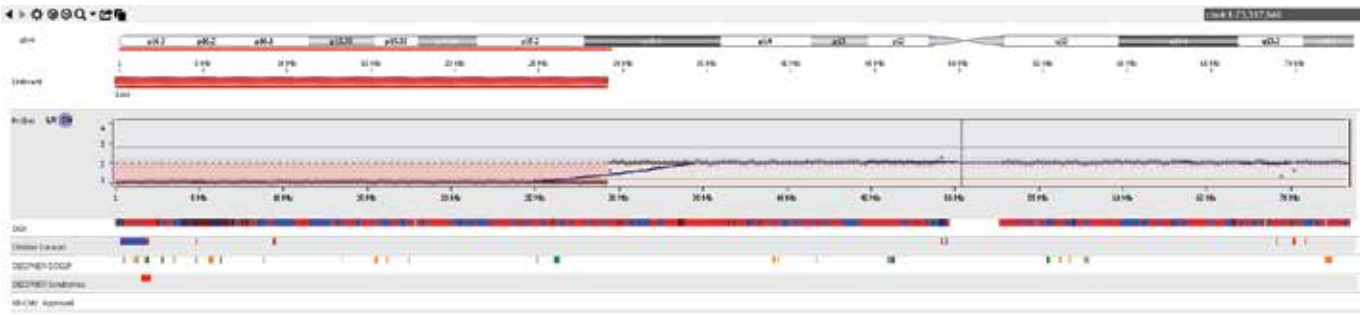
CNSeq & CNSeqHD: Validation Data

	Detected Events – CNVs & Aneuploidies (bp)							
Coriell Controls	10 - 100K	100 - 250K	250 - 500K	500K - 1M	1M - 5M	5M - 30M	>30M	Whole Chr
CNSeq								
NA50324				▣		●▲		
NA21699				●		▲	●	
NA04375						▲		
NA04409				▲		●		
NA03623							●●	
NA11385					▲			
CNSeqHD								
NA21886		●●●▲		▲		▲		
NA04409			●	▲		●		
NA12878		▲▲▲▲▲▲						
PCE-2	▲							
PCE-3	●							
NA21699		▲		●		▲		■

● Gain; ■ Mosaic Gain; ▲ Loss; ◆ Polymorphic event undetected; ▣ Borderline gain event undetected

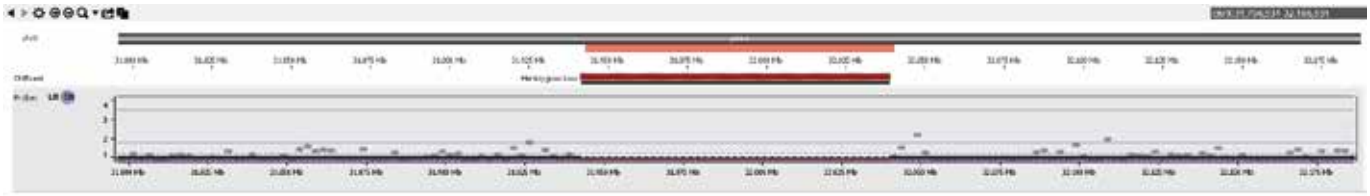
Unique CNVs picked up by CNSeq

Wolf-Hirschhorn Syndrome - Pathogenic loss



Unique CNVs picked up by CNSeqHD

Congenital Heart Defect - **10kb Deletion** Pathogenic Copy Number Loss



Proprietary Platforms

strandomics

Proprietary platform for unparalleled Variant Interpretation & Reporting

strandngs

State-of-the-art platform for Best in class Sequencing

illumina NovaSeq X Plus

World's highest throughput Sequencer for fastest report delivery

Additional Testing Options

- ExomePlus: Exome Sequencing
- MaatriSeq: NIPS
- AneuXpress: Quantitative Fluorescent PCR
- Sanger Based Testing
- Couple Carrier Screening
- Whole Genome Sequencing
- Preimplantation Genetic Testing: PGT - Aneuploidy

24+ YEARS OF EXPERIENCE

80,000+ Genetic Tests Reported

500+ Projects Executed for Genomics Majors Globally

Presence in **20+** Countries

SCAN TO KNOW MORE

CHANNEL PARTNER

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