Genomic Scar Analysis for Homologous Recombination Deficiency (HRD) With N_xClinical™ Software Developed by BioDiscovery

With the latest release of N_xClinical software, we've made it possible to get comprehensive, consistent, automated genomic scar analysis from microarray and next-generation sequencing data. While some other approaches attempt to measure HRD through limited analysis of individual genes, or mutations in genes in HR pathways, N_xClinical software offers a more complete analysis by evaluating the entire genome for large scale genomic instability. We can help reveal more genetic variation that matters in solid tumors, without disrupting existing data pipelines.

Automated, Consistent Scores for Large Scale Genomic Instability

- **LOH: Loss of Heterozygosity**
- **TAI: Telomeric Allelic Imbalance**
- **LST: Large-Scale State Transitions**

Accelerate Your Cancer Research Discovery

- Confidently detect CNVs and LOH from NGS panels or whole exome sequencing data
- Automatically count events that are hallmarks of large-scale genomic instability
- Seamlessly integrate multiple datasets in a single view to build genome-wide profiles for complex cancers

N_xClinical 6.2 software allows you to use data from many widely adopted array and sequencing platforms, including:

Illumina:

- Infinium® GDA-Cyto
- Infinium® CytoSNP-850k
- TruSight™ Oncology 500 Assay

ThermoFisher:

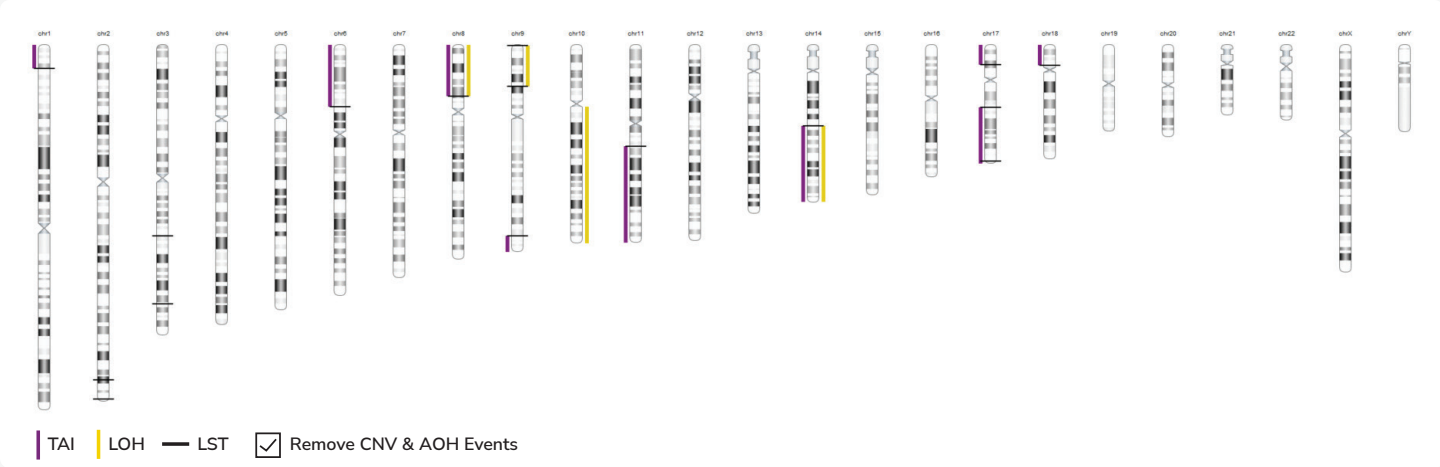
- OncoScan™ CNV Assay
- CytoScan™ HD Array

To learn more, visit: **biodiscovery.com/genomic-scar-scoring**

Decode Cancer Complexity with Enhanced Transparency and Clarity

The visual display for genomic scar analysis for HRD in N_xClinical 6.2 lets you see more genomic variation that matters. Our karyogram shows regions with genetic scarring events in a simple, convenient view, with full transparency to chromosomal regions affected. Our algorithm merges and smooths data into a unified representation that combines similar event types and small gaps to select events meeting the criteria of each genomic scar. This analysis is easily exported for reporting, creating a scalable, reliable way for laboratories to routinely include genomic scar analysis in tumor evaluation.

Figure 1: N_xClinical 6.2 karyogram highlighting regions of TAI, LOH, and LST across the genome.



N_xClinical: Powering Discovery in Cancer Research

For more than 20 years, BioDiscovery, now a Bionano Genomics company, has enabled laboratories around the world to visualize, interpret, and report on genomic data. N_xClinical's core capabilities let you:

Easily implement new analyses at scale with an off-the-shelf solution

Quickly obtain critical insights from NGS and CNV data

Automatically create an internal oncology knowledgebase from your own samples

Want to Learn More?

Contact your Bionano Software Regional Business Manager to get started.

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FLY-00001_Rev.01_NX Clinical 6.2 Launch Sales Flyer
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