

Genomic Scar Analysis for Homologous Recombination Deficiency (HRD) with NxClinical™ Software

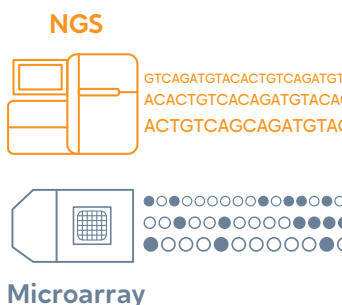
With the latest release of NxClinical software, it is possible to get comprehensive, consistent, automated genomic scar analysis from microarray and next-generation sequencing data. While some other approaches only measure HRD through limited analysis of individual genes, or mutations in genes in HR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

Automated, Consistent Measurement of 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

NxClinical 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: bionano.com/hrd-testing/

Decode Cancer Complexity with Enhanced Transparency and Clarity

The visual display for genomic scar analysis for HRD in NxClinical 6.2 lets you see more genomic variation that matters. A karyogram shows regions with genetic scarring events in a simple, convenient view, with full transparency to chromosomal regions affected. The integrated 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.

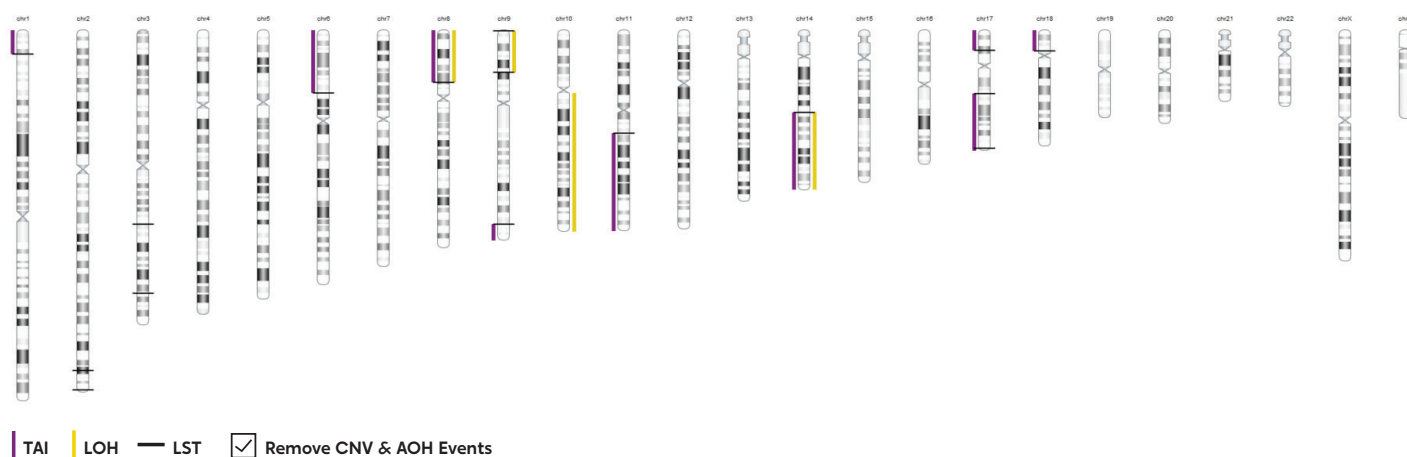


Figure 1: NxClinical 6.2 karyogram highlighting regions of TAI, LOH, and LST across the genome.

NxClinical: Powering Discovery in Cancer Research

NxClinical enables laboratories around the world to visualize, interpret, and report on genomic data with core capabilities that 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

Contact your Bionano Regional Business Manager to get started.

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