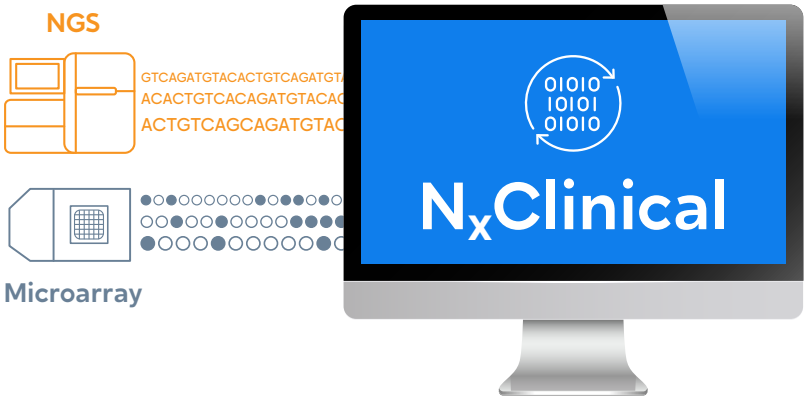
bionano

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

With the latest release of N_xClinical 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, N_xClinical software offers a more complete analysis by evaluating the entire genome for large scale genomic instability. N_xClinical 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

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: bionano.com/genomic-scar-scoring

bionano

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.

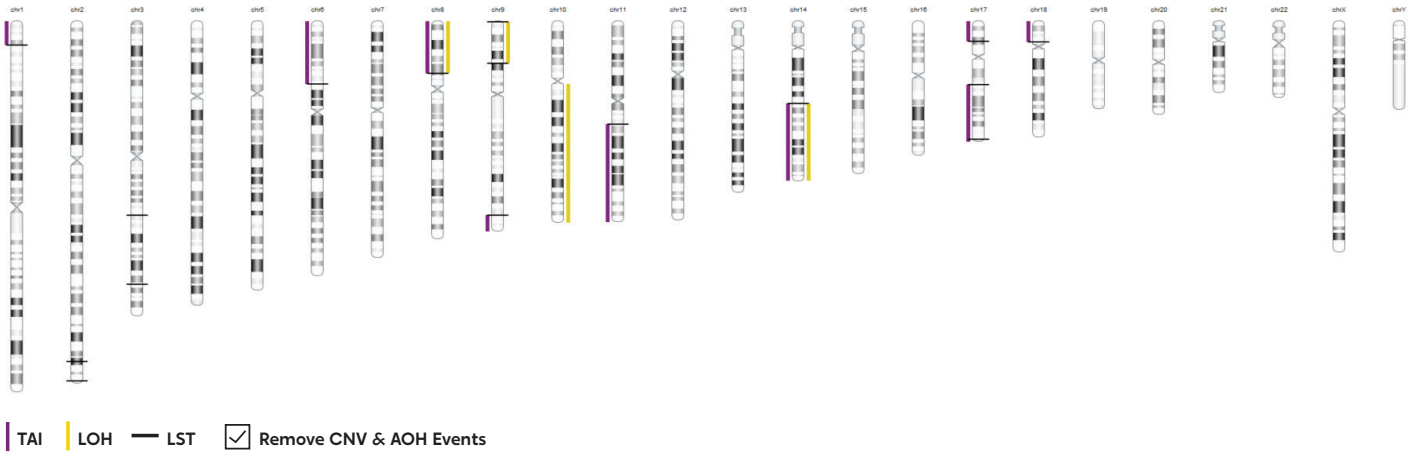


Figure 1: NxClinical 6.2 karyogram highlighting regions of TAI, LOH, and LST across the genome.

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.

+1 310.414.8100
info@bionano.com
bionano.com

FLY-00001_Rev.01_NX Clinical 6.2 Launch Sales Flyer Effective: 2/14/23