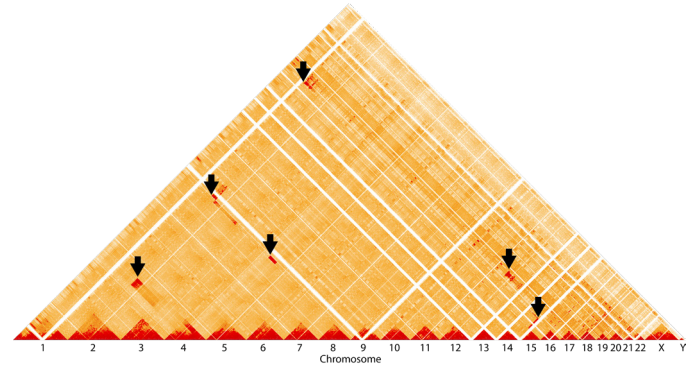
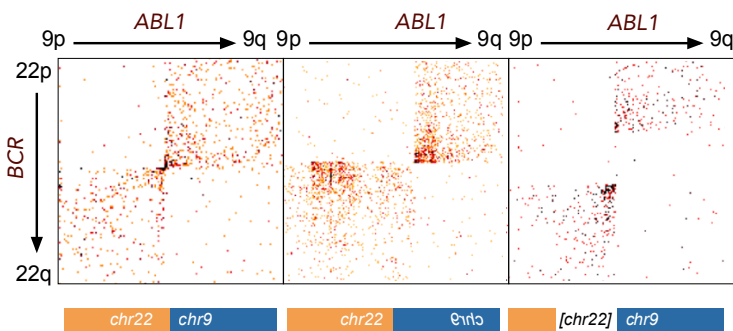


Comprehensive Cytogenetics of Fresh, Frozen, and FFPE Tissue with a Single Assay

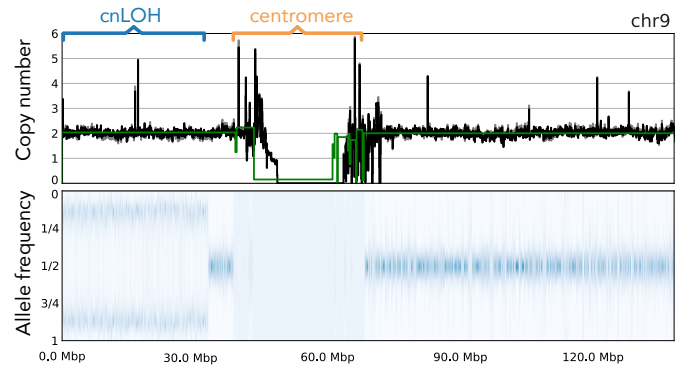
- Surpass the breadth and depth of karyotyping, FISH, and CMA with a single, NGS-based assay
- Genome-wide cytogenetic information from a wide variety of sample types, including blood and FFPE tissue
- Scalable, fast, and cost-effective—no cell culture or dedicated instrumentation required
- Integrated sample-to-report product, no advanced NGS experience needed



Genome-wide view of large-scale changes in chromosome structure

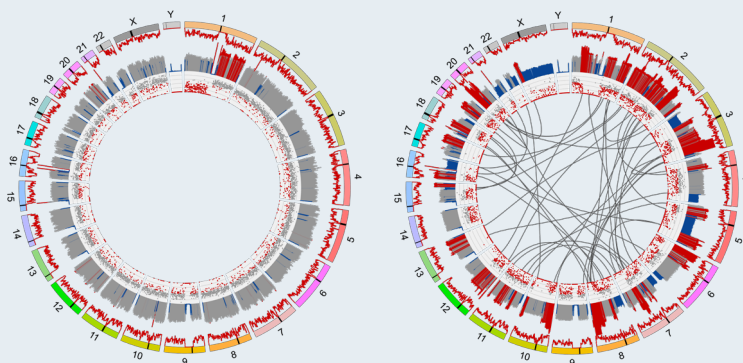


High-resolution mapping of genomic breakpoints



Chromosome-scale mapping of deletions, amplifications, and allele frequency

Homologous Recombination Deficiency (HRD) Assessment

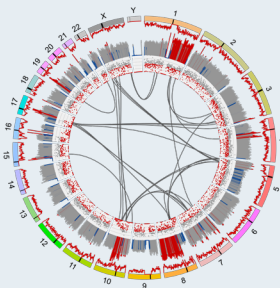


Comprehensively capture genomic scarring

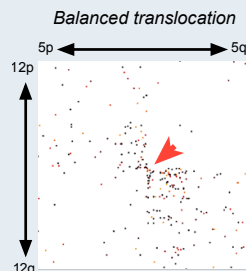
Cancers that demonstrate phenotypic homologous recombination deficiency (HRD) are candidates for treatment with drugs that exploit synthetic lethality. The CytoTerra® Platform captures the range of genomic scars that result from HRD, including those that are difficult to detect with whole genome sequencing.

FFPE Applications

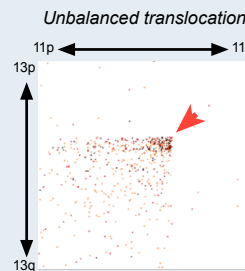
- The CytoTerra® Platform enables high-resolution cytogenetic analysis of solid tumors—samples that are unsuitable for traditional cytogenetics
- Identify balanced and unbalanced chromosomal aberrations including copy-neutral loss of heterozygosity (cnLOH); all with a fraction of sequencing costs associated with whole genome sequencing
- Identify novel and known druggable gene fusions and other indications for precision oncology therapies
- Recover genome-wide insights from as little as 2 x 5 µm FFPE curls



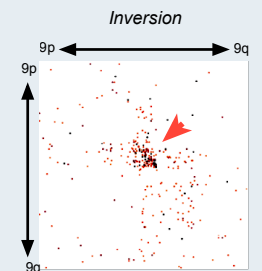
High complexity breast tumor sample



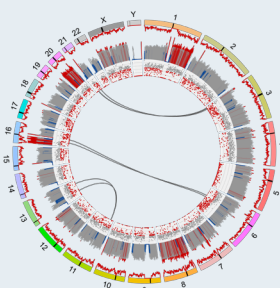
Balanced translocation
NPM1-ALK1 fusion; Crizotinib



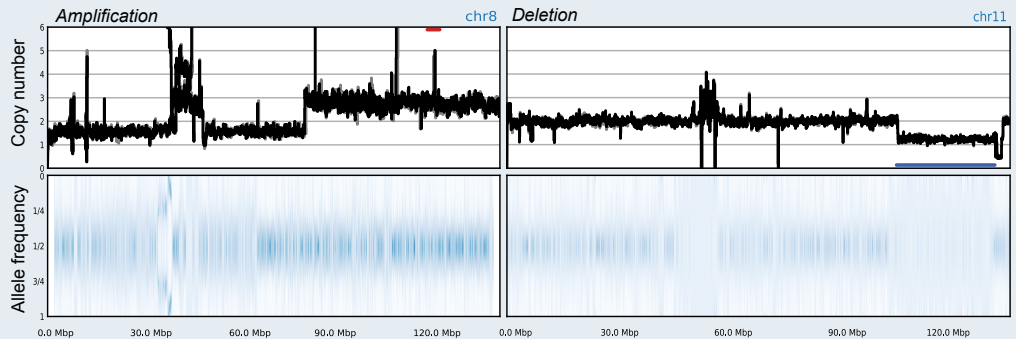
Unbalanced translocation
RB1 disruption; Volasertib



Inversion
Novel NTRK2 fusion; Entrectinib



Intermediate complexity breast tumor sample



MYC amplification; Omomyc

BRCA2 deletion; Olaparib

Learn more



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