

**BIONANO GENOMICS SEMINAR**

You're Invited!

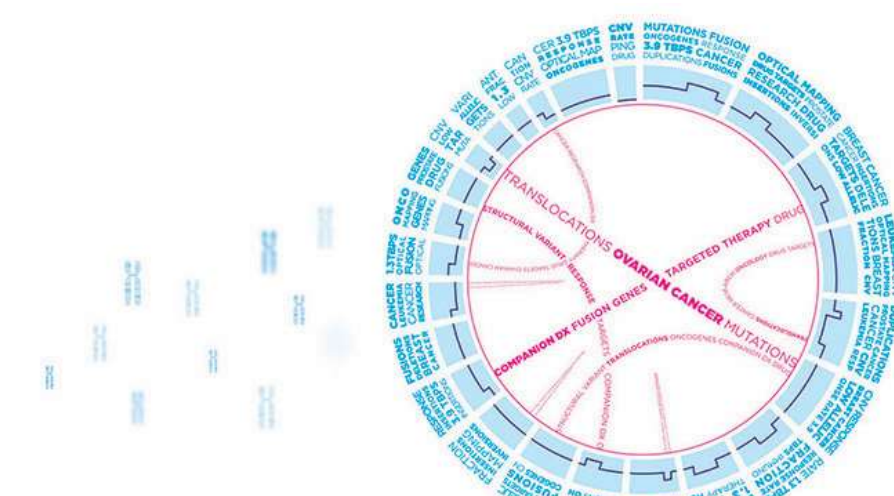
**Next-Generation Cytogenomics: High-throughput Mapping of Structural Variation in Cancer Research and Clinical Oncology**

The promise of personalized medicine in cancer remains elusive, because no single technology can comprehensively detect all the rearrangements in the cancer genome.

Bionano Genomics' platform for whole genome mapping offers an extremely long-read technology, providing unmatched sensitivity to detect structural variation, genome wide, at low cost. Our de novo maps can resolve complex repetitive regions, identify Copy Number Variations, and elucidate genome-wide structural variation like balanced/unbalanced translocations, inversions, and indels with much higher sensitivity and precision than sequencing-based methods.

For heterogeneous cancer samples, Bionano's extremely high coverage depth allows for the detection of any type of structural variant with more than 90% sensitivity, present in as little as 5% allele fraction, genome wide, and completely unbiased.

Examples will be presented of how Bionano's platform elucidates genomic rearrangements in cancer that are missed by NGS and cytogenetic methods.



**Event Info**

**DATE:**

Wednesday, February 12th, 2020

**TIME:**

2:00 PM – 3:00 PM

**LOCATION:**

Boardroom 1

Level 6

The Alfred Centre Building, Monash Central Clinical School

99 Commercial Rd, Melbourne

**SPEAKER:**

Yingying Wu | Scientific Affairs Manager | BioNano Genomics

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**THANKS TO:**

Prof Mark Shackleton | Director of Oncology | The Alfred Centre

Vikki Marshall | Program Manager-Precision Oncology | Monash Partners Comprehensive Cancer Consortium



**For more information about the Saphyr® System, please visit [www.bionanogenomics.com](http://www.bionanogenomics.com)**