BIONANO GENOMICS LUNCH AND LEARN

You're Invited!

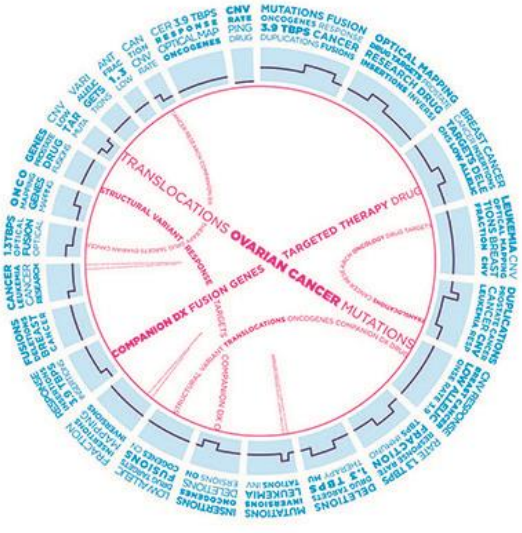
Next-Generation Cytogenomics: High-throughput Mapping of Structural Variation in Cancer Research and Clinical Oncology

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.



Lunch will be provided

Event Info

DATE:

Friday 14th Feb

TIME:

7:15 – 8:15am

LOCATION:

Cumberland Lorne Resort, top floor workshop room

CONTACT:

Josh Warburton

Josh.Warburton@decodescence.com.au

Speakers:

Professor Vanessa Hayes, Garvan Institute of Mdedial Research

Yingying Wu, Medical Affairs Manager, Bionano Genomics

For more information about the Saphyr® System, please visit www.bionanogenomics.com

BIONANO GENOMICS LUNCH AND LEARN

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Next-Generation Cytogenomics: High-throughput Mapping of Structural Variation in Genetic Disease

The diagnostic yield in genetic disease has seen very little improvement over the last few decades, despite the introduction of whole genome sequencing.

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 mosaic samples, Bionano's high coverage depth allows for the detection of any type of structural variant with more than 90% sensitivity, present in as little as 10% of the cells, genome wide, and completely unbiased.

Examples will be presented of how Bionano's platform is helping provide a molecular diagnosis for patients with a variety of genetic disorders by detecting genomic rearrangements and structural variants missed by NGS and cytogenetic methods.

Lunch will be provided

Event Info

DATE:

Monday, April 29th, 2019

TIME:

12:00 PM – 1:00 PM

LOCATION:

Room #1013 (lobby)
Sanford Consortium for Regenerative Medicine | 2800 Torrey Pines Scenic Dr. | La Jolla, CA | 92037

CONTACT:

Heather Mashoodi
hmashhoodi@bionanogenomics.com

RSVP VIA: Please scan the QR code with your smartphone camera to access the link

THANKS TO:

Kristen Jepsen, PhD | Director, IGM Genomics Center | UC San Diego

Elsa Molina, PhD| Stem Cell Genomics Core Director | UC San Diego Stem Cell Program

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You're Invited!

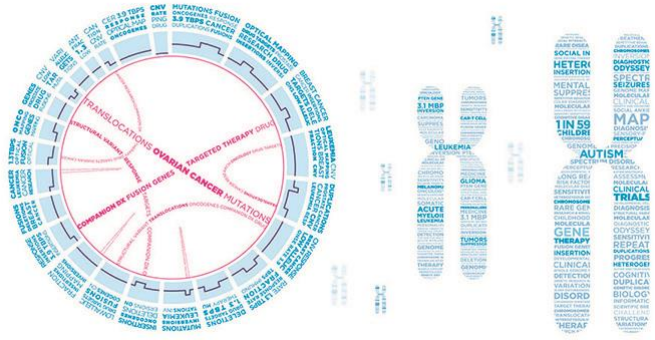
Next-Generation Cytogenomics: High-throughput Mapping of Structural Variation in Cancer and Genetic Disease

The diagnostic yield in genetic disease has seen very little improvement over the last few decades, despite the introduction of whole genome sequencing. 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 or mosaic patient cases, 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% of the cells, genome wide, and completely unbiased.

Examples will be presented of how Bionano's platform is helping provide a molecular diagnosis for patients with undiagnosed genetic disorders, and how it elucidates genomic rearrangements in cancer that are missed by NGS and cytogenetic methods.



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