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I was blind, but now I see: Genomic insights revealed by optically mapping the 3q29 deletion interval

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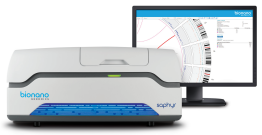
Arranged by:

Emory Integrated Genomics Core
Emory Integrated Core Facilities

Friday, September 20th, 2019
10:00 am-11:00 am
SOM-178P, School of Medicine

bionano GENOMICS

Seminar, followed by Q&A. Please join us!
Light refreshments served



3q29 deletion syndrome is caused by a recurrent, typically de novo 1.6 Mb hemizygous deletion and is associated with mild to moderate intellectual disability, autism, and an astonishing 40-fold increased risk for schizophrenia. This deletion sits at the intersection of two properties that make it a high-value target for interrogation: it has one of the largest effect sizes for neuropsychiatric phenotypes, and the region itself has reduced complexity compared to other genomic disorder intervals. Despite this reduced complexity, the genomic structure of the 3q29 interval has not been extensively mapped, and the factors that predispose to genomic rearrangement are not understood. At other loci, the presence of inversion polymorphisms, and the arrangement and composition of flanking low copy repeat (LCR) sequence have been reported to be risk factors for genomic rearrangement, but these studies have been laborious, expensive, and inefficient. Technical barriers have rendered complex genomic structures such as inversions and LCRs all but undetectable by high-throughput whole-genome methods. With the advent of new optical mapping strategies, such as the Bionano Saphyr, these regions are now accessible for interrogation, and we have applied such strategies to investigate the 3q29 interval. Using Bionano optical mapping technology, we identified multiple inversions at the 3q29 locus and also found a high degree of previously undocumented variation at the LCRs that flank the region. These data fuel new hypotheses about the mechanism by which deletions at the 3q29 interval may arise and highlight the value of shining light on the "unseen" parts of the human genome.