

# GWAS Seminar Series

## Next-gen Genotyping. Now.

Building on the HapMap Project, massive re-sequencing efforts, such as the 1000 Genomes Project, are delivering a catalogue of human variation at an unprecedented scale. These data are already offering a much richer understanding of the true spectrum of genetic variation across human populations.

Up to 50% more coverage of common and rare variants. Maximum power for any population. Multiple product paths and flexible points of entry. Always the latest content. Enabling bioinformatic solutions. It's Next-gen GWAS and genotyping with the whole genome in mind.

At this seminar series, we will provide an overview of our Omni family of microarrays and the bioinformatics applications we provide to address the data management challenges of next gen GWAS and sequencing.

**THURSDAY, AUGUST 19, 2010**

Hyatt Regency Hotel Auckland  
Regatta Room B&C  
Cnr Waterloo Quadrant and Princes St  
Auckland

Please RSVP your attendance for catering purposes to Gretchen Weightman on [gweightman@illumina.com](mailto:gweightman@illumina.com)

### SEMINAR SCHEDULE

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|-------|---|--|
| 9:45  | Registration  |  |
| 10:00 | Introduction  | Karl Sluis, Regional Account Manager, Illumina New Zealand         |
| 10:05 | The New Era of Higher Density MicroArrays for Rare Variant Discovery                      | Dr Jennifer Stone, Product Manager, Illumina San Diego             |
| 11:05 | MORNING TEA   |  |
| 11:25 | Next-Generation Informatics: An overview of Illumina's array and sequencing data analysis | Dr Jason Blue-Smith, Product Manager Informatics, Illumina Hayward |
| 12:30 | Conclusion  |  |