



Impact of Next Generation Sequencing

**Coral Ballroom 2.
Hilton Hawaiian Village
Honolulu, HI, USA**

20th October 2009



7.45 – 8.30 Speakers arrive and hand in presentations
Poster Mounting
Registration

8.30 – 8.35 **President's Welcome**
Graham R. Taylor

Session I

Chair: Graham Taylor

8.35 – 9.20

INVITED SPEAKER

Matt Hurles

Genomic Approaches to Elucidating the Genetics of Rare Disorders

9.20 – 9.40

Peter Nagy

Diagnosis of Rare Genetic Disorders With Combination of High Resolution Comparative Genomic Hybridization and Array Capture Assisted High Throughput Parallel Sequencing

9.40 – 10.00

Christophe Bérout

Distinguish neutral variations from pathogenic mutations using bioinformatics tools

10.00 – 10.30 **COMPANY LECTURE**

Roche

Timothy Harkins

From Whole Exon Sequencing to 1000 Base-Pair Sequencing Reads:
Technology Advancements with the 454 Genome Sequencer FLX

10.30 – 11.00

Coffee Break & Poster Session

Poster presenters to stand by their poster

Session 2

Chair: William Oetting

11.00 – 11.30

INVITED SPEAKER

George Grills

Implementation of Next Generation Sequencing Technologies as Shared
Research Resources

11.30 – 11.50

Graham Taylor

Sensitive high-throughput gene-centric analysis in familial breast cancer
and TP53 using the Illumina GAII clonal sequencer

11.50 – 12.10

Etienne Rouleau

CDH1 large rearrangements in breast cancer predisposition: case report,
prescreening method, and zoom-in CGH-array screening

12.10 – 12.30

Bruce Gottlieb

The Impact of Next Generation Sequencing on the Genetics of
Multifactorial Disease and Genome Wide Association Studies

12.30 – 13.00

COMPANY LECTURE

Illumina

Jeremy Preston

The Illumina Genome Analyzer Iix: Genome Sequencing Simplified

13.00 – 14.10

Lunch – Coral Ballroom 1

Session 3	Chair: Richard Cotton
14.10 – 14.40	INVITED SPEAKER Harry Cuppens Next Generation Genetic Tests: From Artisan Genetic Testing To Uniform, Streamlined, Fully Quality-Assured And Automated Processing of Genetic Tests Using Next Generation Sequencing
14.40 – 15.00	Sandro Rossetti Comparison of two next-generation sequencing platforms (Illumina GA and Roche 454) for the deep sequencing of the PKD1 and PKD2 genes in Autosomal Dominant Polycystic Kidney Disease (ADPKD)
15.00 – 15.20	Vanessa Hayes Determining population diversity without a reference genome: Next Generation Sequencing enables genome-wide diversity studies
15.20 – 15.35	COMPANY LECTURE Helicos BioSciences Avak Kahvejian Helicos Single Molecule Sequencing: Delivering Accurate, Quantitative Information for Genome Biology
15.35 – 15.55	Steven Brenner Prospects for personal genome interpretation with next-generation sequencing: opportunities and challenges
15.55 – 16.05	Concluding Remarks, Graham Taylor
16.05 – 16.30	Coffee Break
16.30 – 18.30	HGVS ANNUAL GENERAL MEETING Non-members are welcome