

## CGET 2006 Conference Program

### Sunday, Oct 1

6:00-9:00 Exhibitor Set-up  
6:00-8:00 Registration & Poster Set-up

### Monday, October 2

7:30-8:45 Registration & Poster Set-up  
8:55-9:00 Patrice Morin Welcome and Introductions

### Session 1: Genetic Analyses and Epigenetic Profiling in Human Cancer Chair: Kornelia Polyak

9:00-9:30	Kornelia Polyak	Genome-wide methylation profiling using MSDK
9:30-10:00	Marco A. Marra	Mapping genome rearrangements in follicular lymphoma
10:00-10:30	Victor Velculescu	Genomic analyses of human cancer
10:30 - 10:45	Break	
10:45-11:15	Andrew Futreal	Exon resequencing in human cancers - understanding natural history and identification of new suspects
11:15 -11:45	Tim Hui-Ming Huang	Global profiling of epigenetic alterations using CpG island microarray
12:00-1:30	Lunch Buffet	
1:30-2:00	Tian-Li Wang	Applying digital karyotyping to explore cancer genomes
2:00-2:45	3 short talks selected from abstracts:	
	Bin Feng	Comparing detection of DNA copy number aberrations by six microarray platforms
	Victoria Boyd	Methylation Determination using Fragment Analysis and Sequencing of PCR Amplicons from bisulfite-converted gDNA
	Sarah Wheelan	Another man's treasure: The Transposon Insertion site Profiling chip (TIP-chip)

- 2:45-4:00 View Posters & Exhibits
- 4:00-5:00 4 short talks selected from abstracts:
- |                   |  |
|-------------------|--|
| Levi Garraway     | High-throughput oncogene mutation detection in human cancers                     |
| Michail Shipitsin | Genomic characterization of putative breast cancer stem cells                    |
| Jonas Ekblom      | A new generation of transfection reagents for functional studies of cancer genes |
| Trevor Pugh       | Genome structural fidelity of whole genome amplification & tissue archival       |
- 5:15-6:15 Wine Reception with Exhibitors
- 6:15-7:30 Open
- 7:30-9:30 Dinner Buffet

## **Tuesday, October 3**

**8:30-9:30 Keynote Speaker: Jeffrey Trent**  
**Systems medicine in cancer therapeutics**

### **Session 2: Functional Analyses of Cancer Genes** **Chair: Alberto Bardelli**

- 9:30-10:00 Yijun Ruan Genome-wide interrogation of transcriptional regulatory networks in cancer cells
- 10:00-10:30 2 short talks selected from abstracts:
- |                   |   |
|-------------------|---|
| JM Cummins        | MiRAGE: Using SAGE methodology to explore the human microRNAome   |
| Ashani Weeraratna | Wnt5a mediates motility in melanoma cells via the inhibition of metastasis suppressors, and initiation of the epithelial to mesenchymal transition. |
- 10:30 - 10:45 Break
- 10:45-11:15 Alberto Bardelli Dissecting oncogenic signaling pathways by mutational and functional profiling of gene families

### **Session 3: New Genomics Technologies**

**Chair: Victor Velculescu**

11:15-11:45	Frank Baas	Locked Nucleic Acid: A tool for modulating gene expression in vivo
11:45-12:15	Andrew B Sparks	Affymetrix array technologies for high-resolution analysis of cancer genetics
12:15 - 1:30	Lunch Buffet	
1:30-2:00	Stanley N. Lapidus	Multiple genomic perspectives of cancer using single molecule sequencing
2:00-2:30	George M Church	Single cell, RNA, and chromosome sequencing technologies
2:30-3:00	Gina Costa	Sequencing by Oligo Ligation and Detection
3:00-3:15	Break	
3:15-3:45	John Quackenbush	Extracting biological meaning from high-dimensional datasets
3:45-4:15	Jonathan Rothberg	454 Sequencing: Moore's law comes to sequencing, beyond the \$100,000 genome, implications to understanding cancer
4:15-4:45	Gary Schroth	Cost effective discovery and quantification of mRNA and microRNA using the Solexa 1G Genetic Analyzer System
4:45-5:15	Open	
5:15-5:30	Board Bus for Dinner Cruise	
5:30	Bus Departs	
6:30-10:00	Dinner Cruise	

**Wednesday, October 4**

**Session 4: Cancer Therapeutic Targeting and Drug Resistance**

**Chair: Greg Riggins**

8:45-9:15	Greg Riggins	Using genomics to identify pathway targeted inhibitors for brain cancers
9:15-9:45	Todd R Golub	Genomic views of cancer
9:45-10:15	Charles L. Sawyers	Kinase inhibitors in cancer: Lessons from Chronic Myeloid Leukemia
10:15-10:30	Break	
10:30-11:00	Paul S Meltzer	A close look at the breast cancer genome
11:00-11:30	Matthew Meyerson	Genomic studies of human cancer
11:30-12:00	2 short talks selected from abstracts:	
	Ben Ho Park	High throughput isogenic cell line screening identifies compounds that target p21 null Tamoxifen resistant breast epithelial cells
	Minjung Kim	Comparative oncogenomics identifies NEDD9 as a melanoma metastasis gene
12:00-12:10	Closing Remarks	

**Applied Biosystems Lunch**

12:20-1:30 Lunch Buffet

**Sponsored by:**

