

The Biology of Genomes

Session 1 COMPUTATIONAL GENOMICS

WEDNESDAY 5/10/2006, 7:30 PM

T. Hubbard / M. Kellis

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
1	Hubbard	Reference vertebrate genome annotation at the genome camps—Ever closer union	15
2	Bansal	Evidence for inversion polymorphisms from unusual linkage disequilibrium patterns in the HapMap data	12
3	Keibler	Effects of SNPs on gene predictions	12
4	Neafsey	Transcription need not imply translation—Evidence of selection for reduced translational efficiency	12
5	Kellis	Sequencing and comparative analysis of <i>Drosophila</i> genomes	15
6	Siepel	Lineage-specific conserved elements and evolutionary turnover in ENCODE regions	12
7	Koller	Genetic variation and regulatory networks—Mechanisms and complexity	12
8	Schwarz	Cis-regulatory analysis of three <i>Caenorhabditis</i> genomes	12

Session 2 FUNCTIONAL GENOMICS

THURSDAY 5/11/2006, 9:00 AM

L. Pennachio / P. Fraser

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
9	Pennacchio	In vivo enhancer analysis of extremely conserved human noncoding sequence	15
10	Pavan	A sensitized mouse mutagenesis screen for novel loci regulating mammalian neural crest development	12
11	Bejerano	A tetrapodal distal enhancer and a mammalian ultraconserved exon are both derived from a novel "living fossil" retroposon	12
12	Mikkelsen	Epigenetic landscape of conserved gene deserts	12
13	Fraser	Preferential, transcription-dependent co-associations of specific genes in transcription factories reveal 3D transcriptional networks	15
14	Snyder	The transcriptional regulatory landscape of the human ENCODE regions	12
15	DePace	Building a 3-dimensional atlas of gene expression in multiple <i>Drosophila</i> species	12
16	Murray	Single-cell gene expression profiling in <i>C. elegans</i>	12

Session 3 POSTER SESSION I

THURSDAY 5/11/2006, 2:00 PM

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
17	Agarwal	Composition analysis of <i>N. equitans</i> reveals traits of hyperthermophilic adaptation	
18	Ahsan	5'SAGE-based micro RNA prediction	

19	Alejandro Osorio	The role of the histone deacetylase Rpd3p in coordinating the environmental stress response in yeast
20	Alfoldi	The huge repeat array—An extensive segmental duplication on the mouse Y chromosome
21	Alvarez	DNA sequencing with 454—New data type, new tools and new applications
22	Ambrosini	Human subtelomeric structure and variation
23	Amemiya	What does it take to make an adaptive immune system?—Genomics and the VLR system in the jawless vertebrates
24	Ananiev	Whole genome methylomic profiling via single molecule analysis
25	Apodaca	Comparative genomics of oxygen regulation in <i>E. coli</i> and phytopathogenic <i>Erwinia</i>
26	Estivill	Population-specific abnormal high density of HapMap phase II QC-SNPs in ENCODE regions
27	Arumugam	Pairagon—A program for accurate cDNA to genome alignment
28	Jaillon	A model for the analysis of whole genome duplications—The genome of <i>P. tetraurelia</i>
29	Avraham	Applications of plant ontology for describing and comparing phenotypes and gene expression in plant databases
30	Kent	VisiGene—A virtual microscope for in situ images
31	Barker	Genomic analyses of <i>Coccidioides</i> , a cryptically sexual human pathogenic fungus
32	Bassetti	A benchtop system for automated total gene synthesis
33	Baum	DNA pooling for whole genome association studies on the Illumina Infinium assay arrays
34	Belov	Towards a catalogue of marsupial immune genes—The marsupial antimicrobial gene repertoire
35	Benton	Measuring the dose-dependent global transcriptional response of <i>S. cerevisiae</i> to various DNA-damaging agents
36	Bhinder	High density genome scanning using Affymetrix and Illumina chips—Using the HapMap to evaluate performance
37	Bird	Exploring the role of noncoding DNA in the function of the human genome through variation
38	Bischof	Genome-wide identification of pseudogenes capable of disease-causing gene conversion
39	Brown	Informatics for next-generation DNA sequencing using single-molecule clusters and sequencing-by-synthesis (SBS)
40	Brown	What should we sequence next?—Predicting the utility of genome sequences for comparative gene prediction
41	Bult	The power of genomic data integration—Disease gene discovery in the laboratory mouse
42	Bustamante	Quantifying the distribution of selective effects among newly arising mutations in the human genome
43	Butler	Progress on ALLPATHS, a new assembly algorithm

44	Butler	Comprehensive testing of common variation in eight BBS genes for a role in obesity and short stature
45	Cain	The generic model organism database project
46	Campbell	Using F1 mice to detect the effects of <i>cis</i> -acting variants reveals complexities in gene expression
47	Carlborg	The role of epistasis in maintaining long-term selection response
48	Chen	Identifying and analyzing human Bardet-Biedl syndrome genes using <i>C. elegans</i> as a comparative genomics platform
49	Chen	Application of transgenic mice model in functional study of a novel putative oncogene <i>ALC-1</i>
50	Church	Analysis of the mouse reference (C57BL/6J) and non-reference assemblies
51	Stein	Aspects of large-scale chromatin structures can be predicted from the DNA sequence
52	Clamp	A human gene catalog based on comparative genomics revises the protein-coding gene count to under 20,000
53	Clark	An inventory of sequence polymorphisms for <i>Arabidopsis</i>
54	Collins	Investigations into the mechanism of bi-directional promoter activity
55	Cooper	Identifying direct binding sites of serum response factor in human transcriptional promoters
56	Bernardi	An isochore map of human chromosomes
57	Cruz	Launching a medical sequencing pipeline at the NIH Intramural Sequencing Center (NISC)—Initial computational challenges
58	Kellis	Sequencing and comparative analysis of <i>Candida</i> genomes
59	De La Vega	A genome-wide direct association study of Chron's Disease with 19,772 putative functional coding SNPs
60	Deakin	Analysis of MHC paralogous regions in the opossum
61	DeCaprio	A haplotype map for <i>P. falciparum</i>
62	Delaney	Gene copy number variants, the limits of detection using Affymetrix® SNP genotype chips
63	Deo	Phylogenetic application to complex psychiatric phenotypes
64	Dermitzakis	Interrogating functional variation in the ENCODE regions
65	Derrien	A revised canine gene repertoire inferred from gene-order conservation analysis and confirmed by sequence similarity search
66	Ding	Software developments for high-throughput medical sequencing data analysis
67	Down	Genome-wide prediction of transcription factor binding sites
68	Dunham	Comprehensive mutation discovery in experimentally evolved yeast
70	Ehm	The design and performance of a genome-wide association study to identify genetic predispositions to rare adverse drug reactions
71	Eppig	From sequence to disease—Mining for mouse models

72	Feuk	Assembly comparisons to discover copy number variants and DNA sequences not present in the human reference genome
73	Fiedler	WormBook—A software suite for online biological literature
74	Flicek	EGASP—The human ENCODE genome annotation assessment project
75	Flicek	Functional genomics and Ensembl
76	Forrest	A comprehensive investigation of alternative splicing on human chromosomes 20 and 22
77	Fulton	A look at the sequence improvement pipeline at the Genome Sequencing Center in St. Louis
78	Furey	Genome-wide sequence and functional analysis of early replicating DNA in normal human fibroblasts
79	Furey	Identifying genes potentially hypermethylated in cancer using genome sequence features
80	Giardine	Phenocode—Paving the path between phenotype and genome
81	Gibbs	The Bovine Genome Project
82	Gibbs	High throughput genomics at the Baylor College of Medicine Human Genome Sequencing Center
83	Gibbs	A second non-human primate genome
84	Giresi	FAIRE for the isolation of accessible DNA from human chromatin
85	Glasscock	The chimpanzee genome, swinging the other way with comparative analysis
86	Glavina Del Rio	JGI sequencing projects—The process of ensuring efficiency and quality from initiation to completion
87	Goel	The relationship between the closest blast matches and the nearest tree neighbors—Koski-Golding incompatibilities and what to make out of them
88	Gogarten	Evolutionary dynamics of the olfactory receptor subgenome
89	Hameister	Precise characterization of the macro- and microchromosomal differences that distinguish human and chimpanzee genomes
90	Milosavljevic	Genboree open hosting system for genome research
91	Dirks	'Zomes—Tools for phylogenomic exploration and analysis of animals, plants, and fungi
92	Goodwin	Implementing project management at the Joint Genome Institute
93	Gopinathrao	Reactome—Not just another pathway database
94	Grabherr	Quality metrics for draft genomes
95	Alarcon-Riquelme	A common haplotype of interferon regulatory factor 5 (IRF-5) regulates mRNA splicing and expression, and is associated with increased genetic risk in human SLE
96	Estivill	Tag SNP genotyping of neurotrophin signaling pathways in neuropsychiatric disorders
97	Grosse	Vombat—A web server for predicting transcription factor binding sites using variable order Bayesian trees
98	Graves	Exploring genomes of alternative mammals

99	Green	Analysis of over 1 megabase of the Neandertal genome
100	Griffith	Characterization of alternative splicing events in the druggable genome using splicing microarrays
101	Griffith	A novel method for identification of deregulated genes using differential coexpression analysis—A prostate cancer case study
102	Grosse	Reconstruction of Bayesian networks from mRNA and metabolite expression data
103	Guigo	The transcriptional landscape of the ENCODE regions
104	Wortman	Automated annotation and classification of alternatively spliced transcripts using TIGR's PASA pipeline
105	Hallgrimsdottir	Two-locus affected sib-pair linkage analysis
106	Hardison	Prediction and experimental validation of erythroid <i>cis</i> -regulatory modules
107	Milosavljevic	Reconstruction of the genome of the human-chimpanzee ancestor and the events in the last six million years of human genome history
108	Harris	WormBase, a highly curated resource of nematode biology
109	Harrow	Improving genome annotation—Lessons from ENCODE
110	Harrow	Vega—A unique multi-species annotation resource
111	Havlak	RepeatMasker hides too much—K-masker for fast screening of frequent sequences before searching
112	Heger	Predictions and analyses of genes from 10 fruit fly genomes
113	Herschleb	Discovering structural variants in cancer genomes via single molecule analysis
114	Hicks	Functional genomics of breast cancer using ROMA-CGH
115	Hilger	Towards a levitated droplet ion source for electrospray ionization mass spectrometry
116	Hill	A novel method for rapid <i>de novo</i> repeat masking improves blast search speed 5 to 10 times
117	Hill	Determining the minimum subtree prune and regraft (SPR) distance between unrooted binary trees
118	Hirst	Characterizing the expressed genome of human embryonic stem cells through deep longSAGE profiling coupled with high-throughput race rescue of novel transcripts
119	Charlier	Power of genome-wide association studies in cattle—Identification of a mutation in ATP2A1 responsible for congenital muscular dystony in the Belgian blue breed
120	Huntley	Cataloging and comparing KRAB-ZNF transcription factors encoded in vertebrate genomes
121	Hurwitz	Variation between four wild rice genomes and the <i>O. sativa</i> genome
122	Iazvovskaia	NCBI probe database—A centralized archive of nucleotide probes and experimental results
123	Wadelius	A major effect of the histone deacetylase inhibitor butyrate is a paradoxical decrease in promoter histone acetylation and decrease in gene activity
124	Ishikawa	Global detection of copy number variations in human genome by Affymetrix 500K mapping arrays

Session 4 GENOMICS OF NON-HUMAN SPECIES

THURSDAY 5/11/2006, 7:30 PM

L. Andersson / P. Andolfatto

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
125	Andersson	Domestic animals—A treasure trove for exploring genotype-phenotype relationships	15
126	Georges	A mutation revealing an illegitimate miRNA target site in the myostatin gene is a quantitative trait nucleotide with major effect on muscularity in sheep	12
127	Ecker	Mapping and functional analysis of the epigenome in <i>Arabidopsis</i>	12
128	Worley	The Honey Bee Genome Project	12
129	Andolfatto	Constraint and adaptive evolution in coding and non-coding DNA of <i>Drosophila</i>	15
130	Durbin	The yeast population genome re-sequencing project—Initial results	12
131	Richards	Informing biology with model insect genomics—New insights into embryonic development and a facile model for cloning complex genetic trait loci	12
132	Sidow	Regulatory architecture, function, and evolution—Insights from motif level dissection of ten <i>Ciona</i> gene regulatory regions	12

Session 5 EVOLUTIONARY GENOMICS

FRIDAY 5/12/2006, 9:00 AM

J. Graves / H. Kaessmann

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
133	Graves	Application of the E-painting technique for karyotype reconstructions and breakpoint characterization	15
134	Lindblad-Toh	Insights from the first high coverage marsupial genome sequence	12
135	Haussler	Feasibility of reconstructing the 100 million year history of the human genome	12
136	Rokhsar	Our squishy cousins—Genome evolution across the animal tree of life	12
137	Kaessmann	Origin and evolution of retrogenes in the human genome	15
138	Carbone	A high-resolution map of synteny breakpoints indicates a strong correlation between human segmental duplications and gibbon translocation regions	12
139	Jiang	Evolutionary reconstruction of segmental duplications reveals genomic cores of human gene innovation	12
140	Paabo	Pleistocene genomics	12

Session 6 POSTER SESSION II

FRIDAY 5/12/2006, 2:00 PM

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
141	Jackson	Evolution of chromosomes in the genus <i>Oryza</i>	
142	Jaeger	PrimerDesign script, database and website—An optimized tool for primer development	
143	Jaffe	Assembly of genomes from microreads	

144	Jeong	Transcriptional consequences of DNA gyrase inhibition in <i>E. coli</i>
145	Jiang	Development of high resolution human fosmid arrays
146	Johnson	Genome-wide analysis of transcription
147	Kalafus	Bacterial and mammalian genome resequencing using pyrosequencing
148	Kamal	A large family of ancient repeat elements in the human genome is under strong selection
149	Kanin	A regulatory network map of bacterial transcription regulation
150	Karlsson	Genome-wide association mapping of three traits in dogs using 20,000 SNPs
151	Karro	Time-average neutral substitution rate variation over the genomes of modern mammals and the mammalian ancestor
152	Thorisson	Biomart—A query-oriented data management system for fast and flexible access to biological data
153	Kathiresan	Value of multiple measurements of phenotype in heritability estimation—An example of lipid phenotypes serially measured over 30 years in the Framingham heart study
154	Kato	MotifCombinator—A web tool to search for <i>de novo</i> combinations of cis-regulatory motifs in mammalian genomes
155	Katoh	Human WNT-ome project
156	Kawashima	Analysis of polymorphism in the genome of the chordate, <i>C. intestinalis</i>
157	Kern	A population genetic Hidden Markov Model for detecting genomic regions under selection
158	King	Constraint in mammalian transcriptional regulatory regions
159	Kingsford	Rapidly finding intrinsic transcription terminators in bacteria
160	Kirby	A haplotype-variation map of 50 inbred strains of mice
161	Kitts	Detecting foreign sequences in genome assemblies
162	Dunham	Maps of histone modifications in 1% of the human genome
163	Kohler	Simultaneous discovery and testing of small segregating deletions for association with disease in SNP genotyping studies
164	Kokocinski	Improving Ensembl gene annotation with ditags
165	Kouprina	Segmental human genome cloning to characterize gene function, structural variants, long-range haplotypes, and evolutionary changes
166	Krause	Multiplex amplification of the mammoth mitochondrial genome and the evolution of Elephantidae
167	Grosse	Prediction of genetic mapping positions using sequence alignments
168	Hattori	Metagenomics of microbial community in human intestine
169	Kuroki	Construction of a physical map for Tammar wallaby X chromosome comparative analysis
170	Kvikstad	Contribution of insertion/deletion events to sex chromosome architecture as inferred from human-chimpanzee genomic alignments

171	Kwitek	Developing rat knockouts for cardiovascular and pulmonary disease
172	Landry	Mutational variance of gene expression in yeast
173	Larkin	Ancient reuse chromosome breakpoints and large homologous synteny blocks revealed by multispecies comparison of vertebrate genomes
174	Larsson	Early vertebrate chromosome duplications generated the NPY receptor paralogon
175	Latreille	The <i>A. vinelandii</i> sequencing project
176	Lee	Highly conserved syntenic blocks and conserved non-coding sequences at the vertebrate Hox loci
177	Lee	The TIGR Rice Genome Annotation
178	Lehner	Systematic mapping of genetic interactions in <i>C. elegans</i> suggests a new paradigm for human genetic disease
179	Lette	Allelic imbalance in human cell lines and tissues
180	Lewis	Isotope-assisted differential metabolomics—A new strategy for high throughput analysis of global metabolic profiles
181	Liang	Comparative genome analysis in Gramene
182	Limborska	Association study of neurotransmission gene polymorphisms in Parkinson Disease patients from Russia by the use of APEX technology
183	Lin	Comparative gene identification in fungal, fly and mammalian genomes using a classification-based approach
184	Smith	Differential male and female contributions from Africans and Europeans to African Americans—Consequences for admixture gene discovery
185	Lipovich	Global computational and expression profiling of the human cis-antisense subtranscriptome
186	Little	Genetic variation and the individual landscape of gene expression
187	Liu	Differential turn-over patterns of transposable elements account for the genome size differences among cattle, dog and human
188	Lombard	Identifying putative candidate genes through data-mining—Fetal alcohol syndrome as a model
189	Lunter	Adaptive evolution of non-coding elements expressed in brain
190	Lyon	Reproducibility of human obesity associations
191	MacArthur	Evolution of binding sites for transcription factors controlling early development in <i>Drosophila</i>
192	Magrini	Applications development for the 454 GS20 sequencer
193	Maher	Evolution of plant microRNAs
194	Mandir	Flap endonuclease cycling on a surface
195	Margulies	Exploring the relationship between evolutionary sequence conservation and sequence function

196	Friddle	Texas Institute for Genomic Medicine (TIGM)—Knocking out all murine genes in embryonic stem cells
197	Marshall	Genomic structural variation in patients with autism and developmental verbal dyspraxia
198	Mathavan	Comparative genomics approach for identifying regulatory regions in genes that express in the forebrain
199	Matysiak	New developments in microarray technology
200	McCarroll	An initial genome-wide map of common, multikilobase human deletion polymorphisms
201	McKay	An interactive web-based karyotype viewer and image generator
202	McKay	Positional clustering of human metabolic pathway genes
203	Arndt	The evolution of the human genome—Prevalence of segmental duplications on small scales
204	Micklem	Flymine—An integrated database of <i>Drosophila</i> and <i>Anopheles</i> genomics
206	Devine	An initial map of insertion and deletion (INDEL) variation in the human genome
207	Moffat	A lentiviral RNAi library targeting human and mouse genes—Construction, characterization and application to a high content arrayed screen
208	Grosse	Computational identification of transcription factor binding sites in seed specific promoters in <i>A. thaliana</i>
209	Phillips	Development of high throughput genotyping assays for pharmacogenomics using multiple technology platforms
210	Montgomery	In silico approach to the identification of regulatory polymorphisms within promoter regions of <i>H. sapiens</i> using comparative genomics, regulatory feature and sequence composition metrics
211	Thomas	Interspecies pre-mRNA splicing in the chicken DT40 cell line
212	Mortazavi	Towards a better model of the NRSF PSFM and of its in vivo targets
213	Muzny	Strategies for upgrading genomes
214	Myers	Integrated analysis of multiple experimental datasets reveals novel human promoters with no existing cDNA evidence
215	Nakatani	Genome evolution of medaka, <i>Tetraodon</i> , and zebrafish
216	Levanon	RNA editing level in the mouse is determined by the genomic repeat repertoire
217	Nelson	Development of a densely genotyped population reference sample—A resource for population, disease, and pharmacological genetics research
218	Newman	A human genome structural variation project
219	Newton-Cheh	Reproducible genetic associations with cardiovascular traits in the Framingham heart study
220	Ng	Structure and function revealed by the nucleotide sequence and genome analysis of a novel hyperthermophilic marine archaeon
221	Ng	Capturing common human variation on a single SNP beadchip

222	Nguyen	Influence of effective population size on selection for human and mouse copy number variants
223	Nikolaev	Early history of mammalian evolution is elucidated with the ENCODE multiple species sequencing data
224	Nilsson	Genotyping single DNA molecules in situ
225	Noguchi	Genome comparison between false killer whale and human
226	Noonan	Genomewide and targeted sequencing of Neandertal and cave bear DNA from metagenomic libraries
227	Oh	Evidence for positive selection among <i>Saccharomyces</i> genes
228	Okamura	Rapid diversification of genes by frameshift translation
229	Olivier	Quantitative proteomic profiling of vascular endothelial cells from consomic rat strains during angiogenesis—The NHLBI National Center for Proteomics Research at the Medical College of Wisconsin
230	Sachidanandam	Gviz—Psephology of genes
231	Pan	Exploration of genome conservation—Conserved clusters of homologous genes in plant genomes
232	Pangilinan	High-throughput eukaryotic whole-genome shotgun assembly
233	Papenfuss	Comparative analysis of the eukaryotic actin-ome reveals the specialized core proteins of apicomplexan motility
234	Bina	Transcription factor binding and functional properties of conserved and not conserved DNA sequence elements in genomic DNA
235	Park	Unique genomic landscape underlies human X inactivation profile
236	Ostrander	Phylogenetic studies in the domestic dog facilitates genetic studies of complex traits
237	Parra	Estimating gene prediction parameters in naked genomes from universal genes
238	Pasternak	The Maize Genome Sequence Browser
239	Riethman	Cloning and characterization of mouse telomere fragments
240	Feuillet	Chromosome based strategies to decipher the hexaploid wheat genome—Chromosome 3B, a case study
241	Petri	The Pathway Ontology—A new controlled vocabulary for biological pathways developed at Rat Genome Database
242	Elnitski	Development of a high throughput assay for negatively-acting transcriptional regulators in mammalian sequences
243	Ponjavic	Transcriptional and structural impact of TATA-initiation site spacing in mammalian core promoters
244	Salzberg	Assembling diverse mixtures of genomes
245	Prabhakar	Accelerated evolution of conserved noncoding sequences in the human genome
246	Pruitt	The conserved CDS (CCDS) project—A collaboration to facilitate use of genome annotation results

Session 8 POPULATION GENOMIC VARIATION

FRIDAY 5/12/2006, 7:30 PM

J. Pritchard / J. Sebat

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
248	Pritchard	A scan for recent selection in the human genome	15
249	Frazer	Phase II of The HapMap Project—Genotyping and analysis	12
250	Mullikin	Unbiased inferences about human demographic history from HapMap data	12
251	Majewski	Alternative splicing variation in humans	12
252	Sebat	High-resolution analysis of genome copy number variation in autism	15
253	Hurles	Global genomic variation in copy number	12
254	Hall	Copy number variation and genetic drift in the inbred mouse	12
255	Aitman	Copy number polymorphism in <i>Fcgr3</i> predisposes to glomerulonephritis in rats and humans	12

Session 9 STATISTICAL GENOMICS AND ASSOCIATION STUDIES

SATURDAY 5/13/2006, 9:00 AM

K. Roeder / L. Cardon

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
256	Roeder	Using weights to improve power of genome-wide association	15
257	Kimmel	Rapid and accurate significance evaluation in disease association tests of SNPs and haplotypes	12
258	Teslovich	Likelihood association tests for real-life studies	12
259	Oleksyk	Human genomic regions that display footprints of historic natural selection	12
	Cardon	No Abstract	15
260	Hallgrimsdottir	Identification of shared haplotypes for gene mapping	12
261	Stranger	Genome-wide associations of gene expression variation in humans	12
262	Baross	Genome copy number analysis of idiopathic mental retardation using high-density oligonucleotide microarrays	12

Session 10 POSTER SESSION III

SATURDAY 5/13/2006, 2:00 PM

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
263	Qu	Paralog evolution in two fishes medaka (<i>O. latipes</i>) and <i>Tetraodon</i>	
264	Sutter	Genetics of hip dysplasia in the domestic dog	
265	Marth	A computational tool for polymorphism detection in DNA resequencing data	
266	Haussler	Infinite sites models of genome evolution	

267	Rasmussen	SINDR—A probabilistic framework for genome-wide phylogeny and ortholog determination
268	Elsik	BeeBase—Supporting biologists in development of a new model organism, the honey bee
270	Richardson	Genedesign—Rapid, automated design of multikilobase synthetic genes
271	Robison	The identification of genes related to silicon metabolism in the marine diatom, <i>T. pseudonana</i> using tiling microarrays
272	Ruan	Genome-wide interrogation of transcriptional regulatory networks in cancer and stem cells
273	Wei	Transcriptome complexity of embryonic stem cells
274	Sabo	A high-resolution map of human chromatin accessibility in vivo
275	Hausler	Genome-wide scan for the most evolutionarily accelerated regions in the human genome reveals a novel RNA structural gene expressed in early neocortical development
276	Salamov	Genomic complexity of the basal cnidarian - <i>N. vectensis</i>
277	Miller	Spatial clustering of ultra-conserved sequence
278	Sasaki	Two <i>O. latipes</i> genomes reveal positive selection and multiple motifs around transcription start sites
279	Schein	Physical map of a follicular lymphoma genome—Identification and sequencing of genomic rearrangements
280	Scherer	Candidate gene medical sequencing—Fast identification of causative variant candidates in genetically heterogeneous cardiac disease
281	Serre	Allele-specific expression in the human genome
282	Ureta-Vidal	Untangling complex gene evolution in metazoa
283	Sharp	Heritability and linkage disequilibrium of copy number polymorphisms and identification of pathogenic rearrangements within duplicated regions of the human genome
284	Shaw	Chemical profiling of human cells to reveal functional consequences of disease mutations
285	Sachidanandam	Insights into splicing through comparative genomics
286	Delaney	An examination of sequence biases in large scale gene expression profiling data
287	Sikela	Genome-wide detection of human gene copy number variation by cDNA aCGH
288	Small	Genome wide characterization of extreme polymorphism in the urochordate <i>C. savignyi</i>
289	Smirnov	Influence of the mutations in the <i>ATM</i> gene on cellular processes prior and following cellular exposure to ionizing radiation
290	Smith	Cis-regulatory modules controlling gene expression in pancreas, kidney, and liver
291	Sodergren	The Sea Urchin Genome Project
292	Sodergren	Pooling BAC clones for sequencing the sea urchin and bovine genomes
293	Shen	The Atlas assembler integrates BAC derived data and adjusts for highly polymorphic genomes
295	Cheung	True and false positive results in genome-wide association analysis

296	Stamatoyannopoulos	Chromatin and replication architecture of the human ENCODE regions
297	Stapleton	The <i>Drosophila</i> ORFeome
298	Stark	Regulatory motif discovery in flies by comparative analysis of 9 <i>Drosophila</i> species
299	Stemers	Whole genome genotyping
300	Stein	Comparative mapping of an orthologous region of rice, maize, and sorghum
301	Stromberg	A novel methodology for the automatic detection of somatic mutations
302	Sugnet	Detection of alternative splicing and gene level summaries using exon micorarrays
303	Sundararajan	Measuring the dynamics of a transcriptional response using reverse transfection cell arrays
304	Sunkin	The Allen Brain Atlas—A genome-scale anatomically comprehensive atlas of gene expression in the mouse central nervous system
305	Sunyaev	Widely distributed non-coding selection in the human genome
306	Suzuki	Identification, comparative studies and experimental characterization of alternative promoters of human genes
307	Talkowski	Complete sequencing and comprehensive evaluation of the dopamine D3 receptor gene (<i>DRD3</i>) suggests an association with schizophrenia in 2 large samples
308	Tanaka	Comparative genome analysis between rice and <i>Arabidopsis</i> based on the curated annotation data of the Rice Annotation Project (RAP)
309	Taylor	Universe framework—Toward effortless tool integration and intelligent interfaces in genome biology
310	Taylor	Learning alignment patterns to identify functional elements
311	Tenney	Base calling for traces derived from multiple templates
312	Grosse	Computational mapping of crop plant ESTs
313	Thurman	Discovery of higher-order functional features in large genomes
314	Tischler	Combinatorial RNA interference in <i>C. elegans</i> reveals that redundancy between gene duplicates can be maintained for more than 80 million years of evolution
315	Totoki	Identification of novel human genes expressed in an extremely low level
316	Miller	Functional annotations of micro- and ultra-conserved sequence in human/dog/frog intersections
317	Tsung	A coalescent-based marker selection tool for clinical association studies
318	Twigger	Physiological genomics at the Rat Genome Database (RGD)
319	Urban	High resolution mapping of DNA copy alterations in human chromosome 22 using high density tiling oligonucleotide arrays
320	Valouev	An efficient algorithm for the whole-genome restriction map reconstruction from single DNA molecular restriction maps
321	Vavouri	Comparative analysis of conserved non coding elements in vertebrate and nematode genomes

323	Vignal	Radiation hybrid and genetic maps of GGA25, a microchromosome absent from the first draft chicken genome assembly
324	Villani	The familial Mediterranean fever gene (MEFV) as a disease susceptibility gene in inflammatory bowel disease (IBD)
325	Vinckenbosch	Evolutionary fate of retroposed gene copies in the human genome
326	Vinson	Gene prediction using conditional random fields
327	Visel	An in vivo dataset of human enhancers
328	Volik	Structural sequence, and functional analysis of tumor genomes and transcriptomes using end sequence profiling
329	Wade	Deep resequencing of 15 mouse strains
330	Wadhawan	Dual coding genes in human genome
331	Wakefield	Reconstructing the X with ancestral mammals
332	Wang	Darwin's fingerprint—Accelerated recent adaptive evolution in humans
333	Wang	Evidence of influence of genomic DNA sequence on human X chromosome inactivation
334	Warburton	Bioinformatic analysis of the evolutionary history of mammalian transposable elements by defragmentation and insertional analysis
335	Warby	Detailed haplotype analysis of the HD gene
336	Webber	Influences of chromatin status and G+C on the mammalian genomic landscape
337	Wheelan	Hunting transposon insertions in vivo—The TIP-chip
338	Wheeler	Mining genetic diversity from mammalian genomes
339	Williams	Normalization can profoundly influence identity of linkage in expression genetics studies
340	Wu	Expression QTL mapping in diverse mouse inbred strains
341	Zhang	Comparative genomics analysis facilitates the identification of functional exonic splicing enhancer elements in human genes
342	Xie	Families of conserved noncoding elements in the human genome related to ancient transposable elements
343	Xuan	Mammalian promoter database and its application
344	Yahyanejad	Predicting impact of missense substitutions by evaluating rejected substitutions in protein alignments
345	Yamada	PrimerStation—A highly specific multiplex genomic PCR primer design server for the human genome
346	Yamada	<i>De novo</i> repeat detection on the medaka genome
347	Yang	Combined assembly strategies for sequencing genomes with both 454 and 3730 reads
348	Yeang	A general model for coevolution of biosequences
349	Yorke	Improving genome assemblies using "reliable" overlaps

350	Kenmochi	Evolution of spliceosomal introns—Inferred from the ribosomal protein gene analysis
351	Zhang	A clustering property of highly-degenerate transcription factor binding sites in the mammalian genome
352	Zhang	Computational support of community annotation
353	Zhao	Boosting for predicting non-CpG related promoters
354	Zhao	Assessment of reference organism selection in the phylogenetic profiles for prediction of protein-protein interactions
355	Zheng	Identification and characterization of pseudogenes in the ENCODE regions
356	Zhou	Chimera gene detection improves genome annotation quality
357	Zhu	An in silico drug development framework for new antimalarials
358	Zimin	Assembly reconciliation—Improving drafts of genomes by combining several assemblies

SATURDAY 5/13/2006, 4:30 PM

GUEST SPEAKERS

David Cox, Perlegen Sciences

Nancy Wexler, Columbia University

Session 11 HIGH THROUGHPUT GENOMICS

SUNDAY 5/14/2006, 9:00 AM

J. Rogers / M. Uhlen

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
359	Rogers	Evaluation of new sequencing technologies	15
360	Arnaout	Profiling sequence dynamics in the adaptive immune system using 454	12
361	Crawford	DNase-chip—A high resolution method to identify DNase hypersensitive sites using tiled microarrays	12
362	Gresham	Genome-wide detection of single nucleotide polymorphisms with a single DNA microarray	12
363	Uhlen	A protein atlas based on the human genome sequence	15
364	McPherson	Medical resequencing—High-throughput detection of sequence variants associated with disease	12
365	Wiemann	High throughput cellular assays and the MIACA standard for disease research	12
366	Bentley	Human genome sequencing with next-generation technology	12