

# The Biology of Genomes

## Session 1 FUNCTIONAL AND CANCER GENOMICS

TUESDAY 5/6/2008, 7:30 PM

R. Wilson / M. Dean

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
	Wilson	No title	20
1	Futreal	Identification of somatic mutations in human cancer—Whole genome shotgun sequencing of a small cell lung cancer and matching constitutional genome	15
2	Hodges	Refined platforms for selective re-sequencing of genomic regions associated with breast cancer	15
3	Pleasance	Genomic rearrangements in cancer identified using massively parallel paired-end sequencing	15
4	Dean	Genome wide association studies of breast cancer	20
5	Edwards	Novel approach to whole genome methylation profiling applied to epigenetic alterations in breast cancer	15
6	Dermitzakis	Population genetics and genomics of human gene expression	15
7	McVean	Identification of a DNA sequence motif associated with hotspots for genome instability	15

## Session 2 GENETICS OF COMPLEX TRAITS

WEDNESDAY 5/7/2008, 9:00 AM

M. Georges / A. DiRienzo

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
8	Georges	Searching for rare Crohn's Disease susceptibility variants	20
9	Hurles	The contribution of common and rare copy number variants to disease risk in seven common diseases	15
10	Spielman	Heritable gene expression responses to endoplasmic reticulum (ER) stress in humans	15
11	Gabriel	Variant discovery in WGAS follow-up—Towards complete characterization of rare and common variation	15
12	DiRienzo	Adaptations to climate in candidate genes for common metabolic disorders	20
13	Speliotes	Meta analysis of genome wide association data for body mass index from over 32,000 individuals confirms two loci and identifies additional strong candidate loci	15
14	Riveira	A deletion of the late cornified envelope (LCE) 3C and 3B genes is a common susceptibility factor for psoriasis	15
15	Nica	Using gene expression to investigate the genetic basis of complex disorders	15

## Session 3 POSTER SESSION I

WEDNESDAY 5/7/2008, 2:00 PM

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
16	Abras	Effect of nematic fields on DNA elongation	

17	Absher	Genome-wide characterization of 51 human populations from the human genome diversity project
18	Ahsan	High throughput 5' end mRNA data analysis pipeline
19	Akagi	Extensive variation between inbred mouse strains due to endogenous L1 retrotransposition
20	Albert	Development of an optimized oligonucleotide microarray for capturing the entire human exome for high throughput sequencing
21	Albrechtsen	Relatedness mapping and tracts of relatedness for genome-wide data in the presence of linkage disequilibrium
22	Zhi	Recombination-associated sequence homogenization of neighboring Alu elements—The signature of nonallelic gene conversion
23	Andersson	Meta-genomic screening for new viruses—Exploration of the human virome
24	Wadelius	Functional SNP candidates identified by genome wide ChIP analyses
25	Andres	Balancing selection in the human genome—From genomic signals to evolution of individual genes
26	Andreassen	ROC curves of bootstrap samples used to predict type 2 diabetes status using validated SNPs
27	Antonacci	Discovery and characterization of human/great-ape inversion polymorphisms
28	Apodaca	Evolution of the transcriptional response to oxygen limitation in the enterobacteria
29	Yancopoulos	Bounds on generalized transpositions in genome rearrangements using the double cut and join (DCJ)
30	Avraham	The Plant Ontology database—A community resource for plant structure and developmental stages controlled vocabulary and annotations
31	Bachtrog	Pervasive adaptive evolution on a newly formed X chromosome
32	Bainbridge	Genome-wide exon-specific variation discovery in a HapMap trio with array capture and high-throughput sequencing
33	Barnes	Association testing with common copy number variants
34	Barnett	Whole-genome, complete mutational profiling using next-generation short-read sequencing
35	Estivill	Spectrum of genomic structural variation in human populations
36	Bell	Towards a complete planarian gene catalog
37	Bellott	Convergent evolution of the human and chicken sex chromosomes
38	Benovoy	Effect of polymorphisms within probe target sequences on oligonucleotide microarray experiments
39	Berlin	Sequencing and defining diversity of rare HCV genotypes using 454
40	Bird	Spatial gene expression of human paralogs
41	Ophoff	Genomic survey of DNA methylation in twin pairs reveals large degree of genetic control and independent strong effects of age and gender

42	Borel	The genetic control of microRNA expression variation in humans
43	Boycheva	Construction of a <i>pilA</i> gene knockout mutant of <i>A. temperans</i>
44	Furey	High-resolution mapping and characterization of open chromatin across the genome
45	Boyle	F-Seq—A feature density estimator for high-throughput sequence tags
46	Bradley	Ancestral reconstruction of proteins and ncRNAs
47	Bradley	Genome-wide survey for mRNA localization signals in <i>Drosophila</i>
48	Brejova	A probabilistic model of gene structure evolution
49	Busby	An informatics pipeline for miRNA profiling using next-generation sequencing platforms
50	Cain	A complete system for community genome annotation
51	Carbone	The Gibbon—A genomic puzzle
52	Carlborg	Multi-locus epistasis leads to hybrid inferiority in domestic fowl
53	Carninci	Cap-analysis gene expression (CAGE) analysis of transcriptional complexity and regulation
54	Carter	Whole genome sequence variation in 70 <i>Saccharomyces</i> strains
55	Carvalho Silva	Merging gene sets to validate vertebrate genomes
56	Caspi	Noncoding genome variation contributes to measures of selection in plasmodium genes
57	Chen	Detection of indels and novel splice variants using Illumina reads from cDNA libraries
58	Cherukuri	Predicting intolerance of amino acid alterations in conserved domains
59	Fujiyama	Joint <i>Porphyra</i> genome project to reveal early development of plant systems
60	Church	The Genome Reference Consortium
61	Galagan	Integrated genomics for tuberculosis drug resistance and metabolism
62	Thompson	Single molecule sequencing for human cancer genes
63	Conrad	A comprehensive map of common copy number variation
64	Cooper	Systematic assessment of copy-number variant detection via genome-wide SNP genotyping
65	Cooper	Profiling of small molecule metabolites in <i>S. cerevisiae</i>
66	Cotsapas	Towards a 'functional HapMap' with genetic dissection of drug metabolism in vivo and in vitro
67	Cox	Informatics of whole human genome sequencing
68	Cuomo	Comparative analysis of 8 pathogenic and non-pathogenic <i>Candida</i> species
69	De La Vega	SNP identification and genotyping by short-read next generation sequencing
70	Degenhardt	Increased <i>CCL3L</i> copy number is protective against simian AIDS in rhesus macaque
71	Di Palma	All creatures great and small—Vertebrate genome sequencing at the Broad Institute

72	Djebali	Efficient targeted transcript discovery via array-based normalization of race libraries
73	Diehl	A new method for identifying regulatory sequences under lineage-specific selection
74	Dimas	Exploring epistatic effects between regulatory and protein-coding variation
75	Dolan	MouseCyc—A curated biochemical pathways database for the laboratory mouse
76	Donato	Binding site specificity in genomes—The role of allosteric DNA modulation in protein-DNA assembly
77	Durbin	The 1000 Genomes Project—Obtaining a deep catalog of human genetic variation with new sequencing technology
78	Stein	Sequence information encoded in DNA that may influence long-range chromatin structure correlates with human chromosome function
79	Erlich	Machine-learning approach to improving the accuracy of next-generation sequencing
80	Carninci	Repetitive elements are globally expressed in mammalian cells
81	Fernandez-Banet	Improvements in Ensembl human genome annotation
82	Feuk	The database of genomic variants (DGV)—Annotating structural genomic variation
83	Flicek	Extending ENCODE annotation to the entire genome
84	Coller	A search for conserved sequences in coding regions reveals that microRNAs target coding regions and suggests a mechanistic difference in coding regions versus 3'UTRs
85	Forman	A method for mining arbitrarily large multiple alignments finds evidence for DNA sequence motifs under recent positive selection
86	Chuang	Universality in regional mutation rates and silent site selective pressures
87	Fredman	Reconstructing the evolutionary history of genomic regulatory blocks
88	Friedli	An in vivo unbiased screen for enhancer activity using lentivector-mediated transgenesis
89	Fu	SOLiD™ sequencing and 2-Base encoding
90	Gaffney	Quantifying the evolution of alternative splicing in mammals using exon arrays
91	Gao	Identifying the optimal number of clusters via the Deviance Information Criterion
92	Garber	A new statistical framework for detecting functional constraint using comparative genomics
93	Navarro	Copy number variation in the great apes
94	Tenenbaum	Using RNA-binding proteins and microRNA targeting to study the mRNP code
95	Gibbs	Genome biology at the Baylor College of Medicine Human Genome Sequence Center
96	Gonzales-Garay	Genboree Discovery System and its application in The Cancer Genome Atlas (TCGA) project
97	Goode	A consistent effect of constraint on sequence variation in the human genome
98	goodson	Identifying functional biases within QTL datasets
99	Goodstadt	Extensive changes to the mouse gene repertoire

100	Gordon	Using Consed and Cross_match in resequencing projects
101	Goto	Evolution of X-degenerate Y chromosome genes in greater apes—Conservation of gene content in human and gorilla, but not chimpanzee
102	Grabherr	Finding signatures of adaptive evolution in populations of three-spine sticklebacks
103	Kelso	A complete Neanderthal mitochondrial genome sequence
104	Grundberg	Population variation in <i>cis</i> -regulation of gene expression in human primary cells
105	Gundem	Intogen—Integrating different types of oncogenomic data
106	Haas	Genome dynamics in the potato blight organism may define aspects of pathogenesis
107	Milosavljevic	Comprehensive basepair-level map of chromosomal aberrations in the MCF-7 breast cancer cell line yields insights into the clonal evolution of a cancer genome
108	Han	Genome-wide target site triplication of <i>Alu</i> elements in the human genome
109	Zhao	CpG islands density and its correlations with genomic features in mammalian genomes
110	Hansoul	Phenotype prediction using animal breeding methodology—Application to Crohn's Disease
111	Hardison	Determinants of DNA occupancy by mammalian transcription factors—History and current events
112	Harismendy	Comparative study between Solexa and Sanger sequencing
113	Harris	Design of a primate comparative methylation array
114	Harris	Towards integrative customizable displays for a model organism database
115	Hashimoto	High-resolution analysis of the 5'-end transcriptome in a colon cancer cell line treated with epigenetic drugs
116	Haynes	Reverse engineering transcriptional networks from static and dynamic data
117	Hazkani-Covo	Numt insertion mechanism involves reduced loss of chromosomal nucleotides
118	Hellmann	CpG dinucleotides in primate evolution
119	Reese	What can we learn from an individual genome—Dr. Watson's sequence analyzed for disease-predisposing alleles
120	Reymond	Copy number variants and gene expression in the mouse
121	Higasa	Impact of definitive haplotypes for detecting recent positive selection
122	Himmelbauer	BeetSeq—A reference genome sequence for sugar beet

**Session 4 HIGH THROUGHPUT GENOMICS AND GENETICS**

WEDNESDAY 5/7/2008, 7:30 PM

M. Vidal / S. Celniker

<b>#</b>	<b>Iname</b>	<b>Title</b>	<b>Talk Length</b>
123	Celniker	The modENCODE (model organism Encyclopedia of DNA Elements) Project	20
124	Segre	Core diversity profile of human skin microbiome in health and disease	15

125	Margulies	De novo genome sequencing and assembly using short sequence reads and reduced representation libraries	15
126	Nusbaum	Biological applications and process development for massively parallel sequencing technologies	15
	Vidal	No title	20
127	Lister	Sequencing the genome, transcriptome, methylome and smRNAome of the <i>Arabidopsis</i> ecotype, Cape Verde Island	15
128	Kapranov	New classes of RNAs associated with 5' ends of non-coding transcripts	15
129	Green	Transcriptional profiles of male and female <i>D. melanogaster</i> as revealed by deep sequencing	15
130	Guttman	Chromatin structure reveals thousands of highly conserved, large non-coding RNAs in mammals	15
131	Durbin	The 1000 Genomes Project—Obtaining a deep catalog of human genetic variation with new sequencing technology	15

**Session 5 COMPUTATIONAL GENOMICS**

THURSDAY 5/8/2008, 9:00 AM

S. Salzberg / S. Lewis

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
132	Salzberg	Gene-boosted assembly of very short reads	20
133	Sorek	Sequencing gaps in bacterial genomes harbor antimicrobial peptides, restriction enzymes and toxic small RNAs	15
134	Herrero	ENREDO, PECAN and ORTHEUS, accurate and realistic genome wide alignment and ancestor reconstruction	15
135	Kellis	Comparative genomics of <i>Drosophila</i> and mammalian species	15
	Lewis	No title	20
136	Batzer	L1 recombination-mediated deletions generate human genetic variation	15
137	Li	Inference of human population history from whole genome sequence of a single individual	15
138	Arndt	Mutagenic processes associated with transcription	15

**Session 6 POSTER SESSION II**

THURSDAY 5/8/2008, 2:00 PM

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
139	Hoffman	The properties of natural selection in mammalian promoters	
140	Hong	Genetics and genomics of mammalian pigment patterns— <i>Tortoiseshell</i> , <i>calico</i> , and Ohno's law	
141	Huang	A benchmarking platform for next-generation sequence read assembly and polymorphism discovery tools	
142	Hubner	Identification and mapping of single nucleotide polymorphisms for genetic analysis in the rat	
143	Clark	Inference from short-reads to tandem gene arrays	

144	Hurle	Comparative genomic studies of the kallikrein and <i>WFDC</i> loci provide insights about primate genome evolution
145	Hussin	Haplotype allelic classes in the lactase persistence locus
146	Hyland	Whole genome sequencing of a Yoruba sample—54,000 small indels in a Yoruba sample are highly underrepresented in coding regions and are overrepresented in certain genes
147	Slesarev	The supragenome of <i>Methanopyrus</i> isolates
148	Imamura	Is the local mutation rate different in orthologous mammalian locations?
149	Irie	The correlation analysis between primary DNA sequences and transcriptional activities in HEK293 cells
150	Ishikawa	CNV detection by microfluidic digital array
151	Iskow	A novel assay to detect recent transposon insertions in the human genome
152	Peltonen	The genome-wide patterns of variation exposes significant substructure in a founder population
153	Jeffares	Selective constraint in the small and compact genomes of malaria parasites ( <i>Plasmodium</i> sp.)
154	Johansson	Selector and extractor probes for multiplex targeted copy-number and sequence analyses
155	Johnson	Estimating recombination rate in microbial populations
156	Johnston	Population demographic history can cause the appearance of recombination hotspots
157	Joseph	The actinome of <i>D. discoideum</i> in comparison to actins and actin-related proteins from other organisms
158	Zdobnov	Amniote CNC slowdown—Selection or a drift?
159	Katzman	UCSC Genome Browser display of 1000 genomes
160	Kemkemer	An ancient addition to the ancestral part of the mammalian X chromosome was already enriched for brain specific genes
161	Kim	Association mapping study for circadian clock variation of <i>N. crassa</i> natural population
162	Kirkness	Evaluation of paired-end tags for detection of variation between human genome sequences
163	Kitts	NCBI resources for genome assemblies defined in AGP format
164	Kokocinski	Enhanced UTR definition using additional evidence
165	Smith	Genome wide admixture mapping identifies a major effect risk gene for focal segmental glomerulosclerosis and hypertensive end-stage kidney disease in African Americans
166	Kordis	Synapsid paleogenomics—The enormous impact of the end-Permian ecological catastrophe on the genome structure and evolution of mammals
167	Kramer	wikiLIMS—Developing a laboratory information management system for next generation sequencing data
168	Kukita	Detection of human copy number variations using a collection of complete hydatidiform moles—A strategy of CNV-detection using human haploid genomes

169	Kulevich	Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry for top-down proteomics
170	Hattori	Comparative metagenomics revealed commonly enriched gene sets in human intestine
171	Kuroki	Comprehensive analyses of Y chromosomes toward understanding of the male-specific genome functions
172	Kuroshu	Short read multiclonal assembly accelerates sequencing full-length cDNA clones
173	Kuruville	Integrated genotype calling and association analysis of SNPs, common copy number polymorphisms, and rare CNVs
174	Kuttykrishnan	A dynamic model of the glucose transport network in <i>S. cerevisiae</i>
175	Kvikstad	Ride the wavelet—Scale-specific dynamic of genomic contexts flanking small insertions and deletions
176	Kwan	Genome-wide analysis of tissue-specific genetic variation in transcript isoform processing
177	Bujold	GenoByte—A high performance storage engine for high-throughput genotyping
178	Pe'er	A genomic survey of preferential allelic amplification in lung and breast cancer
179	Lappalainen	Signatures of genetic drift, admixture and natural selection in the genomic landscape of North European populations
180	Larkin	Evidence for adaptive and negatively selected chromosome rearrangements in amniote evolution
181	Lawson	Connecting genotype to phenotype—The molecular evolution of craniofacial growth and development
182	Lee	Comparison of elephant shark, human and teleost fish genomes reveals evolutionary changes in the regulatory regions of teleost fishes
183	Lee	The fine-scale and complex architecture of 1086 human copy number variant (CNV) regions as defined by custom high-density oligonucleotide microarrays
184	Lefebvre	InfRec—A heuristic tool to analyze recombination rate at the sequence level
185	Lenhard	Type 2 diabetes susceptibility variants fall within anciently conserved chromosomal domains of transcriptional regulator genes
186	Levin	Identifying somatic mutations in cancer and expression level changes with Illumina cDNA sequencing
187	Li	MAQ—Mapping and assembling short read sequences using quality scores
188	Li	Bayesian mixture models for case-control genome-wide association studies
189	Li	Association studies involving over 90,000 samples demonstrate that common variants near to <i>MC4R</i> influence fat mass, weight and risk of obesity
190	Liang	Evidence-based gene builds in plant genomes
191	Li	GADEM—A Genetic Algorithm guided formation of spaced Dyads coupled with an Em algorithm for Motif discovery
192	Lieberman	Transposons are a major force spreading insulators across the mammalian genome
193	Limborska	Analysis of PARK2 and LRRK2 defects in sporadic Parkinson's patients from Russia

194	Lin	Exploring legumen genome evolution by sequence analysis of homeologous regions of soybean and legume species
195	Lister	Highly integrated single base resolution maps of the epigenome in <i>Arabidopsis</i>
196	Liu	Antibiotic resistance genes database (ARDB)
197	Liu	Analysis of cattle copy number variation reveals insights into the evolution of ruminants
198	Liu	CpG island methylation on mammalian X chromosomes
199	Logsdon	A statistical framework for inferring pathway structure from gene expression data
200	Lopez-Bigas	Genome-wide analysis of the H3K4 histone demethylase RBP2 reveals a transcriptional program controlling differentiation
201	Lowe	Select extant species harbor ancient mobile elements exapted by humans
202	Lu	Cross-species cDNA-to-genome alignment—Program accuracy depends on evolutionary distance
203	Tello-Ruiz	Using HapMap population data to reconstruct chromosome-length phased contigs from an individual's diploid genome
204	Lunter	10% of the human genome is evolutionarily conserved
205	Hausler	Reconstructing ancestral genomes using the infinite sites model of genome evolution
206	MacArthur	Recent positive selection on a common human null allele associated with athletic performance
207	Eisen	Transcription factors bind promiscuously, but are they doing anything?
208	Maguire	Improved and applied quality scores for new DNA sequencing technologies
209	Maia	Studying susceptibility to breast cancer using allelic variation of gene expression
210	Maier	Optimizing phylogenetic substitution models for N-SCAN gene prediction
211	Malcolm	Identifying functional CNEs using enhancer trap-containing BACs as transgenes in zebrafish
212	Marques	Functional diversification of duplicate genes through subcellular adaptation of encoded proteins
213	Marth	Informatics tools for human genome resequencing
214	Boffelli	Phyloepigenomic comparison of human and chimpanzee
215	Navarro	The role of genetic heterogeneity in inter-population replication trials of disease risk variants
216	Matsumoto	Construction and end-sequence of full-length cDNA clones from a malting barley—Towards understanding of barley transcriptome
217	McEwen	The effect of sequence quality on comparative genomics analyses
218	McGuire	Cross-kingdom patterns of alternative splicing and splice recognition
219	McKay	The Genetic Genome Browser—New features

220	McLaughlin	Large-scale SNP detection in a human genome achieved by sequencing of fragment and paired-end libraries
221	Wu	Cloning of long PCR amplicons and difficult DNAs in a linear plasmid
222	Meador	Applying the neutral indel model to real and simulated genomes for diverse metazoans
223	Zwick	Evaluating microarray-based genomic selection (MGS) of targeted human X-chromosome sequences
224	Mersha	A candidate gene discovery procedure for obesity-related linkage studies
225	Meyer	Allele-specific upregulation of <i>FGFR2</i> increases susceptibility to breast cancer
226	Meynert	An explanatory model for vertebrate enhancers
227	Mezey	Genome-wide association analysis of genotype by cigarette smoking interactions affecting small airway epithelium gene expression
228	Zhang	Targeted sequencing of megabase regions in the human genome by combining microarray based genomic selection and high-throughput sequencing
229	Devine	1.7 million structural variants in the genomes of diverse humans
230	Montgomery	Implications of <i>trans</i> -acting regulatory interactions in lymphoblast cells on the functional and structural organization of the human genome
231	Morgante	Genome proteome and transcriptome of the grapevine ( <i>V. vinifera</i> ) improved using new sequencing technologies
232	Morgante	Resequencing of a second grapevine genome reveals frequent SNP and structural variation
233	Mori	Extreme sequence conservation of 16S rRNA gene copies
234	Mueller	The mouse X chromosome is enriched for multi-copy testis genes exhibiting post-meiotic expression
235	Dolan	Describing biological regulation in the gene ontology
236	Muralidhara	Singular value decomposition analysis of 16S rRNA sequence alignments reveals phylogenetic subgroups and corresponding characteristic sites
237	Muzny	Multi-platform mammalian assemblies using next generation technology
238	Nadeau	Testing haplotype allelic classes by coalescence simulations
239	Nagarajan	Framework for cost-effective, hybrid assembly of genomes using Sanger and 454 sequencing
240	Nakatani	Clear chromosome-wide synteny conservation between chicken ( <i>G. gallus</i> ) microchromosomes and silkworm ( <i>B. mori</i> ) chromosomes
241	Navratilova	<i>Cis</i> -regulatory activity of conserved non-coding elements residing in megabase and multigene regions around transcription factor genes
242	Nayak	Identifying gene expression regulatory networks in lymphoblastoid cells
243	Negrete	DNA nanotechnology via DNA microarrays
244	Parnell	Identifying genetic variants underlying differential response to the diet

245 Nowick Rapid divergence of KRAB-ZNF expression between human and chimpanzee B-lymphoblasts

**Session 8 EVOLUTIONARY GENOMICS**

THURSDAY 5/8/2008, 7:30 PM

J. Noonan / S.L. Baldauf

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
246	Noonan	Human-specific gain of function in a developmental enhancer	20
247	Marques-Bonet	Characterization of great ape and human specific duplications reveals a burst of activity in the common ancestor	15
248	Paabo	The Neanderthal genome project	15
249	Pollard	Accelerated evolution in the upstream regions of ape-specific duplicated genes	15
	Baldauf	No title	20
250	Kozyavkin	Triplex DNA in <i>T. thermophilus</i> siphoviruses and genome fragility	15
251	Rosso	Enhanced mitochondrial targeting of the hominoid-specific glutamate dehydrogenase driven by positive Darwinian selection	15
252	Dagan	Modular networks and cumulative impact of lateral transfer in prokaryote genome evolution	15

**Session 9 GENETICS AND GENOMICS OF NON-HUMAN SPECIES**

FRIDAY 5/9/2008, 9:00 AM

G. Barsh / W. Warren

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
253	Barsh	Evolutionary history and molecular basis of adaptive melanism in arctic wolves—Reverse gene transfer	20
254	Bustamante	Sign, sign, everywhere a sign—High density haplotype maps of the dog, human, and cow genomes reveal extensive human reorganization of domesticated genomes	15
255	Andersson	A Cis-acting regulatory mutation causes premature hair graying and susceptibility to melanoma in the horse	15
256	Charlier	Highly effective SNP-based association mapping and management of recessive defects in livestock	15
257	Warren	Gaining evolutionary insight from the platypus genome	20
258	Werren	The Nasonia genome and applications to microevolutionary studies and QTL cloning	15
259	Symer	Extensive variation between inbred mouse strains due to endogenous LTR retrotransposition	15
260	Ptak	Bonobo genome sequencing	15

**Session 10 POSTER SESSION III**

FRIDAY 5/9/2008, 2:00 PM

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
261	Haghighi	DNA methylation profiling of major depression	
262	Oleksyk	Evolution and worldwide distribution of <i>APOL1</i> , <i>APOL2</i> , <i>APOL3</i> , <i>APOL4</i> and <i>MYH9</i> In human populations	

263	Omberg	Integrative analysis of genome-scale expression data from yeast cell cycle time courses under different oxidative stress conditions
264	Ong	Approaches to combining and analyzing time-series expression data
265	Pang	Identification of structural variation using clone-end sequence mapping
266	Parker	No dog is an island—Mapping fixed traits in purebred domestic dogs
267	Parla	High-throughput genetic resequencing of target genomic regions
268	Peckham	A high-resolution structural variation map of a human genome by next-generation, high-throughput paired-end sequencing
269	Pertea	OperonDB—A comprehensive database of predicted operons in microbial genomes
270	Petri	Pathway data at the Rat Genome Database
271	Elnitski	Detection and characterization of silencers and enhancer-blockers in the greater CFTR region
272	Phanstiel	Quantitation of protein expression in human IPS cells using iTRAQ, ETD, and beam-type CAD on an Orbitrap mass spectrometer
273	Plagnol	Assessing association with common chromosomal inversions in seven common diseases
274	Ponjavic	Non-coding and protein-coding transcripts co-localize in the developing brain as well as on the genome
275	Marques	Chromosomal gene movements reflect the recent origin and biology of therian sex chromosomes
276	Pravenec	Genetic deficiency in the renal expression of Cd36 increases blood pressure in the spontaneously hypertensive rat
277	Pruefer	Biases in the analysis of ancient DNA sequences
278	Qin	New sequencing technology evaluation for human microbiome reference genome sequencing
279	Quinlan	Rare allele discovery and frequency estimation using current sequencing technologies
280	Rabinowicz	analysis of the castor bean genome reveals a large ricin gene family, few segmental duplications, and synteny with poplar
281	Rabionet	Genomic structural variation in patients with multiple sclerosis
282	Regulski	PCR-based enrichment of genomic targets for high-throughput sequencing
283	Reichwald	Initial genome characterization of <i>N. furzeri</i> —A new vertebrate model for aging research
284	Reid	microRNA variation and schizophrenia
285	Richards	Whole genome re-sequencing strategies in <i>Drosophila</i> —Short reads vs. long reads vs. assembled sequence
286	Rinkwitz	A genomic screen reveals principles of developmental gene regulation and genome architecture
287	Ripatti	Tackling gene-environment interactions—GWA in monozygotic twins exposes potential variability genes for serum lipids in females

288	Ritter	CNEviewer—A biotactic webtool of vertebrate conserved non-coding DNA elements
289	Robyrt	Functional interactions of conserved non-coding (CNC) sequences with other CNC using circular chromosome conformation capture (4C)
290	Rosenbloom	The ENCODE Data Coordination Center at UC Santa Cruz
291	Rosenfeld	Determination of enriched histone modifications in non-genic parts of the human genome
292	Rosso	Birth and rapid subcellular adaptation of a hominoid-specific CDC14 protein
293	Ruzanov	Sage protocol combined with Illumina flow-cell sequencing (Tag-Seq) improves detection of rare transcripts associated with longevity in <i>C. elegans</i>
294	Saito	UTGB shell—An open-source browser framework for the integration of biological data
295	Salmela	Genome-wide analysis of population structure in northern Europe
296	Sambriski	A mesoscale model of DNA and its application to the encapsidation of genomes in bacteriophage
297	Bruhn	Genome-wide oligonucleotide array-based measurements of copy number variations
298	Schatz	Genome assembly forensics—Finding the elusive mis-assembly
299	Scherer	Human variation discovery validation strategies
300	Schneider	Clone finding tools at NCBI
301	Schramm	A single molecule system for discovery of structural alteration and sequence information
302	Schueler	Chasing change—Primate centromere evolution
303	Scott	Meta-analysis of genome-wide association data and large-scale replication identifies several additional susceptibility loci for type 2 diabetes
304	Sen	Non-allelic homologous recombination between <i>Alu</i> elements contributes to genomic diversity between human populations
305	Serre	Metagenomic analyses of the microbial communities in a cheese sample and their temporal variations
306	Shadding	GSC Undergraduate Scholars—A cohort study on retention and increasing minorities in STEM
307	Shaikh	Genomewide copy number variation and its impact on the assessment of genotype-phenotype correlations in genetic disorders
308	Worley	Extensions of the Atlas genome assembly suite address issues in genome assembly and analysis
309	Smith	The obesity/metabolic syndrome portal at RGD
310	Shin-i	Whole transcriptome analysis of the nematode <i>C. elegans</i>
311	Shirts	Genes, herpes viruses, and cognitive function in schizophrenia
312	Shlyakhter	De novo assembly of microbial genomes from Illumina whole-genome shotgun data
313	Siddiqui	SuRFing the genome—A common standard for DNA sequence data
314	Sindi	Identification of inversion polymorphisms from single nucleotide polymorphism data

315	Cheung	Ataxia telangiectasia—A complex disorder?
316	Smith	Developmentally regulated rearrangement of the lamprey genome
317	Smith	Annotated datasets—Customizing your data at RGD
318	Soranzo	A genome-wide scan of adult human stature and skeletal size
319	Sougnéz	Approaches for somatic mutation discovery using Illumina sequencing technology
320	Sparsø	Haplotypes in <i>KLF7</i> associate with obesity assessed by BMI
321	Stein	Data coordination for the modENCODE project
322	Stewart	SPANNER—A tool for structural variation discovery from paired-end reads
323	Meyer	High-throughput targeted sequencing of ancient and forensic DNA
324	Stromberg	MOSAİK—A reference-guided assembler for next-generation sequencing platforms
325	Donnelly	A Bayesian multipoint allele sharing method for genome-wide association studies
326	Davuluri	A high-resolution map of alternative promoters that are active in different mouse tissues
327	Suzuki	Large-scale identification and characterization of alternative promoters of human genes using Solexa
328	Swaney	Decision tree-driven tandem mass spectrometry for shotgun proteomics
329	Tadepally	The Knockout Mouse Project (KOMP) Data Coordination Center
330	Tanaka	Transcriptome-based annotation of the rice genome and comparative analysis of transcription start sites
332	Tatsuno	Identification of precise recombination points using high-density SNP array and their impact on IBD estimation and linkage analysis
333	Taylor	Galaxy workflows—Enabling complex computational analysis for experimental biologists
334	Teytelman	Surprises in heterochromatin evolution of budding yeasts—Hyperdivergence of silenced DNA and hyperconservation of a silencer
335	Thomas	The white-throated sparrow—A natural model uniting genetics, evolution, and behavior
336	Tietjen	Challenging the dogma of RNA polymerase II CTD phosphorylation
337	Guigo	Splicing simulation based on a reduced set of putative splicing regulatory sequences
338	Sidow	The short read sequencing revolution in functional genomics—A case study from the intersection of ChIP-Seq data with tailored computational approaches
339	Pastinen	Common cis variants alter expression of complex disease genes
340	Vinar	Reconstructing duplication histories of complex tandem arrays in multiple primate species
341	Nekrutenko	Short-read analysis with Galaxy—Windshield genomics and beyond
342	Wang	Genome-wide discovery of genomic imprinting in mouse
343	Ward	Comparing genomic transcription factor affinity landscapes—An alternative to phylogenetic footprinting for identifying regulatory connectivity

344	Ware	Sequence and analysis of the maize B73 genome
345	Watkins-Chow	A sensitized mouse mutagenesis screen for modifiers of Sox10 neurocristopathies
346	Webber	Reduced purifying selection prevails over positive selection in human copy number variant evolution
347	Webber	Association of neurological disease genes with de novo copy number variants in mental retardation
348	Webster	Hotspots of biased nucleotide substitutions in human genes
349	Hoffmann	Region capture for next generation sequencing
350	Wheeler	Comparative analysis of genome-wide polymorphisms in two humans
351	White	Comparative metagenomics of organic and conventional apple tree microflora
352	Willer	Genome-wide association meta-analysis identifies new loci associated with height
353	Williams	Jumping libraries for paired end sequencing on Illumina's next generation sequencing platform
354	Sodergren	Evolution of the human microbiome project at WUGSC
355	Wu	Random shear BAC libraries for improved genome finishing
356	Wu	Sheep whole-genome RH comparative mapping for aiding its genome assembling
357	Xing	Analyses of human genetic structure using SNP microarrays
358	Xu	Integrating GWAs and candidate gene information with a functional SNP selection algorithm—An example in the genetic determinants of prostate cancer aggressiveness
359	Yeang	Combinatorial patterns of somatic gene mutations in cancer
360	Young	Assembly of genomes from new sequencing technologies
361	Yu	Understanding the full spectrum of genetic variants—2nd phase ENCODE re-sequencing in 805 individuals from 11 ethnicities
362	Zerbino	Velvet—Large assemblies using only short reads
363	Zhang	A new gram-based approach to identify interaction indicators between proteins from domain-domain interaction data yeast
364	Zhang	Characterization of cereal microRNA genes
365	Scacheri	Epitope tagging of endogenous proteins in somatic cells for genome wide ChiP-chip studies
366	Zhang	Constraint and turnover in sex-biased gene expression in the genus <i>Drosophila</i>
367	Zhang	Comprehensive analysis of a QTL revealed casual genes for lipid disorders in an obese cohort
368	Sanborn	UCSC cancer genomics browser

Michael Levin, University of California, Berkeley

Michael Lynch, Indiana University, Bloomington

**Session 11 POPULATION GENOMIC VARIATION**

SATURDAY 5/10/2008, 9:00 AM

E. Eichler / M. Przeworski

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
369	Przeworski	Variation in recombination patterns among humans	20
370	Neafsey	Widespread selection and frequent recombination in the genome of <i>P. falciparium</i> malaria	15
371	Bentley	Sequencing and analysis of an African human genome	15
372	Eichler	Ancient introgression and evolutionary recurrence of human genome structural variation	20
373	McVicker	Background selection explains patterns of neutral diversity in primate genomes	15
374	McCarroll	Genome-wide analysis of SNP and copy number variation in 1,170 individuals from multiple populations	15
375	Kidd	"New" human genome sequences that are variable among individuals	15