

# The Biology of Genomes

## Session 1 HIGH-THROUGHPUT BIOLOGY

WEDNESDAY 5/11/2005, 7:30 PM

E. Green / B. Andrews

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
1	Green	The ENCyclopedia Of DNA Elements (ENCODE) Project—An overview	15
2	Guigo	Towards the set of all protein coding genes in the ENCODE regions	12
3	Trinklein	The effects of genomic methylation on promoter activity and transcription factor binding in 1% of the human genome	12
4	Wadelius	Dissection of gene regulatory networks in liver cells using chromatin immunoprecipitation and high resolution genomic arrays of the ENCODE regions	12
5	Forrest	Biological interpretation of gene expression variation in the human genome	12
6	Andrews	Constructing genetic networks and exploring gene function using yeast functional genomics	15
7	Hubner	Integrated gene expression profiling and linkage analysis for identification of genes underlying disease	12
8	Little	Tissue specificity and the influence of genetic variation on gene expression	12
9	Dermitzakis	Adaptive evolution and selective constraints in conserved non-coding sequences in the human genome	12
10	McCallion	Efficient functional examination of human noncoding sequences in transgenic	12

## Session 2 COMPUTATIONAL GENOMICS

THURSDAY 5/12/2005, 9:00 AM

D. Haussler / E. Eichler

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
11	Haussler	Computational reconstruction of an ancient mammalian chromosome	15
12	Kellis	Regulatory motif discovery in human—Promoters, 3'-UTRs and microRNAs	12
13	Cutler	Whole genome association analysis, EATDT and beyond	12
14	Jaffe	Recent progress in genome assembly	12
15	Stein	The Reactome knowledgebase of biological processes	12
16	Eichler	Fine-scale structural variation of the human genome	15
17	Teague	Validation of mammalian genome sequence using optical maps	12
18	Birney	Using variation data to classify functional elements	12
19	Asimenos	A reference mammalian whole-genome alignment	12
20	Kent	New data, research and tools at genome.ucsc.edu	12

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
21	Agarwal	Genomic distribution of genes encoding 68 cytoplasmic ribosomal protein families	
22	Ak	DNA duplex destabilization at yeast regulatory regions—Genome-wide analysis reveals a highly conserved property	
23	Alejandro-Osorio	The role of chromatin remodeling proteins in the regulation of gene expression in response to environmental stress	
24	Alfoldi	The sequence of the mouse Y chromosome	
25	Alioto	Prediction of genes with U12-dependent introns in the human genome	
26	Riethman	Analysis of human subtelomeric duplicon structure and organization	
27	Ananiev	A single molecule approach for analysis of genome-wide methylation profiles	
28	Anderson	CGHScan—A novel algorithm for establishing deletion boundaries using comparative genomic hybridization data	
29	Andersson	Development of a chicken 10k SNP panel and its application to genome biology	
30	Annilo	Variation patterns in genes involved in the blood pressure regulation in human	
31	Antonarakis	Sequencing the short arm of human chromosome 21	
32	Attanasio	The majority of mammalian conserved non-coding sequences are not classical transcription regulators	
33	Bacha	High throughput SNP mining and functional testing of human chromosome 22	
34	Balija	Examining the 5'-end annotation of genes and gene predictions in the ENCODE	
35	Barr	Retroviral DNA integration and construction of the chicken genome	
36	Bassetti	Progress in the development of an automated gene synthesis method	
37	Bell	Design of oligonucleotide microarrays for vertebrate chromatin immunoprecipitation—From promoters to whole genomes	
38	Bennett	SVA retrotransposition in human cells	
39	Benton	//S. cerevisiae// as living biosensors for the detection of genotoxicity	
40	Bilusic	Double congenic BN.GH2.18—An animal model for threshold effect in	
41	Bina	A contextual analysis of sequences in proximal promoters of human genes	
42	Biro	Hidden messages in hidden sub-sequences—A study on collagens	
43	Birtle	Duplication and positive selection among hominid-specific PRAME genes	

44	Bonnen	Haplotype map for an isolated population in Micronesia—Evaluating potential for whole genome studies
45	Bray	Multiple alignment with MAVID v2.0
46	Zhao	Molecular and functional diversity in the maize genome
47	Brown	Begin at the beginning—Predicting genes with 5'UTRs
48	Burt	Comparative analysis of CpG islands in the genome sequences of chicken and
49	Cai	Large genomic segmental polymorphisms in inbred mouse strains detected using whole genome BAC arrays
50	Cain	The generic model organism database project
51	Rowen	The sea urchin hox cluster—Gene order and organization
52	Cantarel	From similarities to phylogenies—Exploring the relationship between evolutionary distance and accurate phylogenetic trees
53	Chapman	One million reads of maize
54	Chatterjee	Trimming both ends of large DNA inserts cloned in pBACe3.6 and related vectors using wild type and mutant 511 loxP transposons
55	Mandir	Direct SNP genotyping on surface invasive cleavage arrays
56	Chen	Brownian dynamics simulation of DNA conformation and dynamics in microfluidic
57	Chen	Shape encoded particles for high-throughput biological analysis
58	Stein	Predicting unusual chromatin structures in mouse liver from the genomic DNA
59	Clark	Population genetics of the metabolic syndrome
60	Cooper	Characterization of the effects of purifying selection in a sample of the human
61	Crawford	Genome-wide mapping of DNase I hypersensitive sites by massively parallel signature sequencing (MPSS)
62	Cunningham	Linkage disequilibrium data in Ensembl
64	Das	Genome-wide prediction of methylation landscape of the human genome
65	Das	Computational prediction of methylation status of the human genome
66	de Bakker	Selection and evaluation of tag SNPs in genetic association studies
67	Dehal	Two rounds of whole genome duplication in the ancestral vertebrate genome
68	Dehal	Tree based orthology and paralogy determination—Phylogenetically inferred groups (PHIGS)
69	Delaney	Progress in SAGE bioinformatics
70	Dirks	MetaZome
71	Doi	Gene prediction by 5' SAGE

72	Down	Discovery of regulatory motifs in large sets of sequence data
73	Drmanac	Universal chips for rapid gene resequencing
74	Du	Genome sequencing of //N. crassa// using 454 sequencing technology
75	Eisenberg	A-to-I RNA editing in mouse
76	Elsik	Insects that exhibit systemic RNA interference have SID-1 homologs
77	Engel	Increasing refinement of the //S. cerevisiae// genome annotation
78	Lipovich	Cis-antisense and bidirectionally promoted gene pairs in the mouse genome—From complex multipair chains to global cis-regulatory networks?
79	Eppig	Mouse models—Mutant phenotypes and human disease
80	Estivill	High throughput SNPlex genotyping of the BDNF gene in anorexia and bulimia
81	Farnoud	High-resolution analysis of genomic imbalance related to mental retardation (MR)
82	Fife	Novel interleukin 6 (IL-6) haplotypes and disease association
83	Force Aldred	New twists on enhancer and promoter trapping—Techniques ready for genome scale application
84	Friedberg	Calibrating genomic distance via universal operation
85	Gabriel	High throughput genotyping for the human Hap Map
86	Galver	A high density SNP panel in the MHC region
87	Gan	Towards a comprehensive functional and expression map of the proximal 75Mb of mouse chromosome 5
88	Ganko	Systematic identification of polymorphic transpositions in yeast
89	Sellers	Transforming cancer treatment through genome discovery
90	Giardine	Galaxy metaserver for integrative bioinformatic analysis of genomic data
91	Gibbs	Challenges in genome sequencing
92	Gilchrist	Systematic identification of pseudo-allele gene pairs in an allotetraploid amphibian by reference to a closely related diploid species
93	Gnerre	Assembly of 2X mammalian shotgun data sets, assisted by other mammalian
94	Milosavljevic	Genboree—Support for collaborative online sharing and development of genome annotations and related data
95	Goodstadt	Gene orthology and duplications in the dog and human genomes
96	Gunnarsson	Cloning of integration sites of ALVE using an AFLP-based approach

**Session 4 PERTURBATIONS OF GENOME SYSTEMS**

THURSDAY 5/12/2005, 7:30 PM

A. Fraser / C. Austin

<b>#</b>	<b><u>Iname</u></b>	<b><u>Title</u></b>	<b><u>Talk Length</u></b>
97	Austin	The NIH Chemical Genomics Center and Molecular Libraries Roadmap	15
98	Clemons	Multidimensional screening—Probing relationships between small molecules, assay measurements and cell states	12
99	Shaw	Novel phenotype discovery using systematic chemical perturbation and cell-based	12
100	Kanin	Chemical genomics offers unexpected insight into mechanisms of global transcription control	12
101	Roth	Analysis of the //S. cerevisiae// synthetic lethal genetic network	12
102	Fraser	RNAi screens to examine genetic interactions in //C. elegans// development	15
103	Root	High-content screening of a lentiviral RNAi library for genes required for mitosis	12
104	Schuler	New databases for molecular probe sequences and RNA interference results	12
105	Bucan	70 lethals, 700 genes and 7000 phenotypes in 70 Mb of the mouse genome	12
106	Kappen	Genome-wide discovery of gene regulatory elements	12

**Session 5 HAPLOTYPE VARIATION AND INTRASPECIES RESEQUENCING**

FRIDAY 5/13/2005, 9:00 AM

T. Hudson / E. Mardis

<b>#</b>	<b><u>Iname</u></b>	<b><u>Title</u></b>	<b><u>Talk Length</u></b>
107	Hudson	The 5kb HapMap—A haplotype map of the human genome with one million SNPs	15
108	Donnelly	A fine-scale genetic map of the human genome	12
109	Stone	High density SNP typing of ~1200 founder chromosomes reveals greater than expected haplotype diversity	12
110	Schaffner	Evidence for natural selection in the human genome using data from the International Haplotype Map Project	12
111	Pe'er	Reconciled estimates of linkage disequilibrium	12
112	Kasai	Developing a comprehensive approach to mutational profiling studies of the human genome	15
113	Nguyen	The signature of adaptation among human copy number polymorphisms	12
114	Feuk	Inversion events in recent primate evolution and discovery of human inversion polymorphisms	12
115	Arking	Genome-wide SNP association study of QT-interval	12
116	Stuve	Examination of linkage disequilibrium between common deletions and single nucleotide polymorphisms in the human genome	12

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
117	Metzker	Association of sequence variation in diabetes	
118	Hameister	From fishes, birds and mammals to the bony vertebrate proto-karyotype—A comparative study	
119	Hansen	Evolution of a targeted comparative mapping and sequencing pipeline	
120	Harris	Evolution of sequence conservation in vertebrates	
121	Elnitski	A //bird's eye view// of vertebrate promoters gleaned from human-chicken alignment	
122	Milosavljevic	Rhesus macaque genome yields insights into the natural history of human and chimpanzee genomes	
123	Harris	WormBase, a comprehensive resource for nematode comparative genomics	
124	Hartman	Identification and analysis of promoters in the ENCODE regions	
125	Herschleb	Single molecule analysis of genomic variation within karyotypically stable and unstable genomes—MCF-7 breast cancer and human embryonic stem cell lines	
126	Higasa	Periodicity of SNP distribution around transcription start sites	
127	Hirschmann	Natural variation in human meiotic recombination	
128	Hirst	The mammalian gene collection—Closing the gap	
129	Hoehe	High resolution haplotypes, the HapMap and haplotype approaches to disease gene discovery	
130	Hughes	Preservation of the Y chromosome during human evolution as revealed by comparative sequencing in the chimpanzee	
131	Hurle	Evolutionary dynamics of the Rapidly Evolving Substrate for Transglutaminase (REST) locus in primates	
132	Ihara	Many-body interaction networks from literature mining	
133	Ishikawa	Dissecting copy number polymorphisms by integrating allelic information	
134	Devine	Genetic variation caused by transposons in humans and other primates	
135	Jacob	Rat Genome Database—Tools and strategies for physiological genomics	
136	Roest Crolius	Genome evolution from an ancestral vertebrate to modern human, chicken and	
137	Johnson	Gene family evolution in divergent land plant lineages—An HMM approach	
138	Johnson	//morpheus//—A dynamic model for gene and genome evolution among primates	
139	Jones	Ultra-high density microarray-based SNP genotyping	
140	Karlsson	Fine scale analysis of haplotype structure in the domestic dog population	

141	Karro	Removing duplications for the reconstruction of the placental mammalian ancestor
142	Kasahara	Whole genome shotgun sequencing of medaka ( <i>O. latipes</i> )
143	Kaufman	Genomic organization leads to evolution of gene function, and other lessons from the chicken MHC
144	Enard	Parallel patterns of evolution in the genomes and transcriptomes of humans and chimpanzees
145	Kim	Estimating historical demographic dynamics via combinatoric-set likelihood analysis of population genetic diversity summary statistics
146	Kimura	Analysis of 1.4 million one-pass sequence data from oligo-capped human full-length cDNAs
147	Kitts	Automating the design of gene-specific probes for use in the mouse GENSAT project
148	Kleber	ALLPATHS—A new genome assembly algorithm that preserves intrinsic ambiguity
149	Kodzius	Transcriptional starting site complexity as investigated by high-throughput 5'-RACE
150	Kondoh	Trans-phylogenetic analysis of regulatory sequence sets—The <i>Sox2</i> locus as an
151	Krzywinski	Fingerprint profiling—Whole genome discovery of balanced rearrangements in cancer using restriction digest BAC fingerprints
152	Ware	Progress of the Oryza Map Alignment Project (OMAP)
153	Kuroki	Sequencing the chimpanzee Y chromosome to understand its evolutionary and biological characteristic
154	Kwitek	HPD—Toward a human phenome database for complex disease
155	Larkin	Dynamics of mammalian chromosome evolution inferred from multispecies comparative maps
156	Down	Searching for functional motifs in exons
157	Lewis	Automated filtering of NMR spectra—A new tool for the discovery of metabolites associated with type 2 diabetes
158	Limborska	Gene polymorphism analysis from sporadic amyotrophic lateral sclerosis patients from Russia
159	Makalowski	Origin and evolution of U12-dependent introns
160	Lipovich	GISCAP—Genome Institute of Singapore Cis-Antisense Program
161	Locke	Copy number variation in regions of segmental duplication between humans and great apes
162	Loytynoja	Alignment of sequences with an internal structure—Application to phylogenetic gene finding
163	Lynn	The detection of positive selection in cattle using site-specific models of evolution
164	Ma	Reconstructing an ancient chromosome

165	Maher	Analysis of microRNAs in plant genomes
166	Makalowska	Evolution of overlapping genes in vertebrates
167	Makova	Strong and weak male mutation bias at different sites of the primate genomes—Lessons from the human-chimpanzee comparison
168	McCarroll	Using the HapMap to identify structural polymorphisms in the human genome
169	McPherson	High-throughput cloning of full-length open reading frames representing human and mouse genes
170	Gnirke	Reduced representation bisulfite sequencing (RRBS)—A large scale method for high resolution DNA methylation analysis
171	Merriman	Comparing gene expression patterns between Vervet and human brain
172	Merriman	Identity-by-descent mapping using high density SNP genotyping
173	Meyer	Automated gene annotation pipeline for sequenced genomes
174	Montpetit	A 5kb haplotype map of human chromosomes 2 and 4p
175	Moreno-Quinn	Overlapping congenics for the dissection of the genetic determinants of blood
176	Morgante	Helitron-like elements mediate extensive gene duplications and exon shuffling in
177	Mortazavi	Assessment of the network-level conservation of cis-regulatory elements using
178	Mudge	The importance of manual annotation in gene families
179	Mulle	Large-scale SNP association study of chromosome 13q32 and schizophrenia
180	Nefedov	New recombination proficient BAC libraries for targeted knock out genomic
181	Nekrutenko	Oscillating evolution of a mammalian locus with overlapping reading frames—An //XLas/ALEX// relay
182	Hirschhorn	Genetic evidence from HapMap data for functional importance of conserved noncoding regions in humans
183	Newman	A fosmid paired-end strategy to identify large-scale structural variation between the human and chimpanzee genome
185	Noguchi	Whale-land mammal genome comparison
186	Noonan	Genomic sequencing of pleistocene cave bears
187	Oleksyk	Identifying selected regions in humans from allele frequencies and population
188	Olinski	Single gene, segmental as well as genome duplications gave rise to the insulin/relaxin gene family and to the chromosomal regions in which they reside
189	Olivier	SNP analysis of lipid QTL regions in the human metabolic syndrome—How representative are HapMap data for other populations?
190	Ophoff	Integrated genetic and physical mapping resources for the vervet monkey (//C. aethiops//)—Refinement of genetic map and identification of SNPs

191	Ostrander	The canine genome—Low-pass sequencing and dense radiation hybrid map construction as an alternative and cost-effective method for navigating mammalian
192	Ovcharenko	Evolution of ancient gene deserts
193	Parra	Deriving accurate gene prediction training sets from naked genomes
194	Pasternak	Bioinformatics tools for managing genotyping data for the HapMap Project
195	Pe'er	Towards whole-genome association studies with high density arrays
196	Peiffer	Phylogenetic footprinting and genome scanning identifies vertebrate BMP response elements and new target genes
197	Pollard	Survey of the human genome to find short segments with the most dramatically accelerated evolution since divergence with chimp
198	Putnam	Assembling mosaic genomes from uncultivated archaeal populations

## ELSI Panel Discussion

Friday, 5/13/2005, 4:30 pm

### Session 8 SNPs AND THEIR RELATIONSHIP TO BIOLOGY

FRIDAY 5/13/2005, 7:30 PM

V. Cheung / R. Gibbs

<b>#</b>	<b><u>Iname</u></b>	<b><u>Title</u></b>	<b><u>Talk Length</u></b>
199	Cheung	Genetic variation in human gene expression	15
200	Stranger	Dissecting the genetic basis of gene expression variation in the human genome	12
201	Cotsapas	Genetic dissection of gene regulation in multiple mouse tissues	12
202	Chiba-Falek	The role of NACP-Rep1 polymorphic site and its binding factor PARP-1 in the regulation of !a!-synuclein expression—Implications for Parkinson's disease	12
203	Kelley	The adaptive landscape of the human genome	12
204	Gibbs	Uncovering causative human mutations in epilepsy and other disorders with complex underlying genetics	15
205	Ogorelkova	Interparalog gene conversion patterns of HBII-52 C/D box snoRNAs cluster at human chromosome 15q11-q12	12
206	Reich	The first admixture association scans and a novel risk locus for multiple sclerosis	12
207	Saxena	A framework for comprehensive association testing of common mitochondrial DNA variants to disease and application to type 2 diabetes	12
208	Sebat	Analysis of large-scale copy number variation in the HapMap	12

**Session 9 NON-HUMAN SPECIES INCLUDING COMPARATIVE GENOMICS OF**

SATURDAY 5/14/2005, 9:00 AM

R. Hardison / K. Lindblad-Toh

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
209	Hardison	Using vertebrate genome comparisons to find gene regulatory elements	15
210	Rubin	Comparative metagenomics of microbial communities	12
211	Galagan	Insights into eukaryotic biology through the genome comparison of three Aspergilli	12
212	Rokhsar	I think that I shall never see, a genome lovely as a tree's—The genome of the black cottonwood //P. trichocarpa//	12
213	Celniker	Functional genomics in //Drosophila//	12
214	Lindblad-Toh	A unique haplotype structure of the dog genome and implications for mapping of disease genes	15
215	Hellsten	Big frog, little frog—Whole genome duplication in //Xenopus//	12
216	Nakatani	Comparative analysis of Medaka genome	12
217	Ponting	Comparisons of dog and human genomes	12
218	Stamatoyannopoulos	Organization, evolution and natural variation of functional elements defined by DNaseI hypersensitive sites in the human genome	

**Session 10 POSTER SESSION III**

SATURDAY 5/14/2005, 2:00 PM

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
219	Galibert	The dog olfactory repertoire—Inventory and comparison with the rat olfactory	
220	Rangel-Filho	Gene hunt for seemingly unrelated phenotypes reveals a possible syndrome in the fawn-hooded hypertensive rat	
221	Chowdhury	Regulatory regions of prokaryotes are enriched in G4 DNA elements	
222	Pandey	Annotation of the human genome using mass spectrometry	
223	Rozen	Widespread architectural polymorphism among human Y chromosomes, but limited variation in gene copy number	
224	Reslewic	Uncovering novel human genome variation by single molecule analysis	
225	Richards	Sequencing of //T. castaneum// the red flour beetle—A progress report	
226	Richter	Large-scale automated SNP discovery reveals biases in resequencing for variation discovery	
227	Robertson	High-throughput //cis//-regulatory element prediction in mammalian genomes	
228	Robison	DNA microarray analysis of diatom cell wall synthesis	
229	Roe	Sequencing the //M. truncatula// genome	
230	Roedder	The mediability of genomes—A story from the "book of life"	
231	Bentley	Exon sequencing to identify variants in human genomes	
232	Rogers	Detection and analysis of putative primate-specific promoter elements	
233	Rotmistrovsky	Recent improvements in UniGene—Genome-based clustering and expression	

234	Salama	Identification of non-coding transcripts in ultraconserved regions of the genome
235	Sampas	Detection of genomic aberrations using total genomic data with 60mer oligonucleotide arrays
236	Sasaki	Fast and accurate multiple alignment derivation for large-scale whole genome shotgun assembly
237	Sasaki	The DNA sequence of medaka chromosome LG22
238	Salzberg	Improving genome assemblies without sequencing
239	Scherer	Generating a genetic map for //Xenopus//
240	Schnerch	Global transcriptome analysis of undifferentiated human embryonic stem cells
241	Schueler	Progressive proximal expansion of the primate X chromosome centromere
242	Dubchak	SNP-VISTA—An interactive SNPs visualization tool
243	She	Comparative analyses of segmental duplications among primate genomes—Recent genome expansions and accelerated substitution rates
244	Shearman	Estrogen receptor $\alpha$ gene variation is associated with risk of myocardial infarction in 7,517 men
245	Sorek	Processed pseudogenes at the service of current transcriptome research
246	Siddiqui	A quantitative and comprehensive atlas of gene expression in mouse development
247	Sikela	Genome-wide survey of intra- and inter-specific human gene copy number variation using cDNA aCGH
248	Small	Whole genome haplotype alignment of //C. savignyi//
249	Smith	Sequencing and initial analysis of five //Drosophila// genomes
250	Smith	Cloned single-molecule arrays™ for genome-wide resequencing
251	Smith	Chimpanzee chromosome 23 vs. human 22—Genomic insertion, deletion and ancestral indel polymorphisms
252	Spier	Selecting SNPs for genetic association studies based on the genome-wide patterns of linkage disequilibrium inferred from the HapMap Project data
253	Stalker	The Ensembl genome annotation and presentation system
254	Sugnet	ExonWalk—Building full length alternative transcripts from partial evidence
255	Sunkin	High-throughput gene expression mapping in the mouse brain
256	Suzuki	Generating sequence and experimental data resources for the comprehensive understanding of the transcriptional network of human genes
257	Taylor	Clustering genomic sequences by short alignment patterns
258	Thomas	HapMap data in the UCSC Genome Browser
259	Thomas	The analysis of ENCODE data at UCSC

260	Thomas	Phylogenomic characterization of the HPRT1 locus across eighteen vertebrate orders
261	Todd	Genome-wide disease association mapping using a large panel of non-
262	Tordoir	Computational prediction of miRNA-mediated allelic trans-interactions at the Dlk1-Gtl2 and other imprinted domains
263	Totoki	Identification of novel human genes predicted by combining gene-finders
264	Toyoda	Comparative BAC-end sequence analysis of the Japanese macaque, <i>M. fuscata</i>
265	Tsung	A computational tool for HapMap-based marker prioritization for clinical association
266	Urban	Detection of deletions and amplifications and breakpoint mapping in human chromosome 22q using ultra-high resolution fine-tiling array CGH (FT-CGH)
267	Velikanov	Modeling mammalian introns in TWINSKAN using explicit length distributions
268	Venkatesh	Elephant shark genome—A model basal vertebrate genome
269	Vignal	Mapping chicken sequence of unknown location with the ChickRH6 radiation hybrid
270	Vinson	Assembly of polymorphic genomes—Algorithms and application to <i>C. savignyi</i>
271	Wade	Dog SNP discovery—A map of the dog genome and a glimpse into dog history
272	Wagner	A chemical-genomic investigation of adipogenesis
273	Hayashizaki	Noncoding RNAs as transcriptome modulators by a S/AS mechanism
274	Wang	Global landscape of recent inferred Darwinian selection for <i>H. sapiens</i>
275	Boffelli	Identification of primate-specific regulatory elements of cholesterol homeostasis
276	Kirkness	SINEs are a major source of canine genomic diversity
277	Wang	Sequence features associated with human X-chromosome inactivation
278	Webber	Hotspots for mutation, selection and breakage in human and dog genomes
279	Whelan	A new and effective heuristic for tree topology estimation in phylogenetics
280	Holt	Identification by full coverage BAC array CGH of DNA segments gained in the human lineage since divergence from the human/chimp common ancestor
281	Winter	Mammalian <i>BEX</i> , <i>WEX</i> and <i>GASP</i> genes—Coding and non-coding chimaerism sustained by gene convergence events
282	Weng	Computational analysis of mammalian core promoters
283	Xiao	Systematic evaluation and comparison of multiple whole genome microarray
285	Xu	Co-evolution of bacteroides in the human intestinal ecosystem
286	Xuan	Improve non-CpG-related promoter prediction with tissue-specific features
287	Yamada	dsCheck—Sensitive off-target search software for dsRNA-mediated RNAi
289	Yeang	Experimental design for validating and refining pathway models of gene regulation

290	Yoshinaga	Human haplotype-specific sequencing of megabase-regions predisposing to ALS
291	Young	Striking between-species change in the V1R pheromone receptor and olfactory receptor gene families
292	Yu	Positive selection of a pre-expansion CAG repeat of the human //SCA2// gene
293	Zhang	Discovery of a novel gene evolution mechanism through analysis of invalid "SNPs" in the mouse genome
294	Zhao	Analysis of sequence context surrounding single nucleotide polymorphic sites in the mouse genome

## KEYNOTE SPEAKERS

Saturday, 5/14/2005, 4:30 pm

Thomas Gingeras, Affymetrix

Aravinda Chakravarti, Johns Hopkins University School of Medicine

## Session 11 EVOLUTIONARY BIOLOGY INCLUDING COMPARATIVE

SUNDAY 5/15/2005, 9:00 AM

C. Langley / T. Mikkelsen

<u>#</u>	<u>Iname</u>	<u>Title</u>	<u>Talk Length</u>
295	Langley	//Drosophila simulans// and //yakuba//—A first step toward population genetics	15
296	Clamp	Systematic identification of functional elements in the human genome by low-redundancy comparative sequencing—Initial progress and observations	12
297	Carninci	The transcriptional landscape of the mammalian genome	12
298	Sutter	Size sexual dimorphism is regulated by interacting QTLs in dog	12
299	Salama	Characterization of ultraconserved elements in the POLA-ARX region of the genome	12
300	Mikkelsen	Neutral and accelerated protein evolution in the lineages leading to human, mouse	15
301	Margulies	Comparative sequence analysis in the ENCODE project	12
302	McVean	The signature of selection in the human genome	12
303	Pedersen	Genome wide identification and classification of conserved RNA secondary	12
304	Sharp	Segmental duplications and copy number variation in the human genome assessed by array comparative genomic hybridization	12