Research

Letters

Human embryonic stem cells have a unique epigenetic signature
Marina Bibikova, Eugene Chudin, Bonnie Wu, Lixin Zhou,
Eliza Wickham Garcia, Ying Liu, Soojung Shin, Todd W. Plaia,
Jonathan M. Auerbach, Dan E. Arking, Rodolfo Gonzalez,
Jeremy Crook, Bruce Davidson, Thomas C. Schulz, Allan Robins,
Aparna Khanna, Peter Sartipy, Johan Hyllner, Padmavathy Vanguri,
Smita Savant-Bhonsale, Alan K. Smith, Aravinda Chakravarti,
Anirban Maitra, Mahendra Rao, David L. Barker, Jeanne F. Loring,
and Jian-Bing Fan

An ~140-kb deletion associated with feline spinal muscular atrophy
implies an essential LIX1 function for motor neuron survival
John C. Fyfe, Marilyn Menotti-Raymond, Victor A. David,
Lars Brichta, Alejandro A. Schäffer, Richa Agarwala,
William J. Murphy, William J. Wedemeyer, Brittany L. Gregory,
Bethany G. Buzzell, Meghan C. Drummond, Brunhilde Wirth,
and Stephen J. O’Brien

Identification of potential regulatory motifs in odorant receptor
genes by analysis of promoter sequences
Jussara S. Michaloski, Pedro A.F. Galante, and Bettina Malnic

Phylogenetic analyses of cyanobacterial genomes: Quantification
of horizontal gene transfer events
Olga Zhaxybayeva, J. Peter Gogarten, Robert L. Charlebois,
W. Ford Doolittle, and R. Thane Papke

Hemizygous subtelomeres of an African trypanosome chromosome
may account for over 75% of chromosome length
Sergio Callejas, Vanessa Leech, Christopher Reitter,
and Sara Melville

Common inheritance of chromosome Ia associated with clonal
expansion of Toxoplasma gondii
Asis Khan, Ulrike Böhme, Krystyna A. Kelly, Ellen Adlem,
Karen Brooks, Mark Simmonds, Karen Mungall, Michael A. Quail,
Claire Arrowsmith, Tracey Chillingworth, Carol Churcher,
David Harris, Matthew Collins, Nigel Fosker, Audrey Fraser,
Zahra Hance, Kay Jagels, Sharon Moule, Lee Murphy, Susan O’Neil,
Marie-Adele Rajandream, David Saunders, Kathy Seeger,
Sally Whitehead, Thomas Mayr, Xuan Xuan, Junichi Watanabe,
Yutaka Suzuki, Hiroyuki Wakaguri, Sumio Sugano,
Chihiro Sugimoto, Ian Paulsen, Aaron J. Mackey, David S. Roos,
Neil Hall, Matthew Berriman, Bart Barrell, L. David Sibley,
and James W. Ajioka

(continued)
Methods and Resources

Methods

Predicting essential genes in fungal genomes
Michael Seringhaus, Alberto Paccanaro, Anthony Borneman, Michael Snyder, and Mark Gerstein

High-resolution genomic profiling of chromosomal aberrations using Infinium whole-genome genotyping

STAC: A method for testing the significance of DNA copy number aberrations across multiple array-CGH experiments

SyMAP: A system for discovering and viewing syntenic regions of FPC maps
Carol Soderlund, William Nelson, Austin Shoemaker, and Andrew Paterson

Græmlin: General and robust alignment of multiple large interaction networks
Jason Flannick, Antal Novak, Balaji S. Srinivasan, Harley H. McAdams, and Serafim Batzoglou

Resource

An initial map of insertion and deletion (INDEL) variation in the human genome
Ryan E. Mills, Christopher T. Luttig, Christine E. Larkins, Adam Beauchamp, Circe Tsui, W. Stephen Pittard, and Scott E. Devine

Open Access paper.

Cover The cover photo shows a purebred Maine coon cat affected by spinal muscular atrophy. Genetic analysis of the feline disorder implicates a novel disease gene and illustrates the maturity of current resources for genomic analysis in this species. (Photo: William Lassaline. [For details, see Fyfe et al., pp. 1084–1090.])

The Editors regret that the DNA that appeared on the August 2006 issue cover was printed incorrectly as a left-handed rather than a right-handed helix.