Commentary and Review

Review
Copy number variation: New insights in genome diversity
Jennifer L. Freeman, George H. Perry, Lars Feuk, Richard Redon, Steven A. McCarroll, David M. Altshuler, Hiroyuki Aburatani, Keith W. Jones, Chris Tyler-Smith, Matthew E. Hurles, Nigel P. Carter, Stephen W. Scherer, and Charles Lee

Research

Articles
Extensive low-affinity transcriptional interactions in the yeast genome
Amos Tanay

Letters
Heterozygous carriers of Nijmegen Breakage Syndrome have a distinct gene expression phenotype
Vivian G. Cheung and Warren J. Ewens

Genomic signatures of positive selection in humans and the limits of outlier approaches
Joanna L. Kelley, Jennifer Madeoy, John C. Calhoun, Willie Swanson, and Joshua M. Akey

Relaxation of selective constraint on dog mitochondrial DNA following domestication
Susanne Björnerfeldt, Matthew T. Webster, and Carles Vilà

Tissue-specific expression and regulation of sexually dimorphic genes in mice
Xia Yang, Eric E. Schadt, Susanna Wang, Hui Wang, Arthur P. Arnold, Leslie Ingram-Drake, Thomas A. Drake, and Aldons J. Lusis

Genomic clusters, putative pathogen recognition molecules, and antimicrobial genes are induced by infection of C. elegans with M. nematophilum
Delia O’Rourke, Dilair Baban, Maria Demidova, Richard Mott, and Jonathan Hodgkin

Adaptive evolution in two large families of ubiquitin-ligase adapters in nematodes and plants
James H. Thomas

(continued)
Skewed genomic variability in strains of the toxigenic bacterial pathogen, *Clostridium perfringens*


**Methods and Resources**

*RNA expression profiling at the single molecule level*

Jan Hesse, Jaroslaw Jacak, Maria Kasper, Gerhard Regl, Thomas Eichberger, Martina Winklmayr, Fritz Aberger, Max Sonnleitner, Robert Schlapak, Stefan Howorka, Leila Muresan, Anna-Maria Frischauf, and Gerhard J. Schütz

Comparative isoschizomer profiling of cytosine methylation: The HELP assay

Batbayar Khulan, Reid F. Thompson, Kenny Ye, Melissa J. Fazzari, Masako Suzuki, Edyta Stasiek, Maria E. Figueroa, Jacob L. Glass, Quan Chen, Cristina Montagna, Eli Hatchwell, Rebecca R. Selzer, Todd A. Richmond, Roland D. Green, Ari Melnick, and John M. Greally

*Resource*

A molecular-properties-based approach to understanding PDZ domain proteins and PDZ ligands

Cosmas Giallourakis, Zhifang Cao, Todd Green, Heather Wachtel, Xiaohui Xie, Marco Lopez-Illasaca, Mark Daly, John Rioux, and Ramnik Xavier

**Erratum**

**Retraction**

*Cover* A fundamental question in genetics is whether carriers of recessive disorders have distinctive phenotypes. Using genomic approaches (represented by the microarray fluorescent hybridization image in the background), a distinct gene expression phenotype (represented by a sphere as clustered output of microarray data) was identified for carriers of an autosomal recessive disease, Nijmegen Breakage Syndrome (NBS). This expression phenotype allows identification of carriers of NBS from noncarriers and also from carriers of a similar syndrome, Ataxia Telangiectasia. The result implies that there are phenotypic characteristics that define carriers of an autosomal recessive disease and suggest that heterozygosity for recessive disorders contributes to variation in human gene expression. (Cover illustration by Alethea Andrews and Michael Morley. [For details, see Cheung and Ewens, pp. 973–979.])