Research

Genomic regulatory blocks encompass multiple neighboring genes and maintain conserved synteny in vertebrates
Hiroshi Kikuta, Mary Laplante, Pavla Navratilova,
Anna Z. Komisarczuk, Pär G. Engström, David Fredman,
Altuna Akalin, Mario Caccamo, Ian Sealy, Kerstin Howe,
Julien Ghislain, Guillaume Pezron, Philippe Mourrain,
Staale Ellingsen, Andrew C. Oates, Christine Thisse, Bernard Thisse,
Isabelle Foucher, Birgit Adolf, Andrea Geling, Boris Lenhard,
and Thomas S. Becker

Functionality or transcriptional noise? Evidence for selection within long noncoding RNAs
Jasmina Ponjavic, Chris P. Ponting, and Gerton Lunter

The modifier of Min 2 (Mom2) locus: Embryonic lethality of a mutation in the Atp5a1 gene suggests a novel mechanism of polyp suppression
Amy A. Baran, Karen A. Silverman, Joseph Zeskand, Revati Koratkar,
Ashley Palmer, Kristen McCullen, Walter J. Curran Jr.,
Tina Bocker Edmonston, Linda D. Siracusa, and Arthur M. Buchberg

Identification of mouse Duffy Antigen Receptor for Chemokines (Darc) as a BMD QTL gene
Bouchra Edderkaoui, David J. Baylink, Wesley G. Beamer,
Jon E. Wergedal, Ryan Porte, Asok Chaudhuri,
and Subburaman Mohan

Letters

Fine mapping of a swine quantitative trait locus for number of vertebrae and analysis of an orphan nuclear receptor, germ cell nuclear factor (NR6A1)
Satoshi Mikawa, Takeya Morozumi, Shin-Ichi Shimanuki,
Takeshi Hayashi, Hirohide Uenishi, Michiko Domukai,
Naohiko Okumura, and Takashi Awata

The mode and tempo of genome size evolution in eukaryotes
Matthew J. Oliver, Dmitri Petrov, David Ackerly, Paul Falkowski,
and Oscar M. Schofield

Distinct mechanisms for trans-mediated mobilization of cellular RNAs by the LINE-1 reverse transcriptase
José L. García-Perez, Aurélien J. Doucet, Alain Bucheton,
John V. Moran, and Nicolas Gilbert

Rapid evolution of an X-linked microRNA cluster in primates
Rui Zhang, Yi Peng, Wen Wang, and Bing Su

Fast-X on the Z: Rapid evolution of sex-linked genes in birds
Judith E. Mank, Erik Axellson, and Hans Ellegren

(continued)
CpG methylation is targeted to transcription units in an invertebrate genome
Miho M. Suzuki, Alistair R.W. Kerr, Dina De Sousa, and Adrian Bird

A large number of novel coding small open reading frames in the intergenic regions of the Arabidopsis thaliana genome are transcribed and/or under purifying selection
Kousuke Hanada, Xu Zhang, Justin O. Borevitz, Wen-Hsiung Li, and Shin-Han Shiu

Methods and Resources

Methods
X chromosome cDNA microarray screening identifies a functional PLP2 promoter polymorphism enriched in patients with X-linked mental retardation
Lilei Zhang, Chunfa Jie, Cassandra Obie, Fatima Abidi, Charles E. Schwartz, Roger E. Stevenson, David Valle, and Tao Wang

Efficient target-selected mutagenesis in Caenorhabditis elegans: Toward a knockout for every gene
Edwin Cuppen, Eelke Gort, Esther Hazendonk, Josine Mudde, José van de Belt, Isaäc J. Nijman, Victor Guryev, and Ronald H.A. Plasterk

Resources
PolyScan: An automatic indel and SNP detection approach to the analysis of human resequencing data
Ken Chen, Michael D. McLellan, Li Ding, Michael C. Wendl, Yumi Kasai, Richard K. Wilson, and Elaine R. Mardis

OA Open Access paper.

Cover An H&E stain illustrating the undulating pattern of crypts and villi from the proximal small intestine of a C57BL/6j ApcMin/+ mouse compared to the sequence of a portion of exon 3 from the Atp5a1 gene isolated from a Mom2R/+ mouse. The chromatograph displays the 4 base pair duplication found in exon 3 of the Atp5a1 gene, the candidate gene for the modifier of Min 2 (Mom2) locus. The Mom2R mutation suppresses intestinal polyposis by ~90% in ApcMin/+ mice. (Cover illustration by Amy A. Baran and Arthur M. Buchberg. [For details, see Baran et al., pp. 566–576.])