Commentary and Review

Perspectives

Genome-wide analyses of alternative splicing in plants: Opportunities and challenges
W. Brad Barbazuk, Yan Fu, and Karen M. McGinnis

Research

Letters

Pervasive positive selection on duplicated and nonduplicated vertebrate protein coding genes
Romain A. Studer, Simon Penel, Laurent Duret, and Marc Robinson-Rechavi

CpG dinucleotides and the mutation rate of non-CpG DNA
Jean-Claude Walser, Loïc Ponger, and Anthony V. Furano

A deletion in nephronophthisis 4 (NPHP4) is associated with recessive cone-rod dystrophy in standard wire-haired dachshund
Anne Caroline Wiik, Claire Wade, Tara Biagi, Ernst-Otto Ropstad, Ellen Bjerkås, Kerstin Lindblad-Toh, and Frode Lingaas

A novel mode of enhancer evolution: The Tal1 stem cell enhancer recruited a MIR element to specifically boost its activity
Aileen M. Smith, Maria-Jose Sanchez, George A. Follows, Sarah Kinston, Ian J. Donaldson, Anthony R. Green, and Berthold Göttgens

Long noncoding RNAs in mouse embryonic stem cell pluripotency and differentiation

On the origin of new genes in Drosophila
Qi Zhou, Guojie Zhang, Yue Zhang, Shiyu Xu, Ruoping Zhao, Zubing Zhan, Xin Li, Yun Ding, Shuang Yang, and Wen Wang

A diverse set of microRNAs and microRNA-like small RNAs in developing rice grains
Qian-Hao Zhu, Andrew Spriggs, Louisa Matthew, Longjiang Fan, Gavin Kennedy, Frank Gubler, and Chris Helliwell

Relaxation of yeast mitochondrial functions after whole-genome duplication
Huifeng Jiang, Wenjun Guan, David Pinney, Wen Wang, and Zhenglong Gu

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Genome sequence of the β-rhizobium *Cupriavidus taiwanensis* and comparative genomics of rhizobia
Claire Amadou, Géraldine Pascal, Sophie Mangenot, Michelle Glew, Cyril Bontemps, Delphine Capela, Sébastien Carrère, Stéphane Cruveiller, Carole Dossat, Aurélie Lajus, Marta Marchetti, Vérona Poinsot, Zoé Rouy, Bertrand Servin, Maged Saad, Chantal Schenowitz, Valérie Barbe, Jacques Batut, Claudine Médiagne, and Catherine Masson-Boivin

Very small mobile repeated elements in cyanobacterial genomes
Jeff Elhai, Michiko Kato, Sarah Cousins, Peter Lindblad, and José Luis Costa

Impacts of protein–protein interaction domains on organism and network complexity
Kai Xia, Zheng Fu, Lei Hou, and Jing-Dong J. Han

**Methods and Resources**

**Methods**

*RNA-seq: An assessment of technical reproducibility and comparison with gene expression arrays*
John C. Marioni, Christopher E. Mason, Shrikant M. Mane, Matthew Stephens, and Yoav Gilad

**Resources**

*An integrated resource for genome-wide identification and analysis of human tissue-specific differentially methylated regions (tDMRs)*

Tracking the complex flow of chromosome rearrangements from the Hominioidea Ancestor to extant *Hylobates* and *Nomascus* Gibbons by high-resolution synteny mapping
Doriana Misceo, Oronzo Capozzi, Roberta Roberto, Maria P. Dell’Oglio, Mariano Rocchi, Roscoe Stanyon, and Nicoletta Archidiacono

**EagleView: A genome assembly viewer for next-generation sequencing technologies**
Weichun Huang and Gabor Marth

**Erratum**

OAOpen Access paper.

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**Cover** EagleView visualization of next-generation genome assembly. In many applications of next-generation sequencing technologies, data visualization is essential for (1) identification of different types of errors from sequencing, read mapping, and assembly; (2) validation of candidate polymorphisms; (3) software development and testing; and (4) data interpretation and hypothesis generation. The illustration shows a genome assembly of 33-bp Illumina reads. Below the genome coordinates is the genome feature annotation bar with different colors representing promoter regions (pink), exons (cyan), and introns (yellow). The small pink rectangle above the features is the navigation cursor, and the small red rectangle below indicates a single nucleotide polymorphism site. (Cover illustration by Weichun Huang. [For details, see Huang and Marth, pp. 1538–1543.])