

## Perspective

- Assembly of large genomes using second-generation sequencing 1165  
Michael C. Schatz, Arthur L. Delcher, and Steven L. Salzberg

## Research

- The initial peopling of the Americas: A growing number of founding mitochondrial genomes from Beringia 1174<sup>OA</sup>  
Ugo A. Perego, Norman Angerhofer, Maria Pala, Anna Olivieri, Hovirag Lancioni, Baharak Hooshiar Kashani, Valeria Carossa, Jayne E. Ekins, Alberto Gómez-Carballa, Gabriela Huber, Bettina Zimmermann, Daniel Corach, Nora Babudri, Fausto Panara, Natalie M. Myres, Walther Parson, Ornella Semino, Antonio Salas, Scott R. Woodward, Alessandro Achilli, and Antonio Torroni
- Susceptibility to chronic pain following nerve injury is genetically affected by *CACNG2* 1180  
Jonathan Nissenbaum, Marshall Devor, Ze'ev Seltzer, Mathias Gebauer, Martin Michaelis, Michael Tal, Ruslan Dorfman, Merav Abitbul-Yarkoni, Yan Lu, Tina Elahipanah, Sonia delCanho, Anne Minert, Kaj Fried, Anna-Karin Persson, Hagai Shpigler, Erez Shabo, Benjamin Yakir, Anne Pisanté, and Ariel Darvasi
- An 8q24 gene desert variant associated with prostate cancer risk confers differential in vivo activity to a *MYC* enhancer 1191<sup>OA</sup>  
Nora F. Wasserman, Ivy Aneas, and Marcelo A. Nobrega
- Gene amplification as double minutes or homogeneously staining regions in solid tumors: Origin and structure 1198  
Clelia Tiziana Storlazzi, Angelo Lonoce, Maria C. Guastadisegni, Domenico Trombetta, Pietro D'Addabbo, Giulia Daniele, Alberto L'Abbate, Gemma Macchia, Cecilia Surace, Klaas Kok, Reinhard Ullmann, Stefania Purgato, Orazio Palumbo, Massimo Carella, Peter F. Ambros, and Mariano Rocchi
- MicroRNA, mRNA, and protein expression link development and aging in human and macaque brain 1207<sup>OA</sup>  
Mehmet Somel, Song Guo, Ning Fu, Zheng Yan, Hai Yang Hu, Ying Xu, Yuan Yuan, Zhibin Ning, Yuhui Hu, Corinna Menzel, Hao Hu, Michael Lachmann, Rong Zeng, Wei Chen, and Philipp Khaitovich
- Chickens possess centromeres with both extended tandem repeats and short non-tandem-repetitive sequences 1219  
Wei-Hao Shang, Tetsuya Hori, Atsushi Toyoda, Jun Kato, Kris Popendorf, Yasubumi Sakakibara, Asao Fujiyama, and Tatsuo Fukagawa
- Patching gaps in plant genomes results in gene movement and erosion of colinearity 1229  
Thomas Wicker, Jan P. Buchmann, and Beat Keller

Function annotation of the rice transcriptome at single-nucleotide resolution by RNA-seq 1238<sup>OA</sup>  
Tingting Lu, Guojun Lu, Danlin Fan, Chuanrang Zhu, Wei Li, Qiang Zhao, Qi Feng, Yan Zhao, Yunli Guo, Wenjun Li, Xuehui Huang, and Bin Han

Genome-wide mapping of nuclear mitochondrial DNA sequences links DNA replication origins to chromosomal double-strand break formation in *Schizosaccharomyces pombe* 1250  
Sandrine Lenglez, Damien Hermand, and Anabelle Decottignies

## Methods

High-throughput sequencing reveals extensive variation in human-specific LI content in individual human genomes 1262  
Adam D. Ewing and Haig H. Kazazian, Jr.

Methylation profiling in individuals with uniparental disomy identifies novel differentially methylated regions on chromosome 15 1271  
Andrew J. Sharp, Eugenia Migliavacca, Yann Dupre, Elisavet Stathaki, Mohammad Reza Sailani, Alessandra Baumer, Albert Schinzel, Deborah J. Mackay, David O. Robinson, Gilda Cobellis, Luigi Cobellis, Han G. Brunner, Bernhard Steiner, and Stylianos E. Antonarakis

Bisulfite Patch PCR enables multiplexed sequencing of promoter methylation across cancer samples 1279  
Katherine Elena Varley and Robi David Mitra

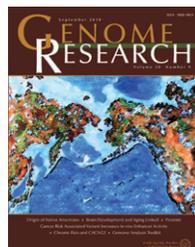
High-throughput profiling of amino acids in strains of the *Saccharomyces cerevisiae* deletion collection 1288  
Sara J. Cooper, Gregory L. Finney, Shauna L. Brown, Sven K. Nelson, Jay Hesselberth, Michael J. MacCoss and Stanley Fields

## Resources

The Genome Analysis Toolkit: A MapReduce framework for analyzing next-generation DNA sequencing data 1297  
Aaron McKenna, Matthew Hanna, Eric Banks, Andrey Sivachenko, Kristian Cibulskis, Andrew Kernytsky, Kiran Garimella, David Altshuler, Stacey Gabriel, Mark Daly, and Mark A. DePristo

Structural and operational complexity of the *Geobacter sulfurreducens* genome 1304  
Yu Qiu, Byung-Kwan Cho, Young Seoub Park, Derek Lovley, Bernhard Ø. Palsson, and Karsten Zengler

<sup>OA</sup>Open Access paper.



**Cover** General consensus among scientists from different disciplines is that Native American populations trace their gene pool to Asian groups who colonized northeast Siberia, including parts of Beringia—the land-bridge that connected North Asia to Alaska during the last glacial period. During that time, these ancestral populations probably retreated into refugia, where their genetic variation was reshaped. In the millennia after the initial Paleo-Indian migrations, other groups also from Beringia or eastern Siberia expanded into North America, contributing at least 15 distinct founder mitochondrial genomes that have survived to the present time. (Cover illustration by Dr. Valeria Carossa, valeria.carossa@unipv.it. [For details, see Perego et al., pp. 1174–1179.]