GENOME RESEARCH
Volume 20 Issue 1 January 2010

Research

Letters

Ecological adaptation determines functional mammalian olfactory subgenomes 1
Sara Hayden, Michaël Bekaert, Tess A. Crider, Stefano Mariani, William J. Murphy, and Emma C. Teeling

Extreme variability among mammalian VIR gene families 10
Janet M. Young, Hillary F. Massa, Li Hsu, and Barbara J. Trask

A novel active endogenous retrovirus family contributes to genome variability in rat inbred strains 19
Yongming Wang, František Liška, Claudia Gosele, Lucie Šedová, Vladimír Křen, Drahomíra Křenová, Zoltán Ivics, Norbert Hubner, and Zsuzsanna Izsvák

An integrative genomic analysis identifies *Bhmt2* as a diet-dependent genetic factor protecting against acetaminophen-induced liver toxicity 28
Hong-Hsing Liu, Peng Lu, Yingying Guo, Erin Farrell, Xun Zhang, Ming Zheng, Betty Bosano, Zhaomei Zhang, John Allard, Guochun Liao, Siyu Fu, Jinzhi Chen, Kimberly Dolim, Ayako Kuroda, Jonathan Usuka, Janet Cheng, William Tao, Kevin Welch, Yanzhou Liu, Joseph Pease, Steve A. de Keczer, Mohammad Masjedizadeh, Jing-Shan Hu, Paul Weller, Tim Garrow, and Gary Peltz

Genome-wide mapping of SMAD target genes reveals the role of BMP signaling in embryonic stem cell fate determination 36
Teng Fei, Kai Xia, Zhongwei Li, Bing Zhou, Shanshan Zhu, Hua Chen, Jianping Zhang, Zhang Chen, Huasheng Xiao, Jing-Dong J. Han, and Ye-Guang Chen

Genome-wide mapping of alternative splicing in *Arabidopsis thaliana* 45
Sergei A. Filichkin, Henry D. Priest, Scott A. Givan, Rongkun Shen, Douglas W. Bryant, Samuel E. Fox, Weng-Keen Wong, and Todd C. Mockler

A novel strategy of transcription regulation by intragenic nucleosome ordering 59
Cédric Vaillant, Leonor Palmeira, Guillaume Chevereau, Benjamin Audit, Yves d'Aubenton-Carafa, Claude Thermes, and Alain Arneodo

(continued)

Methods and Resources

Methods

Inferring tumor progression from genomic heterogeneity — 68[OA]
Nicholas Navin, Alexander Krasnitz, Linda Rodgers, Kerry Cook, Jennifer Meth, Jude Kendall, Michael Riggs, Yvonne Eberling, Jennifer Troge, Vladimir Grubor, Dan Levy, Pär Lundin, Susanne Månér, Anders Zetterberg, James Hicks, and Michael Wigler

Targeted chromosomal deletions in human cells using zinc finger nucleases — 81
Hyung Joo Lee, Eunji Kim, and Jin-Soo Kim

High-resolution nucleosome mapping reveals transcription-dependent promoter packaging — 90[OA]
Assaf Weiner, Amanda Hughes, Moran Yassour, Oliver J. Rando, and Nir Friedman

Estimating population genetic parameters and comparing model goodness-of-fit using DNA sequences with error — 101[OA]
Xiaoming Liu, Yun-Xin Fu, Taylor J. Maxwell, and Eric Boerwinkle

Detection of nonneutral substitution rates on mammalian phylogenies — 110[OA]
Katherine S. Pollard, Melissa J. Hubisz, Kate R. Rosenbloom, and Adam Siepel

Reconstructing ancestral gene content by coevolution — 122
Tamir Tuller, Hadas Birin, Uri Gophna, Martin Kupiec, and Eytan Ruppin

Resources

A single-base resolution map of an archaeal transcriptome — 133
Omri Wurtzel, Rajat Sapra, Feng Chen, Yiwen Zhu, Blake A. Simmons, and Rotem Sorek

ProPhylER: A curated online resource for protein function and structure based on evolutionary constraint analyses — 142
Jonathan Binkley, Kalpana Karra, Andrew Kirby, Midori Hosobuchi, Eric A. Stone, and Arend Sidow

[OA]Open Access paper.

Cover Suspended over a liver and sectioned liver tissue background are the structural formulas for acetaminophen (*right*) and *S*-methylmethionine (SMM) (*over* lobe filled with capsules). SMM, a Chinese herbal medicine and dietary metabolite abundant in all flowering plants, is the substrate of BHMT2, an enzyme identified to confer protection against acetaminophen-induced liver injury in vivo. (Cover illustration by Myriam Kirkman-Oh, KO Studios, http://www.kostudios.com. [For details, see Liu et al., pp. 28–35.])