Commentary and Review

Forum

Don’t throw the baby out with the bathwater: Enabling a bottom-up approach in genome-wide association studies
Sean E. McGuire and Amy L. McGuire

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Defensins and the dynamic genome: What we can learn from structural variation at human chromosome band 8p23.1
Edward J. Hollox, John C.K. Barber, Anthony J. Brookes, and John A.L. Armour

Research

Articles

Copy number variation and evolution in humans and chimpanzees
George H. Perry, Fengtang Yang, Tomas Marques-Bonet, Carly Murphy, Tomas Fitzgerald, Arthur S. Lee, Courtney Hyland, Anne C. Stone, Matthew E. Hurles, Chris Tyler-Smith, Evan E. Eichler, Nigel P. Carter, Charles Lee, and Richard Redon

Letters

Reduced purifying selection prevails over positive selection in human copy number variant evolution
Duc-Quang Nguyen, Caleb Webber, Jayne Hehir-Kwa, Rolph Pfundt, Joris Veltman, and Chris P. Ponting

Copy number variation at the breakpoint region of isochromosome 17q
Claudia M.B. Carvalho and James R. Lupski

Unexpected complexity at breakpoint junctions in phenotypically normal individuals and mechanisms involved in generating balanced translocations (t(1;22)(p36;q13)
Marzena Gajecka, Andrew J. Gentles, Albert Tsai, David Chitayat, Katherine L. Mackay, Caron D. Glotzbach, Michael R. Lieber, and Lisa G. Shaffer

Dispensability of mammalian DNA
Cory McLean and Gill Bejerano

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Evolution of the mammalian transcription factor binding repertoire via transposable elements
Guillaume Bourque, Bernard Leong, Vinsensius B. Vega, Xi Chen, Yen Ling Lee, Kandhadayar G. Srinivasan, Joon-Lin Chew, Yijun Ruan, Chia-Lin Wei, Huck Hui Ng, and Edison T. Liu

E2F in vivo binding specificity: Comparison of consensus versus nonconsensus binding sites
Alina Rabinovich, Victor X. Jin, Roman Rabinovich, Xiaojin Xu, and Peggy J. Farnham

Reconfiguration of genomic anchors upon transcriptional activation of the human major histocompatibility complex

In-depth characterization of the microRNA transcriptome in a leukemia progression model
Florian Kuchenbauer, Ryan D. Morin, Bob Argiriopoulos, Oleh I. Petriv, Malachi Griffith, Michael Heuser, Eric Yung, Jessica Piper, Allen Delaney, Anna-Liisa Prabhu, Yongjun Zhao, Helen McDonald, Thomas Zeng, Martin Hirst, Carl L. Hansen, Marco A. Marra, and R. Keith Humphries

Transcription of foreign DNA in Escherichia coli
René L. Warren, John D. Freeman, Roger C. Levesque, Duane E. Smailus, Stephane Flibotte, and Robert A. Holt

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Methods
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Bo Wen, Hao Wu, Hans Bjornsson, Roland D. Green, Rafael Irizarry, and Andrew P. Feinberg

Enredo and Pecan: Genome-wide mammalian consistency-based multiple alignment with paralogs
Benedict Paten, Javier Herrero, Kathryn Beal, Stephen Fitzgerald, and Ewan Birney

Genome-wide nucleotide-level mammalian ancestor reconstruction
Benedict Paten, Javier Herrero, Stephen Fitzgerald, Kathryn Beal, Paul Flicek, Ian Holmes, and Ewan Birney

Nested Patch PCR enables highly multiplexed mutation discovery in candidate genes
Katherine Elena Varley and Robi David Mitra

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Mapping short DNA sequencing reads and calling variants using mapping quality scores
Heng Li, Jue Ruan, and Richard Durbin

Erratum

Open Access paper.