

Commentary and Review

Insight/Outlook

Ethical, legal, and social considerations in conducting the Human Microbiome Project

1861

Amy L. McGuire, James Colgrove, Simon N. Whitney,
Christina M. Diaz, Daniel Bustillos, and James Versalovic

Research

Letters

Analysis of copy number variants and segmental duplications in the human genome: Evidence for a change in the process of formation in recent evolutionary history

1865^{OA}

Philip M. Kim, Hugo Y.K. Lam, Alexander E. Urban, Jan O. Korbel,
Jason Affourtit, Fabian Grubert, Xueying Chen, Sherman Weissman,
Michael Snyder, and Mark B. Gerstein

Active *Alu* retrotransposons in the human genome

1875

E. Andrew Bennett, Heiko Keller, Ryan E. Mills, Steffen Schmidt,
John V. Moran, Oliver Weichenrieder, and Scott E. Devine

Characterization of the bovine pseudoautosomal boundary: Documenting the evolutionary history of mammalian sex chromosomes

1884

Anne-Sophie Van Laere, Wouter Coppieters, and Michel Georges

Transcriptional enhancement by GATA1-occupied DNA segments is strongly associated with evolutionary constraint on the binding site motif

1896^{OA}

Yong Cheng, David C. King, Louis C. Dore, Xinmin Zhang,
Yuepin Zhou, Ying Zhang, Christine Dorman,
Demesew Abebe, Swathi A. Kumar, Francesca Chiaromonte,
Webb Miller, Roland D. Green, Mitchell J. Weiss,
and Ross C. Hardison

Genome-wide relationship between histone H3 lysine 4 mono- and tri-methylation and transcription factor binding

1906^{OA}

A. Gordon Robertson, Mikhail Bilenky, Angela Tam,
Yongjun Zhao, Thomas Zeng, Nina Thiessen, Timothee Cezard,
Anthony P. Fejes, Elizabeth D. Wederell, Rebecca Cullum,
Ghia Euskirchen, Martin Krzywinski, Inanc Birol, Michael Snyder,
Pamela A. Hoodless, Martin Hirst, Marco A. Marra,
and Steven J.M. Jones

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	Pathogen corruption and site-directed recombination at a plant disease resistance gene cluster	1918
	Ervin D. Nagy and Jeffrey L. Bennetzen	
	Many or most genes in <i>Arabidopsis</i> transposed after the origin of the order Brassicales	1924
	Michael Freeling, Eric Lyons, Brent Pedersen, Maqsudul Alam, Ray Ming, and Damon Lisch	
	DNA methylation and heterochromatinization in the male-specific region of the primitive Y chromosome of papaya	1938
	Wenli Zhang, Xiue Wang, Qingyi Yu, Ray Ming, and Jiming Jiang	
Methods		
Methods	Unraveling ancient hexaploidy through multiply-aligned angiosperm gene maps	1944
	Haibao Tang, Xiyin Wang, John E. Bowers, Ray Ming, Maqsudul Alam, and Andrew H. Paterson	
	Multigenome DNA sequence conservation identifies <i>Hox</i> <i>cis</i> -regulatory elements	1955
	Steven G. Kuntz, Erich M. Schwarz, John A. DeModena, Tristan De Buyscher, Diane Trout, Hiroaki Shizuya, Paul W. Sternberg, and Barbara J. Wold	
	DNA methylation profile of tissue-dependent and differentially methylated regions (T-DMRs) in mouse promoter regions demonstrating tissue-specific gene expression	1969
	Shintaro Yagi, Keiji Hirabayashi, Shinya Sato, Wei Li, Yoko Takahashi, Tsutomu Hirakawa, Guoying Wu, Naoko Hattori, Naka Hattori, Jun Ohgane, Satoshi Tanaka, X. Shirley Liu, and Kunio Shiota	
	Gene prediction in novel fungal genomes using an ab initio algorithm with unsupervised training	1979
	Vardges Ter-Hovhannisyan, Alexandre Lomsadze, Yury O. Chernoff, and Mark Borodovsky	
Resources		
Resources	Finding friends and enemies in an enemies-only network: A graph diffusion kernel for predicting novel genetic interactions and co-complex membership from yeast genetic interactions	1991 ^{OA}
	Yan Qi, Yasir Suhail, Yu-yi Lin, Jef D. Boeke, and Joel S. Bader	
	Genome-scale spatiotemporal analysis of <i>Caenorhabditis elegans</i> microRNA promoter activity	2005
	Natalia J. Martinez, Maria C. Ow, John S. Reece-Hoyes, M. Inmaculada Barrasa, Victor R. Ambros, and Albertha J.M. Walhout	

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Haplotype sorting using human fosmid clone end-sequence pairs

2016

Jeffrey M. Kidd, Ze Cheng, Tina Graves, Bob Fulton,
Richard K. Wilson, and Evan E. Eichler

Sequencing of natural strains of *Arabidopsis thaliana* with short reads2024^{OA}

Stephan Ossowski, Korbinian Schneeberger, Richard M. Clark,
Christa Lanz, Norman Warthmann, and Detlef Weigel

Author Index

2034

Reviewer Index

2039

^{OA}Open Access paper.



Cover Female papaya trees with homogametic sex chromosome genotype XX. In this issue, four knob-like heterochromatin structures specific to the male-specific region of the “young” papaya Y chromosome are reported. The DNA sequences associated with these heterochromatic knobs are highly divergent and heavily methylated compared to those of its X chromosome counterpart, suggesting that DNA methylation and heterochromatinization play an important role in the early stage of sex chromosome evolution in papaya. (Photo: Qingyi Yu. [For details, see Zhang et al., pp. 1938–1943.])