Commentary

An emerging toolkit for targeted cancer therapies
Gordon B. Mills

Perspectives

Translational genomics: The challenge of developing cancer biomarkers
James D. Brooks

Translating cancer ‘omics’ to improved outcomes
Emily A. Vucic, Kelsie L. Thu, Keith Robison, Leszek A. Rybaczyk, Raj Chari, Carlos E. Alvarez, and Wan L. Lam

Research

Whole genome sequencing of matched primary and metastatic acral melanomas

Whole-exome sequencing of human pancreatic cancers and characterization of genomic instability caused by MLH1 haploinsufficiency and complete deficiency

Genomic analysis of circulating cell-free DNA infers breast cancer dormancy

Assessment of palindromes as platforms for DNA amplification in breast cancer
Jamie Guenthoer, Scott J. Diede, Hisashi Tanaka, Xiaoyu Chai, Li Hsu, Stephen J. Tapscott, and Peggy L. Porter

Global DNA hypomethylation coupled to repressive chromatin domain formation and gene silencing in breast cancer

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Tumor-specific retargeting of an oncogenic transcription factor chimera results in dysregulation of chromatin and transcription

Mukund Patel, Jeremy M. Simon, Michael D. Iglesia, Sam B. Wu, Andrew W. McFadden, Jason D. Lieb, and Ian J. Davis

Genome-scale analysis of aberrant DNA methylation in colorectal cancer

Toshinori Hinoue, Daniel J. Weisenberger, Christopher P.E. Lange, Hui Shen, Hyang-Min Byun, David Van Den Berg, Simeen Malik, Fei Pan, Houtan Noushmehr, Cornelis M. van Dijk, Rob A.E.M. Tonnaar, and Peter W. Laird

Unique DNA methylome profiles in CpG island methylator phenotype colon cancers

Yaomin Xu, Bo Hu, Ae-Jin Choi, Banu Gopalan, Byron H. Lee, Matthew F. Kalady, James M. Church, and Angela H. Ting

Genomic analysis identifies association of *Fusobacterium* with colorectal carcinoma


*Fusobacterium nucleatum* infection is prevalent in human colorectal carcinoma

Mauro Castellarin, René L. Warren, J. Douglas Freeman, Lisa Dreolini, Martin Krywinski, Jaclyn Strauss, Rebecca Barnes, Peter Watson, Emma Allen-Vercoe, Richard A. Moore, and Robert A. Holt

Acetylation of H2A.Z is a key epigenetic modification associated with gene deregulation and epigenetic remodeling in cancer

Fátima Valde’s-Mora, Jenny Z. Song, Aaron L. Statham, Dario Strbenac, Mark D. Robinson, Shalima S. Nair, Kate I. Patterson, David J. Tremethick, Clare Stirzaker, and Susan J. Clark

Cooperation between Polycomb and androgen receptor during oncogenic transformation

Jonathan C. Zhao, Jianjun Yu, Christine Runkle, Longtao Wu, Ming Hu, Dayong Wu, Jun S. Liu, Qianben Wang, Zhaohui S. Qin, and Jindan Yu

Genetic variation in radiation-induced cell death

Denis A. Smirnov, Lauren Brady, Krzysztof Halasa, Michael Morley, Sonia Solomon, and Vivian G. Cheung

Methods

Single-step capture and sequencing of natural DNA for detection of *BRCA1* mutations

John F. Thompson, Jeffrey G. Reifenberger, Eldar Giladi, Kristen Kerouac, Jaime Gill, Erik Hansen, Avak Kahvejian, Philipp Kapranov, Travis Knope, Doron Lipson, Kathleen E. Steinmann, and Patrice M. Milos

Estimation of rearrangement phylogeny for cancer genomes


Calling amplified haplotypes in next generation tumor sequence data

Ninad Dewal, Yang Hu, Matthew L. Freedman, Thomas LaFramboise, and Itsik Pe’er

De novo discovery of mutated driver pathways in cancer

Fabio Vandin, Eli Upfal, and Benjamin J. Raphael

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Integrating genetic and gene expression evidence into genome-wide association analysis of gene sets
Qing Xiong, Nicola Ancona, Elizabeth R. Hauser, Sayan Mukherjee, and Terrence S. Furey

Mutual exclusivity analysis identifies oncogenic network modules
Giovanni Ciriello, Ethan Cerami, Chris Sander, and Nikolaus Schultz

Resource
A DNA methylation fingerprint of 1628 human samples

Open Access paper.

Cover Genome Research presents a Cancer Genomics special issue that highlights insights gained from cutting-edge genomic and epigenomic analyses of cancer. The cover is an artist’s rendering of the transformation from normal genome to cancer genome, depicting the cell cycle in the format of a Zen spiritual exercise in which the enso (“circle”) is drawn daily. The first enso is representative of normal growth and division, progressing as carcinogenesis “redraws” the genome until it is another creature entirely. (Illustration © Victor O. Leshyk, 2011, www.victorleshyk.com.)