Highlights of This Issue  955

CHROMATIN, GENE, AND RNA REGULATION

957  A YAP/TAZ-Regulated Molecular Signature Is Associated with Oral Squamous Cell Carcinoma
Samantha E. Hiemer, Liye Zhang, Vinay K. Kartha, Trevor S. Packer, Munirah Almershed, Vikki Noonan, Maria Kukuruzinska, Manish V. Bais, Stefano Monti, and Xaralabos Varelas

969  A Protein Interaction between β-Catenin and Dnmt1 Regulates Wnt Signaling and DNA Methylation in Colorectal Cancer Cells
Jing Song, Zhanwen Du, Mate Ravaš, Bohan Dong, Zhenghe Wang, and Rob M. Ewing

DNA DAMAGE AND REPAIR

982  EphB1 Suppression in Acute Myelogenous Leukemia: Regulating the DNA Damage Control System

GENOMICs

993  Homologous Mutation to Human BRAF V600E Is Common in Naturally Occurring Canine Bladder Cancer—Evidence for a Relevant Model
Brennan Decker, Heidi G. Parker, Deepika Dhawan, Erika M. Kwon, Eric Karlins, Brian W. Davis, José A. Ramos-Vara, Patty L. Bonney, Elizabeth A. McNiel, Deborah W. Knapp, and Elaine A. Ostrander

ONCOGENES AND TUMOR SUPPRESSORS

1003  AKT1 E17K in Colorectal Carcinoma Is Associated with BRAF V600E but Not MSI-H Status: A Clinicopathologic Comparison to PIK3CA Helical and Kinase Domain Mutants
Jadyn F. Hechtman, Justyna Sadowska, Jason T. Huse, Laetitia Borsu, Rona Yaeger, Jinrit Shia, Efsevia Vakiani, Marc Ladanyi, and Maria E. Arcila

1009  Anti–miR-21 Suppresses Hepatocellular Carcinoma Growth via Broad Transcriptional Network Deregulation

1022  COX-2 Elevates Oncogenic miR-526b in Breast Cancer by EP4 Activation
Mousumi Majumder, Erin Landman, Ling Liu, David Hess, and Peeyush K. Lala

SIGNAL TRANSDUCTION

1034  The Role of Nitric Oxide Synthase Uncoupling in Tumor Progression

1044  Endophilin A2 Promotes TNBC Cell Invasion and Tumor Metastasis
Tomas Baldassarre, Kathleen Watt, Peter Truesdell, Jania Meens, Mark M. Schneider, Sandip K. Sengupta, and Andrew W. Craig
ABOUT THE COVER

The cover shows a heat map of oral squamous cell carcinoma (OSCC) tumor expression data from “The Cancer Genome Atlas (TCGA)” projected onto the YAP/TAZ-activated transcriptional signature identified from microarray studies performed by Hiemer and colleagues (beginning on page 957). Hierarchical clustering identified two tumor-associated sub-clusters which were enriched in either cell-cycle genes or genes responding to cancer-related signaling pathways.