Addressing Genetic Tumor Heterogeneity through Computationally Predictive Combination Therapy ..........166
B. Zhao, J.R. Pritchard, D.A. Lauffenburger, and M.T. Hemann

Précis: Computational modeling enables design and optimization of chemotherapeutic drug combinations that minimize tumor cell subpopulation outgrowth in heterogeneous tumors.

Tolerance of Whole-Genome Doubling Propagates Chromosomal Instability and Accelerates Cancer Genome Evolution ............175

Précis: Genome doubling is an early event in colorectal cancer development that is associated with an increased tolerance for chromosomal instability and poor prognosis.

Epithelial-to-Mesenchymal Transition Rewires the Molecular Path to PI3K-Dependent Proliferation ...............186
M.B. Salt, S. Bandyopadhyay, and F. McCormick

Précis: EMT removes an autocrine ERBB3 loop in NSCLC, leading to a reduction in proliferation that can be rescued by restoring PI3K signaling through divergent mechanisms.

Radiogenomics: Using Genetics to Identify Cancer Patients at Risk for Development of Adverse Effects Following Radiotherapy ..........155
S.L. Kerns, H. Ostrer, and B.S. Rosenstein

Précis: BCR-ABL activates a MEK-dependent negative feedback pathway that persistently inhibits growth factor receptor signaling and leads to apoptotic commitment upon BCR-ABL inhibition.
Patients with triple-negative breast cancer who do not experience a pathologic complete response following neoadjuvant chemotherapy have a poor prognosis due to a high rate of recurrence of metastatic disease. Balko and colleagues performed genomic analyses of residual triple-negative breast cancers after neoadjuvant chemotherapy to identify potential targets for adjuvant therapy and found that over 90% of residual triple-negative breast cancers harbored an actionable alteration in a targetable pathway. Molecular profiling of residual triple-negative breast cancers after neoadjuvant chemotherapy could thus potentially guide the use of adjuvant targeted therapies aimed at preventing disease recurrence. For details, please see the article by Balko and colleagues on page 232.

For more News and Research Watch, visit Cancer Discovery online at http://CDnews.aacrjournals.org. Online-only News stories include the following:

- BCL-2 Inhibitor Yields High Response in CLL and SLL
- Anastrozole May Aid Breast Cancer Prevention
- PIK3CA Mutation Predicts Resistance to Breast Cancer Therapy
- Positive Results for Drug Combo in I-SPY 2 Trial
- Endoxifen Shows Promise in Breast Cancer

See commentary, p. 152

Précis: Mutated genes in PAX fusion-negative rhabdomyosarcomas are enriched for PAX fusion protein targets.

Précis: Genomic analysis of chemotherapy-resistant triple-negative breast cancer cells may guide use of adjuvant targeted therapies to prevent recurrence of metastatic disease.

Précis: FGFR dependency in FGFR1-amplified lung cancer is defined by multiple genetic factors including ligand-mediated FGFR signaling and MYC overexpression.

See commentary, p. 152

See commented, p. 152
<table>
<thead>
<tr>
<th>Updated version</th>
<th>Access the most recent version of this article at: <a href="http://cancerdiscovery.aacrjournals.org/content/4/2">http://cancerdiscovery.aacrjournals.org/content/4/2</a></th>
</tr>
</thead>
<tbody>
<tr>
<td>E-mail alerts</td>
<td>Sign up to receive free email-alerts related to this article or journal.</td>
</tr>
<tr>
<td>Reprints and Subscriptions</td>
<td>To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at <a href="mailto:pubs@aacr.org">pubs@aacr.org</a>.</td>
</tr>
<tr>
<td>Permissions</td>
<td>To request permission to re-use all or part of this article, contact the AACR Publications Department at <a href="mailto:permissions@aacr.org">permissions@aacr.org</a>.</td>
</tr>
</tbody>
</table>