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## ON-LINE
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## VIEWS
In The Spotlight

**It Takes a Village to Unmask HSTL**
N. Yoshida and D.M. Weinstock
See article, p. 369

**Exploring the Link between the Germline and Somatic Genome in Cancer**
P. Geeleher and R.S. Huang
See article, p. 410

**Anaphase-Promoting Complex Adaptor FZR1/CDH1 Blocks BRAF Signaling Both by Targeting BRAF for Proteolytic Degradation and by Disrupting BRAF Dimerization**
C. Zhang and G. Bollag
See article, p. 424

## MINI REVIEW
The Epitranscriptome of Noncoding RNAs in Cancer 359
M. Esteller and P.P. Pandolfi

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## RESEARCH BRIEFS

**The Genetic Basis of Hepatosplenic T-cell Lymphoma**

Précis: In-depth genetic characterization of the genomic landscape of hepatosplenic T-cell lymphoma identifies SETD2 as a tumor suppressor and STAT5B and PIK3CD as drivers of hepatosplenic T-cell lymphoma.
See commentary, p. 352

**PTEN Regulates Glutamine Flux to Pyrimidine Synthesis and Sensitivity to Dihydroorotate Dehydrogenase Inhibition**

Précis: PTEN-mutant tumor cells require glutamine-dependent de novo pyrimidine synthesis for their enhanced proliferation and survival, creating a vulnerability that may be targeted with DHODH inhibitors to induce DNA damage and cell death.
See related article, p. 380

**Adaptive Reprogramming of De Novo Pyrimidine Synthesis Is a Metabolic Vulnerability in Triple-Negative Breast Cancer**
K.K. Brown, J.B. Spinelli, J.M. Asara, and A. Toker

Précis: Chemotherapy activates the de novo pyrimidine synthesis pathway to elevate pyrimidine nucleotide levels in TNBC, suggesting that targeting de novo pyrimidine synthesis may enhance chemotherapeutic efficacy.
See related article, p. 380
Safety and Antitumor Activity of the Multitargeted Pan-TRK, ROS1, and ALK Inhibitor Entrectinib: Combined Results from Two Phase I Trials (ALKA-372-001 and STARTRK-1) ...................................... 400


Précis: The multikinase inhibitor entrectinib is well tolerated and has antitumor activity in patients with TKI-naïve NTRK1/2/3, ROS1, or ALK-rearranged tumors, including those with CNS disease.

Interaction Landscape of Inherited Polymorphisms with Somatic Events in Cancer ........................................ 410


Précis: A pan-cancer genome-wide association study of data from The Cancer Genome Atlas identifies genetic risk variants that affect cancer-specific somatic alterations and influence tumor site of origin.

See commentary, p. 354

To discover interactions between germline variants and somatic events in cancer, Carter and colleagues performed a genome-wide association study, evaluating genomic data from The Cancer Genome Atlas (TCGA) including more than 5,900 tumors and 22 cancer types. Association studies that compared tumor-specific SNPs identified loci that were significantly associated with specific tumor types, while association testing of SNPs in TCGA samples and the alteration status of 138 cancer driver genes identified 35 associations between 28 germline loci and 20 cancer driver genes. Analysis of mutational heterogeneity based on germline loci identified 20 candidate cancer driver genes, 15 of which had not previously been shown to be frequently mutated. In addition to providing a resource of germline–somatic interactions in cancer, these findings demonstrate that inherited risk variants can alter the somatic evolution of cancer. For details, please see the article by Carter and colleagues on page 410.