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.

PTEN-regulated glutamine flux to pyrimidine synthesis and sensitivity to dihydroorotate dehydrogenase inhibition.

Adaptive reprogramming of de novo pyrimidine synthesis is a metabolic vulnerability in triple-negative breast cancer.

The epitranscriptome of noncoding RNAs in cancer.
**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 multitargeted kinase inhibitor entrectinib is well tolerated and has antitumor activity in patients with TKI-naive 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

**The APC/C E3 Ligase Complex Activator FZR1 Restricts BRAF Oncogenic Function** 424


**Précis:** The putative tumor suppressor FZR1 negatively regulates BRAF kinase activity via APC/C-dependent ubiquitination and subsequent proteolysis in nontransformed cells and APC/C-independent disruption of BRAF dimerization in cancer cells.

See commentary, p. 356

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.