Research

Single-cell gene expression analysis reveals regulators of distinct cell subpopulations among developing human neurons

Jiaxu Wang, Piroon Jenjaroenpun, Akshay Bhinge, Vladimir Espinosa Angarica, Antonio Del Sol, Intawat Nookaew, Vladimir A. Kuznetsov, and Lawrence W. Stanton

Assessing the reliability of spike-in normalization for analyses of single-cell RNA sequencing data

Aaron T.L. Lun, Fernando J. Calero-Nieto, Liora Haim-Vilmovskay, Berthold Göttgens, and John C. Marioni

Disease-specific biases in alternative splicing and tissue-specific dysregulation revealed by multtissue profiling of lymphocyte gene expression in type I diabetes


Nascent RNA sequencing reveals a dynamic global transcriptional response at genes and enhancers to the natural medicinal compound celastrol

Noah Dukler, Gregory T. Booth, Yi-Fei Huang, Nathaniel Tippens, Colin T. Waters, Charles G. Danko, John T. Lis, and Adam Siepel

Altered hydroxymethylation is seen at regulatory regions in pancreatic cancer and regulates oncogenic pathways

Sanchari Bhattacharyya, Kith Pradhan, Nathaniel Campbell, Jozef Mazdo, Aparna Vasantkumar, Shahina Maqbool, Tushar D. Bhagat, Sonal Gupta, Masako Suzuki, Yiting Yu, John M. Greally, Ulrich Steidl, James Bradner, Meelad Dawlaty, Lucy Godley, Anirban Maitra, and Amit Verma

Methods

Co-expression networks reveal the tissue-specific regulation of transcription and splicing

Ashis Saha, Yungil Kim, Ariel D.H. Gewirtz, Brian Jo, Chuan Gao, Ian C. McDowell, The GTEx Consortium, Barbara E. Engelhardt, and Alexis Battle

Identifying cis mediators for trans-eQTLs across many human tissues using genomic mediation analysis

Fan Yang, Jiebiao Wang, The GTEx Consortium, Brandon L. Pierce, and Lin S. Chen

Quantifying the regulatory effect size of cis-acting genetic variation using allelic fold change

Pejman Mohammadi, Stephane E. Castel, Andrew A. Brown, and Tuuli Lappalainen

Single-cell sequencing data reveal widespread recurrence and loss of mutational hits in the life histories of tumors

Jack Kuipers, Katharina Jahn, Benjamin J. Raphael, and Niko Beerenwinkel

(continued)
Detection of long repeat expansions from PCR-free whole-genome sequence data

High-throughput single-molecule telomere characterization
Jennifer McCaffrey, Eleanor Young, Katy Lassahn, Justin Sibert, Steven Pastor, Harold Riethman, and Ming Xiao

The Mobile Element Locator Tool (MELT): population-scale mobile element discovery and biology

Accounting for GC-content bias reduces systematic errors and batch effects in ChIP-seq data
Mingxiang Teng and Rafael A. Irizarry

HiCRep: assessing the reproducibility of Hi-C data using a stratum-adjusted correlation coefficient
Tao Yang, Feipeng Zhang, Galip Gürkan Yardımcı, Fan Song, Ross C. Hardison, William Stafford Noble, Feng Yue, and Qunhua Li

Resource
A genome-wide interactome of DNA-associated proteins in the human liver
Ryne C. Ramaker, Daniel Savic, Andrew A. Hardigan, Kimberly Newberry, Gregory M. Cooper, Richard M. Myers, and Sara J. Cooper

Cover Pancreatic cancer is characterized by altered distribution of 5-hydroxymethylcytosine (5-hmC) marks. 5-hmC regulates many oncogenic transcripts, including that of the gene encoding the bromodomain-containing transcription factor BRD4. BRD4 inhibition leads to in vivo pancreatic tumor growth inhibition. (Cover illustration by Carlie Hruban. [For details, see Bhattacharyya et al., pp. 1830–1842.])