Research

Slightly deleterious genomic variants and transcriptome perturbations in Down syndrome embryonic selection

Saturation mutagenesis reveals manifold determinants of exon definition
Shengdong Ke, Vincent Anquetil, Jorge Rojas Zamalloa, Alisha Maity, Anthony Yang, Mauricio A. Arias, Sergey Kalachikov, James J. Russo, Jingyue Ju, and Lawrence A. Chasin

Discovery of noncanonical translation initiation sites through mass spectrometric analysis of protein N termini
Chan Hyun Na, Mustafa A. Barbhuiya, Min-Sik Kim, Steven Verbruggen, Stephen M. Eacker, Olga Pletnikova, Juan C. Troncoso, Marc K. Halushka, Gerben Menschaert, Christopher M. Overall, and Akhilesh Pandey

H3S10ph broadly marks early-replicating domains in interphase ESCs and shows reciprocal antagonism with H3K9me2
Carol C.L. Chen, Preeti Goyal, Mohammad M. Karimi, Marie H. Abildgaard, Hiroshi Kimura, and Matthew C. Lorincz

Deep experimental profiling of microRNA diversity, deployment, and evolution across the Drosophila genus
Jaaved Mohammed, Alex S. Flynt, Alexandra M. Panzarino, Md Mosharraf Hossein Mondal, Matthew DeCruz, Adam Siepel, and Eric C. Lai

DNA mismatch repair preferentially protects genes from mutation
Eric J. Belfield, Zhong Jie Ding, Fiona J.C. Jamieson, Anne M. Visscher, Shao Jian Zheng, Aziz Mithani, and Nicholas P. Harberd

Methods

SIDR: simultaneous isolation and parallel sequencing of genomic DNA and total RNA from single cells
Kyung Yeon Han, Kyu-Tae Kim, Je-Gun Joung, Dae-Soon Son, Yeon Jeong Kim, Areum Jo, Hyo-Jeong Jeon, Hui-Sung Moon, Chang Eun Yoo, Woosung Chung, Hye Hyeon Eum, Sangmin Kim, Hong Kwan Kim, Jeong Eon Lee, Myung-Ju Ahn, Hae-Ock Lee, Donghyun Park, and Woong-Yang Park

(continued)
Genome-wide DNA methylation profiling using the methylation-dependent restriction enzyme LpnPI

Ruben Boers, Joachim Boers, Bas de Hoon, Christel Kockx, Zeliha Ozgur, Anco Molijn, Wilfred van IJcken, Joop Laven, and Joost Gribnau

ABCA4 midigene reveals the full splice spectrum of all reported noncanonical splice site variants in Stargardt disease

Riccardo Sangermano, Mubeen Khan, Stéphanie S. Cornelis, Valerie Richelle, Silvia Albert, Alejandro Garanto, Duaa Elmelik, Raheel Qamar, Dorien Lugtenberg, L. Ingeborgh van den Born, Rob W.J. Collin, and Frans P.M. Cremers

SelexGLM differentiates androgen and glucocorticoid receptor DNA-binding preference over an extended binding site

Liyang Zhang, Gabriella D. Martini, H. Tomas Rube, Judith F. Kriebelbauer, Chaitanya Rastogi, Vincent D. FitzPatrick, Jon C. Houtman, Harmen J. Bussemaker, and Miles A. Pufall

Resources

Impact of regulatory variation across human iPSCs and differentiated cells


The landscape of miRNA editing in animals and its impact on miRNA biogenesis and targeting

Lishi Li, Yulong Song, Xinrui Shi, Jianheng Liu, Shaolei Xiong, Wanying Chen, Qiang Fu, Zichao Huang, Nannan Gu, and Rui Zhang

Corrigendum

Corrigendum: Discovery and genotyping of structural variation from long-read haploid genome sequence data


Cover  Per aspera ad astra. Two men are climbing up the tree of life, representing two different genomes that are expressing themselves starting from the level of double helix (trunk), nucleosomes (fruits), and chromatin (leaves). The tree crown is growing up toward the cosmos, toward an unknown future. The climbing is much more difficult for the man on the left since he carries a heavy backpack—representing a severe mutation, such as trisomy 21 in Down syndrome individuals. However, both have progressed above the clouds, which represent natural embryonic selection. In this issue, a study suggests that only a highly fit climber (i.e., with a deficit of slightly deleterious variants) is able to climb successfully with a backpack. (Cover illustration is a watercolor painting by Viktoria Polomoshnova, a student of the Immanuel Kant Baltic Federal University, Russia. [For details, see Popadin et al., pp. 1–10.])