

## Research

The human ribosomal DNA array is composed of highly homogenized tandem clusters	1971 <sup>OA</sup>
Yutaro Hori, Akira Shimamoto, and Takehiko Kobayashi	
Embryonic LTR retrotransposons supply promoter modules to somatic tissues	1983
Kosuke Hashimoto, Eeva-Mari Jouhilahti, Virpi Töhönen, Piero Carninci, Juha Kere, and Shintaro Katayama	
Mutational bias in spermatogonia impacts the anatomy of regulatory sites in the human genome	1994 <sup>OA</sup>
Vera B. Kaiser, Lana Talmane, Yatendra Kumar, Fiona Semple, Marie MacLennan, Deciphering Developmental Disorders Study, David R. FitzPatrick, Martin S. Taylor, and Colin A. Semple	
Nuclease deficiencies alter plasma cell-free DNA methylation profiles	2008 <sup>OA</sup>
Diana S.C. Han, Meng Ni, Rebecca W.Y. Chan, Danny K.L. Wong, Linda T. Hiraki, Stefano Volpi, Peiyong Jiang, Kathy O. Lui, K.C. Allen Chan, Rossa W.K. Chiu, and Y.M. Dennis Lo	
RBFOX splicing factors contribute to a broad but selective recapitulation of peripheral tissue splicing patterns in the thymus	2022 <sup>OA</sup>
Kathrin Jansen, Noriko Shikama-Dorn, Moustafa Attar, Stefano Maio, Maria Lopopolo, David Buck, Georg A. Holländer, and Stephen N. Sansom	
Positive selection in noncoding genomic regions of vocal learning birds is associated with genes implicated in vocal learning and speech functions in humans	2035 <sup>OA</sup>
James A. Cahill, Joel Armstrong, Alden Deran, Carolyn J. Khoury, Benedict Paten, David Haussler, and Erich D. Jarvis	
Genome-wide oscillations in G + C density and sequence conservation	2050
Zarmik Moqtaderi, Susan Brown, and Welcome Bender	
Cellular abundance shapes function in piRNA-guided genome defense	2058
Pavol Genzor, Parthena Konstantinidou, Daniel Stoyko, Amirhossein Manzouriolajdad, Celine Marlin Andrews, Alexandra R. Elchert, Constantinos Stathopoulos, and Astrid D. Haase	
Shared evolutionary trajectories of three independent neo-sex chromosomes in <i>Drosophila</i>	2069 <sup>OA</sup>
Masafumi Nozawa, Yohei Minakuchi, Kazuhiro Satomura, Shu Kondo, Atsushi Toyoda, and Koichiro Tamura	

(continued)

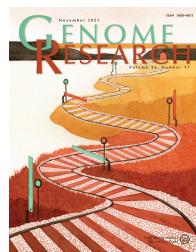
## Methods

Effective sequence similarity detection with strobemers Kristoffer Sahlin	2080 <sup>OA</sup>
Cancer-associated dynamics and potential regulators of intronic polyadenylation revealed by IPAFinder using standard RNA-seq data Zhaozhao Zhao, Qiushi Xu, Ran Wei, Weixu Wang, Dong Ding, Yu Yang, Jun Yao, Liye Zhang, Yue-Qing Hu, Gang Wei, and Ting Ni	2095 <sup>OA</sup>
Variational inference using approximate likelihood under the coalescent with recombination Xinhao Liu, Huw A. Ogilvie, and Luay Nakhleh	2107
Targeted regulation of transcription in primary cells using CRISPRa and CRISPRi Trine I. Jensen, Nanna S. Mikkelsen, Zongliang Gao, Johannes Foßeleder, Gabriel Pabst, Esben Axelgaard, Anders Laustsen, Saskia König, Andreas Reinisch, and Rasmus O. Bak	2120
Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes George Armstrong, Kalen Cantrell, Shi Huang, Daniel McDonald, Niina Haiminen, Anna Paola Carrieri, Qiyun Zhu, Antonio Gonzalez, Imran McGrath, Kristen L. Beck, Daniel Hakim, Aki S. Havulinna, Guillaume Méric, Teemu Niiranen, Leo Lahti, Veikko Salomaa, Mohit Jain, Michael Inouye, Austin D. Swafford, Ho-Cheol Kim, Laxmi Parida, Yoshiki Vázquez-Baeza, and Rob Knight	2131

## Resource

A systematic analysis of <i>Trypanosoma brucei</i> chromatin factors identifies novel protein interaction networks associated with sites of transcription initiation and termination Desislava P. Staneva, Roberta Carloni, Tatsiana Auchyannikava, Pin Tong, Juri Rappaport, A. Arockia Jeyaprakash, Keith R. Matthews, and Robin C. Allshire	2138 <sup>OA</sup>
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<sup>OA</sup>Open Access paper



**Cover** Cell-free DNA in plasma consists of fragments of DNA and has been used for noninvasive prenatal testing, cancer liquid biopsies, and transplantation monitoring. In this issue, Han et al. demonstrate the interrelationships between nucleases, cell-free DNA fragmentation, and DNA methylation, which are depicted in this artistic illustration. The railroad (representing DNA) enters a red tunnel (representing a blood vessel) in the distant mountain. The railroad has red and green sign posts, denoting methylated cytosines and unmethylated cytosines on the DNA, respectively. Barriers of different colors are different nucleases, preferring to cleave (down position) or not cleave (up position) the DNA. DNASE1 (red barriers) prefers to cleave at unmethylated cytosines, while DNASE1L3 (green barriers) prefers to cleave at methylated cytosines. Thus, nuclease-mediated cell-free DNA fragmentation is informed by underlying DNA methylation. (Cover art using watercolor and colored pencils on paper by Carmen Ng [<https://www.carmen-ng.com/>], based on a concept from Dennis Lo. [For details, see Han et al., pp. 2008–2021.]])