

## Research

**Mosaic loss of Chromosome Y in aged human microglia** 1795<sup>OA</sup>  
 Michael C. Vermeulen, Richard Pearse, Tracy Young-Pearse, and Sara Mostafavi

**Physiological intron retaining transcripts in the cytoplasm abound during human motor neurogenesis** 1808<sup>OA</sup>  
 Marija Petrić Howe, Hamish Crerar, Jacob Neeves, Jasmine Harley, Giulia E. Tyzack, Pierre Klein, Andres Ramos, Rickie Patani, and Raphaëlle Luisier

**Diverse environmental perturbations reveal the evolution and context-dependency of genetic effects on gene expression levels** 1826<sup>OA</sup>  
 Amanda J. Lea, Julie Peng, and Julien F. Ayroles

**Functional characterization of enhancer activity during a long terminal repeat's evolution** 1840<sup>OA</sup>  
 Alan Y. Du, Xiaoyu Zhuo, Vasavi Sundaram, Nicholas O. Jensen, Hemangi G. Chaudhari, Nancy L. Saccone, Barak A. Cohen, and Ting Wang

**Natural variation in *C. elegans* short tandem repeats** 1852<sup>OA</sup>  
 Gaotian Zhang, Ye Wang, and Erik C. Andersen

**A butterfly pan-genome reveals that a large amount of structural variation underlies the evolution of chromatin accessibility** 1862  
 Angelo A. Ruggieri, Luca Livraghi, James J. Lewis, Elizabeth Evans, Francesco Cicconardi, Laura Hebberecht, Yadira Ortiz-Ruiz, Stephen H. Montgomery, Alfredo Ghezzi, José Arcadio Rodriguez-Martinez, Chris D. Jiggins, W. Owen McMillan, Brian A. Counterman, Riccardo Papa, and Steven M. Van Belleghem

**Methods**

**Target-enriched nanopore sequencing and de novo assembly reveals co-occurrences of complex on-target genomic rearrangements induced by CRISPR-Cas9 in human cells** 1876  
 Keyi Geng, Lara G. Merino, Linda Wedemann, Aniek Martens, Małgorzata Sobota, Yerma P. Sanchez, Jonas Nørskov Søndergaard, Robert J. White, and Claudia Kutter

**Spatially resolved whole transcriptome profiling in human and mouse tissue using Digital Spatial Profiling** 1892<sup>OA</sup>  
 Stephanie M. Zimmerman, Robin Fropf, Bridget R. Kulasekara, Maddy Griswold, Oliver Appelbe, Arya Bahrami, Rich Boykin, Derek L. Buhr, Kit Fuhrman, Margaret L. Hoang, Quoc Huynh, Lesley Isgur, Andrew Klock, Alecksandr Kutchma, Alexa E. Lasley, Yan Liang, Jill McKay-Fleisch, Jeffrey S. Nelson, Karen Nguyen, Erin Piazza, Aric Rininger, Daniel R. Zollinger, Michael Rhodes, and Joseph M. Beechem

(continued)

A model-based constrained deep learning clustering approach for spatially resolved single-cell data 1906

Xiang Lin, Le Gao, Nathan Whitener, Ashley Ahmed, and Zhi Wei

A statistical physics approach for disease module detection 1918

Xu-Wen Wang, Dandi Qiao, Michael H. Cho, Dawn L. DeMeo, Edwin K. Silverman, and Yang-Yu Liu

Surveying mutation density patterns around specific genomic features 1930

Hui Yu, Scott Ness, Chung-I Li, Yongsheng Bai, Peng Mao, and Yan Guo

## Resources

A high-resolution map of small-scale inversions in the gibbon genome 1941

Ludovica Mercuri, Donato Palmisano, Alberto L'Abbate, Pietro D'Addabbo, Francesco Montinaro, Claudia Rita Catacchio, Patrick Hasenfeld, Mario Ventura, Jan O. Korbel, Ashley D. Sanders, Flavia Angela Maria Maggiolini, and Francesca Antonacci

The western redcedar genome reveals low genetic diversity in a self-compatible conifer 1952<sup>OA</sup>

Tal J. Shalev, Omnia Gamal El-Dien, Macaire M.S. Yuen, Shu Shengqiang, Shaun D. Jackman, René L. Warren, Lauren Coombe, Lise van der Merwe, Ada Stewart, Lori B. Boston, Christopher Plott, Jerry Jenkins, Guifen He, Juying Yan, Mi Yan, Jie Guo, Jesse W. Breinholt, Leandro G. Neves, Jane Grimwood, Loren H. Rieseberg, Jeremy Schmutz, Inanc Birol, Matias Kirst, Alvin D. Yanchuk, Carol Ritland, John H. Russell, and Joerg Bohlmann

## Corrigenda

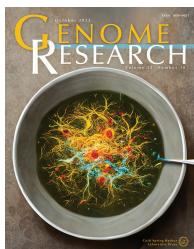
Corrigendum: Cell cycle arrest explains the observed bulk 3D genomic alterations in response to long-term heat shock in K562 cells 1965

Bingxiang Xu, Xiaomeng Gao, Xiaoli Li, Yan Jia, Feifei Li, and Zhihua Zhang

Corrigendum: Diversifying the genomic data science research community 1965

The Genomic Data Science Community Network

<sup>OA</sup>Open Access paper



**Cover** This piece of digital artwork, named "Brain Soup," represents the process of Y Chromosome loss in human brain tissue. The ceramic bowl represents the skull. The noodles are a magnified, cellular interpretation of brain tissue encompassing cell types including neurons (yellow and blue) and microglia (red). The spoon represents the blood-brain barrier and the connection between the brain and peripheral immune system. Note the Y-shaped alphabet noodles—these represent lost Y Chromosomes recently ejected from the genome of their cell-of-origin. In this issue, a cell type-specific investigation of Y Chromosome loss explores human brain tissue and reveals a strong enrichment of Y loss in the microglia of aging and Alzheimer's-affected men. The image was generated using a combination of two large-scale text-to-image generation models: Midjourney and OpenAI's DALLE-2, the draft versions of which were reviewed, edited, and revised by the author who takes ultimate responsibility for the content. (Cover artwork by Michael Vermeulen. [For details, see Vermeulen et al., pp. 1795–1807.])