

## Review

- Advancements in prospective single-cell lineage barcoding and their applications in research 2147<sup>OA</sup>  
Xiaoli Zhang, Yirui Huang, Yajing Yang, Qi-En Wang, and Lang Li

## Research

- Global identification of mammalian host and nested gene pairs reveal tissue-specific transcriptional interplay 2163<sup>OA</sup>

Bertille Montibus, James A. Cain, Rocio T. Martinez-Nunez, and Rebecca J. Oakey

- Convergent relaxation of molecular constraint in herbivores reveals the changing role of liver and kidney functions across mammalian diets 2176

Matthew D. Pollard, Wynn K. Meyer, and Emily E. Puckett

- Analyzing super-enhancer temporal dynamics reveals potential critical enhancers and their gene regulatory networks underlying skeletal muscle development 2190

Song Zhang, Chao Wang, Shenghua Qin, Choulin Chen, Yongzhou Bao, Yuanyuan Zhang, Lingna Xu, Qingyou Liu, Yunxiang Zhao, Kui Li, Zhonglin Tang, and Yuwen Liu

- A low-abundance class of Dicer-dependent siRNAs produced from a variety of features in *C. elegans* 2203

Thiago L. Knittel, Brooke E. Montgomery, Alex J. Tate, Ennis W. Deihl, Anastasia S. Nawrocki, Frederic J. Hoerndl, and Taiowa A. Montgomery

- Hydra* has mammal-like mutation rates facilitating fast adaptation despite its nonaging phenotype 2217<sup>OA</sup>

Arne Sahm, Konstantin Riege, Marco Groth, Martin Bens, Johann Kraus, Martin Fischer, Hans Kestler, Christoph Englert, Ralf Schaible, Matthias Platzer, and Steve Hoffmann

- Characterization of DNA methylation reader proteins in *Arabidopsis thaliana* 2229

Jonathan Cahn, James P.B. Lloyd, Ino D. Karemaker, Pascal W.T.C. Jansen, Jahnvi Pflueger, Owen Duncan, Jakob Petereit, Ozren Bogdanovic, A. Harvey Millar, Michiel Vermeulen, and Ryan Lister

## Methods

- Inferring ancestry with the hierarchical soft clustering approach tangleGen 2244

Klara Elisabeth Burger, Solveig Klepper, Ulrike von Luxburg, and Franz Baumdicker

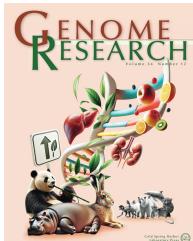
- MCHelper automatically curates transposable element libraries across eukaryotic species 2256<sup>OA</sup>

Simon Orozco-Arias, Pío Sierra, Richard Durbin, and Josefa González

(continued)

Resolving the chromatin impact of mosaic variants with targeted Fiber-seq	2269
Stephanie C. Bohaczuk, Zachary J. Amador, Chang Li, Benjamin J. Mallory, Elliott G. Swanson, Jane Ranchalis, Mitchell R. Vollger, Katherine M. Munson, Tom Walsh, Morgan O. Hamm, Yizi Mao, Andre Lieber, and Andrew B. Stergachis	
Structure-optimized sgRNA selection with PlatinumCRISPr for efficient Cas9 generation of knockouts	2279 <sup>OA</sup>
Irmgard U. Haussmann, Thomas C. Dix, David W.J. McQuarrie, Veronica Dezi, Abdullah I. Hans, Roland Arnold, and Matthias Soller	
Ultrasensitive allele inference from immune repertoire sequencing data with MiXCR	2293 <sup>OA</sup>
Artem Mikelov, George Nefediev, Alexander Tashkeev, Oscar L. Rodriguez, Diego Aguilar Ortmans, Valeria Skatova, Mark Izraelson, Alexey N. Davydov, Stanislav Poslavsky, Souad Rahmouni, Corey T. Watson, Dmitriy Chudakov, Scott D. Boyd, and Dmitry Bolotin	
<b>Resources</b>	
An integrative TAD catalog in lymphoblastoid cell lines discloses the functional impact of deletions and insertions in human genomes	2304
Chong Li, Marc Jan Bonder, Sabriya Syed, Matthew Jensen, Human Genome Structural Variation Consortium (HGSVC), HGSVC Functional Analysis Working Group, Mark B. Gerstein, Michael C. Zody, Mark J.P. Chaisson, Michael E. Talkowski, Tobias Marschall, Jan O. Korbel, Evan E. Eichler, Charles Lee, and Xinghua Shi	
Binding profiles for 961 <i>Drosophila</i> and <i>C. elegans</i> transcription factors reveal tissue-specific regulatory relationships	2319
Michelle Kudron, Louis Gevirtzman, Alec Victorsen, Bridget C. Lear, Jiahao Gao, Jinrui Xu, Swapna Samanta, Emily Frink, Adri Tran-Pearson, Chau Huynh, Dionne Vafeados, Ann Hammonds, William Fisher, Martha Wall, Greg Wesseling, Vanessa Hernandez, Zhichun Lin, Mary Kasparian, Kevin White, Ravi Allada, Mark Gerstein, LaDeana Hillier, Susan E. Celniker, Valerie Reinke, and Robert H. Waterston	
<b>Reviewer Index</b>	2335

<sup>OA</sup>Open Access paper



**Cover** Herbivorous mammals in relaxed postures are shown in the foreground. In the distance, nonherbivorous mammals are shown in grayscale. The lack of color in the nonherbivores represents constrained molecular evolution, whereas the color in the herbivores represents a relaxation of evolutionary constraint as mammalian lineages become more herbivorous. A colorful DNA helix emerges from behind the herbivores, surrounded by plant-based foodstuffs and depictions of the liver and kidneys. In this issue, it is reported that genes associated with liver and kidney functions experience reduced evolutionary constraint and functional importance as increasingly herbivorous diets evolved across Mammalia. (Photo collage created by Matthew D. Pollard in Adobe Photoshop, using public domain images from Wikimedia Commons and images generated by DALL-E 3. [For details, see Pollard et al., pp. 2176–2189.])