

## Mini-Review

- Large-scale genomic analysis of the domestic dog informs biological discovery 811<sup>OA</sup>  
Reuben M. Buckley and Elaine A. Ostrander

## Research

- Single-cell discovery of m<sup>6</sup>A RNA modifications in the hippocampus 822<sup>OA</sup>  
Shuangshuang Feng, Maitena Tellaetxe-Abete, Yujie Zhang, Yan Peng, Han Zhou, Mingjie Dong, Erika Larrea, Liang Xue, Li Zhang, and Magdalena J. Koziol

- Single-cell analysis reveals transcriptional dynamics in healthy primary parathyroid tissue 837  
Aarthi Venkat, Maximillian J. Carlino, Betty R. Lawton, Manju L. Prasad, Matthew Amodio, Courtney E. Gibson, Caroline J. Zeiss, Scott E. Youtlen, Smita Krishnaswamy, and Diane S. Krause

- Genome-wide relaxation of selection and the evolution of the island syndrome in Orkney voles 851  
Xuejing Wang and Gerald Heckel

- Causes and consequences of a complex recombinational landscape in the ant *Cardiocondyla obscurior* 863  
Mohammed Errbii, Jürgen Gadau, Kerstin Becker, Lukas Schrader, and Jan Oettler

- Comparative genomics of *Cryptosporidium parvum* reveals the emergence of an outbreak-associated population in Europe and its spread to the United States 877<sup>OA</sup>  
Greta Bellinzona, Tiago Nardi, Michele Castelli, Gherard Batisti Biffignandi, Karim Adjou, Martha Betson, Yannick Blanchard, Ioana Bujila, Rachel Chalmers, Rebecca Davidson, Nicoletta D'Avino, Tuulia Enbom, Jacinto Gomes, Gregory Karadjian, Christian Klotz, Emma Östlund, Judith Plutzer, Ruska Rimhanen-Finne, Guy Robinson, Anna Rosa Sannella, Jacek Sroka, Christen Rune Stensvold, Karin Troell, Paolo Vatta, Barbora Zalewska, Claudio Bandi, Davide Sasseria, and Simone M. Cacciò

- Large-scale investigation of species-specific orphan genes in the human gut microbiome elucidates their evolutionary origins 888  
Nikolaos Vakirlis and Anne Kupczok

## Methods

- Simultaneous assessment of human genome and methylome data in a single experiment using limited deamination of methylated cytosine 904<sup>OA</sup>  
Bo Yan, Duan Wang, and Laurence Ettwiller

- Fast and space-efficient taxonomic classification of long reads with hierarchical interleaved XOR filters 914  
Jens-Uwe Ulrich and Bernhard Y. Renard

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Accurate estimation of pathway activity in single cells for clustering and differential analysis 925<sup>OA</sup>  
Daniel Davis, Avishai Wizel, and Yotam Drier

Accurate allocation of multimapped reads enables regulatory element analysis at repeats 937  
Alexis Morrissey, Jeffrey Shi, Daniela Q. James, and Shaun Mahony

## Resources

DEAD box RNA helicases are pervasive protein kinase interactors and activators 952  
Alexander Hirth, Edoardo Fatti, Eugen Netz, Sergio P. Acebron, Dimitris Papageorgiou, Andrea Švorinić, Cristina-Maria Cruciat, Emil Karaulanov, Alexandr Gopanenko, Tianheng Zhu, Irmgard Sinning, Jeroen Krijgsveld, Oliver Kohlbacher, and Christof Niehrs

Global compositional and functional states of the human gut microbiome in health and disease 967<sup>OA</sup>  
Sunjae Lee, Theo Portlock, Emmanuelle Le Chatelier, Fernando Garcia-Guevara, Frederick Clasen, Florian Plaza Oñate, Nicolas Pons, Neelu Begum, Azadeh Harzandi, Ceri Proffitt, Dorines Rosario, Stefania Vaga, Junseok Park, Kalle von Feilitzen, Fredric Johansson, Cheng Zhang, Lindsey A. Edwards, Vincent Lombard, Franck Gauthier, Claire J. Steves, David Gomez-Cabrero, Bernard Henrissat, Doheon Lee, Lars Engstrand, Debbie L. Shawcross, Gordon Proctor, Mathieu Almeida, Jens Nielsen, Adil Mardinoglu, David L. Moyes, Stanislav Dusko Ehrlich, Mathias Uhlen, and Saeed Shoaie

## Corrigendum

Corrigendum: Centromere RNA is a key component for the assembly of nucleoproteins at the nucleolus and centromere 979  
Lee H. Wong, Kate H. Brettingham-Moore, Lyn Chan, Julie M. Quach, Melissa A. Anderson, Emma L. Northrop, Ross Hannan, Richard Saffery, Margaret L. Shaw, Evan Williams, and K.H. Andy Choo

<sup>OA</sup>Open Access paper



**Cover** With over 350 recognized breeds, the large-scale analysis of canine genomes is uncovering the genetic basis of trait variation with regard to morphology, behavior, and disease susceptibility. In this issue, a mini-review discusses the global genetic diversity of dog breeds and identifies Asia as a source of missing canine genetic variation. Recent innovations in comparative genomics are also revealing the functional role of noncoding variation and its impact on phenotypic diversity. The cover art features the faces of four dog breeds, the Great Dane, Golden Retriever, Boxer, and German Shepherd Dog, highlighting the genetic and phenotypic diversity between breeds. (Cover design by Renée Mackenzie, vector artwork created using Kittl and Canva. [For details, see Buckley and Ostrander, pp. 811–821.])