

## Research

- Pedigree-based estimation of human mobile element retrotransposition rates** 1567<sup>OA</sup>  
Julie Feusier, W. Scott Watkins, Jainy Thomas, Andrew Farrell, David J. Witherspoon, Lisa Baird, Hongseok Ha, Jinchuan Xing, and Lynn B. Jorde
- LTR retroelement expansion of the human cancer transcriptome and immunopeptidome revealed by de novo transcript assembly** 1578<sup>OA</sup>  
Jan Attig, George R. Young, Louise Hosie, David Perkins, Vesela Encheva-Yokoya, Jonathan P. Stoye, Ambrosius P. Snijders, Nicola Ternette, and George Kassiotis
- RNA components of the spliceosome regulate tissue- and cancer-specific alternative splicing** 1591<sup>OA</sup>  
Heidi Dvinge, Jamie Guenthoer, Peggy L. Porter, and Robert K. Bradley
- Transcriptional alterations in glioma result primarily from DNA methylation-independent mechanisms** 1605  
Franck Court, Elisa Le Boiteux, Anne Fogli, Mélanie Müller-Barthélémy, Catherine Vours-Barrière, Emmanuel Chautard, Bruno Pereira, Julian Biau, Jean-Louis Kemeny, Toufic Khalil, Lucie Karayan-Tapon, Pierre Verrelle, and Philippe Arnaud
- The strand-biased mitochondrial DNA methylome and its regulation by DNMT3A** 1622<sup>OA</sup>  
Xiaoyang Dou, Jerome D. Boyd-Kirkup, Joseph McDermott, Xiaoli Zhang, Fang Li, Bowen Rong, Rui Zhang, Bisi Miao, Peilin Chen, Hao Cheng, Jianhuang Xue, David Bennett, Jiemin Wong, Fei Lan, and Jing-Dong J. Han
- Sequence determinants of polyadenylation-mediated regulation** 1635  
Ilya Vainberg Slutskin, Adina Weinberger, and Eran Segal
- Widespread *cis*-regulatory convergence between the extinct Tasmanian tiger and gray wolf** 1648  
Charles Y. Feigin, Axel H. Newton, and Andrew J. Pask
- Dynamic reversal of random X-Chromosome inactivation during iPSC reprogramming** 1659<sup>OA</sup>  
Adrian Janiszewski, Irene Talon, Joel Chappell, Samuel Collombet, Juan Song, Natalie De Geest, San Kit To, Greet Bervoets, Oskar Marin-Bejar, Caterina Provenzano, Lotte Vanheer, Jean-Christophe Marine, Florian Rambow, and Vincent Pasque
- Regional epigenetic differentiation of the Z Chromosome between sexes in a female heterogametic system** 1673  
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- Fitness benefits of loss of heterozygosity in *Saccharomyces* hybrids** 1685  
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Environmentally induced plasticity of programmed DNA elimination boosts somatic variability in *Paramecium tetraurelia* 1693

Valerio Vitali, Rebecca Hagen, and Francesco Catania

## Methods

RNA-seq as a tool for evaluating human embryo competence 1705<sup>OA</sup>

Abigail F. Groff, Nina Resetkova, Francesca DiDomenico, Denny Sakkas, Alan Penzias, John L. Rinn, and Kevin Eggan

A novel assay to screen siRNA libraries identifies protein kinases required for chromosome transmission 1719<sup>OA</sup>

Mikhail Liskovych, Nikolay V. Goncharov, Nikolai Petrov, Vasilisa Aksenova, Gianluca Pegoraro, Laurent L. Ozbun, William C. Reinhold, Sudhir Varma, Mary Dasso, Vadim Kumeiko, Hiroshi Masumoto, William C. Earnshaw, Vladimir Larionov, and Natalay Kouprina

Identifying clusters of *cis*-regulatory elements underpinning TAD structures and lineage-specific regulatory networks 1733<sup>OA</sup>

Seyed Ali Madani Tonekaboni, Parisa Mazrooei, Victor Kofia, Benjamin Haibe-Kains, and Mathieu Lupien

## Resource

Exploration of fine-scale recombination rate variation in the domestic horse 1744

Samantha K. Beeson, James R. Mickelson, and Molly E. McCue

<sup>OA</sup>Open Access paper



**Cover** In this issue, the first direct estimate of retrotransposition rates in a whole-genome sequenced data set of three-generation CEPH pedigrees is calculated. The cover features an old family portrait representing the multigenerational pedigrees in the CEPH reference panel. The wooden frame is in the shape of the state of Utah to represent the large number of Utah families included in CEPH, as well as to pay homage to Raymond White and his contribution to CEPH in Utah. On the outside of the frame, a mobile element is transcribed into an mRNA intermediate, reverse-transcribed, and reinserted into a new location in the genome of a descendant. (Cover artwork by Cecile Avery, [cecile.avery@utah.edu](mailto:cecile.avery@utah.edu). [For details, see Feusier et al., pp. 1567–1577.]