

## Research

- The human genome contains over a million autonomous exons** 1865<sup>OA</sup>  
Nicholas Stepankiw, Ally W.H. Yang, and Timothy R. Hughes
- Characterization of human transcription factor function and patterns of gene regulation in HepG2 cells** 1879<sup>OA</sup>  
Belle A. Moyers, E. Christopher Partridge, Mark Mackiewicz, Michael J. Betti, Roshan Darji, Sarah K. Meadows, Kimberly M. Newberry, Laurel A. Brandsmeier, Barbara J. Wold, Eric M. Mendenhall, and Richard M. Myers
- E4F1 and ZNF148 are transcriptional activators of the –57A > C and wild-type *TERT* promoter** 1893<sup>OA</sup>  
Boon Haow Chua, Nurkaiyisah Zaal Anuar, Laure Ferry, Cecilia Domrane, Anna Wittek, Vineeth T. Mukundan, Sudhakar Jha, Falk Butter, Daniel G. Tenen, Pierre-Antoine Defossez, and Dennis Kappei
- Cellular age explains variation in age-related cell-to-cell transcriptome variability** 1906  
Ming Yang, Benjamin R. Harrison, and Daniel E.L. Promislow
- Transposon wave remodeled the epigenomic landscape in the rapid evolution of X-Chromosome dosage compensation** 1917  
David C.H. Metzger, Imogen Porter, Brendan Mobley, Benjamin A. Sandkam, Lydia J.M. Fong, Andrew P. Anderson, and Judith E. Mank
- miRNA-like secondary structures in maize (*Zea mays*) genes and transposable elements correlate with small RNAs, methylation, and expression** 1932<sup>OA</sup>  
Galen T. Martin, Edwin Solares, Jeanelle Guadardo-Mendez, Aline Muyle, Alexandros Bousios, and Brandon S. Gaut
- Telomeric repeat evolution in the phylum Nematoda revealed by high-quality genome assemblies and subtelomere structures** 1947<sup>OA</sup>  
Jiseon Lim, Wonjoo Kim, Jun Kim, and Junho Lee
- Genome-wide chromatin interaction profiling reveals a vital role of super-enhancers and rearrangements in host enhancer contacts during BmNPV infection** 1958  
Shudi Zhao, Yuedong Li, Guanping Chen, Xingyang Wang, Nan Chen, and Xiaofeng Wu
- Proteome-wide structural analysis quantifies structural conservation across distant species** 1975  
Shijie Zhang, Teng Zhang, and Yuan Fu

(continued)

## Methods

- De novo reconstruction of satellite repeat units from sequence data 1994  
Yujie Zhang, Justin Chu, Haoyu Cheng, and Heng Li
- Integrating SNVs and CNAs on a phylogenetic tree from single-cell DNA sequencing data 2002  
Liting Zhang, Hank W. Bass, Jerome Irianto, and Xian Mallory
- Characterization of meiotic recombination intermediates through gene knockouts in founder hybrid mice 2018<sup>OA</sup>  
Benjamin Davies, Gang Zhang, Daniela Moralli, Samy Alghadban, Daniel Biggs, Chris Preece, Peter Donnelly, and Anjali Gupta Hinch

<sup>OA</sup>Open Access paper



**Cover** In this issue, Moyers et al. report on analyses of 680 transcription factors in the HepG2 cell line. Transcription factors are depicted as characters associated with DNA, regulating the expression of genes. Some carry flags, denoting tagged ChIP-seq experiments. Some associate with one another by holding hands where different regions of DNA loop together, interacting to achieve the connection between the two distal DNA strands. Some characters accumulate in large numbers, depicting High Occupancy Target (HOT) sites on the DNA. A repressive transcription factor character flexes its muscles to keep others away. Histone proteins are larger characters around which DNA wraps. (Cover illustration concept by Cathleen Shaw, [cshaw@hudsonalpha.org](mailto:cshaw@hudsonalpha.org). [For details, see Moyers et al., pp. 1879–1892.])