

Research

Whole-genome long-read sequencing downsampling and its effect on variant-calling precision and recall 2029^{OA}
William T. Harvey, Peter Ebert, Jana Ebler, Peter A. Audano, Katherine M. Munson, Kendra Hoekzema, David Porubsky, Christine R. Beck, Tobias Marschall, Kiran Garimella, and Evan E. Eichler

A DNA methylation haplotype block landscape in human tissues and preimplantation embryos reveals regulatory elements defined by comethylation patterns 2041
Yan Feng, Zhiqiang Zhang, Yuyang Hong, Yi Ding, Leiqin Liu, Siqi Gao, Hai Fang, and Jiantao Shi

A naturally occurring variant of *MBD4* causes maternal germline hypermutation in primates 2053^{OA}
Alexandra M. Stendahl, Rashesh Sanghvi, Samuel Peterson, Karina Ray, Ana C. Lima, Raheleh Rahbari, and Donald F. Conrad

De novo transcriptome assembly of mouse male germ cells reveals novel genes, stage-specific bidirectional promoter activity, and noncoding RNA expression 2060^{OA}
Mark E. Gill, Alexia Rohmer, Serap Erkek-Ozhan, Ching-Yeu Liang, Sunwoo Chun, Evgeniy A. Ozonov, and Antoine H.F.M. Peters

Revisiting chromatin packaging in mouse sperm 2079
Qiangzong Yin, Chih-Hsiang Yang, Olga S. Strelkova, Jingyi Wu, Yu Sun, Sneha Gopalan, Liyan Yang, Job Dekker, Thomas G. Fazzio, Xin Zhiguo Li, Johan Gibcus, and Oliver J. Rando

Cohesin and CTCF do not assemble TADs in *Xenopus* sperm and male pronuclei 2094
Gregor Jessberger, Csilla Várnai, Roman R. Stocsits, Wen Tang, Georg Stary, and Jan-Michael Peters

Spatiotemporal kinetics of CAF-1-dependent chromatin maturation ensures transcription fidelity during S-phase 2108
Boning Chen, Heather K. MacAlpine, Alexander J. Hartemink, and David M. MacAlpine

tRNA-derived small RNAs are embedded in the gene regulatory network instructing *Drosophila* metamorphosis 2119
Junling Shi, Jiaqi Xu, Jun Ma, and Feng He

Evidence for selfing in a vertebrate from whole-genome sequencing 2133
Astrid Böhne, Zeynep Oğuzhan, Ioannis Chrysostomakis, Simon Vitt, Denis Meuthen, Sebastian Martin, Sandra Kukowka, and Timo Thünken

(continued)

Methods

Using long-read CAGE sequencing to profile cryptic-promoter-derived transcripts and their contribution to the immunopeptidome

2143^{OA}

Ju Heon Maeng, H. Josh Jang, Alan Y. Du, Shin-Cheng Tzeng, and Ting Wang

Assessing and mitigating privacy risks of sparse, noisy genotypes by local alignment to haplotype databases

2156^{OA}

Prashant S. Emani, Maya N. Geradi, Gamze Gürsoy, Monica R. Grasty, Andrew Miranker, and Mark B. Gerstein

Reviewer Index

2174

^{OA}Open Access paper



Cover Like origami, DNA is intricately folded inside of a cell's nucleus. DNA compaction differs in distinct cell types, like somatic and germ cells, and is typically tightly controlled by the function of cohesin, a protein complex that mediates sister chromatid cohesion and DNA looping. In this issue, it is shown that in frog and human sperm, genomic DNA is not folded by cohesin, as it is in somatic cells, possibly because in these cells DNA is densely packaged by specialized sperm proteins called protamines. Earlier work by others had reported that in mouse sperm the genome is folded by cohesin but, in a related study (also in this issue), it was found that these data were caused by chromatin contaminations from somatic cells. Together, these two studies suggest that in sperm from all vertebrate species genomic DNA might be packaged very differently from how it is folded in somatic cells. (Cover illustration by Philipp Dexheimer (www.philippdexheimer.com). [For details, see Jessberger et al., pp. 2094–2107 and Yin et al., pp. 2079–2093.]