

## Review

### The structure, function, and evolution of plant centromeres

Matthew Naish and Ian R. Henderson

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## Research

### Differences in molecular sampling and data processing explain variation among single-cell and single-nucleus RNA-seq experiments

John T. Chamberlin, Younghée Lee, Gabor T. Marth, and Aaron R. Quinlan

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### Genomic origin, fragmentomics, and transcriptional properties of long cell-free DNA molecules in human plasma

Huiwen Che, Peiyong Jiang, L.Y. Lois Choy, Suk Hang Cheng, Wenlei Peng, Rebecca W.Y. Chan, Jing Liu, Qing Zhou, W.K. Jacky Lam, Stephanie C.Y. Yu, So Ling Lau, Tak Y. Leung, John Wong, Vincent Wai-Sun Wong, Grace L.H. Wong, Stephen L. Chan, K.C. Allen Chan, and Y.M. Dennis Lo

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### Tyrosine I-phosphorylated RNA polymerase II transcribes PROMPTs to facilitate proximal promoter pausing and induce global transcriptional repression in response to DNA damage

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### Preferential formation of Z-RNA over intercalated motifs in long noncoding RNA

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### RNA Pol II-dependent transcription efficiency fine-tunes A-to-I editing levels

Brigitta Szabo, Therese C. Mandl, Bernhard Woldrich, Gregor Diensthuber, David Martin, Michael F. Jantsch, and Konstantin Licht

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### Pathogenic variants in *CRX* have distinct *cis*-regulatory effects on enhancers and silencers in photoreceptors

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### Dynamic DNA N<sup>6</sup>-adenine methylation (6mA) governs the encystment process, showcased in the unicellular eukaryote *Pseudocohnilembus persalinus*

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### Modeling alternative translation initiation sites in plants reveals evolutionarily conserved *cis*-regulatory codes in eukaryotes

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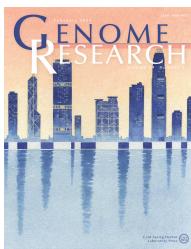
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<sup>OA</sup>Open Access paper



**Cover** Cell-free DNA (cfDNA) in plasma is generally believed to consist of short fragments of DNA. Recently, a previously unexplored population of long cfDNA has been discovered. In this issue, Che et al. demonstrate that such long cfDNA molecules are preferentially originating from euchromatin. Furthermore, the amount of long cfDNA molecules appears to positively correlate with transcriptional activity. The cover art is a stylized version of Figure 1A of the paper by Che et al. The strip of land is drawn to mimic a chromosome ideogram, with white and dark areas representing euchromatin and heterochromatin, respectively. The tall buildings, built on white areas of the strip of land, represent the overrepresentation of long cfDNA. The lit windows of the buildings represent transcriptional activity. The dark reflections of the heterochromatin in the water represent the overrepresentation of short cfDNA. (Cover art using watercolor and colored pencils on paper by Carmen Ng, <https://www.carmen-ng.com/>, based on a concept from Dennis Lo. [For details, see Che et al., pp. 189–200.])