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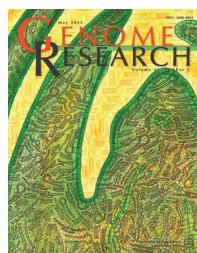
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Erratum: Ultralow-input single-tube linked-read library method enables short-read second-generation sequencing systems to routinely generate highly accurate and economical long-range sequencing information 934

Zhoutao Chen, Long Pham, Tsai-Chin Wu, Guoya Mo, Yu Xia, Peter L. Chang, Devin Porter, Tan Phan, Huu Che, Hao Tran, Vikas Bansal, Justin Shaffer, Pedro Belda-Ferre, Greg Humphrey, Rob Knight, Pavel Pevzner, Son Pham, Yong Wang, and Ming Lei

^{OA}Open Access paper



Cover MicroRNAs (miRNAs) drive spatiotemporal regulation of gene expression. In this issue, patterns of miRNA accumulation and function are assessed across the dynamic developmental environment of the maize shoot apex. The work reveals insights into how the complexity of plant miRNA regulation manifests across developmental contexts. The image shows a longitudinal section through a maize apex, with the stem cell niche at the center of the apex, surrounded by developing leaves. Cell color variations reflect different tissue layers, while a miRNA precursor and duplex pattern across the apex is complemented by representations of two mechanisms of miRNA regulation—target cleavage, represented by a miRNA straddling a broken transcript, and translational repression, represented by a miRNA blocking a transcript in association with another component. These representations are distributed unevenly across tissues, reflecting one of the study's key observations of tissue-specific effects on miRNA transcription, processing, and efficacy. (Cover illustration is created by Tom Denyer with watercolors and ink. [For details, see Ma et al., pp. 811–822.]