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A genome-wide analysis of common fragile sites: What features determine chromosomal instability in the human genome?  
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BRAFV600E remodels the melanocyte transcriptome and induces BANCR to regulate melanoma cell migration  
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Differential DNase I hypersensitivity reveals factor-dependent chromatin dynamics  
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Coding exons function as tissue-specific enhancers of nearby genes  
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Genome-wide phosphoacetylation of histone H3 at Drosophila enhancers and promoters  
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A systematic study of gene expression variation at single-nucleotide resolution reveals widespread regulatory roles for uAUGs

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Unusual combinatorial involvement of poly-A/T tracts in organizing genes and chromatin in *Dictyostelium*

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Sequential ChIP-bisulfite sequencing enables direct genome-scale investigation of chromatin and DNA methylation cross-talk

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Ultra-low-input, tagmentation-based whole-genome bisulfite sequencing

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The origin, global distribution, and functional impact of the human 8p23 inversion polymorphism

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A quantitative atlas of polyadenylation in five mammals

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Transcriptome survey reveals increased complexity of the alternative splicing landscape in *Arabidopsis*  
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**Erratum**

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**Cover** In this issue, the isolation of individual segmented filamentous bacteria (SFB) from the gut of a monocolonized mouse using a microfluidic device, and the sequencing of their genomes, is described. The colored bases in the DNA sequences represent sequence polymorphisms among individual SFB filaments. The filaments represent life cycle stages driven by cell differentiation and include multicellular filaments, holdfasts, and spores. The SFB genomes encode various proteins that facilitate survival in the intestine and interaction with the host; among these is a novel family of ADP-ribosyl transferases, illustrated as hexagons with arrows. (Cover illustration by Sünje J. Pamp. [For details, see Pamp et al., pp. 1107–1119.])