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Ethical, legal, and social considerations in conducting the Human Microbiome Project
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Active Alu retrotransposons in the human genome
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Characterization of the bovine pseudoautosomal boundary: Documenting the evolutionary history of mammalian sex chromosomes
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Transcriptional enhancement by GATA1-occupied DNA segments is strongly associated with evolutionary constraint on the binding site motif
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Genome-wide relationship between histone H3 lysine 4 mono- and tri-methylation and transcription factor binding
A. Gordon Robertson, Mikhail Bilenky, Angela Tam, Yongjun Zhao, Thomas Zeng, Nina Thiessen, Timothee Cezard, Anthony P. Fejes, Elizabeth D. Wederell, Rebecca Cullum, Ghia Euskirchen, Martin Krzywinski, Inanc Birol, Michael Snyder, Pamela A. Hoodless, Martin Hirst, Marco A. Marra, and Steven J.M. Jones

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Methods
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DNA methylation profile of tissue-dependent and differentially methylated regions (T-DMRs) in mouse promoter regions demonstrating tissue-specific gene expression
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Finding friends and enemies in an enemies-only network: A graph diffusion kernel for predicting novel genetic interactions and co-complex membership from yeast genetic interactions
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Haplotype sorting using human fosmid clone end-sequence pairs

Sequencing of natural strains of Arabidopsis thaliana with short reads
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Cover Female papaya trees with homogametic sex chromosome genotype XX. In this issue, four knob-like heterochromatin structures specific to the male-specific region of the “young” papaya Y chromosome are reported. The DNA sequences associated with these heterochromatic knobs are highly divergent and heavily methylated compared to those of its X chromosome counterpart, suggesting that DNA methylation and heterochromatinization play an important role in the early stage of sex chromosome evolution in papaya. (Photo: Qingyi Yu. [For details, see Zhang et al., pp. 1938–1943.])