Genome-wide mapping of human DNA-replication origins: Levels of transcription at ORC1 sites regulate origin selection and replication timing
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GATA3 acts upstream of FOXA1 in mediating ESR1 binding by shaping enhancer accessibility
Vasiliki Theodorou, Rory Stark, Suraj Menon, and Jason S. Carroll

Small noncoding differentially methylated copy-number variants, including lncRNA genes, cause a lethal lung developmental disorder

Birth and expression evolution of mammalian microRNA genes
Julien Meunier, Frédéric Lemoine, Magali Soumillon, Angelica Liechti, Manuela Weier, Katerina Guschaniski, Haiyang Hu, Philipp Khaitovich, and Henrik Kaessmann

Evolutionary dynamism of the primate LRRC37 gene family
Giuliana Giannuzzi, Priscillia Siswara, Maika Malig, Tomas Marques-Bonet, NISC Comparative Sequencing Program, James C. Mullikin, Mario Ventura, and Evan E. Eichler

Modeling of epigenome dynamics identifies transcription factors that mediate Polycomb targeting
Phil Arnold, Anne Schöler, Mikhail Pachkov, Piotr J. Balwierz, Helle Jørgensen, Michael B. Stadler, Erik van Nimwegen, and Dirk Schübeler

Comparative motif discovery combined with comparative transcriptomics yields accurate targetome and enhancer predictions
Marina Naval-Sánchez, Delphine Potier, Lotte Haagen, Máximo Sánchez, Sebastian Munck, Bram Van de Sande, Fernando Casares, Valerie Christiaens, and Stein Aerts

A second-generation assembly of the Drosophila simulans genome provides new insights into patterns of lineage-specific divergence
Tina T. Hu, Michael B. Eisen, Kevin R. Thornton, and Peter Andolfatto

Genome-wide patterns of natural variation reveal strong selective sweeps and ongoing genomic conflict in Drosophila mauritiana
Viola Nolte, Ram Vinay Pandey, Robert Kofler, and Christian Schlötterer

Time series community genomics analysis reveals rapid shifts in bacterial species, strains, and phage during infant gut colonization
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Efficient targeted mutagenesis in the monarch butterfly using zinc-finger nucleases
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RNA sequencing reveals a diverse and dynamic repertoire of the Xenopus tropicalis transcriptome over development
Meng How Tan, Kin Fai Au, Arielle L. Yablonovitch, Andrea E. Wills, Jason Chuang, Julie C. Baker, Wing Hung Wong, and Jin Billy Li

Cover An ink drawing of monarch butterflies migrating through their genetically programmed “internal” landscape. Each fall, millions of monarchs migrate from eastern North America to their overwintering grounds in central Mexico. In this issue, a highly efficient gene-targeting approach, using zinc-finger nucleases, is used to define an essential transcriptional repressor as part of the genetic basis of the long-distance monarch migration, where an intact circadian clock is necessary for proper sun compass navigation. (Cover illustration by Vivian Budnik. [For details, see Merlin et al., pp. 159–168.])