Perspective

Functional transcriptomics in the post-ENCODE era
Jonathan M. Mudge, Adam Frankish, and Jennifer Harrow

Research

The influence of genomic context on mutation patterns in the human genome inferred from rare variants
Valerie M. Schaibley, Matthew Zawistowski, Daniel Wegmann, Margaret G. Ehm, Matthew R. Nelson, Pamela L. St. Jean, Gonçalo R. Abecasis, John Novembre, Sebastian Zöllner, and Jun Z. Li

Derived variants at six genes explain nearly half of size reduction in dog breeds
Maud Rimbault, Holly C. Beale, Jeffrey J. Schoenebeck, Barbara C. Hoopes, Jeremy J. Allen, Paul Kilroy-Glynn, Robert K. Wayne, Nathan B. Sutter, and Elaine A. Ostrander

Identifying multiple causative genes at a single GWAS locus
Michael J. Flister, Shirng-Wern Tsaih, Caitlin C. O’Meara, Bradley Endres, Matthew J. Hoffman, Aron M. Geurts, Melinda R. Dwinell, Jozef Lazar, Howard J. Jacob, and Carol Moreno

The shared genomic architecture of human nucleolar organizer regions
Ioanna Floutsakou, Saumya Agrawal, Thong T. Nguyen, Cathal Seoighe, Austen R.D. Ganley, and Brian McStay

Disclosing the crosstalk among DNA methylation, transcription factors, and histone marks in human pluripotent cells through discovery of DNA methylation motifs
Phuc-Loi Luu, Hans R. Schöler, and Marcos J. Araúzo-Bravo

DNA methylation profiling in human B cells reveals immune regulatory elements and epigenetic plasticity at Alu elements during B-cell activation
Anne Y. Lai, Deepak Mav, Ruchir Shah, Sara A. Grimm, Dhiral Phadke, Katerina Hatzi, Ari Melnick, Cissy Geigerman, Steve E. Sobol, David L. Jaye, and Paul A. Wade

Analysis of variable retroduplications in human populations suggests coupling of retrotransposition to cell division
Alexej Abyzov, Rebecca Iskow, Omer Gokcumen, David W. Radke, Suganthi Balasubramanian, Baikang Pei, Lukas Habegger, The 1000 Genomes Project Consortium, Charles Lee, and Mark Gerstein

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H4K16 acetylation marks active genes and enhancers of embryonic stem cells, but does not alter chromatin compaction
   Gillian C.A. Taylor, Ragnhild Eskeland, Betül Hekimoglu-Balkan, Madapura M. Pradeepa, and Wendy A. Bickmore

Cohesin-based chromatin interactions enable regulated gene expression within preexisting architectural compartments
   Vlad C. Seitan, Andre J. Faure, Ye Zhan, Rachel Patton Mc Cord, Bryan R. Lajoie, Elizabeth Ing-Simmons, Boris Lenhard, Luca Giorgetti, Edith Heard, Amanda G. Fisher, Paul Flicek, Job Dekker, and Matthias Merkenschlager

3' UTR-isoform choice has limited influence on the stability and translational efficiency of most mRNAs in mouse fibroblasts
   Noah Spies, Christopher B. Burge, and David P. Bartel

Distinct global shifts in genomic binding profiles of limb malformation-associated HOXD13 mutations
   Daniel M. Ibrahim, Peter Hansen, Christian Rödelsperger, Asita C. Stiege, Sandra C. Doelken, Denise Horn, Marten Jäger, Catrin Janetzki, Peter Krawitz, Gundula Leschik, Florian Wagner, Till Scheuer, Mareen Schmidt-von Kegler, Petra Seemann, Bernd Timmermann, Peter N. Robinson, Stefan Mundlos, and Jochen Hecht

The altered landscape of the human skin microbiome in patients with primary immunodeficiencies
   Julia Oh, Alexandra F. Freeman, NISC Comparative Sequencing Program, Morgan Park, Robert Sokolic, Fabio Candotti, Steven M. Holland, Julia A. Segre, and Heidi H. Kong

Methods
Single-cell mutational profiling and clonal phylogeny in cancer
   Nicola E. Potter, Luca Ermini, Elli Papaemmanuil, Giovanni Cazzaniga, Gowri Vijayaraghavan, Ian Titley, Anthony Ford, Peter Campbell, Lyndal Kearney, and Mel Greaves

Single-cell methylome landscapes of mouse embryonic stem cells and early embryos analyzed using reduced representation bisulfite sequencing
   Hongshan Guo, Ping Zhu, Xinglong Wu, Xianlong Li, Lu Wen, and Fuchou Tang

Resources
Integrating and mining the chromatin landscape of cell-type specificity using self-organizing maps
   Ali Mortazavi, Shirley Pepke, Camden Jansen, Georgi K. Marinov, Jason Ernst, Manolis Kellis, Ross C. Hardison, Richard M. Myers, and Barbara J. Wold

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A "genetic circuit" represents the complex heritability at a single disease locus. For the past century, it has been widely acknowledged that independently segregating loci contribute to the overall risk of complex diseases, but the possible presence of multiple causative alleles at a single disease locus has been largely unexplored. In this issue, a single GWAS locus for hypertension is shown to harbor multiple alleles that contribute to overall disease risk and susceptibility to end-organ damage. (Cover illustration by Erin Fassbender, erin fassbender design, efassbender@sbcglobal.net. [For details, see Flister et al., pp. 1996–2002.])