GENETICS

A PERIODICAL RECORD OF INVESTIGATIONS
BEARING ON HEREDITY AND VARIATION

Founded in 1916

and published by

THE GENETICS SOCIETY OF AMERICA

VOLUME 182, MAY–AUGUST 2009
Chanet, Soline, Nicolas Vodovar, Véronique Mayau and François Schweiguth, Genome engineering-based analysis of Bearded family genes reveals both functional redundancy and a nonessential function in lateral inhibition in Drosophila ............................................................... 1101—1108

Chau, Johnnie, Laura Shapiro Kulnane and Helen K. Salz, Sex- lethal facilitates the transition from germline stem cell to committed daughter cell in the Drosophila ovary .... 121—132

Chaudhary, Bhupendra, Lex Flagel, Robert M. Stupar, Joshua A. Udall, Neetu Verma, Nathan M. Springer and Jonathan F. Wendel, Reciprocal silencing, transcriptional bias and functional divergence of homeologs in polyploid cotton (Gossypium) ................................................................. 503—517

Chun, Hyonho, and Šundüz Keleş, Expression quantitative trait loci mapping with multivariate sparse partial least squares regression .............................................................................. 79—90

Concha, Carolina, and Maxwell J. Scott, Sexual development in Lucilia cuprina (Diptera, Calliphoridae) is controlled by the transformer gene .......................................................... 785—798

Conde, Francisco, Esther Refolio, Violeta Cordón-Preciado, Felipe Cortés-Ledesma, Luis Aragón, Andrés Aguilera and Pedro A. San-Segundo, The Dot1 histone methyltransferase and the Rad9 checkpoint adaptor contribute to cohesin-dependent double-strand break repair by sister chromatid recombination in Saccharomyces cerevisiae ................................................................. 437—446

Čopić, Alenka, MARIANA DORRINGTON, Silvere Pagant, Justine Barry, Marcus C. S. Lee, Indira Singh, John L. Hartman, IV and Elizabeth A. Miller, Genomewide analysis reveals novel pathways affecting endoplasmic reticulum homeostasis, protein modification and quality control .......................................................................................................................... 757—769

Corrigendum .................................................................................................................... ............. 1399


Cziko, Anne-Marie J., Cathal T. McCann, Iris C. Howlett, Scott A. Barbee, Rebecca P. Duncan, Rene Luedemann, Daniela Zarnescu, Konrad E. Zinsmaier, Roy R. Parker and Mani Ramaswami, Genetic modifiers of dFMRI encode RNA granule components in Drosophila .......................................................................................................................... 1051—1060

Daines, Bryce, Hui Wang, Yumei Li, Yi Han, Richard Gibbs and Rui Chen, High-throughput multiplex sequencing to discover copy number variants in Drosophila ................................................................. 935—941

Da Silva, Jack, Amino acid codification in a functionally important human immunodeficiency virus type 1 protein region is associated with population subdivision .......................................................................................................................... 265—275

Dassah, MaryAnn, Sophie Patzek, Valerie M. Hunt, Pedro E. Medina and Alan M. Zahler, A genetic screen for suppressors of a mutated 5′ splice site identifies factors associated with later steps of spliceosome assembly .............................................................................. 725—734


DeminoFF, Stephen J., Vidhya Ramachandran and Paul K. HERMAN, Distal recognition sites in substrates are required for efficient phosphorylation by the cAMP-dependent protein kinase .......................................................................................................................... 529—539

Deng, Xinjian, S. Kiran Koya, Ying Kong and Victoria H. Meller, Coordinated regulation of heterochromatic genes in Drosophila melanogaster males .......................................................................................................................... 481—491

Dorfman, Marc, José-Eduardo Gomes, Sean O’Rourke and Bruce Bowerman, Using RNA interference to identify specific modifiers of a temperature-sensitive, embryonic-lethal mutation in the Caenorhabditis elegans ubiquitin-like Nedd8 protein modification pathway E1-activating gene rfl-1 .......................................................................................................................... 1035—1049
Dumont, Beth L., Karl W. Broman and Bret A. Payne, Variation in genomic recombination rates among heterogeneous stock mice .......................................................... 1345—1349

Eckert, Andrew J., Andrew D. Bower, Jill L. Wehrzyn, Barnaly Pande, Kathleen D. Jermstad, Konstantin V. Krutovsky, J. Bradley St. Clair and David B. Neale, Association genetics of coastal Douglas fir (Pseudotsuga menziesii var. menziesii, Pinaceae). I. Cold-hardiness related traits .................................................................................................... 1289—1302

Edwards, Alexis C., and Trudy F. C. Mackay, Quantitative trait loci for aggressive behavior in Drosophila melanogaster ........................................................................................................ 889—897

Eismann, Robert C., Melissa A. S. Phelps and Thomas C. Kaufman, Centrosomin: A complex mix of long and short isoforms is required for centrosome function during early development in Drosophila melanogaster .................................................................................. 979—997

Emmons, Richard B., Heather Genetti, Stephen Filandrinos, Jillian Loker and Chaoting Wu, Molecular genetic analysis of Suppressor of zeste identifies key functional domains 999—1013

Favor, Jack, Alan Bradley, Nathalie Conte, Dirk Janik, Walter Pretsch, Peter Reitmeier, Michael Rosemann, Wolfgang Schmahl, Johannes Wienberg and Irmgard Zaus, Analysis of Pax6 contiguous gene deletions in the mouse, Mus musculus, identifies regions distinct from Pax6 responsible for extreme small-eye and belly-spotting phenotypes 1077—1088

Fiumera, Heather L., Maitreya J. Dunham, Scott A. Saracco, Christine A. Butler, Jessica A. Kelly and Thomas D. Fox, Translocation and assembly of mitochondrially coded Saccharomyces cerevisiae cytochrome c oxidase subunit Cox2 by Oxa1 and Yme1 in the absence of Cox18 ........................................................................ 519—528

Forche, Anja, P. T. Magee, Anna Selmeczy, Judith Berman and Georgiana May, Evolution in Candida albicans populations during a single passage through a mouse host ........................................................................................................ 799—811

Gabay-Laughnan, Susan, Evgeny V. Kuzmin, Jessica Monroe, Leah Roark and Kathleen J. Newton, Characterization of a novel thermosensitive restorer of fertility for cytoplasmic male sterility in maize ........................................................................................................ 91—103

Galhardo, Rodrigo S., Robert Do, Masami Yamada, Errol C. Friedberg, P. J. Hastings, Takehiko Nohmi and Susan M. Rosenberg, DinB upregulation is the sole role of the SOS response in stress-induced mutagenesis in Escherichia coli ........................................................................................................ 55—68

Gao, Hong, and Marcus W. Feldman, Complementation and epistasis in viral coinfection dynamics ........................................................................................................................ 251—263


Georis, Isabelle, André Feller, Jennifer J. Tate, Terrance G. Cooper and Evelyne Dubois, Nitrogen catabolite repression-sensitive transcription as a readout of tor pathway regulation: The genetic background, reporter gene and GATA factor assayed determine the outcomes ........................................................................................................................ 927


Gros, Pierre-Alexis, and Olivier Tenailleon, Selection for chaperone-like mediated genetic robustness at low mutation rate: Impact of drift, epistasis and complexity ......................... 555—564

Gros, Pierre-Alexis, Hervé Le Nagard and Olivier Tenailleon, The evolution of epistasis and its links with genetic robustness, complexity and drift in a phenotypic model of adaptation 277—293

Haag, Christoph R., Seanna J. McTaggart, Anaïs Didier, Tom J. Little and Deborah Charlesworth, Nucleotide polymorphism and within-gene recombination in Daphnia magna and D. pulex, two cyclical parthenogens ........................................................................................................ 313—323
Habier, D., R. L. Fernando and J. C. M. Dekkers, Genomic selection using low-density marker panels ................................................................. 343—353
Handel, Adam E., and Sreeram V. Ramagopalan, Public health implications of epigenetics 1397—1398
Hao, Weilong, and G. Brian Golding, Does gene translocation accelerate the evolution of laterally transferred genes? ................................................................. 1365—1375
Hontz, Robert D., Rachel O. Niederer, Joseph M. Johnson and Jeffrey S. Smith, Genetic identification of factors that modulate ribosomal DNA transcription in Saccharomyces cerevisiae 105—119
Howell, Elaine C., Susan J. Armstrong and Dmitry A. Filatov, Evolution of neo-sex chromosomes in Silene clavata .................................................................................. 1109—1115
Huang, Guohong, Stephen D. Dougherty and Scott E. Erdman, Conserved WCPL and CX_{2}C domains mediate several mating adhesin interactions in Saccharomyces cerevisiae .................. 173—189
Ikeda, Hajime, Noriuki Fuji and Hiroaki Setoguchi, Molecular evolution of phytochromes in Cardamine nipponica (Brassicaceae) suggests the involvement of PHYE in local adaptation .............................................................................................................. 603—614
Kerwin, Christine L., and Dennis D. Wykoff, Candida glabrata PHO4 is necessary and sufficient for Pho2-independent transcription of phosphate starvation genes ........................................ 471—479
Kim, Hye-Ryun, Keon-Sang Chae, Kap-Hoon Han and Dong-Min Han, The nsdlC gene encoding a putative C_{2}H_{2}-type transcription factor is a key activator of sexual development in Aspergillus nidulans .............................................................................................................. 771—783
Kopp, Michael, and Joachim Hermisson, The genetic basis of phenotypic adaptation I: Fixation of beneficial mutations in the moving optimum model .............................................................................................................. 233—249
Labbé, Pierrick, Nicolas Sidos, Michel Raymond and Thomas Lenormand, Resistance gene replacement in the mosquito Culex pipiens: Fitness estimation from long-term cline series 303—312
LeBel, Catherine, Emanuel Rosonina, David C. F. Sealey, Fiona Pryde, David Lydall, Laura Maringele and Lea A. Harrington, Telomere maintenance and survival in Saccharomyces cerevisiae in the absence of telomerase and RAD52 .............................................................................................................. 671—684
Legrand, Delphine, Maud I. Tenaillon, Pat Matyot, Justin Gerlach, Daniel Lachaise and Marie-Louise Cariou, Species-wide genetic variation and demographic history of Drosophila sechellia, a species lacking population structure .............................................................................................................. 1197—1206
Li, Wenyun, and Zehua Chen, Multiple-interval mapping for quantitative trait loci with a spike in the trait distribution ................................................................. 337—342
Li, Yubin, and Hugo K. Dooner, Excision of Helitron transposons in maize .............................................................................................................. 399—402
Li, Zheng, Sanwen Huang, Shiqiang Liu, Junsong Pan, Zhonghua Zhang, Qianyi Tao, Quixiang Shi, Zhiqi Jia, Weiwei Zhang, Huiming Chen, Longting Si, Lihuang Zhu and Run Cai, Molecular isolation of the M gene suggests that a conserved-residue conversion induces the formation of bisexual flowers in cucumber plants ................................. 1381—1385
LOHMUELLER, KIRK E., CARLOS D. BUSTAMANTE AND ANDREW G. CLARK, Methods for human demographic inference using haplotype patterns from genomewide single-nucleotide polymorphism data ................................................................. 217—231

LYNCH, MICHAEL, Estimation of allele frequencies from high-coverage genome-sequencing projects .................................................................................................................. 295—301

MANICHAIKUL, ANI, AND KARL W. BROMAN, Binary trait mapping in experimental crosses with selective genotyping ............................................................................................................. 863—874

MARCUS, JEFFREY M., AND TIA M. HUGHES, Drosophila transposon insertions as unknowns for structured inquiry recombination mapping exercises in an undergraduate genetics course 417—422

MATZKIN, LUCIANO M., AND THERÈSE A. MARKOW, Transcriptional regulation of metabolism associated with the increased desiccation resistance of the cactophilic Drosophila mojavensis 1279—1288

MazoUrek, Michael, Elizabeth T. Cirulli, Sarah M. Collier, Laurie G. Landry, BYoung-Cheol Kang, EDMUND A. QUIRING, James M. Bradeen, Peter Moffett and Molly M. Jahn, The fractionated orthology of Bx2 and Rx/Gpa2 supports shared synteny of disease resistance in the Solanaceae .......................................................................................................................... 1351—1364

McGrath, Casey L., Claudio Casola AND Matthew W. Hahn, Minimal effect of ectopic gene conversion among recent duplicates in four mammalian genomes ..................................................................................................................... 615—622

McNamee, Laura M., and Michael H. Brodsky, p53-independent apoptosis limits DNA damage-induced aneuploidy ............................................................................................................................ 423—435

Merritt, Thomas J. S., Caitlin Kuczynski, Efe Sezgin, Chen-TsEh Zhu, Seiji Kumagai and Walter F. Eanes, Quantifying interactions within the NADP(H) enzyme network in Drosophila melanogaster .................................................................................................................................................................................. 565—574

Messer, Philipp W., Measuring the rates of spontaneous mutation from deep and large-scale polymorphism data .................................................................................................................................................................................. 1219—1232

Methods, technology and resources: Drivers of discovery .......................................................................................................................... 1

Moorad, Jacob A., and David W. Hall, Mutation accumulation, soft selection and the middle-class neighborhood .......................................................................................................................................................... 1387—1389

Muirhead, Christina A., and John Wakeley, Modeling multiallelic selection using a Moran model .......................................................................................................................................................................................... 1141—1157

Myrick, Kyi V., François HuT, Stephanie E. Mohr, Inés ÁLVarez-García, Jeffrey T. Lu, Mark A. Smith, Madeline A. Crosby and William M. Gelbart, Large-scale functional annotation and expanded implementations of the P[wHy] hybrid transposon in the Drosophila melanogaster genome ........................................................................................................................................................................ 653—660

Ni, Jian-Quan, Lu-Ping Liu, Richard Binari, Robert Hardy, Hye-Seok Shim, Amanda Cavallaro, Matthew Booker, Barret D. Pfeiffer, Michele Markstein, Hui Wang, Christians Villalta, Todd R. Laverty, Lizabeth A. Perkins and Norbert Perrimon, A Drosophila resource of transgenic RNAi lines for neurogenetics ........................................................................................................................................................................ 1089—1100

O’MILLian, Angela R., and Michael Lynch, Patterns of intraspecific DNA variation in the Daphnia nuclear genome ........................................................................................................................................................................ 325—336

Palstra, Friso P., Michael F. O’Connell and Daniel E. Ruzzante, Age structure, changing demography and effective population size in Atlantic salmon (Salmo salar) ................................................................................................. 1233—1249

PAUKLIN, SIM, JULia S. BURkERT, JULIE Martin, Fekret Osman, Sandra Weller, SIMon J. Boulton, Matthew C. Whitney and Svend K. Petersen-Mahrt, Alternative induction of meiotic recombination from single-base lesions of DNA deaminases ........................................................................................................................................................................ 41—54

Pogorzala, Leah, Shona Mookerjee and ELAINE A. SIA, Evidence that Msh1p plays multiple roles in mitochondrial base excision repair ........................................................................................................................................................................ 699—709
Ratnakumar, Sooraj, Nataley Kacherovsky, Erin Arms and Elton T. Young, Snf1 controls the activity of Adr1 through dephosphorylation of Ser230 .......................................................... 735—745

Ray, Jessica L., Klaus Harms, Odd-Gunnar Wikmark, Irina Starikova, Pál J. Johnsen and Kaare M. Nielsen, Sexual isolation in *Acinetobacter baylyi* is locus-specific and varies 10,000-fold over the genome ........................................................................................................... 1165—1181

Roegiers, Fabrice, Joshua Kavaler, Nicholas Tolwinski, Yu-Ting Chou, Hong Duan, Fernando Bejarano, Diana Zitserman and Eric C. Lai, Frequent unanticipated alleles of *lethal giant larvae* in Drosophila second chromosome stocks .......................................................... 407—410

Rogers, Alan R., and Chad Huff, Linkage disequilibrium between loci with unknown phase .................................................................................................................. 839—844

Saïdou, Abdou-Aziz, Cédric Mariac, Vivianne Luong, Jean-Louis Pham, Gilles Bezançon and Yves Vignouroux, Association studies identify natural variation at *PHYC* linked to flowering time and morphological variation in pearl millet .......................... 899—910

Salathé, Marcel, Jeremy Van Cleve and Marcus W. Feldman, Evolution of stochastic switching rates in asymmetric fitness landscapes ........................................................................ 1159—1164


Sellem, Carole H., Elodie Bovier, Séverine Lorin and Annie Sainsard-Chanet, Mutations in two zinc-cluster proteins activate alternative respiratory and gluconeogenic pathways and restore senescence in long-lived respiratory mutants of *Podospora anserina* .... 69—78

Shalaby, Nevine A., Annette L. Parks, Eric J. Morreale, Marisa C. Osswalt, Kristen M. Pfau, Eric L. Pierce and Marc A. T. Muskavitch, A screen for modifiers of notch signaling uncovers *Amun*, a protein with a critical role in sensory organ development .................................................................................................................. 1061—1076

Shang, Junjun, Yong Tao, Xuewei Chen, Yan Zou, Cailin Lei, Jing Wang, Xiaobing Li, Xianfeng Zhao, Meijun Zhang, Zhike Lu, Jichen Xu, Zhikuan Cheng, Jianmin Wan and Lihuang Zhu, Identification of a new rice blast resistance gene, *Pid3*, by genomewide comparison of paired nucleotide-binding site–leucine-rich repeat genes and their pseudogene alleles between the two sequenced rice genomes .................................................. 1303—1311

Shi, Jiaqin, Ruiyuan Li, Dan Qiu, Congcong Jiang, Yan Long, Colin Morgan, Ian Bancroft, Jianyi Zhao and Jinling Meng, Unraveling the complex trait of crop yield with quantitative trait loci mapping in *Brassica napus* ............................................................................ 851—861

Shringarpure, Suyash, and Eric P. Xing, mStruct: Inference of population structure in light of both genetic admixing and allele mutations ........................................................................... 575—593

Siriaoco, Giorgia, Renate Deuring, Mariacristina Chiода, Peter B. Becker and John W. Tamkun, Drosophila ISWI regulates the association of histone H1 with interphase chromosomes *in Vivo* .......................................................... 661—669

Sivanantharajah, Lovesh, and Anthony Percival-Smith, Analysis of the sequence and phenotype of Drosophila *Sex combs reduced* alleles reveals potential functions of conserved protein motifs of the *Sex combs reduced* protein .................................................................................................................. 191—203

Slatkin, Montgomery, Epigenetic inheritance and the missing heritability problem ......... 845—850

Stamenova, Radostina, Patrick H. Maxwell, Alison E. Kenny and M. Joan Curcio, Rtm3 protects the *Saccharomyces cerevisiae* genome from instability at nascent sites of retrotransposition .................................................................................................................. 711—723

Städler, Thomas, Bernhard Haubold, Carlos Merino, Wolfgang Stephan and Peter Pfabfellhuber, The impact of sampling schemes on the site frequency spectrum in nonequilibrium subdivided populations .................................................................................. 205—216
Steiner, Walter W., Estelle M. Steiner, Angela R. Girvin and Lauren E. Plewik, Novel nucleotide sequence motifs that produce hotspots of meiotic recombination in *Schizosaccharomyces pombe* ................................................................. 459—469

Stinchcombe, John R., Cynthia Weinig, Katy D. Heath, Marcus T. Brock and Johanna Schmitt, Polymorphic genes of major effect: Consequences for variation, selection and evolution in *Arabidopsis thaliana* ........................................................................................................ 911—922

Sun, Song, Otto G. Berg, John R. Roth and Dan I. Andersson, Contribution of gene amplification to evolution of increased antibiotic resistance in *Salmonella typhimurium* .......... 1183—1195

Takano-Kai, Noriko, Hui Jiang, Takahiko Kubo, Megan Sweeney, Takashi Matsumoto, Hiroyuki Kanamori, Badri Padhukasahasram, Carlos Bustamante, Atsushi Yoshimura, Kazuyuki Doi and Susan McCouch, Evolutionary history of GS3, a gene conferring grain length in rice ........................................................................................................ 1323—1334

Taylor, Jesse E., The genealogical consequences of fecundity variance polymorphism ...... 813—837

Traen, Ana, Traude H. Beilharz, Tricia L. Lo, Franziska Lueder, Thomas Preiss and Jörg Heierhorst, The Ccr4-Pop2-NOT mRNA deadenylase contributes to septin organization in *Saccharomyces cerevisiae* ............................................................. 955—966

Tripathi, Namita, Margarete Hoffmann, Detlef Weigel and Christine Dreyer, Linkage analysis reveals the independent origin of poeciliid sex chromosomes and a case of atypical sex inheritance in the guppy (*Poecilia reticulata*) ................................................. 365—374


Valdar, William, Christopher C. Holmes, Richard Mott and Jonathan Flint, Mapping in structured populations by resample model averaging ........................................................................... 1263—1277

Votintseva, Antonina A., and Dmitry A. Filatov, Evolutionary strata in a small mating-type-specific region of the smut fungus *Microbotryum violaceum* .......................................................... 1391—1396

Watanabe, Satoshi, Rumiko Hidestima, Zhengjun Xia, Yasutaka Tsubokura, Shusei Sato, Yumi Nakamoto, Naoki Yamanaka, Ryoji Takahashi, Masao Ishimoto, Toyoaki Anai, Satoshi Tabata and Kyuya Harada, Map-based cloning of the gene associated with the soybean maturity locus *E3* .......................................................................................... 1251—1262

Wegmann, Daniel, Christoph Leuenberger and Laurent Excoffier, Efficient approximate Bayesian computation coupled with Markov chain Monte Carlo without likelihood .... 1207—1218

Weiler, Karen S., The multi-AT-hook chromosomal protein of *Drosophila melanogaster*, *D1*, is dispensable for viability .................................................................................................................. 145—159

Yan, Zhun, Nicolas M. Berbenetz, Guri Giaever and Corey Nislow, Precise gene-dose alleles for chemical genetics ............................................................................................................. 623—626

Yanchukov, Alexey, One- and two-locus population models with differential viability between sexes: Parallels between haploid parental selection and genomic imprinting ............... 1117—1127

Zetterberg, Henrik, Magnus Båth, Madeleine Zetterberg, Peter Bernhardt and Ola Hammarsten, The Szilard hypothesis on the nature of aging revisited ................................................................. 3—9

Zhang, Li-Feng, Yuya Ogawa, Janice Y. Ahn, Satoshi H. Namekawa, Susana S. Silva and Jeannie T. Lee, Telomeric RNAs mark sex chromosomes in stem cells ........................................... 685—698

Zhang, Xu, and Justin O. Borevitz, Global analysis of allele-specific expression in *Arabidopsis thaliana* ............................................................................................................................. 943—954

Zhong, Shengqiang, Jack C. M. Dekkers, Rohan L. Fernando and Jean-Luc Jannink, Factors affecting accuracy from genomic selection in populations derived from multiple inbred lines: A barley case study ................................................................. 355—364
ZHU, CHENGSONG, AND JIANMING Yu, Nonmetric multidimensional scaling corrects for population structure in association mapping with different sample types ........................................... 875—888
A new standard genetic map for the laboratory mouse, pp. 1335–1344
Allison Cox, Cheryl L. Ackert-Bicknell, Beth L. Dumont, Yueming Ding, Jordana Tzenova Bell, Gudrun A. Brockmann, Jon E. Wergedal, Carol Bult, Beverly Paigen, Jonathan Flint, Shing-Wern Tsaih, Gary A. Churchill and Karl W. Broman

Genetic maps continue to be relevant. They remain a critical tool for mapping genes underlying complex traits, and they provide insights into fundamental processes of recombination. This group of investigators produces an improved genetic map of the laboratory mouse genome that is fully integrated with the physical map of the genome. In the process of creating the new map, they correct numerous errors that had accumulated in the mouse map. They demonstrate the impact of these improvements by remapping several historical QTLs.

Genetic modifiers of dFMR1 encode RNA granule components in Drosophila, pp. 1051–1060
Anne-Marie J. Cziko, Cathal T. McCarrn, Iris C. Howlett, Scott A. Barbee, Rebecca P. Duncan, Rene Luedemann, Daniela Zamascu, Konrad E. Zinsmaier, Ray R. Parker and Mani Ramaswami

Fragile-X Mental Retardation Protein (FMRP) is a translational repressor that in neurons probably prevents translation of synaptic RNAs until a threshold of activation is reached. FMRP is also believed to be required for microRNA-mediated translational repression. This article describes a genetic screen that reveals likely new components of the fragile-X pathway that, like FMRP, can modify dendritic structure. The authors come to the unexpected conclusion that FMRP is not essential for microRNA function.

High-throughput multiplex sequencing to discover copy number variants in Drosophila, pp. 935–941
Bryce Daines, Hui Wang, Yumei Li, Yi Han, Richard Gibbs and Rui Chen

This article presents the use of high-throughput DNA sequencing for identifying copy number variation, an approach that promises to become the method of choice for such studies. The authors demonstrate that low sequence coverage is sufficient for identifying and mapping large deletions at kilobase resolution. They show how multiplexing is a good alternative to microarrays because of its greater resolution at a comparable (and rapidly declining) cost.

Domains of heterochromatin protein 1 required for Drosophila melanogaster heterochromatin spreading, pp. 967–979
Karie A. Hines, Diane E. Cryderman, Kaitlin M. Flannery, Hongbo Yang, Michael W. Vitaliini, Tulie Hazelrigg, Craig A. Mozzen and Lori L. Wallrath

Heterochromatin, which makes up a significant fraction of the genome in nearly all eukaryotes, can spread along the chromosomes and silence gene expression. Studying the mechanism of heterochromatin spreading has been challenging due to the repetitive DNA sequences that underlie heterochromatin. These investigators employ the lac repressor to establish heterochromatin domains amenable for analysis of spreading. They identify domains of heterochromatin protein 1 required for spreading, and unexpectedly reveal multiple mechanisms of spreading. Taken together, their findings provide new insights into the mechanisms of transcriptional control by chromatin.

Measuring the rates of spontaneous mutation from deep and large-scale polymorphism data, pp. 1219–1232
Philipp W. Messer

Mutations are the foundation of genetic diversity, yet we remain uncertain about their rates and patterns. This is because new mutations are difficult to assess experimentally, since they occur at extremely low rates in individuals. Indirect estimates of mutation rates from levels of divergence or heterozygosity suffer from unknown selective and demographic biases and disregard deleterious mutations. The author demonstrates how unbiased mutation rate estimates can be obtained from polymorphism data gathered from deep sequencing projects. This promises to facilitate the assessment of several long-standing problems of evolutionary biology.