

## Perspective

- Can I be sued for that? Liability risk and the disclosure of clinically significant genetic research findings 719

Amy L. McGuire, Bartha Maria Knoppers, Ma'n H. Zawati, and Ellen Wright Clayton

## Research

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- Neo-antigens predicted by tumor genome meta-analysis correlate with increased patient survival 743<sup>OA</sup>

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- Evolution of splicing regulatory networks in *Drosophila* 786

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- Tempo and mode of regulatory evolution in *Drosophila* 797<sup>OA</sup>

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| High-resolution mapping defines the cooperative architecture of Polycomb response elements<br>Guillermo A. Orsi, Sivakanthan Kasinathan, Kelly T. Hughes, Sarah Saminadin-Peter,<br>Steven Henikoff, and Kami Ahmad                                                                                                                                                                                                                                                                                                     | 809               |
| Genome methylation in <i>D. melanogaster</i> is found at specific short motifs and is independent<br>of DNMT2 activity<br>Sachiko Takayama, Joseph Dhahbi, Adam Roberts, Guanxiong Mao, Seok-Jin Heo, Lior Pachter,<br>David I.K. Martin, and Dario Boffelli                                                                                                                                                                                                                                                            | 821               |
| Widespread and frequent horizontal transfers of transposable elements in plants<br>Moaine El Baidouri, Marie-Christine Carpentier, Richard Cooke, Dongying Gao, Eric Lasserre,<br>Christel Llauro, Marie Mirouze, Nathalie Picault, Scott A. Jackson, and Olivier Panaud                                                                                                                                                                                                                                                | 831 <sup>OA</sup> |
| Predicting the virulence of MRSA from its genome sequence<br>Maisem Laabei, Mario Recker, Justine K. Rudkin, Mona Aldeljawi, Zeynep Gulay,<br>Tim J. Sloan, Paul Williams, Jennifer L. Endres, Kenneth W. Bayles, Paul D. Fey,<br>Vijaya Kumar Yajjala, Todd Widhelm, Erica Hawkins, Katie Lewis, Sara Parfett, Lucy Scowen,<br>Sharon J. Peacock, Matthew Holden, Daniel Wilson, Timothy D. Read, Jean van den Elsen,<br>Nicholas K. Priest, Edward J. Feil, Laurence D. Hurst, Elisabet Josefsson, and Ruth C. Massey | 839 <sup>OA</sup> |
| A genomic portrait of the genetic architecture and regulatory impact of microRNA<br>expression in response to infection<br>Katherine J. Siddle, Matthieu Deschamps, Ludovic Tailleux, Yohann Nédélec, Julien Pothlichet,<br>Geanncarlo Lugo-Villarino, Valentina Libri, Brigitte Gicquel, Olivier Neyrolles, Guillaume Laval,<br>Etienne Patin, Luis B. Barreiro, and Lluís Quintana-Murci                                                                                                                              | 850               |
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| General approach for in vivo recovery of cell type-specific effector gene sets<br>Julius C. Barsi, Qiang Tu, and Eric H. Davidson                                                                                                                                                                                                                                                                                                                                                                                       | 860               |
| ISMARA: automated modeling of genomic signals as a democracy of regulatory motifs<br>Piotr J. Balwierz, Mikhail Pachkov, Phil Arnold, Andreas J. Gruber, Mihaela Zavolan,<br>and Erik van Nimwegen                                                                                                                                                                                                                                                                                                                      | 869 <sup>OA</sup> |

<sup>OA</sup>Open Access paper



**Cover** Horizontal transfer of genetic material has been demonstrated on a small scale for several organisms. In this issue, this phenomenon is demonstrated to be widespread in the plant kingdom. On the cover is a Pointillist-like view of the horizontal transfer of transposable elements between palm (*top left*) and grape (*bottom right*). The two circles depict the respective DNA molecules and leaf colors indicate the chimeric nature of plants. Horizontal branches on the “tree of life” at the *bottom left* illustrate frequent transfer during the evolution of plants. (Cover illustration by Abdelkebir El Baidouri. [For details, see El Baidouri et al., pp. 831–838.] )