

Perspective

Diversifying the genomic data science research community
The Genomic Data Science Community Network

1231^{OA}

Research

HDAC9 structural variants disrupting *TWIST1* transcriptional regulation lead to craniofacial and limb malformations

1242^{OA}

Naama Hirsch, Idit Dahan, Eva D'haene, Matan Avni, Sarah Vergult, Marta Vidal-García, Pamela Magini, Claudio Graziano, Giulia Severi, Elena Bonora, Anna Maria Nardone, Francesco Brancati, Alberto Fernández-Jaén, Olson J. Rory, Benedikt Hallgrímsson, and Ramon Y. Birnbaum

Extensive protein dosage compensation in aneuploid human cancers

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Compartment-specific and ELAVL1-coordinated regulation of intronic polyadenylation isoforms by doxorubicin

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Cell cycle arrest explains the observed bulk 3D genomic alterations in response to long-term heat shock in K562 cells

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Somatic retrotransposition in the developing rhesus macaque brain

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Multiple *Pristionchus pacificus* genomes reveal distinct evolutionary dynamics between de novo candidates and duplicated genes

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Dynamics of broad H3K4me3 domains uncover an epigenetic switch between cell identity and cancer-related genes

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Epigenomic translocation of H3K4me3 broad domains over oncogenes following hijacking of super-enhancers 1343^{OA}

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High-resolution simulations of chromatin folding at genomic rearrangements in malignant B cells provide mechanistic insights into proto-oncogene deregulation 1355^{OA}

Daniel Rico, Daniel Kent, Nefeli Karataraki, Aneta Mikulasova, Rolando Berlinguer-Palmini, Brian A. Walker, Biola M. Javierre, Lisa J. Russell, and Chris A. Brackley

Dynamic regulatory module networks for inference of cell type-specific transcriptional networks 1367^{OA}

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Identifying cell state-associated alternative splicing events and their coregulation 1385^{OA}

Carlos F. Buen Abad Najar, Prkruthi Burra, Nir Yosef, and Liana F. Lareau

TransMeta simultaneously assembles multisample RNA-seq reads 1398^{OA}

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Zebrafish transposable elements show extensive diversification in age, genomic distribution, and developmental expression 1408^{OA}

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Epigenomic analysis reveals prevalent contribution of transposable elements to *cis*-regulatory elements, tissue-specific expression, and alternative promoters in zebrafish 1424^{OA}

Hyung Joo Lee, Yiran Hou, Ju Heon Maeng, Nakul M. Shah, Yujie Chen, Heather A. Lawson, Hongbo Yang, Feng Yue, and Ting Wang

^{OA}Open Access paper



Cover A digital art illustration entitled “The hijack, identity and Darwin” representing epigenetic changes at oncogenes and the transformation of normal cells to malignant cells. Note how the change of location (from sky to sea) results in a change of color but maintenance of shape. In this issue, three related articles offer insights into how H3K4me3 broad domains are hijacked by oncogenes from cell identity genes. (Cover artwork by Dimple Devadas, <https://www.volvehealth.co.uk/>. [For details, see Belhocine et al., pp. 1328–1342; Mikulasova et al., pp. 1343–1354; and Rico et al., pp. 1355–1366.]