Research

Disclosing pathogenic genetic variants to research participants: Quantifying an emerging ethical responsibility

Christopher A. Cassa, Sarah K. Savage, Patrick L. Taylor, Robert C. Green, Amy L. McGuire, and Kenneth D. Mandl

Interlocus gene conversion events introduce deleterious mutations into at least 1% of human genes associated with inherited disease

Claudio Casola, Ugne Zekonyte, Andrew D. Phillips, David N. Cooper, and Matthew W. Hahn

A transforming KIF5B and RET gene fusion in lung adenocarcinoma revealed from whole-genome and transcriptome sequencing

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Genetic control of gene expression in whole blood and lymphoblastoid cell lines is largely independent

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Tissue type is a major modifier of the 5-hydroxymethylcytosine content of human genes

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Cover A novel transforming KIF5B-RET fusion gene was identified in lung adenocarcinomas analyzed by integration of whole-genome and transcriptome sequencing technologies. Approximately 6% of human lung adenocarcinomas could be caused by the expressed chimeric protein. (Cover Illustration by S.A. Kim and H.J. Min at PTline with Young Seok Ju, Jong-II Kim, and Jeong-Sun Seo at the Genomic Medicine Institute, Seoul National University. [For details, see Ju et al., pp. 436–445.])