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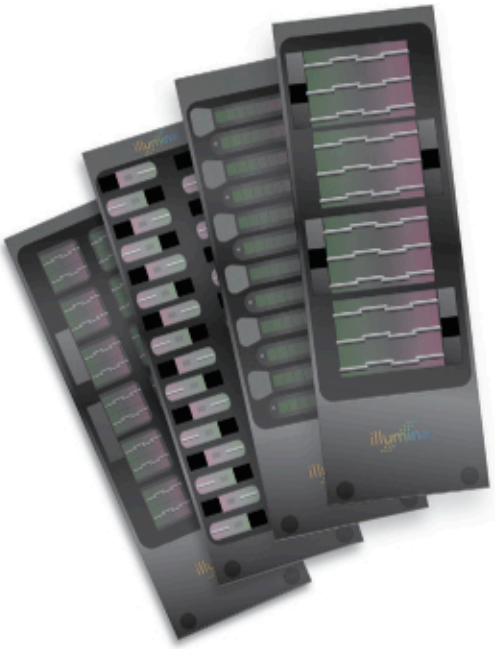

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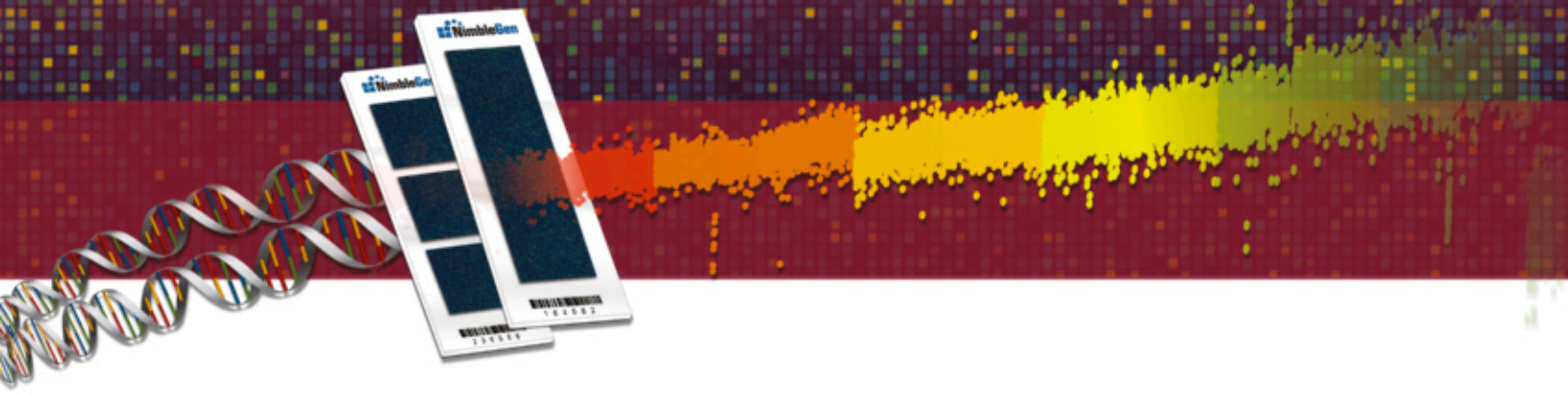

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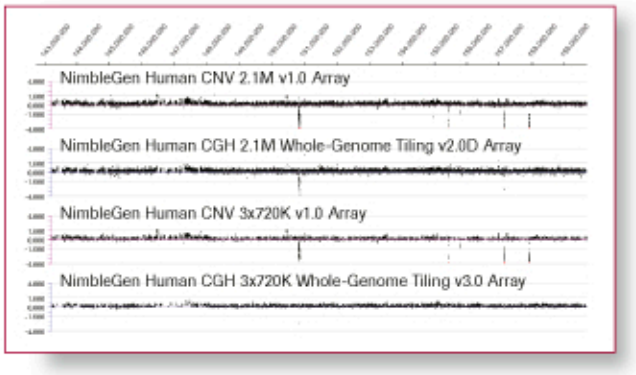

Cross-platform analysis of CNV regions. CNV regions were analyzed from HapMap research sample NA15510 using the NimbleGen Human CNV 2.1M v1.0, NimbleGen Human CGH 2.1M Whole-Genome Tiling v2.0D, NimbleGen Human CNV 3x720K v1.0, and NimbleGen Human CGH 3x720K Whole-Genome Tiling v3.0 arrays, as indicated. A zoom-in region of Chromosome 1 is displayed in SignalMap software, available from Roche NimbleGen.

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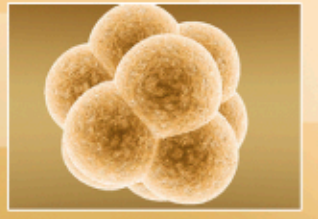

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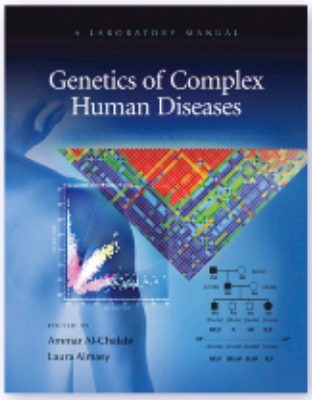

Edited by Ammar Al-Chalabi, *MRC Centre for Neurodegeneration Research, King's College London,* and Laura Almasy, *Southwest Foundation for Biomedical Research, San Antonio, Texas*

Many human diseases—including Alzheimer's disease, schizophrenia, cancer, and cardiovascular disease—show complex inheritance that requires sophisticated analysis. *Genetics of Complex Human Diseases: A Laboratory Manual* brings together the tools that geneticists use to find disease genes with the genetic concepts and statistical theories that underpin these research approaches. Topics covered include basic genetics and Mendelian inheritance, statistical methods, genetic epidemiology, linkage studies, transmission disequilibrium test analysis, variance components analysis, genome-wide association studies, copy-number variation, methods for high-throughput genotyping, the complexity of RNA editing, and genetic computer programs. The book's chapters, written by leading investigators in the field, blend practical information and reviews of each topic, providing both the how and the why of complex disease analysis. *Genetics of Complex Human Diseases* is an important guide for anyone with an interest in human genetics or who uses genetic techniques in the study of diseases with complex inheritance.

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