

Comparison of Comparative Genomic Hybridization Technologies Across Microarray Platforms

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Comparative Genomic Hybridization (CGH) measures DNA copy number differences between a reference genome and a test genome. The DNA samples are differentially labeled and hybridized to an immobilized substrate. In early CGH experiments, the DNA targets were hybridized to metaphase chromosome spreads in FISH assays. This technology later evolved so that the DNA targets are hybridized to microarrays containing complementary DNA (cDNA) fragments or bacterial artificial chromosomes (BACs). Recent commercial offerings from Agilent, Affymetrix, and Illumina derive copy number differences using oligonucleotide microarrays representing 500,000 or more loci. These commercial microarrays are characterized as whole-genome CGH measures obtaining copy number differences in DNA across entire genomes. In the 2007 Association of Biomolecular Resource Facilities (ABRF) Microarray Research Group (MARG) project, we analyzed HL60 and normal female DNA with five platforms representing different chemistries: Agilent, Affymetrix, Illumina, cDNA, and BAC arrays. Data obtained from these platforms were compared for differences in sensitivity, specificity, reproducibility, and concordance using the visualization and statistical tools. All tested platforms detected the known gains and deletions in the HL60 DNA sample. In addition, three novel DNA copy number changes were found on Ch 2, 16, and 19. These analyses identify strengths and weaknesses in each platform. In addition, Affymetrix expression arrays were used for CGH assessment.

This abstract does not necessarily reflect the views of the U.S. Environmental Protection Agency (U.S. EPA).

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