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# BAC to BAC

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Comparative genomic hybridization (CGH) is a useful method for detecting chromosomal imbalances in tumor cells. In the April issue of Nature Biotechnology, Cai *et al.* describe a microarray-based CGH protocol that can reliably identify deletions or amplification in DNA samples from tumors (*Nature Biotechnology* 2002, **20:**393-396). To reduce hybridization background noise they decided to modify the DNA itself, rather than the glass support. They used a bifunctional crosslinker with an epoxide group that covalently attaches to DNA, and deposited the modified DNA - in the form of BACs (bacterial artificial chromosomes) - onto unmodified glass slides. Initial tests showed that the BAC arrays were very uniform and could be used for quantitative analysis of heterozygous deletions. Cai *et al.* constructed arrays consisting of almost 1,000 mouse-DNA BACs and examined loss of heterozygosity (LOH) and amplification events in mouse tumors. The BAC technique could detect chromosomal abnormalities at higher resolution than existing methods, such as microsatellite polymorphism analysis. BAC microarrays could now be easily developed for the analysis of chromosomal abnormalities in human tumors.

# References

1. High resolution analysis of DNA copy number variation using comparative genomic hybridization to microarrays.

2. *Nature Biotechnology*, [http://www.nature.com/nbt/]