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## Amplicon analysis

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The chromosomal region 17q23 is amplified in some cancer cells and is associated with poor prognosis for breast cancer. In the May 8 [Proceedings of the National Academy of Sciences](#), Monni *et al.* describe the use of genomic and microarray analysis to characterize the 17q23 amplicon in breast cancer cells (*Proc Natl Acad Sci USA* 2001, **98**:5711-5716). They constructed a 4 megabase contig covering the amplified region of chromosome 17, containing 17 genes and 26 expressed sequence tags (ESTs) identified from [GeneMap'99](#). They used [tissue microarray-based analysis](#) of 184 primary breast tumor samples to define the extent of 17q23 amplification (the highest amplification frequency was 12.5%). Subsequent microarray analysis of 636 cDNAs from chromosome 17, including 156 transcripts within 17q23, identified five genes that are highly overexpressed in breast cancer cells. Thus, systematic amplicon analysis can identify limited numbers of genes specifically associated with cancer progression.

## References

1. Detection and mapping of amplified DNA sequences in breast cancer by comparative genomic hybridization.
2. *Proceedings of the National Academy of Sciences*, [<http://www.pnas.org>]
3. A New Gene Map of the Human Genome, [<http://www.ncbi.nlm.nih.gov/genemap>]
4. Tissue microarrays for high-throughput molecular profiling of tumor specimens.