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Classifying carcinomas

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In the September 11 [Proceedings of the National Academy of Sciences](#), Sorlie *et al.* show how [cDNA microarray](#) data may be used to define subclasses of [breast carcinomas](#) and to predict clinical outcome (*Proc Natl Acad Sci USA* 2001, **98**:10869-10874). They analysed 78 breast cancer samples (mostly ductal carcinomas) and compared the expression profiles of 456 genes with profiles from normal breast tissue. They then classified the cancers into epithelium-like, ERBB2-overexpressing and normal-breast-like groups, and used different profiling patterns to sub-divide the estrogen-receptor-positive group into two distinct subgroups. Sorlie *et al.* found that the microarray-defined subgroups of patients had different clinical outcomes, suggesting the power of microarray-based studies for determining prognoses.

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1. *Proceedings of the National Academy of Sciences* , [<http://www.pnas.org>]
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3. Molecular portraits of human breast tumours.

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