Expression Profiling of Cancers in Asian Populations

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Abstract

The clinical behaviour and epidemiology of breast cancer differs markedly between Caucasian and Asian populations. Using patient samples of ethnic Chinese origin, we employ microarray technology to identify a set of 20 genes that is able to identify and predict if an unknown breast tissue is normal or malignant. Such minimal genetic identifiers may prove useful in the future development of comprehensive molecular diagnostic assays. We also show that the expression profiles of normal breast tissues are considerably less varied than tumor profiles, suggesting that normal breast tissues can to a first approximation be regarded as a static baseline, from which individual breast cancers arise via diverse tumorigenic pathways.