

OMICS profiling and prognostic significance in cancer

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Genomic abnormalities and gene expression variation have been found in several cancers. The genome-wide analysis and transcriptome analysis by microarray were used to identify peculiar genome and transcriptome signatures associated with cancer patient poor prognosis. Genome signature and/or gene expression profiling have been included in some protocols to evaluate the patient risk and to improve the treatment of cancer. In the last few years the challenge is to integrate genome and transcriptome data. Genome and transcriptome integration will give useful information about the gene function and their abnormal activity in cancer. Finally, miRNA screening by microarray technology has been employed in several cancers to identify miRNA signatures associated with tumor aggressiveness and patient outcome.

Link: http://www.istge.it/dip_tda/on_tr/on_tr.htm