# Cancer signatures uncovered

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A new systematic analysis of the relationship between the neoplastic and developmental transcriptome provides an outline of trends in cancer gene expression. The research, published recently in BioMed Central's open access journal *Genome Biology*, describes how cancers can be divided into three groups distinguished by disparate developmental signatures.

Isaac S Kohane from Children's Hospital Boston and Harvard University, US, led a team of researchers who performed a comprehensive comparison of genes expressed in early developmental stages of various human tissues and those expressed in different cancers affecting these tissues. He says, "Our study reveals potentially clinically relevant differences in the gene expression of different cancer types and represents a reference framework for interpretation of smaller-scale functional studies".

One of the three described groups of cancers has an early developmental phenotype and expresses genes that are characteristic of stem cells. From a developmental perspective, this group presents very homogeneously. A second, more heterogeneous group tends to be more similar to late development and is characterized by an inflammatory signature. The third is a small group of cancers that present as a transition phenotype between these two extremes and displays both characteristics.

According to Kohane, "This segregation of tumors into three groups with distinct expression patterns is surprising. Clearly, the developmental trajectory provides a meaningful background for capturing large-scale

differences in gene expression across diverse conditions".

The study's results will lead towards a better understanding of human disease from a 'macrobiological' approach to analyzing high-throughput data. According to the authors, "Shifting our focus from single sets of genes or processes to the biology of aggregates on the order of the entire transcriptome is likely to be useful in establishing highly robust molecular correlations between seemingly unrelated disease phenotypes".

Source: BioMed Central