

Spotlight

By Caroline Seydel

The Mother of all Microarrays

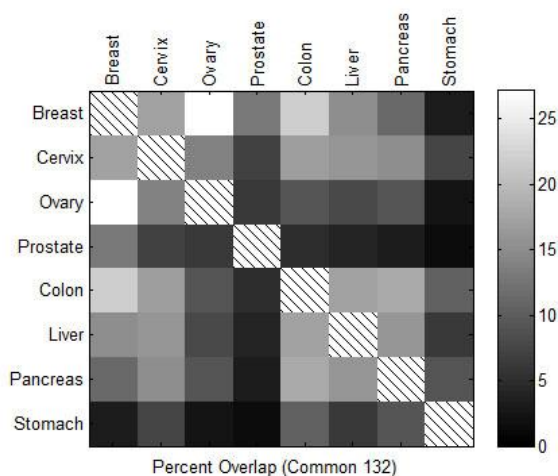
Dawany *et al.*

<http://doi.wiley.com/10.1002/ijc.25854>

Analyzing nearly 6,000 microarray samples, Dawany *et al.* found 329 genes that appeared related to the transformation of cells from normal to cancerous. Many of the genes they identified have been associated with cancer by other methods besides microarray studies.

Huge numbers of cancer-specific microarray samples exist in publicly accessible databases. Because these data are often asymmetric, including cancer samples without controls, or healthy but not cancer tissues, researchers employed a special approach to integrate the data. They used a large-scale approach to integrate microarray data from multiple laboratories by normalizing them together and then using the Significance Analysis of Microarray method to identify the list of genes that are significantly altered in cancer compared to normal.

Using this analysis on data from 84 laboratories, the authors obtained gene lists for 13 human tissues, including breast, prostate, colon, lung, and brain. They found 132 genes present in at least four gene lists, and eleven of these were not previously associated with cancer. Because the genes pertain to multiple cancer types, they might serve as potential targets for new drugs against metastasis.



Heat map showing the degree of commonality among the altered genes identified in different cancer types. For instance, breast and ovarian cancer have many genes in common, but there is little overlap between breast and stomach cancer.