Taking uncertainty out of cancer prognosis

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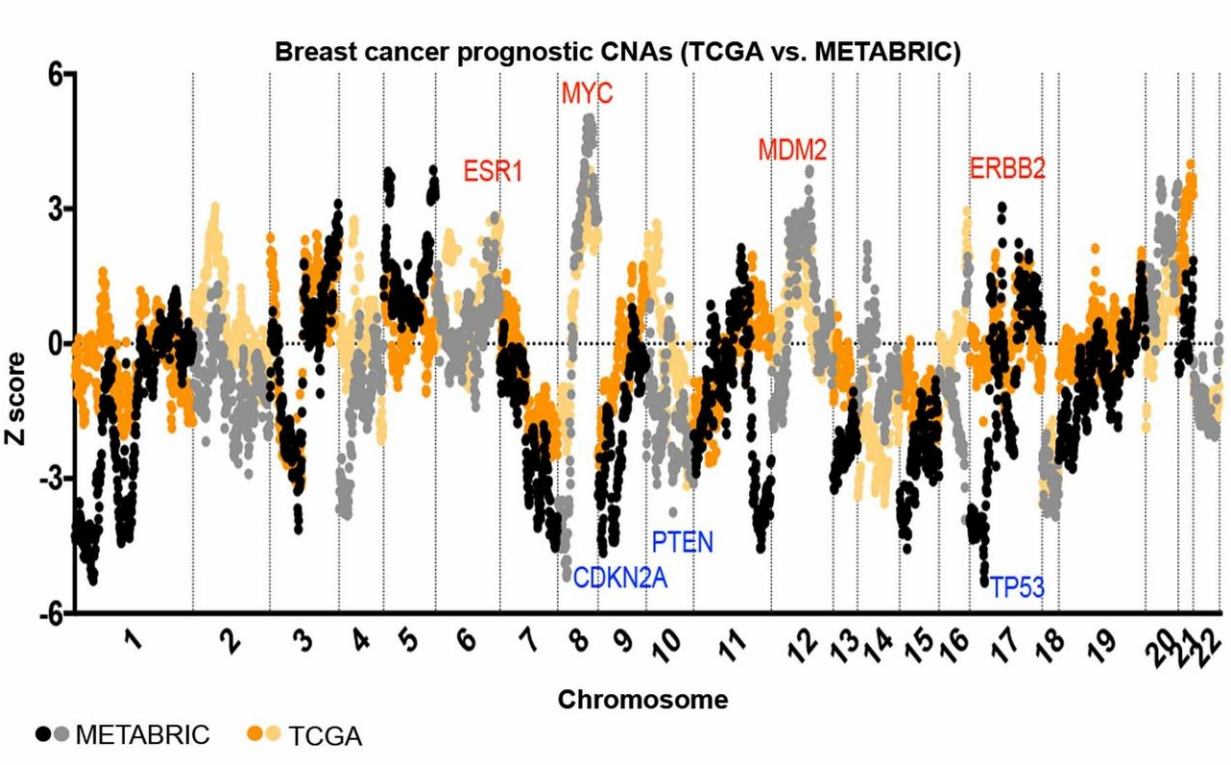

An analysis of breast cancer patient gene reveals that copy number alterations (CNAs) within cancer-causing genes is more likely to accurately indicate the severity of the disease (shown) than simply measuring how many of those genes are actually mutated to cause cancer (not shown). Credit: Sheltzer/CSHL 2018

A cancer diagnosis tells you that you have cancer, but how that cancer will progress is a terrifying uncertainty for most patients. Researchers at Cold Spring Harbor Laboratory (CSHL) have now identified a specific

class of biomarkers that can tell a lot about how aggressive a patient's cancer will be.

"There are undoubtedly dozens or hundreds of mutations that cause cancer, and that can be found in almost any tumor," said CSHL Fellow Jason Sheltzer. "That's why it was surprising to discover that these mutations are pretty evenly distributed in early-stage benign cancer as well as in the really aggressive, highly-malignant cancers."

In other words, the mutations that cause cancer don't actually tell you all that much about who will end up surviving and who will end up dying from cancer.

That's why Sheltzer set out to find other easily identifiable factors that can determine a cancer patient's prognosis. With the aid of software engineer Joan Smith, Sheltzer collected and analyzed the comprehensive history of nearly 20,000 cancer patients.

According to a paper recently published in the journal *eLife*, his team not only traced each patient's outcome—whether it be recovery or tragedy—but also took a closer look at genetic sites commonly associated with cancer causing mutations.

"While there wasn't very much of a difference in the types of mutations that benign and aggressive tumors had," said Sheltzer, "when we looked at copy number changes in these same genes, we found a very significant difference."

Normally, the genetic information in a human cell comes in two copies distributed among 23 pairs of chromosomes. However, cancer cells often gain or lose chromosomes.

"A lot of cancers instead of having two copies of a gene, will have three

copies, four copies, five copies, or only one copy of a gene instead," explained Sheltzer. "We looked at the relationship between these copy number alterations and what happens to cancer patients and found a strong relationship."

Sheltzer now hopes to launch a prospective analysis, closely studying new cancer patients for years after diagnosis. This could highlight which kinds of copy number changes are associated with which outcomes.

"That would be one of the first steps towards taking what we've learned and translating it into a clinically useful tool that could also provide patients with peace of mind," said Sheltzer.

More information: Joan C Smith et al, Systematic identification of mutations and copy number alterations associated with cancer patient prognosis, *eLife* (2018). DOI: 10.7554/eLife.39217

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