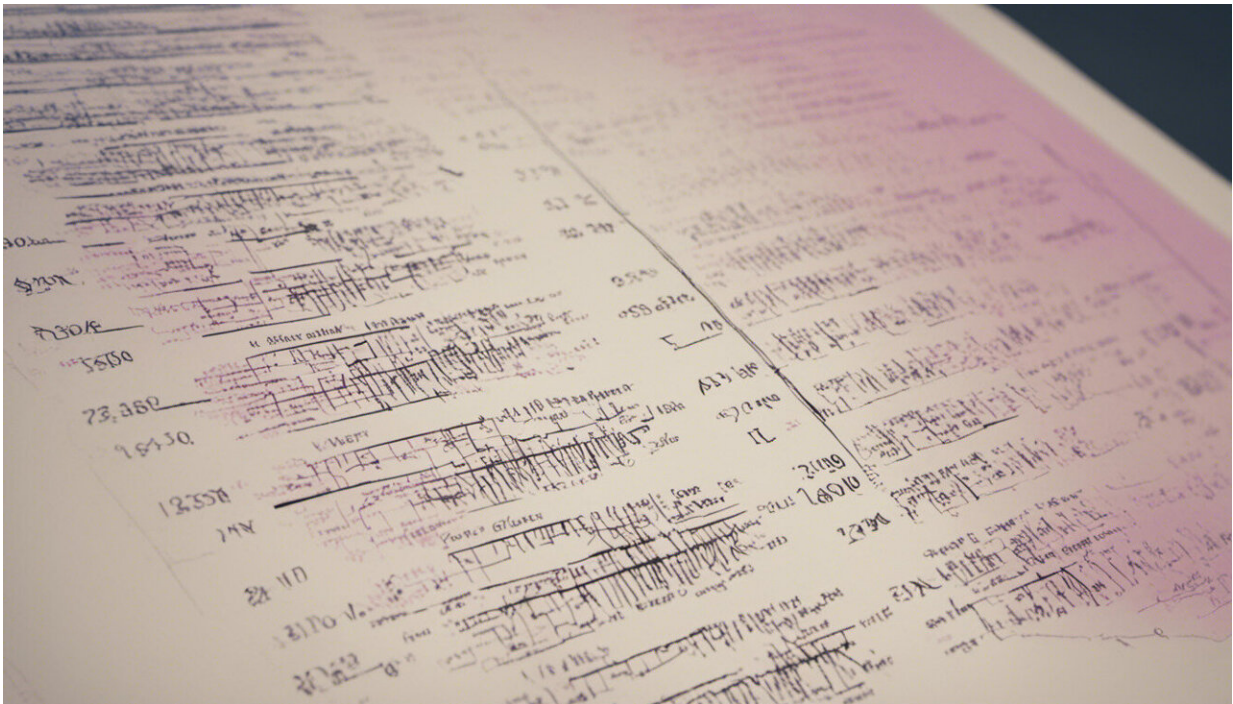# Scientists develop scoring system to calculate prognosis for breast cancer patients

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Credit: AI-generated image (disclaimer)

What if a simple genetic test could tell cancer patients what their odds of survival are? It's an approach that researchers at the Department of Energy's Lawrence Berkeley National Laboratory are developing, and they have made significant inroads in several types of cancer, most recently for breast cancer.

After analyzing large genomic datasets and clinical patient data, scientists at Berkeley Lab found the expression of 381 genes to be significantly associated with relapse-free survival in breast cancer patients.

They further narrowed down the data to a 12-gene signature and developed a scoring system that would help predict patient prognosis. Low scores were linked with higher chances of survival past 20 years, while high scores correlated with lower survival rates. The results were reported recently in the journal *Oncotarget*.

"Distinguishing patients with good prognosis could potentially spare them the toxic side effects associated with adjuvant therapy," said study corresponding author Antoine Snijders, a research scientist at Berkeley Lab's Biological Systems and Engineering Division. "Determining prognosis involves a range of other clinical factors, including tumor size and grade, the degree to which the cancer has spread, and the age and race of the patient. Our scoring system was predictive of survival independent of these other variables."

The signature was most effective for two specific subtypes of breast cancer: HER2 and Luminal A.

Among women in the United States, breast cancer is the most common cancer and the second leading cause of cancer deaths, according to the Centers for Disease Control and Prevention. Death rates have dropped in recent decades; the chance is now 1 in 37 that a woman will die from breast cancer.

"There is obviously a lot of variability in mortality rates, but this paper presents a path towards getting more information specific to an individual," said Snijders.

Researchers have been taking advantage of advances in computational biology and genome-wide screening techniques to identify genetic signatures for cancer prognosis. In 2016, another Berkeley Lab group found a potential new biomarker for early stages of tumor development in a wide variety of cancers.

Such scoring systems could be developed into an additional tool to help doctors and patients make informed decisions about the course of treatment.

The authors of this study included Xuan Mao, Matthew Lee, Jeffrey Zhu and Carissa Zhu, all students from Campolindo High School in Moraga, California, who worked as interns at Berkeley Lab in 2016. Under the supervision of Snijders, they led the programming effort and computational analysis that helped identify the relevant genes and that formed the basis of the scoring system.

Snijders says future steps include multi-center prospective studies to validate the scoring system in clinical settings.

  More information: Genome-wide screen identifies a novel prognostic signature for breast cancer survival. *Oncotarget.* DOI: 10.18632/oncotarget.14776

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