

# 17-gene signature linked to remission after triple-negative breast cancer treatment

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Mayo Clinic researchers have discovered a distinctive pattern in a specific set of 17 genes that may be associated with remission after treatment for triple-negative breast cancer. The multi-omics study, [published](#) in *Breast Cancer Research*, highlights the potential for further investigating this signature as a target for individualized medicine.

Approximately 10–15% of breast cancers fall into the category of "triple-negative," indicating that their growth is not driven through the [hormone receptors](#) for estrogen or progesterone, nor by the human epidermal growth factor receptor 2 (HER2). In contrast, other breast cancers have at least one of these receptors, allowing for treatments that can target or block them to inhibit the cancer's progression.

Triple-negative breast cancer is known for its resistance to targeted therapies, leaving chemotherapy as the primary treatment option. While most patients initially respond well to the standard [neoadjuvant chemotherapy](#), nearly 20% of patients will experience recurrence after treatment.

"It's crucial that we create tools that assist clinicians in making informed treatment decisions," says Krishna Rani Kalari, Ph.D., a lead author of the study and an associate professor of biomedical informatics at the Center for Individualized Medicine. "This 17-gene signature is one of the candidate tools that shows potential. However, for this signature to have clinical utility, there will need to be studies evaluating whether alternative drugs/drug combinations may work in this group of patients."

## Decoding pattern in 17 genes

In their study, the researchers investigated tumor samples before and after treatment of patients with [triple-negative breast cancer](#) who failed to respond to neoadjuvant chemotherapy. Using multi-omics analysis and machine learning technologies, they examined changes in [gene expression](#) to understand the molecular underpinnings driving tumor recurrence.

Multi-omics is an emerging multidisciplinary field of biological sciences that encompasses genomics, proteomics, epigenomics, transcriptomics, metabolomics and more.

The team identified 17 [genes](#) associated with relapse-free survival and found that many of the genes may play a role in triggering inflammation to initiate an immune system response. Dr. Kalari says failure to initiate immune response prevents the clearance of weakened [tumor cells](#), thereby permitting the development of treatment resistance and disease re-occurrence.

## Quest for individualized medicine

The study is an extension of Mayo Clinic's clinical prospective breast cancer study known as Breast Cancer Genome-Guided Therapy Study (BEAUTY). The goal of the study is to determine why some patient's tumors respond to chemotherapy while others don't, and to use that knowledge as a catalyst to develop personalized medicine therapies.

Next, the team plans to further investigate the gene signature and test therapeutic strategies.

**More information:** Xiaojia Tang et al, Integration of multiomics data shows down regulation of mismatch repair and tubulin pathways in triple-negative chemotherapy-resistant breast tumors, *Breast Cancer Research* (2023). [DOI: 10.1186/s13058-023-01656-x](https://doi.org/10.1186/s13058-023-01656-x)

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