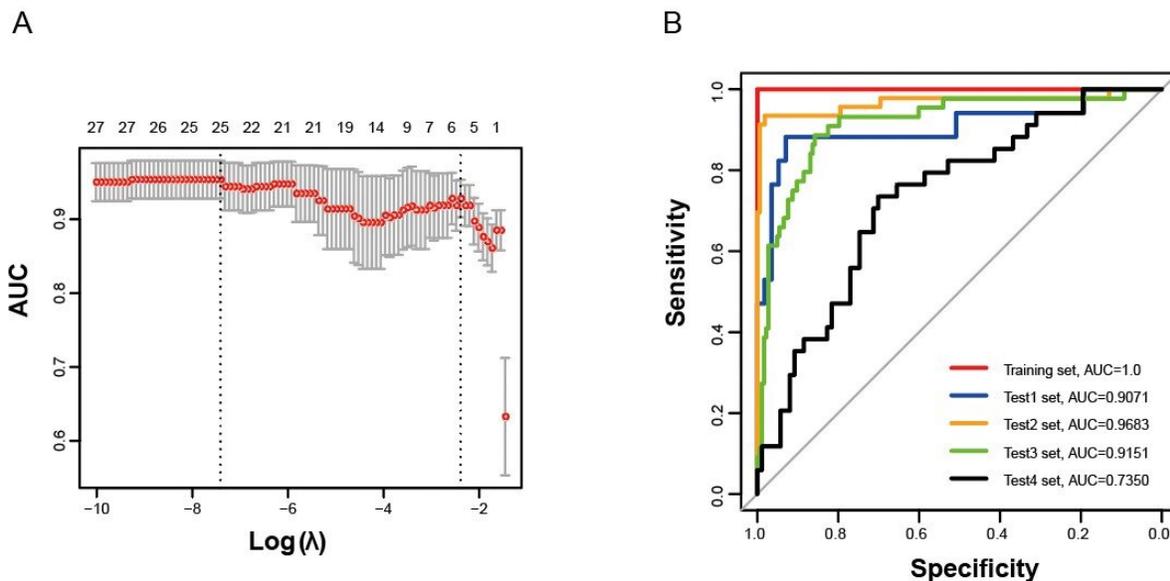


# Novel genomic predictor of chemosensitivity in breast cancer discovered

September 9 2021, by Zhang Nannan



Construction of LASSO Logistic regression model and its predictive power for neoadjuvant therapy. Credit: FU Changfang

A research team by Prof. Yang Wulin and Dai Haiming from the Hefei Institutes of Physical Science (HFIPS) of the Chinese Academy of Sciences recently proposed a genetic classifier that can predict the sensitivity of neoadjuvant chemotherapy for breast cancer in the field of tumor molecular markers.

Breast cancer is a kind of malignant tumor with high clinical and biological heterogeneity. Different subtypes respond to chemotherapy with different clinical characteristics. Therefore, it is important to develop methods to predict treatment sensitivity, which is the basis of precision medicine for [breast cancer](#), so that patients can choose the best treatment strategy and avoid overtreatment.

In this [study](#), the researchers built a [prediction model](#) with 25-gene signature using least absolute shrinkage and selection operator (LASSO) [logistic regression](#) with the help of patient drug response data.

The model has many advantages, "it can predict pathologic complete response to paclitaxel and anthracycline-based [neoadjuvant chemotherapy](#) with high accuracy and is applicable to various subtypes of breast cancer, demonstrating an important contribution of the immune ecosystem to chemotherapeutic sensitivity." said Yang Wulin, who led the research team.

Having shown good predictive abilities for different batches of data and various breast cancer subtypes, and displaying good generalization ability, this gene signature is expected to be promoted as a new diagnostic scheme to predict the sensitive one to chemotherapy in clinical practice.

"It can therefore select the optimal scheme for breast cancer and provide patients with chances of precise treatment," said Yang.

The results have been published in *Frontiers in Immunology*.

**More information:** Changfang Fu et al, An Immune-Associated Genomic Signature Effectively Predicts Pathologic Complete Response to Neoadjuvant Paclitaxel and Anthracycline-Based Chemotherapy in Breast Cancer, *Frontiers in Immunology* (2021). [DOI](#):

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