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Predicting response to immune checkpoint blockade in patients with gynecological cancer

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Abstracts

Immune checkpoint blockade (ICB) has revolutionized cancer treatment and is now one of the standard treatments for many types of cancer. Nevertheless, because the therapeutic efficacy of ICB varies from patient to patient, identifying biomarkers is necessary to predict a patient's response to ICB therapy. PD-L1 expression is currently employed as a biomarker, but it is inadequate for accurately identifying responders, underscoring the need for more robust biomarkers. To tackle this issue, we performed targeted RNA sequencing on 39 patients with cervical, uterine, and ovarian cancers. By employing machine learning techniques, we identified key genes associated with ICB treatment response. We then assessed the performance of these genes using a random forest model, which demonstrated superior predictive accuracy compared to current clinical markers. Furthermore, we evaluated the predictive performance of these key genes in other cancer types using public RNA sequencing datasets. Our findings indicate that these key genes can be clinically utilized to predict ICB treatment response, underscoring their potential as essential tools for personalized medicine in cancer patients.