Abstract

Background

Previous studies of immune genomic signatures (IGSs) in breast cancer have attempted to predict the response to chemotherapy or prognosis and were performed using different patient cohorts. The purpose of this study was to evaluate the predictive functions of various IGSs using the same patient cohort that included data for response to chemotherapy as well as the prognosis after surgery.

Methods

We applied five previously described IGS models in a public dataset of 508 breast cancer patients treated with neoadjuvant chemotherapy. The prognostic and predictive values of each model were evaluated, and their correlations were compared.

Results

We observed a high proportion of expression concordance among the IGS models (r: 0.56-1). Higher scores of IGSs were detected in aggressive breast cancer subtypes (basal and HER2-enriched) ($P < 0.001$). Four of the five IGSs could predict chemotherapy responses and two could predict 5-year relapse-free survival in cases with hormone receptor-positive (HR+) tumors. However, the models showed no significant differences in their predictive abilities for hormone receptor-negative (HR-) tumors.

Conclusions

IGSs are, to some extent, useful for predicting prognosis and chemotherapy response; moreover, they show substantial agreement for specific breast cancer subtypes. However, it is necessary to identify more compelling biomarkers for both prognosis and response to chemotherapy in HR- and HER2+ cases.