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Paper Title: Imaging-proteomics co-profiling reveals biologic pathways underlying prognostic MRI features

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Abstract

Patient selection for neoadjuvant chemotherapy in breast cancer remains an unmet clinical need. While quantitative features from medical imaging have been reported to predict treatment responses, the biological meaning of these features is not well understood, which hinders their clinical use. This study aimed to develop a deep learning signature (DLS) using pre-treatment MRI to predict responses to neoadjuvant chemotherapy and to identify the underlying pathways through paired MRI and proteomic sequencing data. The DLS achieved a prediction accuracy of 0.923 with an AUC of 0.957. Pathways including mitochondrial energy metabolism, vesicle budding and vascular transportation, protein localization to membranes, mRNA processing, and cytoskeleton-dependent trafficking were differentially regulated in patients showing pCR and were significantly correlated with DLS in the validation dataset. This study offers a biologically interpretable DLS for predicting pCR to neoadjuvant chemotherapy in breast cancer patients, which may guide personalized medication.
