

## Prognostic Value of Immune-Related Genes in Esophageal Adenocarcinoma

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**ABSTRACT** Esophageal adenocarcinoma (EAC) is among the most aggressive and lethal malignancies in gastrointestinal tumours. Recently, immunotherapy has gained prominence, highlighting the need for systematic exploration of immune-related genes (IRGs) in EAC to advance treatment and prognostication. Differential gene expression profiles from EAC and adjacent tissues were retrieved through applying the TCGA database. Cross-referencing with immune gene lists from TCGA and GEO (GSE19417) was to identify differentially expressed IRGs (DEIRGs). The researchers established a prognostic mode via employing lasso-penalised Cox regression and this model was validated using GSE19417, which also assessed six tumour-infiltrating immune cell subtypes. A total of 259 DEIRGs were identified, with 10 significantly correlating with overall survival (OS) in EAC. Functional enrichment analysis revealed involvement in extracellular region and cytokine-cytokine receptor interaction. High-risk scores and the AJCC stage were found to be independently linked with worse OS. The study underscores the prognostic relevance of IRGs, informing future EAC prognosis and immunotherapy strategies.