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Identification of key prognosis-associated genes in the lung adenocarcinoma

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Abstract:

Non-small cell lung cancer (NSCLC) is one of the most common causes of cancer-related death globally, and lung adenocarcinoma (LUAD) accounts for almost 40% of all lung cancer cases. In recent years, despite better understanding of the pathogenesis of the disease and achievements in the multimodal treatment of tumors, there is an urgent need to identify new diagnostic and prognostic biomarkers In this study, we aim to identify the potential key genes related to the pathogenesis and prognosis of LUAD by using comprehensive bioinformatics analysis. The gene expression profile was downloaded from The Cancer Genome Atlas (TCGA) database, and we calculated the LUAD immune scores and stromal scores by using the ESTIMATE algorithm. Based on these scores, we further quantified the immune and stromal components and obtained the differentially expressed genes (DEGs) in the tumor. Overall survival analysis could better reflect the impact of genes related to immune and stromal cells on the prognosis. Moreover, Gene Ontology (GO) functional enrichment analysis and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment were conducted, while protein-protein interaction (PPI) network was obtained from STRING. Analysis of the correlation revealed that these genes are mainly involved in the immune/inflammatory response. In conclusion, our study showed that 11 prognostic genes (CD33, IRF8, CD80, CD53, IL16, LY86, CD79B, TYROBP, CD1E, CD1C...

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