

MAGEA Gene Expression Analysis in Hepatocellular Carcinoma

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The MAGEA gene family consists of cancer-testis antigens (CTAs) that are normally restricted to the testis and placenta but become abnormally expressed in various cancers, including Hepatocellular Carcinoma (HCC). This project aims to analyze the expression patterns of MAGEA genes in HCC and explore their potential as diagnostic biomarkers and prognostic indicators. Using RNA-seq data from The Cancer Genome Atlas (TCGA) and clinical metadata from cBioPortal, we perform differential expression analysis to identify significantly overexpressed MAGEA genes in HCC. Further, we conduct Kaplan-Meier survival analysis and Cox proportional hazard modeling to assess correlations between MAGEA expression and clinical outcomes, such as survival rates, recurrence, and tumor stage. The findings from this study will help identify MAGEA genes with strong diagnostic and therapeutic potential, guiding future experimental validation through ELISA/IHC in Dr. Zhang's lab and informing the development of personalized therapies or immunotherapy targets for HCC patients.