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Prognostic value of ubiquitin-conjugating enzyme E2 S overexpression in hepatocellular carcinoma

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Abstract

Previous study has shown that ubiquitin-conjugating enzyme E2 S (UBE2S) is highly expressed in various human cancers. In order to study the clinical value and potential function of UBE2S in hepatocellular carcinoma (HCC), three datasets from the Oncomine database and RNA-seq data from The Cancer Genome Atlas (TCGA) were analyzed. UBE2S expression was found to be significantly higher in HCC samples, which was supported with qPCR validation. Both Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) analyses demonstrated that UBE2S co-expressed genes were involved in cell cycle and DNA replication. Survival analysis showed a significant reduction in overall survival of patients with high UBE2S expression from both the GSE14520 cohort and TCGA Liver hepatocellular carcinoma (LIHC) cohort. Furthermore, Gene set enrichment analysis (GSEA) analysis revealed that high UBE2S expression in HCC patients is associated with increased expression in gene sets associated with decreased survival, increased metastasis and increased recurrence. Finally, qPCR results showed that UBE2S overexpression has diagnostic value in distinguishing between HCC and non-cancerous liver tissue, as the area under the curve (AUC) was 0.8095, and overexpression of UBE2S was significantly associated with decreased overall survival and disease-free survival in HCC patients. In conclusion, UBE2S may hold prognostic value in the treatment of HCC.

Keywords: UBE2S; Prognosis; Hepatocellular carcinoma; Bioinformatics

1. Introduction

Hepatocellular carcinoma (HCC) is a kind of malignant tumor that causes a considerable health burden globally with China accounting for about 50% of the worldwide incidence and mortality each year [1]. Ubiquitination is important in various biological processes such as signal transduction, intracellular transportation and