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5 - 55 Identifification of Therapeutic Targets and Prognostic Biomarkers Among Frizzled Family Genes in Glioma

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The biological functions of the frizzled gene family (FZDs), as the key node of wingless-type MMTV integration site family (Wnt) and mammalian target of rapamycin signaling pathways, have not been fully elucidated in glioma[1,2]. This study aims to identify novel therapeutic targets and prognostic biomarkers for gliomas, which may help us understand the role of FZDs. RNA-sequence data were downloaded from The Cancer Genome Atlas (TCGA) and Genotype-Tissue Expression (GTEx) projects. Survival analyses, Cox regression analyses, nomograms, calibration curves, receiver operating characteristic (ROC) curves, gene function enrichment analyses, and immune cell infifiltration analyses were conducted using *R* statistical language High expressions of FZDs were positively associated with the activation of mTOR signaling. FZD1/2/3/4/5/7/8 was significantly highly expressed in tumor tissues, and the high expression of FZD1/2/5/6/7/8 was significantly positively associated with poorer prognosis. FZD2 and FZD6 positively served as independent predictors of poor prognosis. Gene function analysis showed that FZDs were associated with mTOR signaling, immune response, cytokine-cytokine receptor interaction, extracellular matrix organization, apoptosis, and p53 signaling pathway. Our finding strongly indicated a crucial role of FZDs in glioma. FZD1/2/5/6/7/8 could be an unfavorable prognostic factor in glioma and FZD2 and FZD6 may be novel independent predictors of poor prognosis in glioma.

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