Investigation the expression profile of TC2N Using the TCGA database in gastric cancer

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Abstract

Lung cancer is the leading cause of cancer-related incidents and mortality worldwide, with an estimated 1.8 million new lung cancer cases in 2012 .Tac2-N (TC2N), located on human chromosome 14q32.12, encodes a putative C2 domain-containing protein that belongs to the carboxyl-terminal type (C-type) tandem C2 protein family. TC2N was first cloned in the mouse, and this protein contains two C-terminal C2 domains, C2A and C2B .The C2 domain was originally identified as a protein structural domain of calcium-dependent protein kinase C .Further studies indicated that the function of the C2 domain is not limited to calcium-dependent phospholipid binding, since this motif has been implicated in cellular signal transduction and protein–protein interactions. Moreover, a number of proteins containing C2 domains are involved in the regulation of tumor genesis. For instance, the DOC2B gene functions as a tumor suppressor in cervical cancer through inhibiting cell proliferation, migration and invasion .Myoferlin is an understudied oncogene that increases the metastasis of triple-negative breast cancer. Thus, identification of new functional genes and biomarkers in tumor development and progression may provide valuable insights into the prevention, early detection and treatment of lung cancer patients. In the present study, we investigated the expression profile of TC2N in Lung cancer as well as its association with clinical features and survival to evaluate its prognostic valu. Using the TCGA database in Lung cancer.

Biography

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