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Regulatory network analysis of high expressed long non-coding RNA *LINC00941* in gastric cancer

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Abstract

Accumulating evidence suggests that the aberrant expression of long non-coding RNAs is closely related to the carcinogenesis and progression of gastric cancer (GC), which is a type of prevalent tumor with a high incidence and mortality rate. However, it is still a challenge to find reliable biomarkers and to understand their molecular mechanisms in GC. In this study, we first confirmed that *LINC00941* was up-regulated in GC tumor tissues compared with adjacent normal tissues by RT-PCR, and found that the expression level of *LINC00941* was correlated with invasion depth, lymphatic metastasis, and the TNM stage of patients with GC. Furthermore, by performing enrichment analysis based on the co-expression network and regulatory network, we found that *LINC00941* was associated with cancer related biological processes such as cell cycle, cell communication, cell migration, cell division, as well as processes associated with the immune system. Our results suggested that *LINC00941* may be a potential novel biomarker for therapeutic or diagnostic of GC.

keywords: long non-coding RNA; *LINC00941*; gastric cancer; regulatory network

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