

Accepted Manuscript

Title: Expression of TUSC3 and its Prognostic Significance in Colorectal Cancer

Authors: Zhu Yu Feng, Ming Dong

PII: S0344-0338(18)30531-4
DOI: <https://doi.org/10.1016/j.prp.2018.07.004>
Reference: PRP 52110

To appear in:

Received date: 5-5-2018
Revised date: 14-6-2018
Accepted date: 5-7-2018

Please cite this article as: Feng ZY, Dong M, Expression of TUSC3 and its Prognostic Significance in Colorectal Cancer, *Pathology - Research and Practice* (2018), <https://doi.org/10.1016/j.prp.2018.07.004>

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.



Expression of TUSC3 and its Prognostic Significance in Colorectal Cancer

First author: Zhu YuFeng

China Medical University, Shenyang, Liaoning Province, People's Republic of China

Email: JinZhouzhuyufeng@163.com

***Corresponding author:** Department of Gastrointestinal Surgery, the First Affiliate Hospital of China Medical University, Shenyang, Liaoning Province, People's Republic of China

Email: dongming@cmu.edu.cn

Address: No.92 of Beima Road, Heping District, Shenyang, Liaoning Province, P.R. China

Postal Code: 110001

Abstract

Background: Colorectal cancer (CRC) is one of the most common cancers worldwide. Tumor suppressor candidate 3 (TUSC3) has been reported to be associated with embryogenesis and metabolism. The aim of this study is to investigate the expression of TUSC3 in CRC tissues, and to evaluate the clinical pathological characters and prognostic significance.

Method: First, we performed a bioinformatics analysis by using Oncomine and COEXPEDIA databases. Gene Set Enrichment Analysis (GSEA) was performed using TCGA data set. Then, the protein expression level of TUSC3 was detected by immunohistochemistry in 230 pairs of primary colorectal cancer and corresponding non-tumor tissues.

Result: We investigated Oncomine databases and found that TUSC3 mRNA expression was significantly higher in CRC tissues compared with normal tissues. The immunohistochemistry results demonstrated that TUSC3 was overexpressed in the CRC tissues. Furthermore, TUSC3 overexpression was associated with T stage, lymph node metastasis, and distant metastasis. TUSC3 overexpression was associated with worse overall survival for CRC, and retained significance as an independent prognostic factor for CRC. Bioinformatics analysis indicated that TUSC3 expression was associated with epithelial-mesenchymal transition signaling pathway and TUSC3 co-expression genes were obtained from COEXPEDIA.

Conclusion: TUSC3 may act as an oncogene in the progression of colorectal cancer. Moreover, TUSC3 has potential to be used as prognostic markers or therapeutic targets in CRC.

Keywords: TUSC3; colorectal cancer; immunohistochemistry; clinical significance; prognosis

Download English Version:

<https://daneshyari.com/en/article/8949961>

Download Persian Version:

<https://daneshyari.com/article/8949961>

[Daneshyari.com](https://daneshyari.com)