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# Expression of TUSC3 and its Prognostic Significance in Colorectal Cancer

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## Abstract

**Background:** Colorectal cancer (CRC) is one of the most common cancers worldwide. Tumor suppressor candidate 3 (TUSC3) has been reported 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