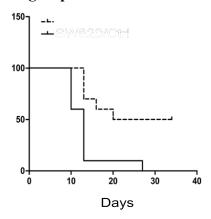
Supplementary Table 1. Clinical features of the $290\ \mathrm{CRC}$ patients involved in the study.

	Value	
Number of patients	290	
Gender		
Male	164/290(57%)	
Female	126/290(43%)	
Age	65.96 ± 12.52	
Dukes stage		
A	44/290(15.2%)	
В	94/290(32.4%)	
C	91/290(31.4%)	
D	61/290(21.0%)	

Supplementary Table 2. Colorectal cancer patient demographics and clinicopathology.

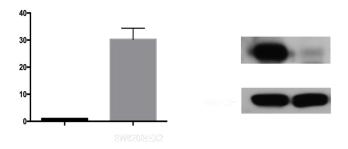
	Value
Number of patients	34
Gender	
Male	18/34(52.9%)
Female	16/34(47.1%)
Age	65.1 ± 11.9
Histology	
Adenocarcinoma	29/34(85.3%)
Mucinous adenocarcinoma	3/34(8.8%)
Neuroendocrine carcinoma	1/34(2.9%)
Signet-ring cell carcinoma	1/34(2.9%)
pTNM stage	
I	10/34(29.4%)
II	7/34(20.6%)
III	7/34(20.6%)
IV	10/34(29.4%)

Supplementary Figure 1. Tumor free survival in SW620/shBEX2 group and the control group.



The tumor free survival of Balb/c athymic nude mice with SW620/shBEX2 cells was significantly longer than that of mice with SW620/Ctrl cells in subcutaneous xenograft model (Log-rank test, p=0.0021). Tumor free survival was measured from the day of tumor inoculation to the day when tumor long axes was less than 2mm and was analyzed by the Kaplan-Meier curve.

Supplementary Figure 2. BEX2 transfection in SW620 cell.



BEX2 was overexpressed in SW620 cell by transfecting the mammalian expression vector pCMV-Myc-BEX2 and the efficiency was verified by qPCR and Western blot analysis. A. *BEX2* mRNA expression was quantified by qPCR. Shown are the relative ratios of over expressed BEX2 in SW620 (SW620/BEX2) to that in SW620 with control vetor (SW620/vetor). *GAPDH* expression was used for normalization. B. BEX2 expression was examined by Western blot analysis. Fold changes (RR) are relative to control.