



**Supplementary information, Figure S1** Bioinformatics analysis of gene expression in 70 human CRC tissues (T) and 12 nontumor tissues (N) from the Hong CRC microarray dataset (GSE9348) available in the Oncomine database. The heatmap shows global gene expression profiling of CRC tissues versus nontumor tissues (fold change > 2,  $P < 0.01$ , FDR < 0.01). Red and green colors represent up-regulation and down-regulation, respectively.