Expression Profile and Prognostic Value of Wnt Signaling Pathway Molecules in Colorectal Cancer

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Supplemental Material includes three Supplemental Tables and two Supplemental Figure

Supplemental Tables

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Figure S1. The expression status of top 10 upregulated CRC-associated genes in the total of 716 samples from six studies.
Figure S2. The prognostic value of mRNA expression level of CRC-associated genes in patients with CRC. The relationship between KRT80 **(A)**, FABP6 **(C)**, FOXQ1 **(B)**, CEMIP **(C)**, and GAS2 **(D)** expression and survival status in 466 TCGA-CRC patients.
Figure S3. The correlation between CTNNB1 and 3 CRC-associated genes in CRC. **(A)-(C)** There was no correlation between CTNNB1 and FABP6, ETV4, or TESC in 275 CRC patients from the TCGA database.

Supplementary Table S1. Sequences of small interfering (si)RNAs and primers

Sequences of siRNAs			
Gene name	**Sense strand (5′-3′)**	**Antisense strand (5′-3′)**	
CTNNB1	CUAUCUGUCUGCUCUAGUATT	UACUAGAGCAGACAGAUAGTT	
NKD2	GCACUCCAGUGUGAUGUCUTT	AGACAUCACACUGGAGUGCTT	
FOXQ1	CCAUCAAACGUGCCUUAAATT	UUUAAGGCACGUUUGAUGGTT	
CEMIP	GGACGGAGUGGUUCGAUCAUGAUAATT	UUAUCAUGAUCGAACCACUCCCGUCCTT	
Sequence of primers			
Gene name	**Forward (5′-3′)**	**Reverse (5′-3′)**	**Melting Temperature (Tm) (°C)**
CTNNB1	TGCTAAATGACGAGGACCAG	TGAGGAGAACGCATGATAGC	54
NKD2	CCTTAGACCCCACTACCCGA	TTTTTCGCCCAGTGCTTTCG	57
FOXQ1	GAGAAAAAGCCCAGCGGAAGA	AGCACCTTGACGAAGCAGTC	57
CEMIP	GCTCTTGAGTTGCATGGACA	ACCGCGTTCAAATACTGGAC	55
GAPDH	AATCCCATCACCATCTTCCA	TGAGTACGTCGTGGAGTCCA	53

Supplementary Table S2. Top 10 up-regulated genes in CRC (GSE21815)

T/N ratio	GENE_SYMBOL	GENE_NAME
108.65	*DPEP1*	dipeptidase 1 (renal)
67.72	*KRT80*	keratin 80
59.75	*FABP6*	fatty acid binding protein 6, ileal
56.90	*NKD2*	naked cuticle homolog 2 (Drosophila)
56.08	*FOXQ1*	forkhead box Q1
51.98	*CEMIP*	cell migration inducing hyaluronan binding protein (also called KIAA1199)
41.53	*ETV4*	ets variant 4
31.95	*TESC*	tescalcin
30.61	*FUT1*	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, H blood group)
30.49	*GAS2*	growth arrest-specific 2

Supplementary Table S3. Univariate and multivariate Cox regression analysis of the 10 CRC-associated genes

Gene Name	Univariate analysis			Multivariate analysis		
	Patient number (N)	Hazard ratio (95% CI)	P	Patient number (N)	Hazard ratio (95% CI)	P
DPEP1						
Low expression	83	0.430	**0.003**	83	0.430	0.003
High expression	143	(0.246-0.751)		143	(0.246-0.750)	
KRT80						
Low expression	211	4.082	**<0.001**	211	0.6067	0.490
High expression	15	(1.907-8.740)		15	(0.147-2.505)	
FABP6						
Low expression	147	0.6723	0.208			
High expression	79	(0.3624-1.247)				
NKD2						
Low expression	44	1.825	0.168			
High expression	182	(0.777-4.289)				
FOXQ1						
Low expression	201	1.727	0.158			
High expression	25	(0.809-3.685)				
CEMIP						
Low expression	152	0.611	0.128			
High expression	74	(0.324-1.152)				
ETV4						
Low expression	152	0.536	0.068			
High expression	74	(0.274-1.046)				
TESC						
Low expression	167	2.083	**0.011**	167	0.849	0.631
High expression	59	(1.182-3.671)		59	(0.434-1.660)	
FUT1						
Low expression	137	1.408	0.230			
High expression	89	(0.805-2.463)				
GAS2						
Low expression	20	0.509	0.099			
High expression	206	(0.228-1.135)				

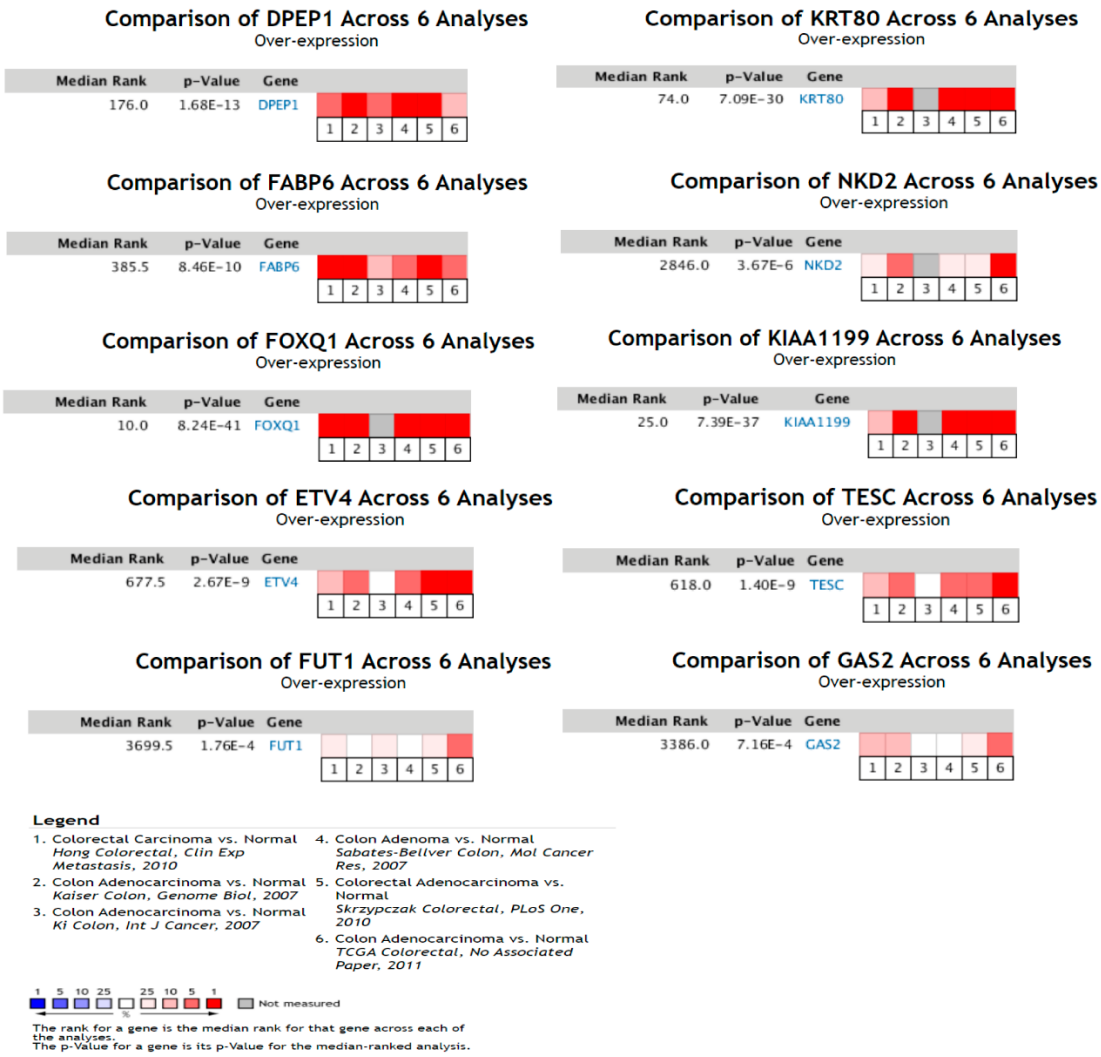


Figure S1. The expression status of top 10 upregulated CRC-associated genes in the total of 716 samples from six studies including, Hong, Kaiser, Ki, Sabates-Bellver, Skrzypczak, and TCGA databases in ONCOMINE by meta-analysis.

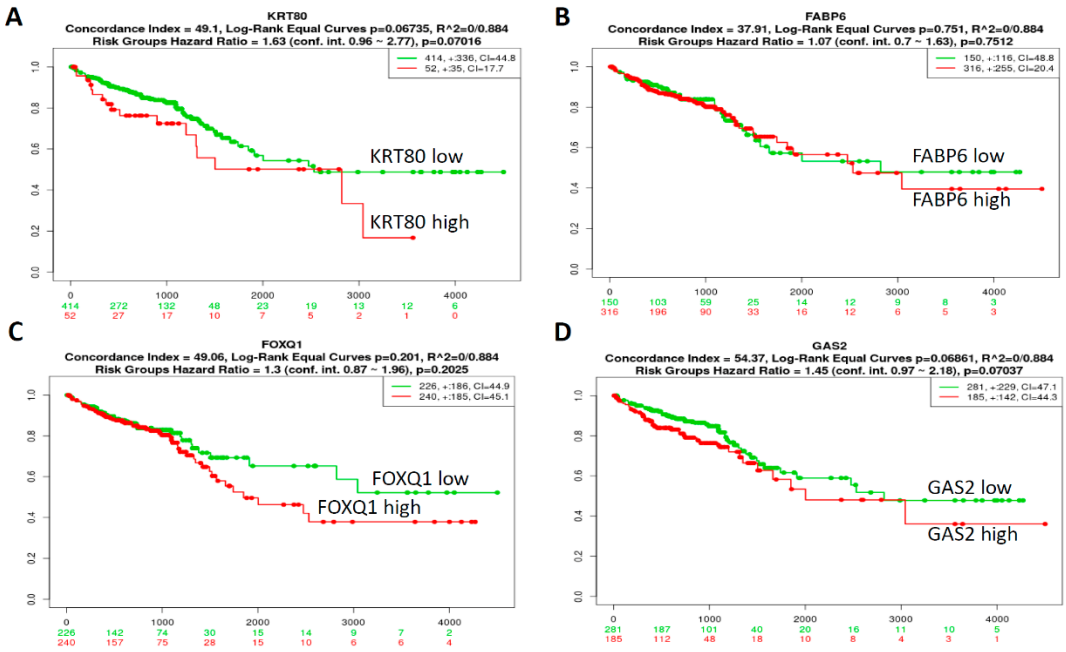


Figure S2. The prognostic value of mRNA expression level of 4 CRC-associated genes in patients with CRC. The relationship between KRT80 **(A)**, FABP6 **(B)**, FOXQ1 **(C)**, and GAS2 **(D)** expression and survival status in 466 TCGA-CRC patients.

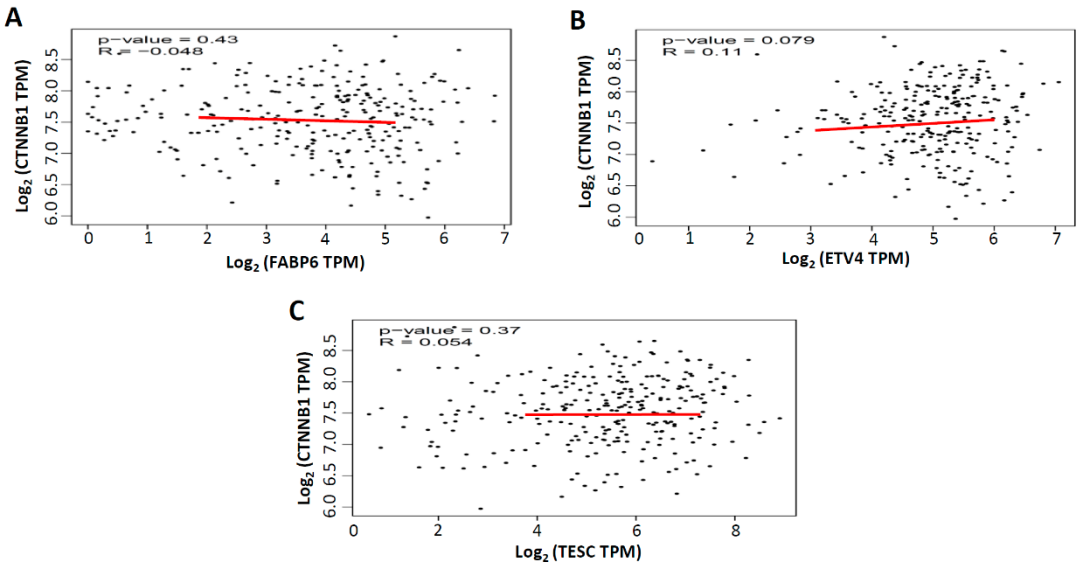


Figure S3. The correlation between CTNNB1 and 3 CRC-associated genes in CRC. **(A)-(C)** There was no correlation between CTNNB1 and FABP6, ETV4, or TESC in 275 CRC patients from the TCGA database.