

**Table S1.** Primer sequences for the reference genes and selected transcripts evaluated by RT-qPCR.

Gene symbol	Primer sequences	Amplicon length
<b>Reference Genes</b>		
<i>GAPDH</i> *	F - 5'TGCACCACCAACTGCTTAG3' R - 5'GATGCAGGGATGATGTTC3'	176bp
<i>GUSB</i> *	F - 5'GAAAATACGTGGTTGGAGAGCTCATT3' R - 5'CCGAGTGAAGATCCCCCTTTTA3'	101bp
<i>RPLP0</i> *	F - 5'GGAGACGCATTACACCTTC3' R - 5'CTTCACCTTAGCTGGGG3'	139bp
<b>Candidate Genes</b>		
<i>BCL2</i>	F - 5'TGTGTGGAGAGCGTCAACCG3' R - 5'TCAGAGACAGCCAGGAGAAATCA3'	181bp
<i>CAV1</i>	F - 5'ACCTCCTCACAGTTTTTCATCCAGC3' R - 5'GCCTTGTTGTTGGGCTTGTAGAT3'	127bp
<i>CD74</i>	F - 5'GCTTTTCCATCCTGGTGA CTCTGC3' R - 5'AGGCTTGGGAGGCTTGGA3'	155bp
<i>COL4A2</i>	F - 5'GGGGTGGAAGGTGACGCT3' R - 5'CCCGTTGATGCCTGCGAA3'	106bp
<i>FZD7</i>	F - 5'TGGAGTTCTTTGAAATGTGCTGGAA3' R - 5'GCTCCCATGATTCTCTGCTAAGCT3'	125bp
<i>ING1</i>	F - 5'GAGTCCCTGCCTTTCGACTTGC3' R - 5'GCGCTCGTAGCACTCGTCTA3'	102bp
<i>LAMB1</i>	F - 5'AAGCTGCCCAAACTCCGGG3' R - 5'CGGCTTTCCTTCTGGCATCAGC3'	177bp
<i>RAC2</i>	F - 5'CACCGACACTCTCCAGGCTC3' R - 5'GTCCACCATCACATTGGCTGAA3'	169bp

F = forward primer; R = reverse primer; \* reference genes

**Table S2.** Antibodies used to investigate the protein expression by immunohistochemistry.

Antibody	Catalog number	Clone	Host	Dilution	Manufacturer
Anti-BCL2	IS61430-2	124	Mouse monoclo- nal	1:300	Dako-Agilent, Santa Clara, CA, USA
Anti-CAV1	ab32577	E249	Rabbit monoclo- nal	1:250	Abcam, Cambridge, UK
Anti-CD74	sc-6262	LN-2	Mouse Monoclo- nal	1:100	Santa Cruz Biotechnology, Dallas, TX, USA
Anti-FZD7	GWB-E6553E	-	Rabbit Polyclo- nal	1:200	Genway Biotech, San Diego, CA, USA
Anti-RAF1	ab181115	EP4969	Rabbit monoclo- nal	1:250	Abcam, Cambridge, UK
Anti-WNT5A	ab235966	-	Rabbit Polyclo- nal	1:300	Abcam, Cambridge, UK
Anti-WNT5B	ab150602	-	Rabbit Polyclo- nal	1:400	Abcam, Cambridge, UK

(-) polyclonal antibodies.

**Table S3.** Relevant biological processes and pathways associated with the differentially expressed genes according to the Enrichr tool analysis. The top 10 enriched terms in the BioCarta, Gene Ontology (GO), Kyoto Encyclopedia of Genes and Genomes (KEGG), and NCI-Nature gene-set libraries are listed.

Enriched terms	Adjusted $p$ -value ( $-\log_{10}$ )	Combined Score ( $\log_2$ )	Genes
<b>BioCarta</b>			
TGF beta signaling pathway	2.263694899	8.280064325	<i>TGFB2; SMAD4; CDH1</i>
IGF-1 Signaling Pathway	2.263694899	8.280064325	<i>MAPK8; IGF1; RAF1</i>
Inhibition of Cellular Proliferation by Gleevec	2.263694899	8.070895405	<i>MAPK8; BCL2; RAF1</i>
CTCF: First Multivalent Nuclear Factor	2.263694899	7.973733049	<i>TGFB2; SMAD4; CDKN1B</i>
Ceramide Signaling Pathway	1.888179013	7.188755253	<i>MAPK8; BCL2; RAF1</i>
NFAT and Hypertrophy of the heart	1.704595592	6.560751421	<i>MAPK8; EDN1; IGF1</i>
Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphorylation	1.704595592	7.800489752	<i>IGF1; RAF1</i>
Melanocyte Development and Pigmentation Pathway	1.704595592	7.800489752	<i>BCL2; RAF1</i>
p53 Signaling Pathway	1.704595592	7.800489752	<i>BCL2; TIMP3</i>
Regulation of p27 Phosphorylation during Cell Cycle Progression	1.704595592	7.800489752	<i>CDKN1B; SKP1</i>
<b>GO</b>			
Cell-cell junction organization	2.897650209	7.935079405	<i>CDH6; TJP1; TGFB2; CDH3; CDH1; CLDN1</i>
Regulation of transforming growth factor beta2 production	2.897650209	11.32001038	<i>SMAD4; TGFB2; CDH3</i>
Extracellular matrix organization	2.897650209	6.772564798	<i>MMP11; POSTN; TGFB2; COL4A2; CDH1; SERPINE1; ICAM3; LAMB1; LOXL2</i>
Regulation of macrophage cytokine production	2.45462084	10.15038089	<i>CD74; TGFB2; WNT5A</i>
Cell morphogenesis	2.45462084	7.718758321	<i>CDH6; TGFB2; CDH3; CDH1; RAC2</i>
Positive regulation of epithelial cell proliferation	2.430283943	7.041373946	<i>CDH3; FZD7; WNT5A; LAMB1; SOX9; IGF1</i>
Negative regulation of cellular process	2.430283943	5.729957251	<i>AZGP1; TGFB2; SMAD4; CDKN1B; FTH1; CAV1; PDCD5; BHLHE40; BCL2; PPT1; RAF1; ING1</i>
Epithelial to mesenchymal transition	2.226162771	7.949843228	<i>TGFB2; WNT5A; SOX9; LOXL2</i>
Regulation of ossification	2.226162771	7.891397721	<i>TGFB2; WNT5A; SOX9; PRKACA</i>
Regulation of calcineurin-NFAT signaling cascade	2.226162771	9.080132971	<i>RCAN1; RCAN3; IGF1</i>
<b>KEGG</b>			
Pathways in cancer	6.466298191	7.236709876	<i>TGFB2; SMAD4; EDN1; CDKN1B; FZD7; WNT5A; LAMB1; IGF1; MAPK8; COL4A2; CDH1; BCL2; RAC2; RAC3; PRKACA; RAF1; SKP1</i>
AGE-RAGE signaling pathway in diabetic complications	5.323196874	8.256314229	<i>TGFB2; SMAD4; EDN1; MAPK8; CDKN1B; COL4A2; SERPINE1; BCL2</i>
Colorectal cancer	4.695419164	8.101592401	<i>MAPK8; TGFB2; SMAD4; RAC2; BCL2; RAC3; RAF1</i>

Focal adhesion	4.463028935	7.111825763	MAPK8; COL4A2; CAV1; BCL2; RAC2; RAC3; LAMB1; IGF1; RAF1
Proteoglycans in cancer	4.463028935	7.08791045	TGFB2; FZD7; CAV1; WNT5A; ITPR1; TIMP3; IGF1; PRKACA; RAF1
Gastric cancer	4.463028935	7.345942753	TGFB2; SMAD4; CDKN1B; CDH1; FZD7; WNT5A; BCL2; RAF1
Wnt signaling pathway	4.337917928	7.20898761	SMAD4; MAPK8; FZD7; WNT5A; RAC2; RAC3; PRKACA; SKP1
Pancreatic cancer	4.213871002	7.84405439	MAPK8; TGFB2; SMAD4; RAC2; RAC3; RAF1
Estrogen signaling pathway	3.808795298	7.040826917	KRT19; KRT15; ITPR1; BCL2; KRT13; PRKACA; RAF1
Hippo signaling pathway	3.414787704	6.675556184	TGFB2; SMAD4; CDH1; YWHAB; FZD7; SERPINE1; WNT5A
<b>NCI-NATURE</b>			
Role of Calcineurin-dependent NFAT signaling in lymphocytes	3.000308833	7.955865881	RCAN1; MAPK8; YWHAB; BCL2; PRKACA
Validated targets of C-MYC transcriptional repression	2.930105281	7.573292518	SMAD4; CDKN1B; FTH1; WNT5A; BCL2
Class I PI3K signaling events mediated by Akt	2.930105281	8.135257715	CDKN1B; YWHAB; PRKACA; RAF1
Signaling events mediated by Stem cell factor receptor (c-Kit)	2.319674044	7.202381679	MAPK8; GRB10; BCL2; RAF1
HIF-1-alpha transcription factor network	2.111786644	6.672375961	EDN1; SMAD4; SERPINE1; BHLHE40
Wnt signaling network	2.111786644	7.545603799	IGFBP4; FZD7; WNT5A
Signaling events mediated by VEGFR1 and VEGFR2	2.111786644	6.605374227	CAV1; GRB10; PRKACA; RAF1
Noncanonical Wnt signaling pathway	2.021480507	7.255617428	MAPK8; FZD7; WNT5A
Signaling events regulated by Ret tyrosine kinase	1.851701712	6.881629075	MAPK8; GRB10; PRKACA
Ceramide signaling pathway	1.777919174	6.560751421	MAPK8; BCL2; RAF1

**Table S4.** Comparison between tumor and normal samples for each transcript and analysis category.

Genes	cDNA microarray		Array dependent validation		Array independent validation	
	Fold# (T/N)	P	Fold# (T/N)	P	Fold# (T/N)	P
<i>BCL2</i>	-6.29	0.005*	-1.47	0.064	-5.10	0.002*
<i>CAV1</i>	6.71	0.005*	2.44	0.045*	1.19	0.516
<i>CD74</i>	-2.56	0.005*	-5.49	0.045*	-8.64	0.006*
<i>COL4A2</i>	5.53	0.005*	16.62	0.045*	3.68	0.023*
<i>FZD7</i>	-10.56	0.005*	-1.70	0.165	-3.62	0.292
<i>ING1</i>	-2.74	0.005*	-1.98	0.123	-2.09	0.019*
<i>LAMB1</i>	4.83	0.005*	2.14	0.045*	4.17	0.029*
<i>RAC2</i>	-4.05	0.005*	-3.42	0.045*	-1.78	0.168

\* Mann-Whitney statistical test significance ( $P < 0.05$ ); \*Fold based on median of tumor (T) and normal samples (N).