

Supplemental Table S1. Clinicopathological characteristics of patients with CC.

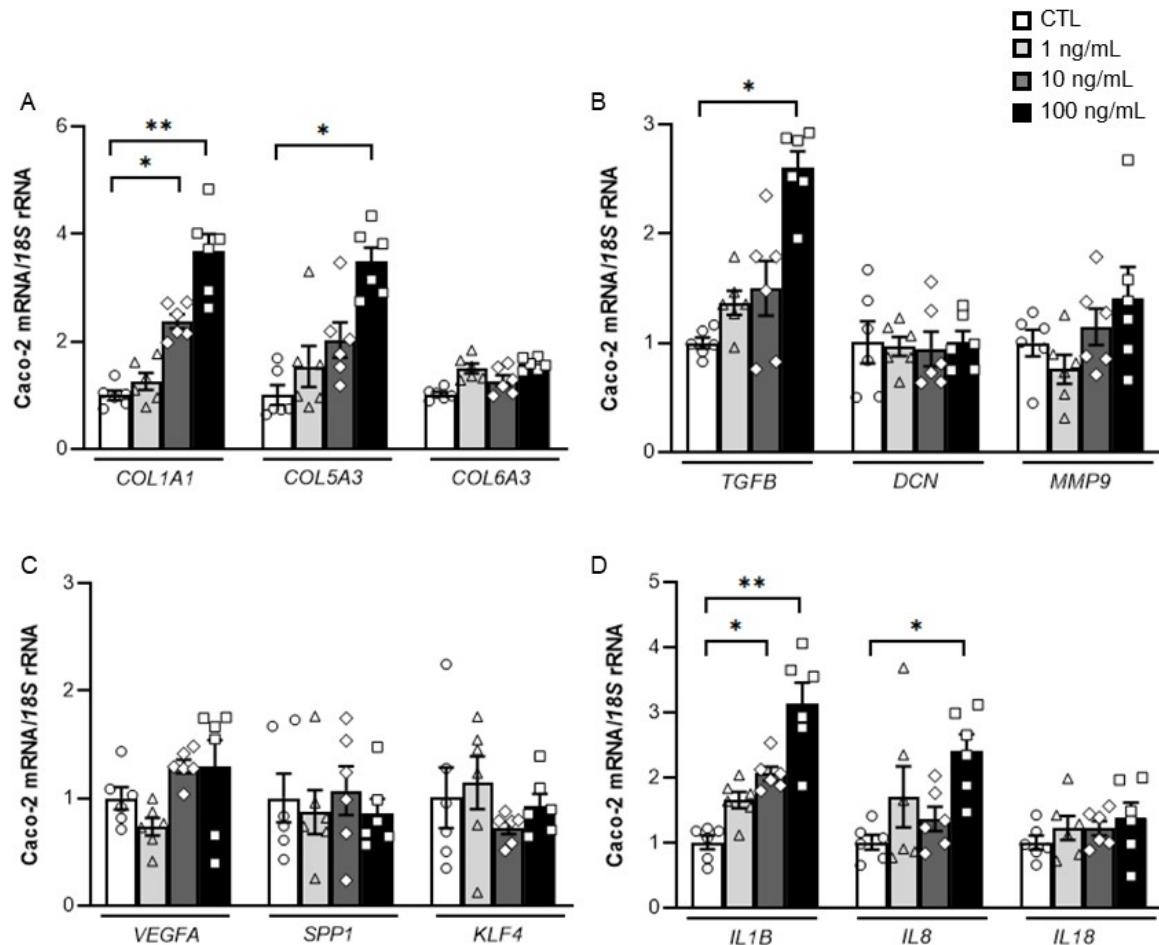
Gender, n	
Male	17
Female	14
Location of primary lesion, n	
Transverse colon	4
Right hemicolon	12
Left hemicolon	13
Missing	2
TNM stage, n	
I	4
II	6
III	15
IV	4
Missing	2
Differentiation, n	
Well	3
Moderately	23
Poorly and undifferentiated	3
Missing	2
Tumor size, n	
< 5 cm	16
> 5 cm	7
Missing	8
Lymph node status, n	
Positive	9
Negative	22

Supplemental Table S2. Sequences of primers and probes.

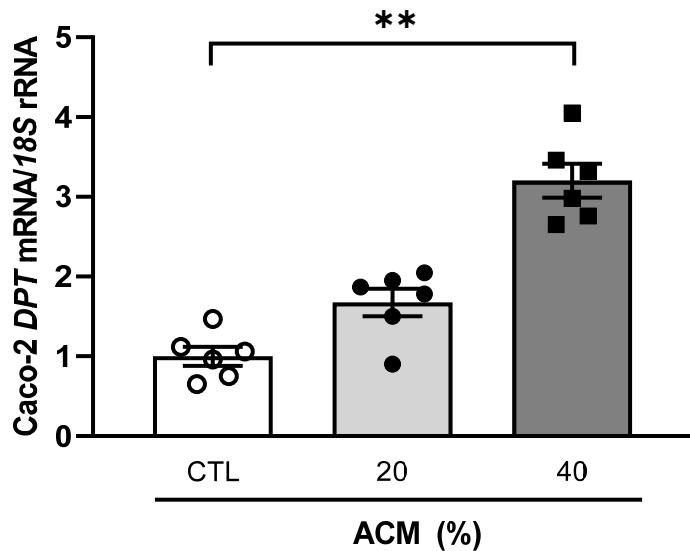
Gene (GenBank accession)	Oligonucleotide sequence (5'-3')
<i>COL1A1</i> (NM_000088.3)	
Forward	CTCCCGGGCCTCAAGGTAT
Reverse	TTGCTCCAGAGGGACCTGTT
TaqMan® Probe	FAM-TCTTCCTGGCCCCTGGTGAACCT-TAMRA
<i>COL5A3</i> (NM_015719.4)	
Forward	GAACAAGGAAATTGGACCTCAAG
Reverse	GATTGGAGCTGGACTCTCTGTCT
TaqMan® Probe	FAM-TCCTGACTCCGCAGAGAACCGACCTC-TAMRA
<i>COL6A3</i> (NM_004369.3)	
Forward	GACGGAGATCTGGCTGATTTACA
Reverse	AGATGCATTAGCCGCTCCAA
TaqMan® Probe	FAM-AGAACCTCCGCCAAGAAGGAGTCCGT-TAMRA
<i>DCN</i> (NM_001920.5)	
Forward	AGAAGCTCTCCTACATCCGCATT
Reverse	CTGCATCAACTCTGCTGATTGT
TaqMan® Probe	FAM-TTCCTCAAGGTCTCCTCCTCCCTACG-TAMRA
<i>DPT</i> (NM_001937.5)	
Forward	GGCAGTTTACTGTTGTCGCTACA
Reverse	CATGTCCATTCTCCTCACCATAGTG
TaqMan® Probe	FAM-TGCCCATATTCTGCTGGCTAACACAG-TAMRA
<i>IL1B</i> (NM_000576)	
Forward	CAGTGGCAATGAGGATGACTTG
Reverse	GTAGTGGTGGTCGGAGATTGTA
TaqMan® Probe	FAM-TGGCCCTAACAGATGAAGTGCTCCTTCC-TAMRA
<i>IL8</i> (NM_000584.3)	
Forward	ACCTTCCACCCAAATTATCA
Reverse	TTCTCAGCCCTCTCAAAAACTTC
TaqMan® Probe	FAM-CCACACTGCGCCAACACAGAAATTATTGTA-TAMRA
<i>IL18</i> (NM_001562)	
Forward	CCAAGGAAATCGGCCTCTATT
Reverse	CCTCTAGGCTGGCTATCTTATACATACT
TaqMan® Probe	FAM-TTCTGACTGTAGAGATAATGCACCCGGAC-TAMRA
<i>KLF4</i> (NM_001314052.1)	
Forward	ACCTACACAAAGAGTCCCACATCTCA
Reverse	GTTCACGGTAGTGCCTGGTCAGTT
TaqMan® Probe	FAM-CCTGCGAACCCACACAGGTGAGAAA-TAMRA
<i>MMP9</i> (NM_004994)	
Forward	GCCC GGACCAAGGATACAGT
Reverse	CCCCTCAGTGAAGCGGTACA
TaqMan® Probe	FAM-ACGCGCTGGCTAGATCATTCCCTCA-TAMRA
<i>SPP1</i> (NM_000582)	
Forward	CATCCAGTACCCTGATGCTACAGA

Reverse	GGCCTTGTATGCACCATTCAA
TaqMan® Probe	FAM-ACATCACCTCACACATGGAAAGCGAGGA-TAMRA
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<i>TGFB</i> (NM_000660)	
Forward	GCCCAGCATCTGCAAAGC
Reverse	TCCTTGCAGAAGTCAATGTACA
TaqMan® Probe	FAM-CACCAACTATTGCTTCAGCTCCACGGGA-TAMRA
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<i>VEGFA</i> (NM_001025250)	
Forward	CAGCACAAACAAATGTGAATGCA
Reverse	ACACGTCTGCAGATCTTGTACA
TaqMan® Probe	FAM-AATCCCTGTGGGCCTTGCTCAGAGC-TAMRA

COL, collagen; *DCN*, decorin; *DPT*, dermatopontin; *IL*, interleukin; *KLF4*, Kruppel-like factor 4; *MMP9*, matrix metalloproteinase 9; *SPP1*, osteopontin; *TGFB*, transforming growth factor- β ; *VEGFA*, vascular endothelial growth factor A.



Supplemental Figure S1. Effect of DPT treatment on the expression levels of A) collagen (*COL*)-*1A1*, *COL5A3* and *COL6A3*; B) transforming growth factor- β (*TGFB*), decorin (*DCN*) and matrix metalloproteinase (*MMP*)-9; C) vascular endothelial growth factor A (*VEGFA*), osteopontin (*SPP1*) and Kruppel-like factor 4 (*KLF4*) and D) interleukin (*IL*)-1*B*, *IL8* and *IL18* in Caco-2 cells. Values are the mean \pm SEM (n = 6 per group). Differences between groups were analysed by one-way ANOVA followed by Dunnett's post hoc tests. * P<0.05 and ** P<0.01.



Supplemental Figure S2. Effect of adipocyte-conditioned media (ACM) on the gene expression levels of *DPT* in Caco-2 cells. Bar graph represents the mean \pm SEM ($n = 6$ per group). Differences were analysed by one-way ANOVA followed by Dunnett's *post hoc* tests. ** $P < 0.01$.