

Supplementary Table 1: Expression of *PTPRR* transcript variants 1 and 2 in colorectal tumors and colorectal cancer cell lines as measured with real time quantitative RT-PCR.

	FOLD CHANGES ¹	
	<i>PTPRR-1</i>	<i>PTPRR-2</i>
POLYPOID ADENOMAS²		
AD-A4*	0.0002	0.048
AD-A26	0.3548	0.416
AD-A36	0.6238	0.067
AD-G5A*	0.037	0.014
AD-G7A	0	0.0152
AD-A27*	0.0004	0.058
AD-Vi.po. 16*	0.025	0.092
AD-Vi.po. 11*	0.0804	0.037
AD-A31*	0.1911	0.057
COLORECTAL CANCERS		
CRC-G9K	0.272	0.206
CRC-G13K	0	0.104
CRC-G15K	0.249	0.445
CRC-G17K	0.538	0.265
CRC-G23K	0.324	0.179
CRC-G25K	0.045	0.3
CRC-G27K	0.0017	0.015
CRC-G29K	0.045	0.369
CRC-G31K	0	0.083
CRC-G35K	0.08	0.688
CRC-G37K	0.675	0.139
COLON CANCER CELL LINES		
Vaco481	0	0.102
Colo205	0	0
SW48	0	0
LS174T	0	0.195
SW620	0	0
HT29	0	0.041
Caco2	0.071	0.12
Colo741	0	0
HCT116	0	0
LS411	0.059	0.118
Lovo	0.105	0.415
SW837	0.057	0
GP5D	0	0
SW480	0	0
CX1	0	0
CO115	0	0.347

¹ Fold changes were calculated as reported in Methods. The level in each tumor was compared with that found in normal mucosa from the same patient; levels in cell lines were compared with a single control level representing the mean found in 9 normal mucosal samples from patients with adenomas. Samples whose values are shown in boldface were found unmethylated by COBRA (Table 1). Each sample was analyzed in duplicate.

² Adenomas marked with asterisks (and corresponding samples of normal mucosa) were collected for a previous study (Sabates-Bellver *et al.*, 2007). All other tumor samples listed in the Table are described in the Methods section.