

Figure S1. Standard curve of methylated *MMP9* from the dilutions of four concentrations of methylated *MMP9* (0.01, 0.1, 1 and 10 ng/ μ l), which was used to convert the Cq values into the concentration of methylated *MMP9*. *MMP9*, matrix metalloproteinase 9.

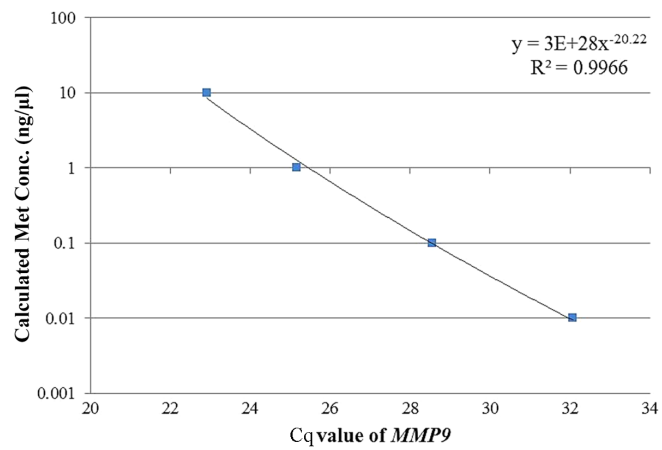


Figure S2. Standard curve of methylated *PLOD1* from the dilutions of four concentrations of methylated *PLOD1* (0.01, 0.1, 1 and 10 ng/ μ l), which was used to convert the Cq values into the concentration of methylated *PLOD1*. *PLOD1*, procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1.

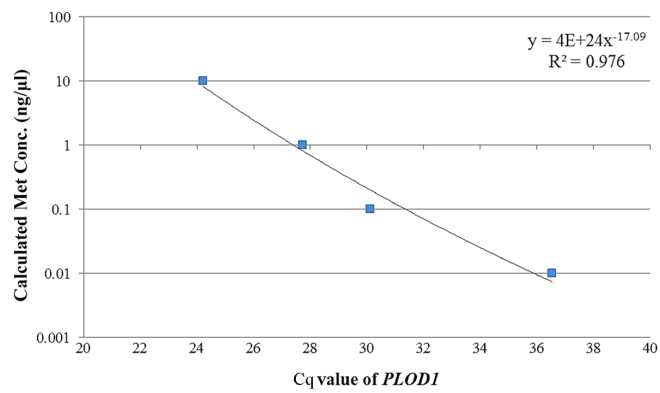


Table SI. Connection up- and downregulation expression analysis of microarrays between DNA methylation changes (GSE110274) and mRNA levels of the white blood cells of patients with colorectal cancer (GSE11545, GSE10715, GSE31023 and GSE47756).

Experiment	MET+, RNA+	MET+, RNA-	MET-, RNA+	MET-, RNA-	Lower 95% CI	Upper 95% CI	OR	P-value
Intragenic_GSE110274_up_GSE11545_up	760	7,252	292	5,369	1.68	2.22	1.93	8.52x10 ⁻²¹
Intragenic_GSE110274_up_GSE10715_up	1,273	8,994	636	6,609	1.33	1.63	1.47	3.70x10 ⁻¹⁴
Upstream_GSE110274_up_GSE10715_up	824	5,556	1,064	9,971	1.26	1.53	1.39	2.17x10 ⁻¹¹
Upstream_GSE110274_up_GSE11545_up	489	5,297	561	7,295	1.06	1.36	1.20	4.54x10 ⁻³
Intragenic_GSE110274_dn_GSE11545_up	699	7,928	353	4,693	1.03	1.34	1.17	1.91x10 ⁻²
Intragenic_GSE110274_up_GSE31023_up	75	6,778	48	5,001	0.80	1.66	1.15	4.44x10 ⁻¹
Upstream_GSE110274_up_GSE47756_up	1,236	6,826	1,888	11,332	1.01	1.17	1.09	3.58x10 ⁻²
Upstream_GSE110274_dn_GSE10715_up	679	5,343	1,209	10,184	0.97	1.18	1.07	1.80x10 ⁻¹
Intragenic_GSE110274_up_GSE47756_up	1,800	10,126	1,341	8,064	0.99	1.15	1.07	8.76x10 ⁻²
Intragenic_GSE110274_dn_GSE47756_up	1,934	10,983	1,207	7,207	0.97	1.14	1.05	2.06x10 ⁻¹
Upstream_GSE110274_dn_GSE10715_dn	1,174	4,848	2,171	9,222	0.95	1.11	1.03	4.84x10 ⁻¹
Upstream_GSE110274_dn_GSE11545_up	458	5,410	592	7,182	0.90	1.17	1.03	6.80x10 ⁻¹
Upstream_GSE110274_up_GSE31023_dn	175	4,592	261	6,858	0.82	1.22	1.00	9.89x10 ⁻¹
Upstream_GSE110274_dn_GSE31023_up	50	4,814	73	6,949	0.69	1.42	0.99	9.51x10 ⁻¹
Intragenic_GSE110274_dn_GSE10715_up	1,162	9,632	747	5,971	0.87	1.06	0.96	4.65x10 ⁻¹
Upstream_GSE110274_dn_GSE47756_up	1,159	6,912	1,965	11,246	0.89	1.04	0.96	3.04x10 ⁻¹
Upstream_GSE110274_dn_GSE11545_dn	372	5,496	515	7,259	0.83	1.10	0.95	5.04x10 ⁻¹
Intragenic_GSE110274_dn_GSE10715_dn	2,027	8,767	1,322	5,396	0.87	1.02	0.94	1.41x10 ⁻¹
Intragenic_GSE110274_up_GSE47756_dn	2,165	9,761	1,809	7,596	0.87	1.00	0.93	4.41x10 ⁻²
Intragenic_GSE110274_dn_GSE31023_dn	256	6,947	180	4,519	0.76	1.12	0.93	4.32x10 ⁻¹
Upstream_GSE110274_dn_GSE47756_dn	1,419	6,652	2,524	10,687	0.84	0.97	0.90	5.50x10 ⁻³
Upstream_GSE110274_up_GSE47756_dn	1,410	6,652	2,533	10,687	0.83	0.96	0.89	2.34x10 ⁻³
Upstream_GSE110274_dn_GSE31023_dn	167	4,697	269	6,753	0.73	1.09	0.89	2.57x10 ⁻¹
Intragenic_GSE110274_dn_GSE31023_up	71	7,132	52	4,647	0.62	1.27	0.89	5.24x10 ⁻¹
Intragenic_GSE110274_dn_GSE47756_dn	2,280	10,637	1,694	6,720	0.79	0.91	0.85	5.36x10 ⁻⁶
Upstream_GSE110274_up_GSE31023_up	44	4,723	79	7,040	0.57	1.20	0.83	3.24x10 ⁻¹
Intragenic_GSE110274_up_GSE10715_dn	1,829	8,438	1,520	5,725	0.76	0.88	0.82	1.55x10 ⁻⁷
Upstream_GSE110274_up_GSE10715_dn	1,088	5,292	2,257	8,778	0.74	0.87	0.80	4.08x10 ⁻⁸
Intragenic_GSE110274_up_GSE31023_dn	225	6,628	211	4,838	0.64	0.94	0.78	1.01x10 ⁻²
Upstream_GSE110274_up_GSE11545_dn	309	5,477	578	7,278	0.62	0.82	0.71	2.34x10 ⁻⁶
Intragenic_GSE110274_dn_GSE11545_dn	461	8,166	425	4,621	0.54	0.70	0.61	1.70x10 ⁻¹²
Intragenic_GSE110274_up_GSE11545_dn	409	7,603	477	5,184	0.51	0.67	0.58	7.82x10 ⁻¹⁵

The results of the analysis are presented as P-values, ORs and 95% CIs. GSE110274 of methylation profiling from co-cultured peripheral blood mononuclear cells; GSE11545 of expression profiling from peripheral blood; GSE10715 of expression profiling from peripheral blood; GSE31023 of expression profiling from peripheral blood; GSE47756 of expression profiling from peripheral blood monocyte. MET+, RNA+ represents the number of genes that were included hypermethylated(up)/hypomethylated(dn) in GSE110274 and up/dn in GSE11545, GSE10715, GSE31023 or GSE47756; MET+, RNA- represents the number of genes that were included hypermethylated(up)/hypomethylated(dn) in GSE110274 and not up/not dn in GSE11545, GSE10715, GSE31023 or GSE47756; MET-, RNA+ represents the number of genes that were included unmethylated in GSE110274 and up/dn in GSE11545, GSE10715, GSE31023 or GSE47756; MET-, RNA- represents the number of genes that were included unmethylated in GSE110274 and not up/dn in GSE11545, GSE10715, GSE31023 or GSE47756. The results of GSE110274, GSE11545 and GSE10715 in OR>1 and P<0.01, which were selected for analysis in the present study. OR, odds ratio; up, upregulated; dn, downregulated.

Table SII. Characteristics of patients with CRC, including age, sex, cancer position, histological grade and cancer stage.

Sample ID	Age	Sex	Position	Grade	Stage
CRC1	79	Male	Rectum	Well-differentiated adenocarcinoma	IIIB
CRC2	82	Male	Rectum	Moderately-differentiated adenocarcinoma	IIA
CRC3	80	Male	Sigmoid	Moderately-differentiated adenocarcinoma	IIA
CRC4	68	Male	Rectum	Moderately-differentiated adenocarcinoma	IIA
CRC5	56	Male	Descending	Moderately-differentiated adenocarcinoma	IIA
CRC6	57	Male	Ascending	Moderately-differentiated adenocarcinoma	N/A
CRC7	67	Female	Recto-sigmoid	Moderately-differentiated adenocarcinoma	IIIA
CRC8	62	Female	Transverse	Moderately-differentiated adenocarcinoma	IVA
CRC9	83	Female	Descending	Moderately-differentiated adenocarcinoma	IIIB
CRC10	64	Female	Rectum	Well-differentiated adenocarcinoma	I
CRC11	46	Female	Recto-sigmoid	Moderately-differentiated adenocarcinoma	I
CRC12	55	Male	Recto-sigmoid	Moderately-differentiated adenocarcinoma	IIIA
CRC13	78	Male	Sigmoid	Moderately-differentiated adenocarcinoma	IIA
CRC14	61	Female	Ascending colon	Poorly differentiated adenocarcinoma	N/A
CRC15	62	Male	Sigmoid	Moderately-differentiated adenocarcinoma	IIA
CRC16	60	Male	Sigmoid	Moderately-differentiated adenocarcinoma	IIA
CRC17	65	Male	Liver-metastatic colonic adenocarcinoma	Well-differentiated adenocarcinoma	IV
CRC18	73	Male	Sigmoid	Moderately-differentiated adenocarcinoma	IIC
CRC19	69	Male	Rectum	Moderately-differentiated adenocarcinoma	IIIC
CRC20	80	Female	Sigmoid	Moderately-differentiated adenocarcinoma	IIIB
CRC21	80	Male	Sigmoid	Moderately-differentiated adenocarcinoma	IIA
CRC22	55	Female	Rectum	N/A	IIA
CRC23	33	Male	Transverse colon	Moderately-differentiated adenocarcinoma	IVA
CRC24	72	Female	Recto-sigmoid	Moderately-differentiated adenocarcinoma	IIIB
CRC25	67	Male	Recto-sigmoid	Well-differentiated adenocarcinoma	IIIB
CRC26	75	Male	Liver-metastatic colonic adenocarcinoma	N/A	IV
CRC27	49	Male	Liver-metastatic colonic adenocarcinoma	N/A	IV
CRC28	65	Male	Descending colon	Moderately-differentiated adenocarcinoma	IIC
CRC29	66	Female	Liver-metastatic colonic adenocarcinoma	N/A	IV
CRC30	63	Male	Rectum	Moderately-differentiated adenocarcinoma	I
CRC31	80	Female	Sigmoid	Well-differentiated adenocarcinoma	I
CRC32	82	Male	Transverse	Well-differentiated adenocarcinoma	N/A

All samples were obtained from patients diagnosed with CRC between January 2016 and January 2018 at Chulalongkorn Memorial Hospital. CRC, colorectal cancer; N/A applicable.