Table S1. Information of patients analyzed in this study

		Right colon cancer	Left colon cancer	Rectal cancer	*p* value	Statistical method
Number of cases		35	36	35		
Age at diagnosis (median ± SD)		68 ± 9.9	69.5 ± 10.1	69 ± 9.2	0.902	Kruskal-Wallis test
Sex (Male : Female)		17:18	21:15	24 :11	0.237	χ^2 test
AJCC cancer stage	Ⅰ	9	6	8	0.762	
	Ⅱ	13	14	10		
	Ⅲ	13	16	17		
	Ⅳ	0	0	0		
Lymph node metastasis	(+)	13	16	17	0.620	
	(-)	22	20	18		
Pathological type	Differentiated	34	36	34	0.547	Fisher's exact test
	Poorly	1	0	1		

AJCC, American Joint Committee on Cancer

Table S2. *KRAS* mutations identified in 106 CRC tissues.

Mutations	Number of tumors	Frequency (%)	Patient ID
G12V	16	15.1%	322, 326, 336, 342, 343, 373, 380, 388, 413, 422, 426, 481, 505, 519, 521, 556
G12D	7	6.6%	275, 316, 361, 410, 444, 464, 558
G12S	3	2.8%	321, 330, 534
G12C	3	2.8%	285, 360, 428
G12A	1	0.9%	472
G13D	9	8.5%	313, 341, 374, 419, 456, 473, 478, 484, 557
G13C	1	0.9%	311
G13R	1	0.9%	425
A59E	1	0.9%	347

Table S3. Relationship between CIMP and *BRAF* or *KRAS* mutations.

	CIMP-positive	CIMP-negative	*p* value	Statistical method
BRAF mut (+)	5	0	0.001	Fisher's exact test
BRAF mut (-)	20	81		
KRAS mut (+)	11	31	0.387	
KRAS mut (-)	14	50		
KRAS G13D (+)	2	7	0.642	
KRAS G13D (-)	23	74		

BRAF mut: *BRAF* mutation (V600E), *KRAS* mut: all *KRAS* mutations

Table S4. MAFG consensus binding sites in the iDMRs.

DMR	Analyzed region[1]	Strand[2]	MAFG consensus binding site[3]	Number of consensus binding sites	Frequency of MAFG consensus binding site per 1 Kb
PPIEL	chr1: 40024626-40025540	-	non	0	0
ARHI-CG1 *ARHI*-CG2	chr1: 68515433-68517545	-	non	0	0
ARHI-CG3	chr1: 68512505-68513486	-	non	0	0
ZDBF2	chr2: 207114583-207136544	-1	ATAGCGCAGAATCTGCTGAAA	5	0.23
		-1	AATTTGCTTAGAGAGCATCAG		
		1	CTGATGCTCTCTAAGCAAATT		
		-1	AAAGTGCTGAGTATGTGTTAT		
		1	ATAACACATACTCAGCACTTT		
NAP1L5	chr4: 89618184-89619237	-	non	0	0
FAM50B	chr6: 3849082-3850359	-1	GATGCGCTGCTTCAGCACCTC	2	1.56
		1	GAGGTGCTGAAGCAGCGCATC		
ZAC	chr6: 144328078-144329888	-1	AGATTGCTTACTTAGCACATG	2	1.10
		1	CATGTGCTAAGTAAGCAATCT		
GRB10-DMR	chr7: 50848726-50851312	-	non	0	0
PEG10	chr7: 94285537-94287960	-	non	0	0
PEG1	chr7: 130130122-130134388	-1	CAAATGCTGATTTAGCACCTA	2	0.47
		1	TAGGTGCTAAATCAGCATTTG		
LOC728024	chr8: 37604992-37606088	-	non	0	0
TRAPPC9	chr8: 141108147-141111081	-	non	0	0
*H19*promoter *H19*DMR	chr11:2018812-2024740	-	non	0	0
IGF2-DMR2	chr11: 2153991-2155112	-	non	0	0
IGF2-DMR0	chr11: 2168333-2169768	-	non	0	0
*Kv*DMR1	chr11: 2719948-2722259	-	non	0	0
RB1	chr13: 48892341-48895763	-	non	0	0
MEG3	chr14: 101290524-101293978	-	non	0	0
MEG8	chr14: 101370741-101371419	-	non	0	0
MAGEL2	chr15: 23892425-23894029	-	non	0	0
NDN	chr15: 23931451-23932759	-	non	0	0
SNRPN	chr15: 25200004-25201976	-1	CCTCTGCTGCGTCTGCGCAAC	2	1.01
		1	GTTGCGCAGACGCAGCAGAGG		
IGF1R	chr15: 99408496-99409650	-	non	0	0
ZNF597 (3')	chr16: 3481801-3482388	-	non	0	0
ZNF597 (TSS)	chr16: 3492828-3494463	-	non	0	0
ZNF331 (1)	chr19: 54040510-54042212	-	non	0	0
ZNF331 (2)	chr19: 54057086-54058425	-	non	0	0
PEG3	chr19: 57348493-57353271	-1	GGTTTGCCGAGTAGGCGCTGT	1	0.21
USP29	chr19: 57629548-57631498	-	non	0	0
L3MBTL	chr20: 42142365-42144040	-	non	0	0
NESP55	chr20: 57414039-57418612	-1	TTTGTGCTGGGTCATCAGAGC	2	0.44
		1	GCTCTGATGACCCAGCACAAA		
NESPAS-GNASXL	chr20: 57425649-57428033	-	non	0	0
GNAS1A	chr20: 57463265-57465201	-	non	0	0
GNASXL	chr20: 57428905-57431463	-	non	0	0
WRB	chr21: 40757510-40758276	-	non	0	0
NHP2L1	chr22: 42077774-42078873	-	non	0	0

[1]The analyzed regions were shown using the UCSC hg19 reference genome.

[2]Foward strand and reverse strand were indicated in 1 and -1, respectively.

[3]MAFG consensus binding site was identified by the JASPAR database. The relative profile score threshold was set at 80%.

Table S5. *IGF2* imprinting status in paired tumors and normal mucosae.

		Tumor			
		MOI	LOI	*p* value	Statistical method
Normal mucosa	MOI	4	3	0.225	Fisher's exact test
	LOI	10	22		

MOI, maintenance of imprinting; LOI, loss of imprinting

Table S6. Relationship between *IGF2*-DMR2 hypomethylation and *IGF2* LOI in tumors.

		Number of MOI cases	Number of LOI cases	*p* value	Statistical method
IGF2-DMR2 hypomethylation	(+)	5	14	0.326	χ^2 test
	(-)	9	13		

MOI, maintenance of imprinting; LOI, loss of imprinting

Table S7. Relationship between clinicopahtological factors and HyMiD status.

		HyMiD-positive	HyMiD-negative	*p* value	Statistical method
Number of cases		55	51		
Age at diagnosis (Median ± SD)		70.0 ± 10.0	68.0 ± 9.8	0.850	Kruskal-Wallis test
Sex	Male	27/55 (49.1%)	35/51 (68.6%)	0.032	Fisher's exact test
	Female	28/55 (50.9%)	16/51 (31.4%)		
Tumor location	Right	18/55 (32.7%)	17/51 (33.3%)	0.567	
	Left	21/55 (38.2%)	15/51 (29.4%)		
	Rectum	16/55 (29.1%)	19/51 (37.3%)		
Pathological type	Differentiated	54/55 (98.2%)	50/51 (98.0%)	0.733	
	Poorly	1/55 (1.8%)	1/51 (2.0%)		
Lymph node metastasis		22/55 (40.0%)	24/51 (47.1%)	0.296	
Lymphatic invasion		28/55 (50.9 %)	27/51 (52.9%)	0.494	
Vascular invasion		16/55 (29.1%)	16/51 (31.4%)	0.482	
AJCC cancer stage	I	17/55 (30.9%)	6/51 (11.8%)	0.053	
	II	16/55 (29.1%)	21/51 (41.2%)		
	III	22/55 (40.0%)	24/51 (47.0%)		
Tumor size (Median ± SD) (mm)		45.0 ±18.6	42.0 ± 16.0	0.556	Mann-Whitney U test
Survival rate		0.992	0.876	0.453	Log-rank test

AJCC, American Joint Committee on Cancer

Table S8. Relationship between clinicopathological factors and *IGF2- DMR0 hypomethylation.*

		IGF2-DMR0 hypomethylation (+)	*IGF2*-DMR0 hypomethylation (-)	*p* value	Statistical method
Number of cases		72	34		
Age at diagnosis (Median ± SD)		69.0 ± 10.2	69.5 ± 8.3	0.572	Kruskal-Wallis test
Sex	Male	42/72 (58.3%)	20/34 (58.8%)	0.566	Fisher's exact test
	Female	30/72 (41.7%)	14/34 (41.2%)		
Tumor location	Right	20/72 (27.8%)	15/34 (44.1%)	0.176	
	Left	28/72 (38.9%)	8/34 (23.5%)		
	Rectum	24/72 (33.3%)	11/34 (32.4%)		
Pathological type	Differentiated	71/72 (98.6%)	33/34 (97.1%)	0.541	
	Poorly	1/72 (1.4%)	1/34 (2.9%)		
Lymph node metastasis		35/72 (48.6%)	11/34 (32.4%)	0.085	
Lymphatic invasion		35/72 (48.6%)	20/34 (58.8%)	0.220	
Vascular invasion		20/72 (27.8%)	12/34 (35.3%)	0.285	
AJCC cancer stage	I	17/72 (23.6%)	6/34 (17.6%)	0.080	
	II	20/72 (27.8%)	17/34 (50.0%)		
	III	35/72 (48.6%)	11/34 (32.4%)		
Tumor size (Median ± SD) (mm)		45.0 ± 18.9	42.5 ± 13.8	0.753	Mann-Whitney U test
Survival rate		0.72	0.66	0.640	Log-rank test

AJCC, American Joint Committee on Cancer

Table S9. Relationship between clinicopathological factors and *IGF2* LOI.

		LOI	MOI	*p* value	Statistical method
Number of cases		25	14		
Age at diagnosis (Median ± SD)		69	69	0.510	Kruskal-Wallis test
Sex	Male	12 (48 %)	6 (42.9 %)	0.511	Fisher's exact test
	Female	13 (52 %)	8 (57.1 %)		
Tumor location	Right	8 (32 %)	5 (35.7 %)	0.458	
	Left	7 (28 %)	6 (42.9 %)		
	Rectum	10 (40 %)	3 (21.4 %)		
Pathological type	Differentiated	10 (40 %)	6 (42.9 %)	0.563	
	Poorly	15 (60 %)	8 (42.9 %)		
Lymph node metastasis		10 (40 %)	5 (35.7 %)	0.534	
Lymphatic invasion		12 (48 %)	8 (57.1 %)	0.416	
Vascular invasion		8 (32 %)	5 (35.7 %)	0.542	
AJCC cancer stage	I	6 (24 %)	3 (21.4 %)	0.915	
	II	9 (36 %)	6 (42.9 %)		
	III	10 (40 %)	5 (35.7 %)		
Tumor size (Median ± SD) (mm)		40 ± 16.9	46 ± 12.1	0.217	Mann-Whitney U test
Survival rate		0.74	0.92	0.218	Log-rank test

LOI: loss of imprinting, MOI: maintenance of imprinting, AJCC: American Joint Committee on Cancer

Table S10. Primers used in this study.

Analysis	Name of iDMR or gene	Primer name	Primer sequence	Location (GRCh37/hg19)	Total number of CpG sites	Number of analyzed CpG sites
Bisulfite-pyrosequencing for iDMRs	*PPIEL*	PPIEL F	Bio-GTTTAGGATGAGTAGGGTTATGGG	Chr 1 : 40,024,626-40,025,540	5	5
		PPIEL R	ACCCCTTCTTTCCTTAATCT			
		PPIEL S	CTAATACCCAATAAAATAAAACAC			
	ARHI-CG1	ARHI-CG1 F	AACTCCCTCTAACTTCTTTCTCCCTTACCT	Chr 1 : 68,510,575-68,510,716	4	4
		ARHI-CG1 R	Bio-GTTTATAGGGTATTGTTGTTAAAATTTGT			
		ARHI-CG1 S	CTTTCTCCCTTACCTAT			
	ARHI-CG2	ARHI-CG2 F	TGGATTAGTTTTTAGATTGTTGTAGATGT	Chr 1 : 68,511,601-68,511,797	3	3
		ARHI-CG2 R	Bio-CCCCAAAAACTCACTCCTCC			
		ARHI-CG2 S	GGTTAGTTTTTTATAGTTGGT			
	ARHI-CG3	ARHI-CG3 F	AGTTTTGGTTTTAAGGAATAGAAGT	Chr 1 : 68,515,139-68,515,364	5	5
		ARHI-CG3 R	Bio-AACCCAACAACTAACAATAAATATTTTCA			
		ARHI-CG3 S	AAGTTTTATAGGAAGATTAGAG			
	ZDBF2	ZDBF2 F	GGTTTTAAATGATTTTGGGTAGTTTG	Chr 2 : 207,125,719-207,125,922	3	3
		ZDBF2 R	Bio-CCCCTAATAACTTTATCTAACTTCTCT			
		ZDBF2 S	GATTTTGGGTAGTTTGG			
	NAP1L5	NAP1L5 F	AGGGTAGTAATAGGAGGAATTTGGTGTAGT	Chr 4 : 89,618,184-89,619,237	4	4
		NAP1L5 R	Bio-AAAACCCAACTCAAAACCTAAAAAAC			
		NAP1L5 S	GGGAGTTTTTTTAGATTT			
	FAM50B	FAM50B F	GGGTTTTGAGGAGAGTGTTAGG	Chr 6 : 3,849,403-3,849,577	3	3
		FAM50B R	Bio-ACCAAAAACCCCTCCTCCAAAATC			
		FAM50B S	GGAAATAGGAAGTGGAG			
	ZAC	ZAC F	ACCTTAACTTTACCCCCAC	Chr 6 : 144,317,462-144,317,725	7	7
		ZAC R	Bio-GGTTGAATGATAAATGGTAGATGT			
		ZAC S	AACCTCCTCCTACCA			
	GRB10-DMR	GRB10 F	GTTAGGTTTTGGAGTATAATAGGAATT	Chr 7 : 50,848,726-50,851,312	6	6
		GRB10 R	Bio-AATTACCATAAAAACCAAAAATCC			
		GRB10 S	GAATTTTAGGATTAAATTTATGTGA			
	PEG10	PEG10 F	TTGGTTTAGGTGTGGGATTTT	Chr 7 : 94,285,537-94,287,960	5	5
		PEG10 R	Bio-AAACATTCTAAAATACTACTCCATCTC			
		PEG10 S	AGGTGTGGGATTTTATTT			
	PEG1 (*MEST*)	PEG1 F	GTGGTTAGGAGTTTGGTATGTTGA	Chr 7 : 130,130,122-130,134,388	6	5
		PEG1 R	Bio-AAACCCACCACCAAACTAAT			
		PEG1 S	GTTGTTGTAAAGGAAATTT			
	LOC728024	LOC728024 F	GGTATGGTTTTTAGGAGTAATTTGA	Chr 8 : 37,604,992-37,606,088	8	7
		LOC728024 R	Bio-AACCTATAACCCTAAACTAATAACTT			
		LOC728024 S	GAAAAATTTTAAGTAAAGAAGAGGG			
	TRAPPC9	TRAPPC9 F	Bio-TTTTGTTGGTAGGGTTGTGT	Chr 8 : 141,108,147-141,111,081	4	4
		TRAPPC9 R	TCATCCTCAAAACCCTATCACC			
		TRAPPC9 S	AAACCTAAATACAAAATCC			
	H19-promoter	H19-Promoter F	GTTTGGGAGAGTTTGTGAGG	Chr 11 : 2,015,729-2,015,932	4	4
		H19-Promoter R	Bio-CCCCAAACCCATTCCCATCCAATTAAC			
		H19-Promoter S	GTTTATAGTTTGTTAGTAGAGTG			
	H19-DMR	H19DMR F	TGGGTATTTTTGGAGGTTTTTTT	Chr 11 : 2,019,871-2,024,740	4	4
		H19DMR R	Bio-ATAAATATCCTATTCCCAAATAA			
		H19DMR S	GTTTYGGGTTATTTAAGTTA			
	IGF2-DMR2	IGF2-DMR2 F	Bio-GGTTTTGGGTGGGTAGAGT	Chr 11 : 2,153,991-2,155,112	5	5
		IGF2-DMR2 R	CCCCAAATACCCCCTAAACAAATTCTTC			
		IGF2-DMR2 S	CCTACCTACCCTCCT			
	IGF2-DMR0	IGF2-DMR0 F	TGAGGATGGGTTTTTGTTTGGTAT	Chr 11 : 2,168,333-2,169,768	3	3
		IGF2-DMR0 R	Bio-TCCTCAATCCACCCAAAATAATAT			
		IGF2-DMR0 S	AAAAGTTATTGGATATATAGT			
	*Kv*DMR1	KvDMR1 F	AGGGAAGTTTTAGGGTGTGAATTTTTAGAG	Chr 11 : 2,719,948-2,722,259	6	6
		KvDMR1 R	Bio-CCAAACCACCCACCTAACAAAAAAC			
		KvDMR1 S	TGGTAATGTTTGGTATTT			
	RB1	RB1 F	GGTAGGGTAGTTTTGGAAATGTTTAAG	Chr 13 : 48,892,341-48,895,763	6	6
		RB1 R	Bio-AACCACAAACCCTTACCC			
		RB1 S	AGTTTTGGAAATGTTTAAGAT			
	MEG3	MEG3-CG7 F	GTTAGGTAGGGTGAATTTAGGTATAATGTGTG	Chr 14 : 101,290,524-101,293,978	7	7
		MEG3-CG7 R	Bio-AACAACCTCTAACTTACATCTAAAAACCAATT			
		MEG3-CG7 S	ATGGTTAAGGTGGGGTTG			
	MEG8	MEG8 F	GAGGGGGATAGTTAAGAGGGA	Chr 14 : 101,370,741-101,371,419	7	7
		MEG8 R	Bio-ACAACTCCCCCAACCTACTACATTACA			
		MEG8 S	TTGGTAGAGGAGTTTTTAATTG			
	MAGEL2	MAGEL2 F	GTTAATTGGAGGTGGATTTTAAGG	Chr 15 : 23,892,425-23,894,029	5	5
		MAGEL2 R	Bio-AAACAACCACCTAAACATTCTCTTCTCTC			
		MAGEL2 S	GAATAGTAGGGAGGTTATAGATAGG			
	NDN	NDN F	GTAGGGTTTTTGAGTTTAGGAGTTTTT	Chr 15 : 23,931,451-23,932,759	7	6
		NDN R	Bio-AATCCCTCTCCCAACAAATAAAACCTC			
		NDN S	GATTTTTGGAGAGGAAG			
	SNRPN	SNRPN F	GGGAGGGAGTTGGGATTTTTG	Chr 15 : 25,200,004-25,201,976	7	7
		SNRPN R	Bio-AAACCACCCACACAACTAACCTTACCC			
		SNRPN S	AGTTGGGATTTTTGTATTG			
	IGF1R	IGF1R F	Bio-TAAGGAGGGGTTGGTTGGAG	Chr 15 : 99,408,496-99,409,650	6	6
		IGF1R R	AACCCCACTCCCTTTTCTAT			
		IGF1R S	CCCAACCTAACCTAAAACCAC			
		ZNF597(2) F	ATGTAGTGGATATGGTTAGGTATATG			

	ZNF597 (3')	ZNF597(2) R ZNF597(2) S	Bio-ATCTCCAACTTAACCACCAACTA ATAGTTTATTTGTTTTAGGAATG	Chr 16 : 3,481,801-3,482,388	5	5
	ZNF597 (TSS)	ZNF597 F ZNF597 R ZNF597 S	GGAGGGGGTTAGGTAGAG Bio-ATCCCTTTAAAAACTATTCTCTCC AGGTATTTAGATTTATTTGGGTT	Chr 16 : 3,492,828-3,494,463	5	5
	ZNF331 (pro)	ZNF331 F ZNF331 R ZNF331 S	Bio-AGGGATTAGGAAGGGTTTAGT CCCAAACCCCCTATTCCAACATACAAC CCCAAACAAAAACCTC	Chr 19 : 54,040,510-54,042,212	5	5
	ZNF331 (int)	ZNF331(2) F ZNF331(2) R ZNF331(2) S	GTTGGGTGAGGGAGGTTTT Bio-CCCCATCACCCCCAATAA GGTGAGGGAGGTTTTTT	Chr 19 : 54,057,086-54,058,425	5	5
	PEG3	PEG3 F PEG3 R PEG3 S	GGTGGTTTTAGGTTAGTTAGAAAGG Bio-ACCAAACTATAAATAATTAATACCTTTT AGATTTTGTAGTAGTTTTTTAGATT	Chr 19 : 57,348,493-57,353,271	5	5
	USP29	USP29 F USP29 R USP29 S	TTTTTAGAGGGAGAGATGGAAGTTGG Bio-ACCACAAACCCCCAAATCTTAAAAAA TGATTGTATTTGGGTTT	Chr 19 : 57,629,548-57,631,498	6	6
	L3MBTL	L3MBTL-CG3 F L3MBTL-CG3 R L3MBTL-CG3 S	TATGAGGAGAAGAGAGGGTTATGGTAT Bio-AAAACCCAACTCAAAACCTAAAAAAC GGGAGTAGTAATTTTTAGATTTTTT	Chr 20 : 42,142,365-42,144,040	5	5
	NESP55	NESP55 F NESP55 R NESP55 S	TTTTTTTTGGGGTTTTGGGGTTTTT Bio-AACAAACCTTAAACTATCCCTCCCC TGGAGTGTTTGGGTATTA	Chr 20 : 57,414,039-57,418,612	7	7
	NESPAS-GNASXL	NESPAS-GNASXL F NESPAS-GNASXL R NESPAS-GNASXL S	GGATATGGGTGGGAGGTTTAA Bio-CCCTAAAACCCCACCTCTC GGGTGGGAGGTTTAATA	Chr 20 : 57,425,649-57,428,033	5	5
	GNAS1A	GNAS 1A F GNAS 1A R GNAS 1A S	TGTTGAAGATGGTTATGAAGTTTAAAGTT Bio-TATCCCAATCAACCCAAACCCTACTC AAGTTTAGGAGGAGGTT	Chr 20 : 57,463,265-57,465,201	8	8
	GNASXL	GNASXL F GNASXL R GNASXL S	ATGAAGGGGTGGTTAGTAG Bio-CTCCCCCAAAAATACCTTCTTAACCTT GGATGTTTTAGTTGGTTTTAGTA	Chr 20 : 57,428,905-57,431,463	6	6
	WRB	WRB F WRB R WRB S	TTGGAGGGGGTTGAGGGTTTA Bio-TACCAATCCTAAAACACCTATACAATAC GGGTTGAGGGTTTAT	Chr 21 : 40,757,510-40,758,276	5	5
	NHP2L1	NHP2L1 F NHP2L1 R NHP2L1 S	Bio-GGATGTTTAGTTTTTAAGAGTAGGAAGTG CCCAACCCCCTTCCTTTAA CCTAATATACCAACTAACCCTAA	Chr 22 : 42,077,774-42,078,873	4	4
Bisulfite-pyrosequencing for CIMP markers	*hMLH1*	hMLH1 F hMLH1 R hMLH1 S	TTGATTGGTATTTAAGTTGTTTAATT Bio-CCAATTCTCAATCATCTCTTTAATA AGTTATAGTTGAAGGAAGAA	Chr 3 : 37,034,823-37,107,380	3	3
	MINT1	MINT1 F MINT1 R MINT1 S	GGTTTTTTGTTAGYGTTTGTATTT Bio-ATTAATCCCTCTCCCCTCTAAACTT TTTAGTAAAAATTTTTTGGG	Chr 5 : 75,378,997-75,649,764	3	3
	MINT2	MINT2 F MINT2 R MINT2 S	AGTGTTAGAAAAATGTGTTG Bio-CTACAATTAAACATCAATTATAT GAATTTTAGTATTTAAGTT	Chr 2 : 58,654,934-59,290,901	3	3
	MINT31	MINT31 F MINT31 R MINT31 S	GTTTAGGGGTGATGGTTTTAGT Bio-AAAACACTTCCCCAACATC GGTGATGGAGGTTAT	Chr 17 : 48,633,568-48,639,469	4	4
	p16	p16 F p16 R p16 S	GGTTGTTTTYGGTTGGTGTTTT Bio-ACCCTATCCCTCAAATCCTCTAAAA GGAGTTAATAGTATTTTT	Chr 9 : 21,967,751-21,995,300	4	4
Bisulfite-pyrosequencing for LINE-1 methylation	LINE-1	LINE-1 F LINE-1 R LINE-1 S	TTTTGAGTTAGGTGTGGGATATA Bio-AAATCAAAAAATTCCCTTTC AGTTAGGTGTGGGATATAGT		4	4
KRAS mutation analysis	*KRAS* exon2	KRAS F1 KRAS R1	GGTGAGTTTGTATTAAAAGGTACTGG CCTTTATCTGTATCAAAGAATGGTC			
	KRAS exon3	KRAS F2 KRAS R2	CCAGACTGTGTTTCTCCCTTC GCATGGCATTAGCAAAGACTC			
Pyrosequencing for BRAF (V600E) mutation analysis	*BRAF*	BRAF F BRAF R BRAF S	ATGCTTGCTCTGATAGGAA Bio-GCATCTCAGGGCCAAA GGTGATTTTGGTCTAGCTAC			
Genotyping of *IGF2* (rs680)	*IGF2*	IGF2 P2-2 IGF2 P5-2	GGACTTTGAGTCAAATTGGC GGGTTGTTGCTATTTTCGGA			
Genotyping of *H19* (rs2839702)	*H19*	H19 331 H19 332	CGGACACAAAACCCTCTAGCTTGGAAATGA AATGGAATGCTTGAAGGCTGCTCCGT			
Pyrosequencing for allelic-specific expression analysis	*IGF2*	IGF2-allele F IGF2-allele R IGF2-allele S	Bio-GGACTTTGAGTCAAATTGGC GGGTTGTTGCTATTTTCGGA GTGCCCACCTGTGATTTCTG			
	H19	H19-allele F H19-allelle R H19-allele S	Bio-CGGACACAAAACCCTCTAGCTTGGAAATGA GCGCTGCTGTTCCGATGGTG GGCTGATGAGGTCTGGTTCC			

F: forward primer, R: reverse primer, S: sequence primer, Bio: biotinylated primer

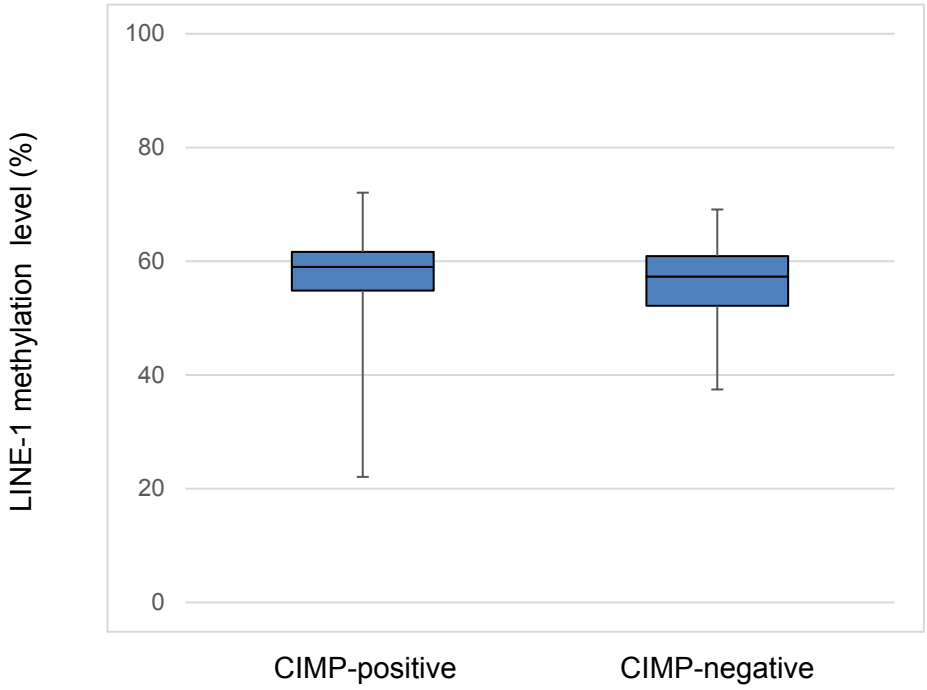

Figure S1. Non-relationship between CIMP status and LINE-1 methylation.

LINE-1 methylation in CIMP-positive tumors (median: 59.0%, ranging from 22.1 to 72.1%) was not significantly different from that in CIMP-negative tumors (median: 57.3%, ranging from 37.5 to 69.1%) (p = 0.235, Mann-Whitney U test).