Table 6. Epigenetic and genetic alterations in 97 CRC patients

Marker	Chr. location	Function	Methylation assay	Mean Methylation level, %	Cases with methylation ≥15%, % of total cases
Classical CIMP markers					
MINT1	5q13-14	SV2C, synaptic vesicle glycoprotein 2C	MCA		38 (39.2)
MINT2	2p22-21	Unknown	MCA		42 (43.3)
MINT27	10q11.22	SYT15 (synaptotagmin XV)	MCA		51 (52.6)
MINT12	7q31-32	Unknown	MCA		35 (36.1)
MINT31	17q21	An island 2kb upstream of CACNA1G	MCA		39 (40.2)
MINT17	12q24.22	HRK (apoptosis regulator)	MCA		28 (28.9)
Type-C genes (genes methylated in cancer only)					
p14	9p21	P53 pathway	COBRA	7.4	21 (21.7)
MLH1	2p22	Mismatch repair	COBRA	8.8	17 (17.5)
THBS1	15q14	Angiogenesis inhibitor	COBRA	2.0	5 (5.2)
THBS2	6q	Angiogenesis inhibitor	COBRA	12.1	37 (38.1)
MGMT	10q26	DNA repair	COBRA	20.6	41 (43.6)
COX2	1q25.2	Cyclooxygenase-2	COBRA	3.3	10 (10.3)
Megalin	1q21.1	phosphodiesterase 4D interacting	COBRA	11.0	30 (30.9)
RIZ1	1p36	Transcription/RB1	MSP	7.3	14 (14.4)

Marker	Chr. location	Function	Methylation assay	Mean Methylation level, %	Cases with methylation ≥15%, % of total cases
p16	9p21	Cell cycle	Pyrosequencing	11.2	22 (23.7)
RASSF1A	3p21.31	RAS association domain family 1A	Pyrosequencing	8.4	16 (17.0)
DAPK	9p34.1	Death associated protein kinase	Pyrosequencing	5.0	8 (8.7)
TIMP3	22q12.1	Metastasis suppressor	Pyrosequencing	16.8	35 (36.1)
hTERT	5p15.33	Telomerase reverse transcriptase	Pyrosequencing	12.9	35 (36.1)
Neurog1	5q31.1	Neurogenin 1	Pyrosequencing	25.3	49 (51.6)
SOCS1	16p13.13	Suppressor of cytokine signaling1	Pyrosequencing	9.5	18 (19.6)
RUNX3	1p36.11	Runt-related transcription factor 3	Pyrosequencing	8.9	20 (21.3)
Type-A genes (genes methylated in both normal and cancer)					
ER alpha	6q25.1	Estrogen receptor	Pyrosequencing	34.1	84 (87.5)
MyoD1	11p15.4	Muscle cell differentiation	Pyrosequencing	39.6	86 (92.5)
N33	8p22	Oligo-saccharyl-transferase	Pyrosequencing	42.4	88 (96.7)
SFRP1	8p12	Secreted frizzled-related protein 1	Pyrosequencing	52.7	92 (98.9)
HPP1	2q32.3	Transmembrane receptor	Pyrosequencing	35.1	76 (87.4)
Genetic					
Genetic Alterations					
BRAF mutant	7q34	serine/threonine-protein kinase	Pyrosequencing		11 (12.6)
KRAS mutant	12p12.1	small GTPase superfamily	MASA*		43 (45.7)
P53 mutant	17p13.1	Nuclear protein, cell cycle	SSCP[#]		44 (47.3)

Marker	Chr. location	Function	Methylation assay	Mean Methylation level, %	Cases with methylation ≥15%, % of total cases
MSI-H		Microsatellite instability-High			22 (22.7)

Chr., Chromosome. *, MASA: mutant allele-specific PCR amplification; #, SSCP: single-strand conformation polymorphism