

Supplemental Table 1. CpG loci are hyper-methylated in SSA/Pa on both the left and right anatomic sides of the bowel.

Probe ID	Gene	Feature	SSA Left	SSA Right	logFC	BH-corrected
			mean	mean		P-value
cg00803088	<i>RET</i>	Body - island	0.49	0.51	0.019	0.96
cg02120582	<i>PDGFD</i>	5'UTR - island	0.49	0.45	-0.033	0.89
cg02485200	<i>JAM2</i>	1stExon - island	0.38	0.44	0.063	0.88
cg03394150	<i>GSG1L</i>	Body - island	0.50	0.51	0.0049	0.99
cg03401096	<i>MIR4493</i>	IGR - island	0.54	0.52	-0.023	0.88
cg03735888	<i>ZNF132</i>	TSS200 - island	0.45	0.40	-0.047	0.92
cg04657205	<i>MIR1233-1</i>	IGR - island	0.38	0.47	0.087	0.88
cg07155336	<i>NTNG1</i>	5'UTR - island	0.40	0.52	0.12	0.81
cg09528825	<i>GSG1L</i>	Body - island	0.49	0.49	-0.0033	0.99
cg14553600	<i>JAM2</i>	1stExon - island	0.41	0.46	0.051	0.89
cg18456523	<i>MCIDAS</i>	IGR - island	0.49	0.56	0.076	0.88
cg20680720	<i>ZNF568</i>	TSS200 - island	0.36	0.43	0.067	0.90
cg21101720	<i>ANKRD13B</i>	Body - island	0.55	0.53	-0.021	0.97
cg22830113	<i>BIN1</i>	IGR - island	0.41	0.55	0.14	0.78
cg24979348	<i>RERG</i>	5'UTR - island	0.35	0.40	0.050	0.93

Benjamini-Hochberg (BH), difference in log odds of methylation (logFC)

Supplemental Table 2. Dysregulated CpG loci differ by CIMP status in The Cancer Genome Atlas (TCGA) data.

Probe ID	Gene	P-value	
		CIMPL vs. CIMP	non-CIMP vs. CIMP
cg00803088	<i>RET</i>	0.0301	< 2e-16
cg02120582	<i>PDGFD</i>	0.00221	5.80E-11
cg02485200	<i>JAM2</i>	0.000672	< 2e-16
cg03394150	<i>GSG1L</i>	0.537	9.81E-09
cg03401096	<i>MIR4493</i>	0.004	1.72E-08
cg03735888	<i>ZNF132</i>	0.171	9.24E-09
cg04657205	<i>MIR1233-1</i>	1.30E-13	< 2e-16
cg07155336	<i>NTNG1</i>	1.20E-05	< 2e-16
cg09528825	<i>GSG1L</i>	0.436	6.94E-09
cg14553600	<i>JAM2</i>	0.00997	3.83E-14
cg18456523	<i>MCIDAS</i>	0.000398	1.24E-06
cg21101720	<i>ANKRD13B</i>	0.847	0.671
cg22830113	<i>BIN1</i>	9.98E-11	< 2e-16
cg24979348	<i>RERG</i>	6.23E-06	9.10E-15