

**Supplementary Table 1.** Tumor Suppressor Genes That Are Frequent Targets of Hypermethylation in CRC

Gene	Methylation frequency (%) in CRC	Function
<i>ALX4</i>	60–70	Homeobox gene
<i>APC</i>	10–30	Wnt signaling
<i>AXIN2</i>	5–10	Wnt signaling
<i>BMP3</i>	70	Bone and cartilage formation
<i>BNIP3</i>	65–70	Apoptosis
<i>CACNA1G<sup>a</sup></i>	20–35	calcium metabolism
<i>CDH1</i>	30–55	Cell adhesion
<i>CDH13</i>	50–60	Cell adhesion
<i>CDKN2A<sup>INK4a</sup> (p14)</i>	10–30	Cell cycle
<i>CDKN2A<sup>A-INK4b</sup> (p15)</i>	30–65	Cell cycle
<i>CDKN2A<sup>ARF</sup> (p16)</i>	20–30	Cell cycle
<i>CDX1</i>	100	Homeobox gene
<i>CHFR</i>	63	Cell cycle
<i>DAPK1</i>	40–50	Apoptosis
<i>DCC</i>	50–60	Axonal guidance
<i>DKK1</i>	10–15	Wnt signaling
<i>EGFR</i>	40–50	Cytokine signaling
<i>EYA2</i>	60–70	Development
<i>EYA4</i>	81	Development
<i>GATA4</i>	70	Transcription factor
<i>GATA5</i>	79	Transcription factor
<i>HIC1</i>	50–80	Transcriptional repressor
<i>HLTF</i>	30–50	Transcription factor
<i>HPP1</i>	60–80	Hyperplastic polyposis
<i>IGF2<sup>a</sup></i>	100	Cell growth
<i>IGFBP3</i>	29	Hormonal signaling
<i>KLF4</i>	25	Transcription factor
<i>MGMT</i>	30–60	DNA repair
<i>MLH1</i>	10–20	Mismatch repair
<i>MMP2</i>	60–70	Protease
<i>MYOD1</i>	>90	Transcription factor
<i>NDRG4</i>	70–85	Putative tumor suppressor gene
<i>NEUROG1<sup>a</sup></i>	20–65	Putative tumor suppressor gene
<i>RAR<math>\beta</math>2</i>	10–40	MAPK signaling
<i>RASSF1A</i>	30–55	RAS signaling
<i>RASSF2A</i>	70	RAS signaling
<i>RUNX3<sup>a</sup></i>	20–35	Transcription factor
<i>SFRP1</i>	82	Wnt signaling
<i>SFRP2</i>	60–90	Wnt signaling
<i>SOCS1<sup>a</sup></i>	20–30	Cytokine signaling
<i>TFAP2E</i>	51	Transcription factor
<i>TIMP3</i>	20–30	ECM component
<i>TWIST1</i>	63	Transcription factor
<i>UNC5C</i>	70–80	Axonal guidance
<i>Vimentin</i>	50–80	Epithelial–mesenchymal transition
<i>WNT5a</i>	48	Wnt signaling

<sup>a</sup>CIMP marker as proposed by Weisenberger et al, 2006.