

Figure W1. Coomassie-stained membranes used to ensure equal quantity of protein sample loading for Western blot analysis shown in Figure 2A.

Table W1. Primer Sequences Used in the Study.

	Sequence	Size (bp)	T_m (°C)
ChIP-PCR			
<i>ADAM19</i> promoter	F: TCACCTCTGAGTGTACCCAAAG R: GATTGTGGTGGACGCGG	133	60
<i>ADAM19</i> exon	F: TTTGTTCCCACGTTCTGCG R: GAACGGCGGAAAGAGAAGC	150	60
<i>ADAM19</i> intron	F: GCTCCATGGGAGCAGTATTCAT R: AGGCCAGGCTAGAGATATGCTG	141	60
RT-PCR			
<i>SMAD4</i>	F: GTCTTTGATTTGCGTCAGTGTTCAT R: CAGCTGACAGACTGATAGCTGGAG	151	60
<i>TGFBR1</i>	F: AGTTAAGGCCAAATATCCCAAACAG R: CCTAGCTGCTCCATTGGCAT	101	59
<i>TGFBR2</i>	F: ATTCCAGCTTCTGGCTCAAC R: CTCACTGAAGCGTTCTGCCAC	123	60
<i>ADAM19</i>	F: CAAGCTGAGGCAACAGTTCAGT R: CGCAGGATTTCCGGAGTGT	132	60
<i>GAPDH</i>	F: CCCCTTCATTGACCTCAACTACAT R: CGTCTCTGAAGATGGTGA	135	60
Bisulfite sequencing			
<i>ADAM19</i> promoter	F: AGAGGGGTTTAGTTTAATTTTGAAG R: CTCAACCATACTACCCACTACCC	340	60
<i>ADAM19</i> exon	F: GGGTAGTGGGTAGGTATGGTTGAG R: CRA CCTCTACCACCTCCAAAAC	347	60
MSP			
<i>ADAM19</i>	MF: AAGGCGTTTGGTATAGTGC MR: AACGCGACCTATAAAAAATCG UF: TTAAAGGTGTTTGGTATAGTGT UR: AACACAACCTATAAAAAATCAAAA	101	60
<i>ADAM19</i>	MF: AAGGCGTTTGGTATAGTGC MR: AACGCGACCTATAAAAAATCG UF: TTAAAGGTGTTTGGTATAGTGT UR: AACACAACCTATAAAAAATCAAAA	101	60
<i>SMAD4</i> mutation			
Exon 9	F: TATTAAGCATGCTATACAATCTG R: CTTCCACCCAGATTTCAATTC seq: TTTTGACAACAAATAGAGCTTTAAGTC	330	58
Exon 11	F: CCAAAAAGTGTGCAGCTTGTTG R: CAGTTTCTGTCTGCTAGGAG seq: TATTTGTAGTCCACCATC	554	58

Table W2. Mutations in *SMAD4* in Ovarian Cancer Cell Lines.

	IOSE	SKOV3	MCP3	MCP2	A2780	CP70
Exon 9	N	N	N	N	Codon 404 (TA insertion)	N
Exon 11	N	Intron/T to C	N	N	N	N

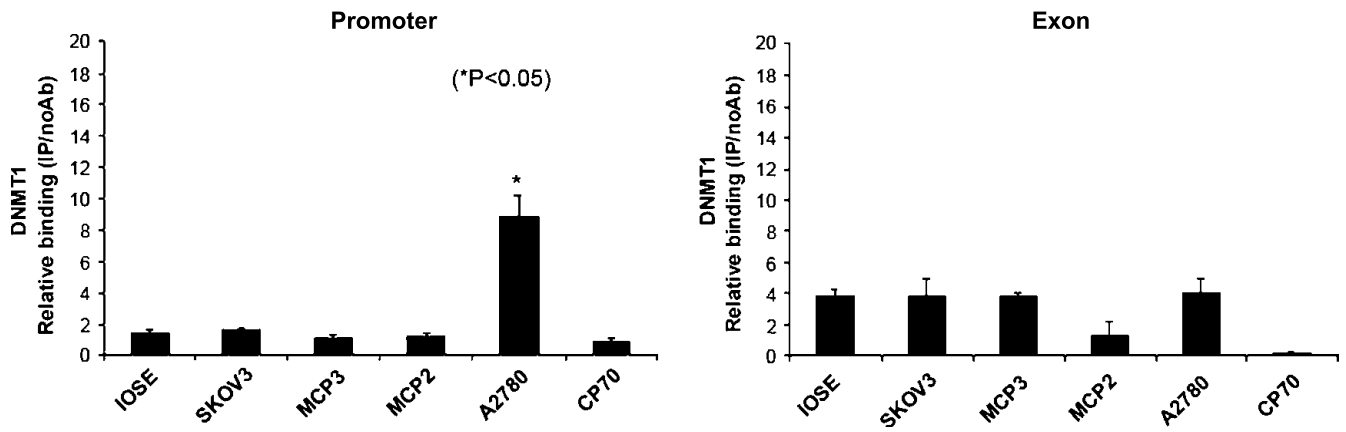


Figure W2. Chromatin immunoprecipitation–PCR analysis of *ADAM19* in ovarian cancer cells. Chromatin immunoprecipitation assays were performed with antibodies directed against DNA methyltransferase 1 (DNMT1; primers used to amplify two regions of *ADAM19* are shown in Figure 2A). The relative binding of each antibody to the corresponding region was measured by quantitative PCR. Error bar indicates SD calculated from triplicates. * $P < .05$.