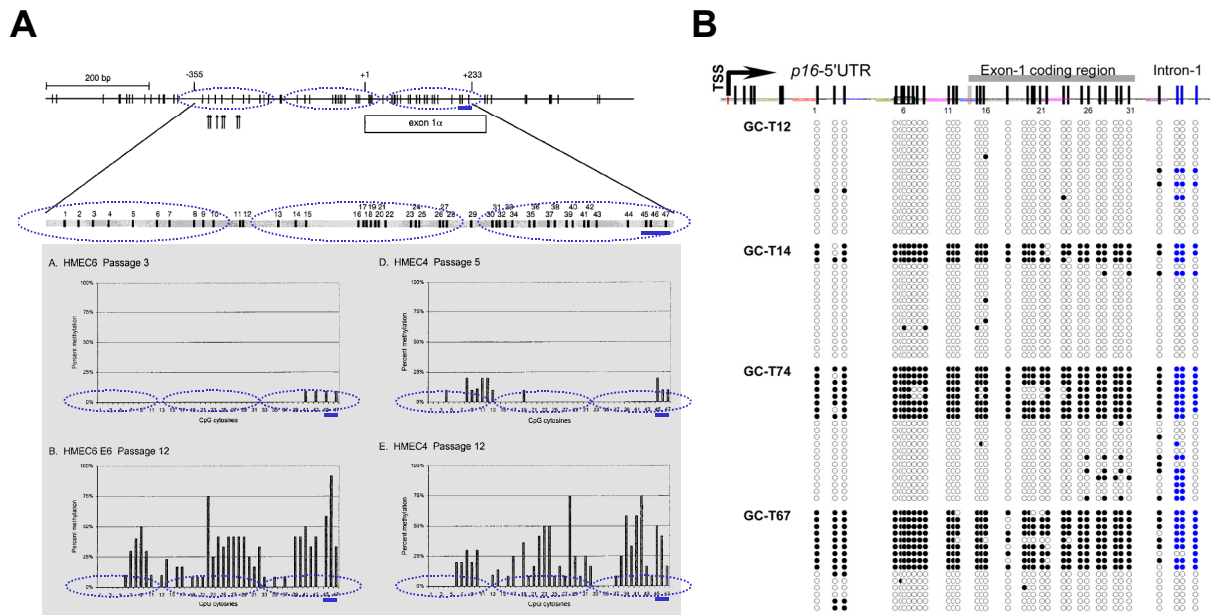
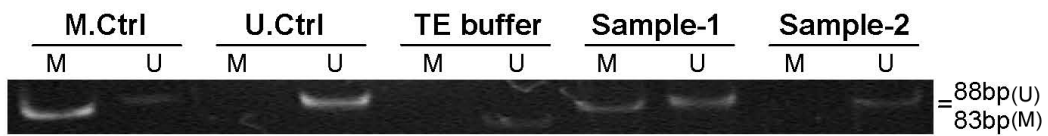


**Table S1.** *p16* Primer sets of quantitative PCR for nucleosome positioning

	<b>Primer sequence (5'→3')</b>	<b>Amplicon size (bp)</b>
Primer-1	F: taggg ggaca ctttc tagtc gtaca gg R: ggtgt ttggt gtcac aggga aa	130
Primer-2	F: ttcc ctatg acacc aaaca cc R: gcgtg ttga gtgcg ttcac tctg	119
Primer-3	F: agtga acgca ctaa acacg c R: gttgg caagg aagga ggact	119
Primer-4	F: agtcct ccttc cttgc caac R: tccga gcact tagcg aatgt g	114
Primer-5	F: acttc agggg tgcca cattc R: accct gtccc tcaaa tectct	124
Primer-6	F: tcccc ttgcc tggaa agata c R: ccacc ctctgg tgacc agc	121
Primer-7	F: caccg gaga agaa agagg a R: ccggc tccat gctgc tc	122
Primer-8	F: agagg gggag agcag gca R: cgccc gcacc tectc tac	127
Primer-9	F: ggggt cgggt agagg aggt R: tgctc ccgct gcaga ccct	113



**Figure S1. Results from bisulfite clone sequencing of the *p16* CpG islands.** (A) The dynamic methylation status of individual CpG site in the whole *p16* CpG island during the immortalization of human mammary epithelial cell strains by stably HPV16 E6/E7 transfection as previously reported [14]. The information of nucleosome positioning (blue dash-line ovals) obtained in the present study was integrated into the published chart. Three seeding methylation sites were under-blue-lined. (B) The methylation status of the 392bp fragment of the *p16* CpG island in primary gastric carcinoma samples as previously reported [29]; Black dots (●) represent methylated-CpG sites open dots (○) represent unmethylated-CpG sites, blue dots (●) represent methylation at the three seeding methylation sites in intron-1. Each black bar represents a CpG site. TSS, transcription start site; the gray vertical bar, translation start site (atg).



		83bp MSP	
		(+)	(-)
sMSP	(+)	<b>33</b>	<b>22</b>
	(-)	<b>1</b>	<b>5</b>

( $p < 0.04$ )

**Figure S2. Results of sMSP were confirmed with those of the 83bp-MSP assay.** The top panel shows the number of PCR products that exhibited methylated- and unmethylated-*p16* of two representative GC samples as determined using the 83bp-MSP assay. The lower panel compares the detection of methylated-*p16* in 61 gastric tissue samples using the 83bp-MSP and sMSP assays. The table indicated that the results of the 83bp-MSP correlated with those of sMSP significantly ( $p < 0.04$ ).