

Supplementary Table 1. Short Tandem Repeat Profiles of the Gastric Cancer Cell Lines

	D3S1358	vWA	FGA	Amelogenin	TH01	TPOX	CSF1P0	D5S818	D13S317	D7S820
AGS	15,2	16,17	23,24	X	6,7	11,12	11,12	9,12	12	10,11
MKN-1	15,17	16	20,23	X	9	8	9,12	11	10,12	10
MKN-45	15,16	19	19	X	7	8	12	10,11	8,11	10,11

Supplementary Table 2. The Individual Primers and Probes for the MethyLight Assay

Gene	Primer/probe	Sequence (5'→3')	Product length, bp	Annealing T _m , °C
<i>miR-200a</i>	Forward primer	CCCTATCCGATCCCGACACC	20	59.5
	Reverse primer	AGGGACGTGGGGTTTCGTTA	20	59.1
	Probe	CCTAACTACTACCGCTCCGATTCTTCCC	29	67.5
<i>miR-200b</i>	Forward primer	AGTGTTTTAGGAGGACGAGGTTT	23	58.3
	Reverse primer	ATACTACCCAATAAAATAACCACGACTA	28	58.0
	Probe	CCGAACTAAATCCGAAAACCGCCCGA	26	66.7

T_m, melting temperature.

Supplementary Table 3. Expression and Promoter Methylation Levels of *miR-200a/b* According to the Subtypes of Gastric Cancer

Type	No.	<i>miR-200a</i>				<i>miR-200b</i>			
		Relative expression	p-value	Promoter methylation	p-value	Relative expression	p-value	Promoter methylation	p-value
Tumor differentiation									
WD	28 (70.0)	0.07 (0.04–0.10)	0.737	40.17 (29.20–59.30)	0.046	0.14 (0.02–0.25)	0.300	22.43 (42.48–12.65)	0.280
MD	9 (22.5)	0.10 (0.05–0.15)		28.40 (18.53–68.07)		0.12 (0.04–1.85)		14.99 (4.50–74.86)	
PD	3 (7.5)	0.07 (NA)		90.03 (NA)		0.01 (NA)		63.71 (NA)	
Gross appearance									
Elevated	4 (10.0)	0.07 (0.03–0.25)	0.450	39.43 (31.01–45.61)	0.671	0.19 (0.03–0.44)	0.979	14.79 (11.38–41.19)	0.469
Flat	7 (17.5)	0.12 (0.03–0.49)		39.12 (24.14–43.98)		0.13 (0.07–0.24)		13.96 (5.03–52.27)	
Depressed	29 (72.5)	0.07 (0.04–0.10)		43.59 (24.71–65.15)		0.10 (0.02–0.39)		28.82 (13.34–46.24)	
Lauren classification									
Intestinal type	39 (97.5)	0.07 (0.04–0.12)	0.722	40.04 (24.43–58.84)	0.528	0.13 (0.02–0.28)	0.595	22.73 (11.10–46.43)	0.718
Diffuse type	1 (2.5)	0.07 (NA)		62.34 (NA)		0.01 (NA)		22.37 (NA)	
Tumor size, cm									
≤1	11 (27.5)	0.05 (0.03–0.12)	0.696	39.12 (17.53–55.18)	0.394	0.07 (0.02–0.24)	0.721	20.29 (3.96–35.93)	0.363
1–2	16 (40.0)	0.08 (0.05–0.18)		47.90 (26.81–68.19)		0.19 (0.01–0.30)		19.82 (14.09–45.57)	
>2	13 (32.5)	0.07 (0.04–0.12)		40.02 (29.37–55.62)		0.12 (0.02–0.36)		31.55 (12.31–56.21)	
Depth of invasion									
Mucosa	37 (92.5)	0.07 (0.04–0.12)	0.709	42.14 (28.72–61.42)	0.111	0.13 (0.02–0.28)	0.651	22.37 (11.66–48.08)	0.514
Submucosa	3 (7.5)	0.10 (NA)		19.53 (NA)		0.09 (NA)		31.55 (NA)	

Data are presented as the number (%) or median (interquartile range).

WD, well differentiated adenocarcinoma; MD, moderately differentiated adenocarcinoma; PD, poorly differentiated adenocarcinoma; NA, not applicable.

Supplementary Table 4. The Promoter Methylation Levels of *miR-200a/b* in the *Helicobacter pylori*-Negative Controls, *H. pylori*-Positive Controls, and *H. pylori*-Positive Gastric Cancer Group

	<i>H. pylori</i> -negative controls (n=20)	<i>H. pylori</i> -positive controls (n=20)	<i>H. pylori</i> -positive gastric cancer patients (n=40)
<i>miR-200a</i>	11.5 (3.0–27.9)	28.4 (8.2–49.2)	40.3 (6.4–100.0)
<i>miR-200b</i>	9.9 (3.0–23.5)	15.3 (3.3–25.5)	22.6 (2.8–100.0)

Data are median (ranges) of percentage of methylated reference.

A

1,167,755 CCGCCAGCCC TGTCCGGTCC CGGCACCACC
1,167,785 CCTGGCTGCT CACCGCTCCG GTTCTTCCCT
1,167,815 GGGCTTCCAC AGCAGCCCT GCCTGCCTGG
1,167,845 CGGGACCCCA CGTCCCTCCC GGGCCCCTGT
1,167,875 GAGCATCTTA CCGGACAGTG CTGGATTTC

B

1,167,015 TGCCTCAGT GCCCCAGGAG GACCGAGGCC
1,167,045 CCCAGCTACT DADCTTCCCA GCGAGTCCCA
1,167,075 TGCAACCCTC AGCCGGGCGG CCCCCGGACC
1,167,105 CAGCTCGGC AGCCGTGGCC ATCTTACTGG
1,167,135 GCAGCATTGG ATGGAGTCAG GTCTTAATA

Supplementary Fig. 1. The sequences of the promoter CpG island region of (A) *miR-200a* and (B) *miR-200b*. The binding sites of the forward and reverse primers were boxed with solid line, and the binding sites of the probe were boxed with dotted line. In this study, methylation status of six CpG sites in the promoter region was analyzed for both *miR-200a* and *miR-200b*, which were highlighted as bold and underline.