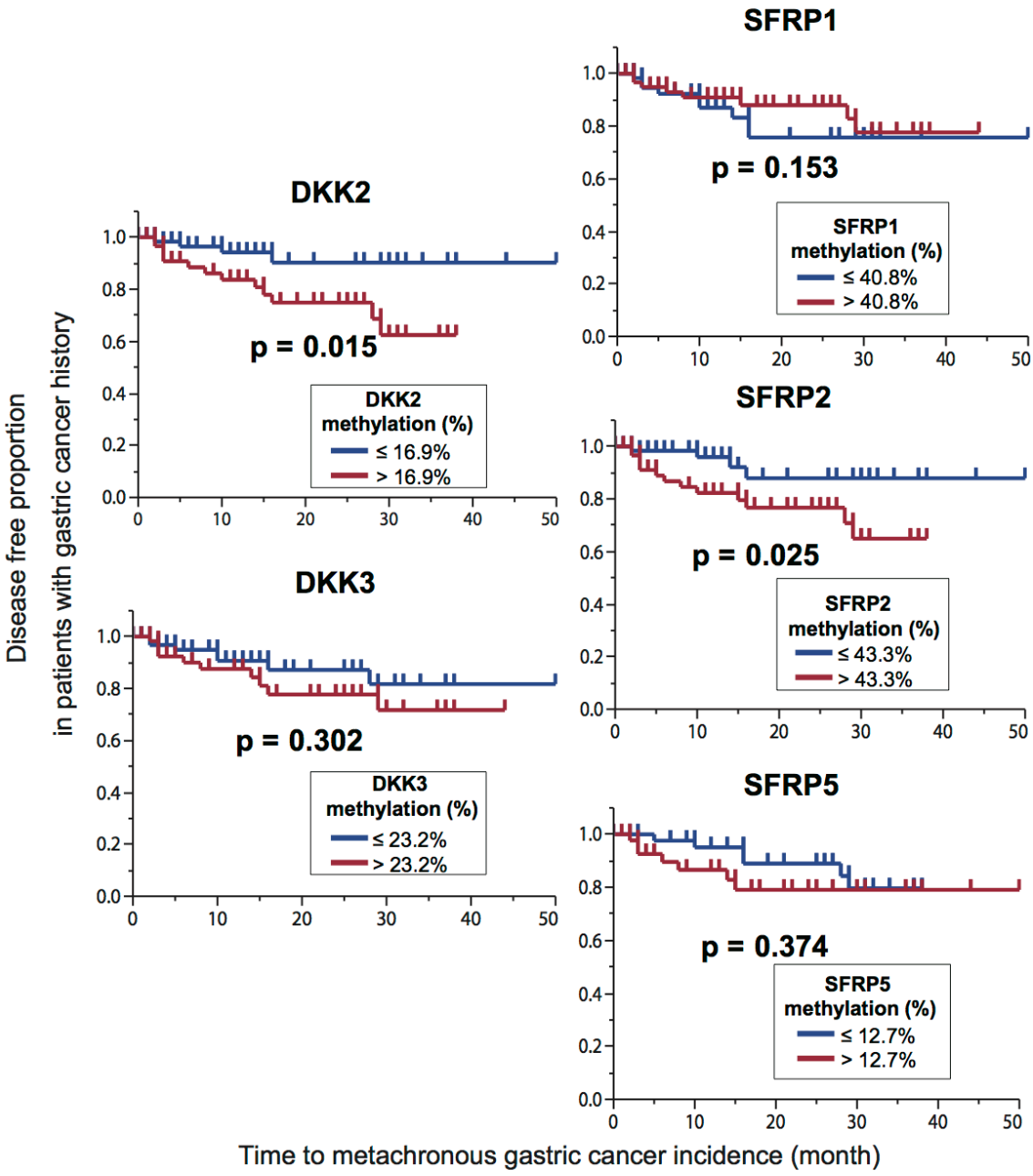
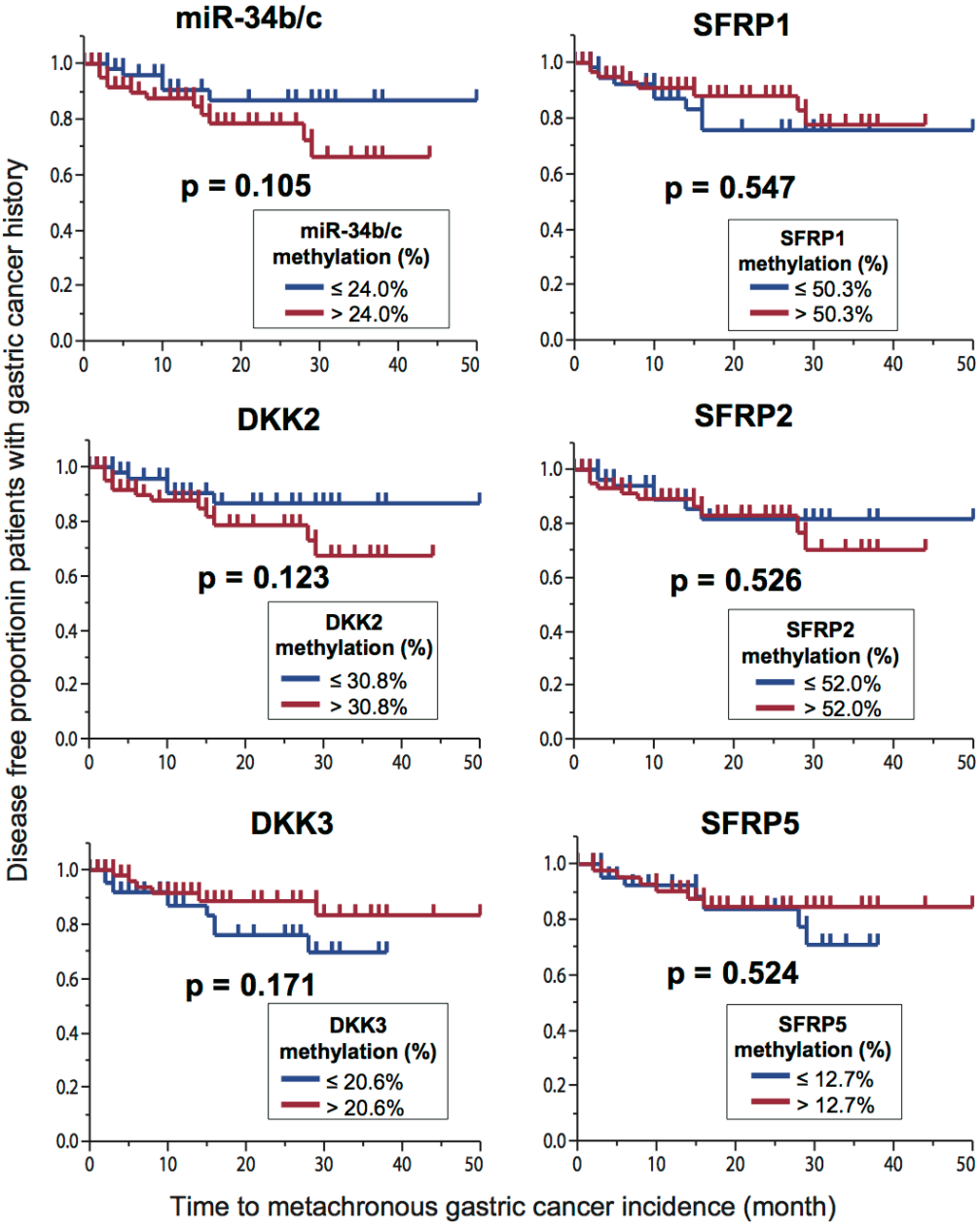
Supplementary Figure 1



Supplementary Figure 1

Kaplan-Meier analysis showing the effect of methylation of the indicated genes in the gastric body on metachronous GC-free survival. Note that higher methylation levels of *SFRP2* and *DKK2* are significantly associated with shorter metachronous GC-free survival.

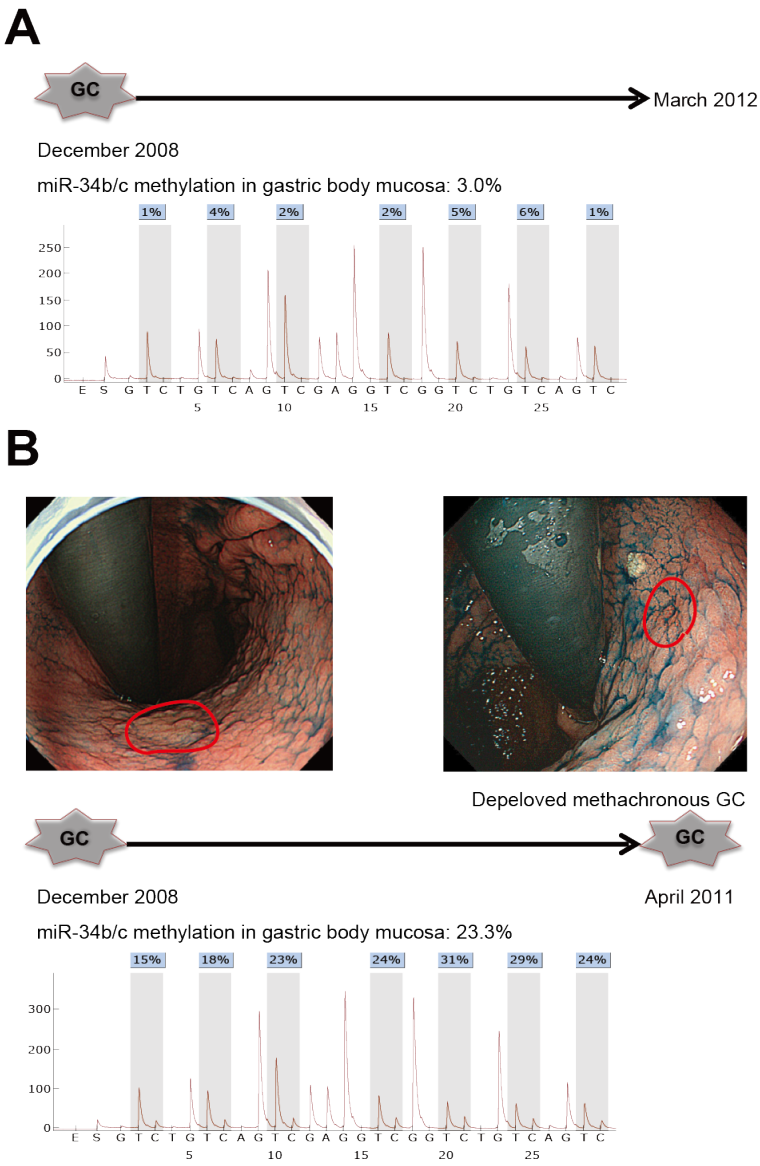
Supplementary Figure 2



Supplementary Figure 2

Kaplan-Meier analysis showing the effect of methylation of the indicated genes in the gastric antrum on metachronous GC-free survival.

Supplemetary Figure 3

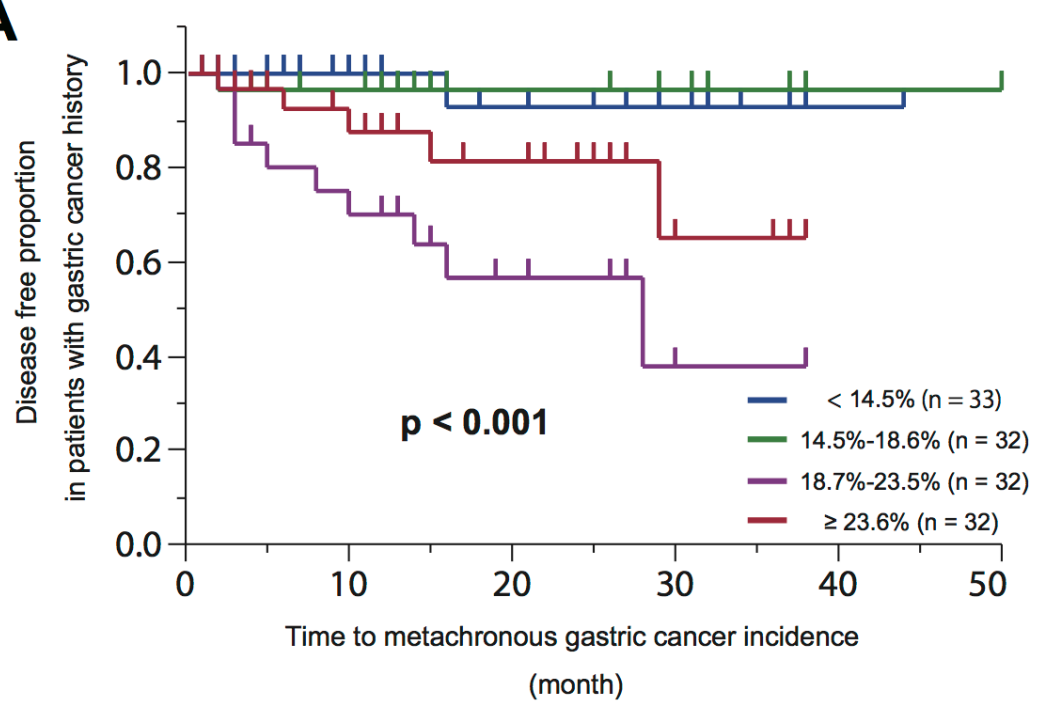


Supplementary Figure 3

Representative patients exhibiting low or high levels of *miR-34b/c* methylation in their gastric body. (A) Patient with a low *miR-34b/c* methylation level (3.0%), who did not develop metachronous GC during the follow-up period. (B) Patient with a high methylation level (23.3%), who developed metachronous GC in the remnant stomach 2 years after curative endoscopic resection.

Supplementary Figure 4

A



B

Methylation (%)	Periods	Total	Non MGC	MGC	incidence rate (%)	95%CI Lower	95%CI Upper
<14.5%	1-year	33	33	0	0.0%	0.0%	10.6%*
	2-year	14	13	1	7.1%	0.0%	20.6%
	3-year	11	11	0	7.1%	0.0%	20.6%
14.5%-18.6%	1-year	32	31	1	3.4%	0.0%	10.1%
	2-year	17	17	0	3.4%	0.0%	10.1%
	3-year	13	13	0	3.4%	0.0%	10.1%
18.7%-23.5%	1-year	32	25	7	29.9%	10.9%	48.9%
	2-year	12	10	2	43.4%	20.7%	66.1%
	3-year	5	4	1	62.3%	28.6%	96.0%
≥23.6%	1-year	32	29	3	7.5%	0.0%	17.7%
	2-year	16	15	1	18.7%	1.6%	35.8%
	3-year	8	7	1	34.9%	3.3%	66.5%

*Calculated by binomial exact method with the number of at risk at the begining.
CI, confidence interval; MGC, metachronous gastric cancer

Supplementary Figure 4

(A) Kaplan-Meier analysis showing the effect of *miR-34b/c* methylation on metachronous GC-free survival. Patients were stratified into four groups according to their level of *miR-34b/c* methylation. (B) Methylation of *miR-34b/c* in noncancerous gastric body mucosa and its association with metachronous gastric cancer.

Supplementary Table1. Sequences of the primers used in this study

		forward	reverse	product size
miR-34b/c	pyroseq PCR	GGTYGAGTGATTGTGGYGGGGG	Bio-CCTCCATCTTCTAAACRTCTCCCTTA	176 bp
	Sequence primer	TAATYGTTTTTGGAATTT		
	Sequence to analyze	YGYGGGTYGAGGGGYGGGGYGGGYGYG		
SFRP1	pyroseq PCR	GTTTTGTTTTTTAAGGGGTGTTGAG	Bio-CTCCRAAAACTACAAAACTAAAATAC	202 bp
	Sequence primer	GYGTTTGGTTTTAGTAAAT		
	Sequence to analyze	TTGYGYGGGGYGGTTTYGAGGGTTYG		
SFRP2	pyroseq PCR	AATTTYGGATTGGGGTAAAATAAGTT	Bio-TTAAACAACAAACAAAAAAACCTAACC	182 bp
	Sequence primer	YGTTTTYGTTAGTATTTGG		
	Sequence to analyze	TYGYGAGGTYGTTYGYG		
DKK2	pyroseq PCR	GGGTTTTTTGATTAATTAAGAGGAGA	Bio-TCTACAATAACTAAAAACAATCAAATAC	179 bp
	Sequence primer	TAATTAAGAGGAGAGTTAAA		
	Sequence to analyze	TYGTYGAGATTTYGGYG		
DKK3	pyroseq PCR	GATTTTGTTGAGTTTAGTTTTTTTTGGT	Bio-CAAACCTCTCTCAACCCCTACCTA	123bp
	Sequence primer	TTTTTTGGTGGATGTG		
	Sequence to analyze	GGGYGGGGYGTTYGAGTAGGATTYGAYG		

Y=C or T, R=A or G