

Risk-Association of DNA Methyltransferases Polymorphisms with Gastric Cancer in the Southern Chinese Population

Supplementary Information

Table S1. OR for case-control study of 10 GC susceptibility loci.

SNP	Model	Genotype	Case n (%)	Control n (%)	OR (95% CI) ^a	p-value	
DNMT1							
rs2114724	Dominant	C/C	132 (54.5)	162 (56.2)	1.00	0.77	
		T/C-T/T	110 (45.5)	126 (43.8)	1.05 (0.74–1.50)		
	Recessive	C/C-T/C	229 (94.6)	263 (91.3)	1.00	0.13	
		T/T	13 (5.4)	25 (8.7)	0.58 (0.29–1.18)		
rs2228611	Log-additive	-	-	-	0.95 (0.72–1.25)	0.70	
		Dominant	G/G	132 (54.5)	160 (56.1)		1.00
	Recessive	A/G-A/A	110 (45.5)	125 (43.9)	1.05 (0.74–1.49)	0.08	
		G/G-A/G	229 (94.6)	259 (90.9)	1.00		
rs8101866	Log-additive	A/A	13 (5.4)	26 (9.1)	0.54 (0.27–1.09)	0.61	
		-	-	-	0.93 (0.71–1.23)		
	Dominant	T/T	130 (53.9)	166 (56.5)	1.00	0.65	
		C/T-C/C	111 (46.1)	128 (43.5)	1.08 (0.76–1.53)		
rs16999593	Recessive	T/T-C/T	228 (94.6)	268 (91.2)	1.00	0.11	
		C/C	13 (5.4)	26 (8.8)	0.57 (0.28–1.15)		
	Log-additive	-	-	-	0.96 (0.73–1.26)	0.76	
		Dominant	T/T	141 (58.3)	196 (66.7)		1.00
rs16999593	Recessive	C/T-C/C	101 (41.7)	98 (33.3)	1.42 (0.99–2.03)	1.00	
		T/T-C/T	230 (95.0)	279 (94.9)	1.00		
	Log-additive	C/C	12 (5.0)	15 (5.1)	1.00 (0.45–2.21)	0.11	
		-	-	-	1.27 (0.94–1.70)		
DNMT2							
rs11254413	Dominant	T/T	57 (23.6)	74 (25.3)	1.00	<0.0001	
		C/T-C/C	185 (76.5)	218 (74.7)	0.34 (0.22–0.52)		
	Recessive	T/T-C/T	178 (73.5)	229 (78.4)	1.00	0.045	
		C/C	64 (26.4)	63 (21.6)	2.00 (1.01–3.98)		
rs11254413	Log-additive	-	-	-	0.65 (0.48–0.87)	0.004	
	DNMT3A						
	rs1550117	Dominant	G/G	157 (64.9)	191 (65.0)	1.00	0.9
A/G-A/A			85 (35.1)	103 (35.0)	0.98 (0.68–1.40)		
Recessive		G/G-A/G	231 (95.5)	284 (96.6)	1.00	0.48	
		A/A	11 (4.5)	10 (3.4)	1.37 (0.57–3.33)		
rs11887120	Log-additive	-	-	-	1.02 (0.75–1.39)	0.89	
		Dominant	T/T	57 (23.6)	74 (25.3)		1.00
	Recessive	C/T-C/C	185 (76.5)	218 (74.7)	1.05 (0.70–1.57)	0.22	
		T/T-C/T	178 (73.5)	229 (78.4)	1.00		
rs11887120	Log-additive	C/C	64 (26.4)	63 (21.6)	1.29 (0.86–1.94)	0.37	
		-	-	-	1.12 (0.87–1.44)		

Table S1. Cont.

SNP	Model	Genotype	Case n (%)	Control n (%)	OR (95% CI) ^a	p-value
rs13420827	Dominant	C/C	167 (69.0)	183 (62.7)	1.00	0.18
		G/C-G/G	75 (31.0)	109 (37.3)	0.78 (0.54–1.12)	
	Recessive	C/C-G/C	228 (94.2)	282 (96.6)	1.00	0.12
		G/G	14 (5.8)	10 (3.4)	1.97 (0.84–4.61)	
	Log-additive	-	-	-	0.92 (0.68–1.24)	0.58
rs13428812	Dominant	A/A	137 (56.6)	160 (55.4)	1.00	0.81
		G/A-G/G	105 (43.4)	129 (44.6)	0.96 (0.68–1.36)	
	Recessive	A/A-G/A	221 (91.3)	266 (92.0)	1.00	0.67
		A/A	21 (8.7)	23 (8.0)	1.14 (0.61–2.15)	
	Log-additive	-	-	-	1.00 (0.76–1.31)	1.00
<i>DNMT3B</i>						
rs2424908	Dominant	T/T	78 (32.2)	99 (33.7)	1.00	0.99
		C/T-C/C	164 (67.8)	195 (66.3)	1.00 (0.69–1.44)	
	Recessive	T/T-C/T	192 (79.3)	238 (81.0)	1.00	0.79
		C/C	50 (20.7)	56 (19.0)	1.06 (0.69–1.64)	
	Log-additive	-	-	-	1.02 (0.80–1.30)	0.89

Note: CI, confidence interval; OR, odds ratio; *p*-values obtained by chi-squared; ^a OR (95% CI) was adjusted by sex and age; Bold mean *p* < 0.05.

Table S2. The D' and *r*² value between SNPs in *DNMT1* and *DNMT3A*.

	L1	L2	D'	LOD	<i>r</i> ²
<i>DNMT1</i>					
	rs2114724	rs2228611	1.0	197.54	0.99
	rs2114724	rs8101866	0.99	190.58	0.976
	rs2114724	rs16999593	1.0	17.45	0.093
	rs2228611	rs8101866	0.99	187.91	0.97
	rs2228611	rs16999593	1.0	17.84	0.094
	rs8101866	rs16999593	1.0	17.96	0.094
<i>DNMT3A</i>					
	rs13420827	rs11887120	0.706	15.9	0.118
	rs13420827	rs13428812	0.233	0.56	0.005
	rs13420827	rs1550117	0.093	1.0	0.009
	rs11887120	rs13428812	0.057	0.13	0.001
	rs11887120	rs1550117	0.097	0.23	0.002
	rs13428812	rs1550117	0.604	4.25	0.032