

SNP–SNP interactions of three new pri-miRNAs with the target gene *PGC* and multidimensional analysis of *H. pylori* in the gastric cancer/atrophic gastritis risk in a Chinese population

SUPPLEMENTARY TABLES

Supplementary Table S1: The baseline of the subjects

Variables	AG vs. CON		GC vs. CON	
	CON(%)	AG(%)	CON(%)	GC(%)
	n=862	n=862	n=729	n=724
Gender	<i>P</i> =0.846		<i>P</i> =0.564	
Male	483(56.0)	487(56.5)	483(66.3)	490(67.7)
Female	379(44.0)	375(43.5)	246(33.7)	234(32.3)
Age	<i>P</i> =0.343		<i>P</i> =0.562	
Mean±SD	54.9±9.2	55.4±9.5	56.1±9.2	56.4±9.8
Median	54	56	56	57
Range	17-85	16-79	17-85	21-81
<i>H. pylori</i>	<i>P</i> <0.001		<i>P</i> <0.001	
Positive	241(28.0)	505(58.6)	201(27.6)	369(51.0)
Negative	621(72.0)	41.4(36.5)	528(72.4)	355(49.0)

Supplementary Table S2: The interaction of miRNA SNP-miRNA SNP in the risk of gastric cancer/atrophic gastritis^a

		let7e rs8111742		miR-365b rs121224	
		GA+GG	AA	CG+CC	GG
AG vs CON (n=862 Vs. 862)					
miR-365b rs121224					
CG+CC	Case/Control	634/649	51/49	/	/
	OR(95%CI)	1(Ref)	1.06(0.71-1.59)	/	/
GG	Case/Control	167/151	10/13	/	/
	OR(95%CI)	1.13(0.88-1.44)	0.78(0.34-1.80)	/	/
		$P_{\text{interaction}}=0.244$		/	
		interaction index=0.55			
miR4795 rs1002765					
GA+GG	Case/Control	668/671	52/56	569/595	151/132
	OR(95%CI)	1(Ref)	0.93(0.63-1.38)	1(Ref)	1.19(0.92-1.55)
AA	Case/Control	133/129	9/6	116/103	26/32
	OR(95%CI)	1.05(0.80-1.37)	1.50(0.53-4.24)	1.20(0.90-1.60)	0.85(0.50-1.44)
		$P_{\text{interaction}}=0.636$		$P_{\text{interaction}}=0.196$	
		interaction index=1.33		interaction index=0.64	
GC vs CON (n=724 Vs. 729)					
miR-365b rs121224					
CG+CC	Case/Control	551/546	46/45	/	/
	OR(95%CI)	1(Ref)	1.01(0.66-1.54)	/	/
GG	Case/Control	115/128	12/10	/	/
	OR(95%CI)	0.88(0.67-1.17)	1.18(0.51-2.76)	/	/
		$P_{\text{interaction}}=0.368$		/	
		interaction index=1.59			
miR4795 rs1002765					
GA+GG	Case/Control	569/568	52/51	512/511	109/108
	OR(95%CI)	1(Ref)	1.01(0.68-1.52)	1(Ref)	1.00(0.75-1.35)
AA	Case/Control	97/106	6/4	85/80	18/30
	OR(95%CI)	0.93(0.69-1.25)	1.49(0.42-5.32)	1.08(0.78-1.51)	0.60(0.33-1.08)
		$P_{\text{interaction}}=0.368$		$P_{\text{interaction}}=0.155$	
		interaction index=1.44		interaction index=0.58	

Note:^a, P for interaction was used Logistic Regression adjusted by gender, age and *H. pylori* infection status. CON:controls; AG: atrophic gastritis; GC:gastric cancer.

Supplementary Table S3: MiRNA-PGC gene interaction models for polymorphisms and for *H. pylori* in gastric cancer and/or atrophic gastritis risk by MDR analysis

Model	Training Bal. Acc.	Testing Bal. Acc.	Sign Test (p)	CV Consistency	P for permutation test
For AG risk					
Two-way interaction					
let-7e rs8111742-PGC rs6458238	0.5344	0.5288	9(0.0107)	9/10	0.0020-0.0025
miR-4795 rs1002765-PGC rs9471643	0.5397	0.5312	9(0.0107)	10/10	0.0015-0.0020
miR-365b rs121224-PGC rs6912200	0.5127	0.4780	3(0.9453)	7/10	0.9660-0.9665
let-7e rs8111742-PGC rs6941539	0.5259	0.5052	5(0.6230)	8/10	0.5390
Three-way interaction					
let-7e rs8111742-PGC rs6458238- <i>H. pylori</i>	0.6707	0.6678	10(0.0010)	5/10	0.0000-0.0005
let-7e rs8111742-PGC rs6941539- <i>H. pylori</i>	0.6547	0.6500	10(0.0010)	10/10	0.0000-0.0005
miR-4795 rs1002765-PGC rs9471643- <i>H. pylori</i>	0.6720	0.6630	10(0.0010)	5/10	0.0000-0.0005
For GC risk					
let-7e rs8111742-PGC rs6458238- <i>H. pylori</i>	0.6883	0.6854	10(0.0010)	10/10	0.0000-0.0005

Note: When the *P* value for the Sign Test <0.05 and *P* for permutation test <0.05 meant a statistical difference. AG, atrophic gastritis; GC, gastric cancer.