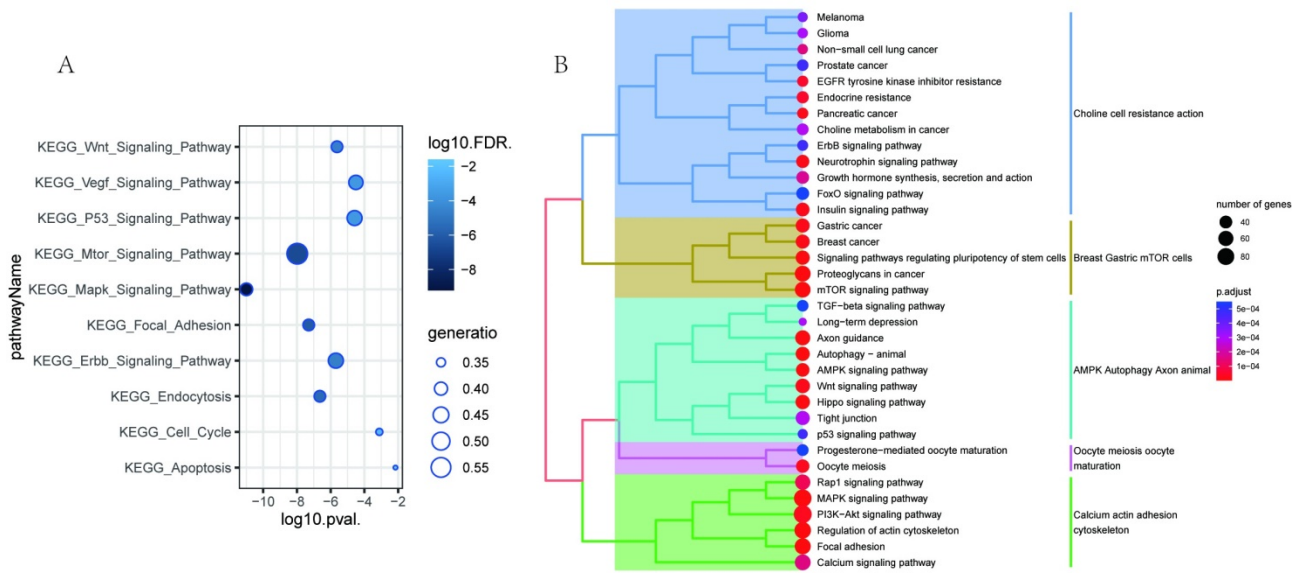


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2 **Fig. S1.** High methylation induces downregulation of miR-497-5p in gastric cancer. A. Expression of  
 3 miR-497-5p in normal gastric epithelial cells and gastric cancer cells determined by RT-qPCR. B.  
 4 Prediction of the presence of a CpG island (highlighted in blue) upstream of the miR-497-5p promoter  
 5 using the MethPrimer database. C. Methylation status of the promoter in gastric cancer tissues and  
 6 normal tissues assessed by MSP. D. Methylation status of the promoter in normal gastric epithelial  
 7 cells and gastric cancer cells determined by MSP. E. Expression of miR-497-5p in HGC-27 cells  
 8 treated with 5-Aza-dc measured by RT-qPCR. F. ChIP experiments examining the interaction between

9 DNMT1/DNMT3 (a/b) and the miR-497-5p promoter. AGS-1 and NCI-N87 groups vs. GES-1 group,  
10  $P < 0.01$ ; HGC-27 group vs. GES-1 group,  $P < 0.05$ ,  $P < 0.001$ ; DMSO group vs. 5-Aza-dc group, \* $P$   
11  $< 0.05$ .

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14 **Fig. S2 A:** mirTarPathway database and the biological function of predicted target genes; B: KEGG

15 pathway analysis of target genes.

16 **Table S1: Correlation between expression level of miR-49-5p and clinical pathology.**

Clinical feature	n	miR-49-5p expression	p
Age			0.399
≤45	27	0.543 ± 0.073	
>45	33	0.561 ± 0.088	
Gender			0.895
Female	27	0.555 ± 0.067	
Male	33	0.552 ± 0.093	
Drinking			0.492
Yes	32	0.560 ± 0.088	
No	28	0.545 ± 0.074	
Smoking			0.116
Yes	35	0.567 ± 0.087	
No	25	0.534 ± 0.071	
Gastric ulcer			0.804
Yes	36	0.551 ± 0.063	
No	24	0.557 ± 0.104	
Duodenal ulcer			0.059
Yes	32	0.535 ± 0.075	
No	28	0.574 ± 0.085	
Stage			0.0001
II	27	0.596 ± 0.073	
IV	33	0.506 ± 0.062	

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