

Figure S1. Sequence information of circPGC.



Home **hsa_circ_0076305 circRNA Mature Sequence**

GTGGCTACTTTGGTGGATGCGCATGCGGAGCTCCACCCAGAACTTCTGCTCTTTTGGACACGG
 GTGGGTGCTCTGTCTACTGCGAGGCGAGGCTGACACAGTCACTCCCGCTTCAACCCAGAGAT
 CGACCATGSSGAGACTTCTCCCTGCAATGSSGATGSSGAGCTCACCGCTCTCTTTGGCTATGAC
 CAGAGCATCCAGGTCCCAACAGAGGTTGGGTTGAGTGGAAATGAGGCTGATGACACTTGGCTTA
 TGGCATGATGGGCTGGCTGACCTGCTCTCTCTCCGTTGATGAGGCGCACACGCTATGCGAGGCAATG
 CCGTCCAGACGCGGCTGTCAGCGTCTACTGACGAAACAGGAGGCTCCAGCGGAGGAGGAGTGTG
 GATAGCGCTGTACAGGAGGAGTACTGAGGCGCTGTACCCAGGAACTACTGCGAGATTGG
 CCTACTGGGCGAGGCTCCCGGCTGAGGTTCTGAGGAGTGGAGGCTGCGAGGAGTGGAGGAGGCT
 TGGCGGAGGAGTGGAGGCTGAGGAGTGGAGGCTGAGGAGTGGAGGCTGAGGAGTGGAGGAGGCT
 AACAGCATTCAGGATGCGGAGCTTGGAGCTTCTGATGAGTGGAGTGGAGTGGAGTGGAGTGGAGT
 CAGTACAGCGCTACTGACCGTGGAGTGGAGGCTGAGGAGTGGAGGCTGAGGAGTGGAGGCTGAG
 GAGTGGTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG
 TGGTGGTGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG
 ATTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG

Length: 1098 nt

B Query: sequence of circPGC Vector **Sbjct: Sequence information matched after BLAST**

circPGC

Score	Expect	Identities	Gaps	Strand
2152 bits(1165)	0.0	1165/1165(100%)	0/1165(0%)	Plus/Minus
Query 1	AAAGGTAAGTACTAATGAC	ATACCTCAGGCTGGCTACTTTGGTGGATCAG		60
Sbjct 1212	AAAGGTAAGTACTAATGAC	ATACCTCAGGCTGGCTACTTTGGTGGATCAG		1153
Query 61	CATCGGGACTCCACCCAGAACT	CTCGGCTCTTTTGGACACGGCTCTCCAACTTGTG		120
Sbjct 1152	CATCGGGACTCCACCCAGAACT	CTCGGCTCTTTTGGACACGGCTCTCCAACTTGTG		1093
Query 121	GGTGGCTCTGCTACTGCCAGAGCCAGGCTGCA	CCAGCTCACTCCCGCTTCAACCCAG		180
Sbjct 1092	GGTGGCTCTGCTACTGCCAGAGCCAGGCTGCA	CCAGCTCACTCCCGCTTCAACCCAG		1033
Query 181	CGAGTCTCCACCTACTCCACCAATGGG	CAGACTTCTCCCGTGCAGTATGGCAGTGGCAG		240
Sbjct 1032	CGAGTCTCCACCTACTCCACCAATGGG	CAGACTTCTCCCGTGCAGTATGGCAGTGGCAG		973
Query 241	CCTCACCGGCTTCTTTGGCTATGACA	CCCTGACAGCATCCAGGTCGCCAACA		300
Sbjct 972	CCTCACCGGCTTCTTTGGCTATGACA	CCCTGACAGCATCCAGGTCGCCAACA		913
Query 301	GGAGTTGGGCTTGAGTGAGAAATGAGC	TGGTACCAACTTGGCTATGCGCAGTTTGCATGC		360
Sbjct 912	GGAGTTGGGCTTGAGTGAGAAATGAGC	TGGTACCAACTTGGCTATGCGCAGTTTGCATGC		853
Query 361	CATCATGGGCTGGCTACCGTCTCTG	TCCTGGATGAGGCCACCAAGCTATGCAGGG		420
Sbjct 852	CATCATGGGCTGGCTACCGTCTCTG	TCCTGGATGAGGCCACCAAGCTATGCAGGG		793
Query 421	CATGGTGCAGGAGGGGCGCTCAC	CCAGGCGCTTTCAGGCTTCACTCAGCAACCCAGCA		480
Sbjct 792	CATGGTGCAGGAGGGGCGCTCAC	CCAGGCGCTTTCAGGCTTCACTCAGCAACCCAGCA		733
Query 481	GGGCTCCAGCGGGGACCGGTTGCT	TTGGGGTGTGGATAGCAGCGCTTACACGGGGCA		540
Sbjct 732	GGGCTCCAGCGGGGACCGGTTGCT	TTGGGGTGTGGATAGCAGCGCTTACACGGGGCA		673
Query 541	CATCTACTGGGCGCTGTACCCAGGAACT	CTACTGGCAGATTGGCATTGAAGAGTTCTCT		600
Sbjct 672	CATCTACTGGGCGCTGTACCCAGGAACT	CTACTGGCAGATTGGCATTGAAGAGTTCTCT		613
Query 601	CATCGCGGGCCAGGCTCCGGCTGGT	TTCTGAGGTTGCCAGGCCATCGGACACAGG		660
Sbjct 612	CATCGCGGGCCAGGCTCCGGCTGGT	TTCTGAGGTTGCCAGGCCATCGGACACAGG		553
Query 661	CACTCTCTGCTCACTGTGCCCCAGCAGT	ACATGAGTCTCTTCTGACGGCCACAGGGCC		720
Sbjct 552	CACTCTCTGCTCACTGTGCCCCAGCAGT	ACATGAGTCTCTTCTGACGGCCACAGGGCC		493
Query 721	CCAGGAGGATGAGTATGGACAGTTTCT	CGTGAAGTAAACAGCATTGAGAACTGCCCCAG		780
Sbjct 492	CCAGGAGGATGAGTATGGACAGTTTCT	CGTGAAGTAAACAGCATTGAGAACTGCCCCAG		433
Query 781	CTTGACCTTCATCATCAATGGTGGAG	TGCTGCGCACTTCTCTCTATATCTCTCAG		840
Sbjct 432	CTTGACCTTCATCATCAATGGTGGAG	TGCTGCGCACTTCTCTCTATATCTCTCAG		373
Query 841	TAACAACGGCTACTGCAACGGTGGAG	TGAGGCCAAGTCTCTCCAGAACGGGCA		900
Sbjct 372	TAACAACGGCTACTGCAACGGTGGAG	TGAGGCCAAGTCTCTCCAGAACGGGCA		313
Query 901	GCCCTGTGATCTCCGGGATGCTTCT	CTCAGGCTCTACTATTCCTCTACGACTTGGG		960
Sbjct 312	GCCCTGTGATCTCCGGGATGCTTCT	CTCAGGCTCTACTATTCCTCTACGACTTGGG		253
Query 961	CACAACAGAGTAGGCTTTGCCACTG	CCGCTAGACTTGTGCTCTGACAGCTGGGCTCC		1020
Sbjct 252	CACAACAGAGTAGGCTTTGCCACTG	CCGCTAGACTTGTGCTCTGACAGCTGGGCTCC		193
Query 1021	CCTCTTCTCTTGAACCTGCAACCT	CTAGGGCAATGATCTGCTTTCCACTCTGGATT		1080
Sbjct 192	CCTCTTCTCTTGAACCTGCAACCT	CTAGGGCAATGATCTGCTTTCCACTCTGGATT		133
Query 1081	CAGCCTCTTTTCTGGACTCTGGACT	TTCTCTAATAAATAAGTCTCTTTACTAAG		1140
Sbjct 132	CAGCCTCTTTTCTGGACTCTGGACT	TTCTCTAATAAATAAGTCTCTTTACTAAG		73
Query 1141	AAGCAAGGAAAAGAAATTAGGCTCGG	1165		
Sbjct 72	AAGCAAGGAAAAGAAATTAGGCTCGG	48		

Table SI. Primer sequences used for PCR.

Gene	Sequence (5'-3')
circPGC-F	TACTTCAGGCTGCCTACTTTGGTGAGATCAG
circPGC-R	CTTGCTTCTTACTAAAGAAGAAGAACTATTTATTATTAGAGAAAAGTCCAGAGTCCAGA
pcDNA (3.1)-F	GTTCTTCTTTAGTAAGAAGCAAGGAAAAGAATTAGGCTCG
pcDNA (3.1)-R	GTAGGCAGCCTGAAGTATAAAAAAAAAAAGTCATTAGTACGTACCT

F, forward; R, reverse.

Table SII. Primer sequences used for quantitative PCR.

Gene	Sequence (5'-3')
hsa_circ_0076305 (qPCR)-F	CCCTCCTAGGGCATTGTATCTG
hsa_circ_0076305 (qPCR)-R	GCCGGTGTCAAAAAGGACCA
hsa_circ_0076304 (qPCR)-F	CCACTCTGGATTACAGCCTTCT
hsa_circ_0076304 (qPCR)-R	TGCCATCAAACCTGCGCATAG
hsa_circ_0000390 (qPCR)-F	GCCGGTGTCAAAAAGGACCA
hsa_circ_0000390 (qPCR)-R	GAGCATCTCATACGGGGAA
PGC mRNA (qPCR)-F	CTGCGACTGCAGAACTCAGA
PGC mRNA (qPCR)-R	CAGCAAGCCCTTCTCCTTCA
GAPDH (qPCR)-F	ACCCACTCCTCCACCTTTGAC
GAPDH (qPCR)-R	TGTTGCTGTAGCCAAATTCGTT

F, forward; R, reverse.

Table SIII. Association between circPGC expression and clinicopathological characteristics of patients with GC.

Characteristic	Number of patients (n=30)	High circPGC expression, n (%) (n=4)	Low circPGC expression, n (%) (n=26)
Age, years			
≥60	22	2 (50)	20 (77)
<60	8	2 (50)	6 (23)
Sex			
Female	6	0 (0)	6 (23)
Male	24	4 (100)	20 (77)
TNM staging			
I/II	13	4 (100)	9 (35)
III/IV	17	0 (0)	17 (65)
Primary focus			
T1/T2	4	2 (50)	2 (8)
T3/T4	26	2 (50)	24 (92)
Lymphatic metastasis			
Yes	21	3 (75)	18 (69)
No	9	1 (25)	8 (31)

CircPGC, CircPGC, hsa_circ_0076305; TNM, tumor-node-metastasis.