

Table S1. The sequences of plasmids used in the luciferase reporter assays

Plasmids	Sequences
pEZX-MT06-Wt-circ_GLG1	GAAGCAAATAAAAAACAGTGAATTGATGGATCCCAAATGCAAACAGATGATAACCAAGCGCC AGATCACCCAGAACACAGATTACCGCTTAAACCCCATGTTAAGAAAAGCCTGTAAAGCTGACA TTCCTAAATTCTGTCACGGTATCCTGACTAAGGCCAAGGATGATTCAGAATTAGAAGGACAAG TCATCTCTTGCCTGAAGCTGAGATATGCTGACCAGCGCCTGTCTT CAGACTGTGAAGACCAGA TCCGAATCATTATCCAGGAGTCCGCCCTGGACTACCGCCTGGATCCTCAGCTCCAGCTGCACT GCTCAGACGAGATCTCCAGTCTATGTGCTGAAGAAGCAGCAGCCCAAGAGCAGACAGGTCAG GTGGAGGAGTGCCTCAAGGTCAACCTGCTCAAGATCAAAACAGAATTGTGTAAAAAG
pEZX-MT06-Mut-circ_GLG1	GAAGCAAATAAAAAACAGTGAATTGATGGATCCCAAATGCAAACAGATGATAACCAAGCGCC AGATCACCCAGAACACAGATTACCGCTTAAACCCCATGTTAAGAAAAGCCTGTAAAGCTGACA TTCCTAAATTCTGTCACGGTATCCTGACTAAGGCCAAGGATGATTCAGAATTAGAAGGACAAG TCATCTCTTGCCTGAAGCTGAGATATGCTGACCAGCGCCTGTCTT GTCTGACTGAAGACCAGA TCCGAATCATTATCCAGGAGTCCGCCCTGGACTACCGCCTGGATCCTCAGCTCCAGCTGCACT GCTCAGACGAGATCTCCAGTCTATGTGCTGAAGAAGCAGCAGCCCAAGAGCAGACAGGTCAG GTGGAGGAGTGCCTCAAGGTCAACCTGCTCAAGATCAAAACAGAATTGTGTAAAAAG
pEZX-MT06-Wt-KRAS	TCTGGGTGTTGATGATGCCTTCTATACATTAGTTCGAGAAATTCGAAAACATAAAGAAAAGATG AGCAAAGATGGTAAAAAGAAGAAAAAGAAGTCAAAGACAAAGTGTGTAATTATGTAAATACA ATTTGTACTTTTTTCTTAAGGCATACTAGTACAAGTGGTAATTTTTGTACATTACCTAAATTATT AGCATTGTGTTTAGCATTACCTAATTTTTTCTGCTCCAT GCAGACTGTTAGCTTTTACCTTAA ATGCTTATTTTAAAATGACAGTGGAAGTTTTTTTTTCTCTAAGTGCCAGTATTCCCAGAGTTTT GGTTTTTGAAGTAGCAATGCCTGTGAAAAAGAACTGAATACCTAAGATTTCTGTCTTGGGGC TTTTGGTGCATGCAGTTGATTACTTCTATTTTTTCTTACCAATTGTGAATGTTGGTGTGAAACAA
pEZX-MT06-Mut-KRAS	TCTGGGTGTTGATGATGCCTTCTATACATTAGTTCGAGAAATTCGAAAACATAAAGAAAAGATG AGCAAAGATGGTAAAAAGAAGAAAAAGAAGTCAAAGACAAAGTGTGTAATTATGTAAATACA ATTTGTACTTTTTTCTTAAGGCATACTAGTACAAGTGGTAATTTTTGTACATTACCTAAATTATT AGCATTGTGTTTAGCATTACCTAATTTTTTCTGCTCCAT CGTCTGACTTAGCTTTTACCTTAA TGCTTATTTTAAAATGACAGTGGAAGTTTTTTTTTCTCTAAGTGCCAGTATTCCCAGAGTTTTG GTTTTTGAAGTAGCAATGCCTGTGAAAAAGAACTGAATACCTAAGATTTCTGTCTTGGGGC TTTTGGTGCATGCAGTTGATTACTTCTATTTTTTCTTACCAATTGTGAATGTTGGTGTGAAACAA

gray area, miR-622-binding sites

Table S2. Relationships between circ_GLG1 expression and clinico-pathological characteristics in 40 patients with colorectal cancer

Factor	Cases	circ_GLG1		
		Low expression	High expression	P value
Age (years)				
≥ 60	24	13	11	0.301
< 60	16	6	10	
Sex				
Male	24	12	12	0.698
Female	16	7	9	
Cancer type				
Colon cancer	19	6	13	0.055
Rectal cancer	21	13	8	
Differentiation				
Poor	8	2	6	0.303
Well & moderate	32	17	15	
Invasion				
T1 & T2	5	4	1	0.172
T3 & T4	35	15	20	
Stage				
I & II	18	10	8	0.356
III	22	9	13	
Nodal status				
Negative	18	10	8	0.356
Positive	22	9	13	

Table S3. TargetScan miRNA predictions

CircRNA Mirbase ID	CircRNA (Top) - miRNA (Bottom) pairing	Site Type	CircRNA Start	CircRNA End	Position	Context + Score	Context + Score Percentile
hsa_circ_0003315 (5' ... 3')	UUGAAGCAAAAUAAAAACAGUGA 	8mer-1a	58	65	-0.1	-0.366	99
hsa-miR-1208 (3' ... 5')	AGGCGGACAGACUUGUCACU						
hsa_circ_0003315 (5' ... 3')	GUCAGGUGGAGGAGUGCCUCAAG 	7mer-m8	431	437	-0.056	-0.158	92
hsa-miR-1304 (3' ... 5')	GUGUAGAGUGACAUCGGAGUUU						
hsa_circ_0003315 (5' ... 3')	AACAGUGAAUUGAUGGAUCCCAA 	8mer-1a	73	80	-0.096	-0.427	99
hsa-miR-769-3p (3' ... 5')	UUGGUUCUGGGGCCUCUAGGGUC						
hsa_circ_0003315 (5' ... 3')	AAACCAUGUUGCAGUGCUUGAAG 	7mer-m8	41	47	-0.056	-0.153	97
hsa-miR-498 (3' ... 5')	CUUUUUGCGGGGGACCGAACUUU						
hsa_circ_0003315 (5' ... 3')	CUCAAGGUCAACCUGCUCAAGAU 	7mer-m8	448	454	-0.058	-0.144	92
hsa-miR-526b (3' ... 5')	UGUCUUUCACGAAGGGAGUUCUC						
hsa_circ_0003315 (5' ... 3')	CAAGGAUGAUUCAGAAUUAGAAG 	7mer-m8	219	225	-0.031	-0.02	91
hsa-miR-576-5p (3' ... 5')	UUUCUGCACCUCUUUAAUCUUA						
hsa_circ_0003315 (5' ... 3')	ACCAGCGCCUGUCUUCAGACUGU 	7mer-m8	278	284	-0.034	-0.188	94
hsa-miR-622 (3' ... 5')	CGAGGUUGGAGUCGUCUGACA						
hsa_circ_0003315 (5' ... 3')	ACACAGAUUACCGCUUAAACCCC 	7mer-m8	134	140	-0.043	-0.157	96
hsa-miR-629 (3' ... 5')	UCAAGAGGGUUGCAUUUGGGU						

Table S3. Continued

CircRNA Mirbase ID	CircRNA (Top) - miRNA (Bottom) pairing	Site Type	CircRNA Start	CircRNA End	Position	Context + Score	Context + Score Percentile
hsa_circ_0003315 (5' ... 3')	GCUGAAGAAGCAGCAGCCCAAGA 	8mer-1a	400	407	-0.096	-0.38	97
hsa-miR-635 (3' ... 5')	CCUGUAACAAAGUCACGGGUUCA						
hsa_circ_0003315 (5' ... 3')	AACAGUGAAUUGAUGGAUCCCAA 	7mer-1a	73	79	-0.042	-0.233	96
hsa-miR-638 (3' ... 5')	CGGCGGUGGGCGGGCGCUAGGGA						
hsa_circ_0003315 (5' ... 3')	CUGUAAAGCUGACAUCCUAAAU 	7mer-1a	171	177	-0.031	-0.095	91
hsa-miR-651 (3' ... 5')	UUUCAGUUCGAAU AGGAUUU						
hsa_circ_0003315 (5' ... 3')	GAGUGCCUCAAGGUCAACCUGCU 	7mer-m8	442	448	-0.058	-0.203	93
hsa-miR-657 (3' ... 5')	GGAUCUCUCCACUCUUGGACGG						