Figure S1

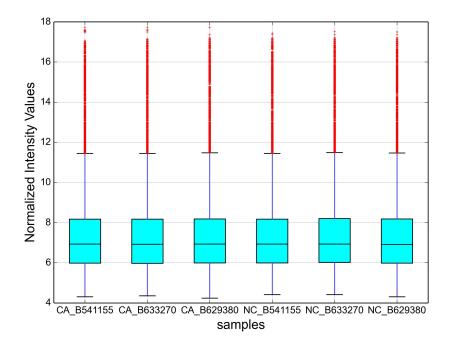
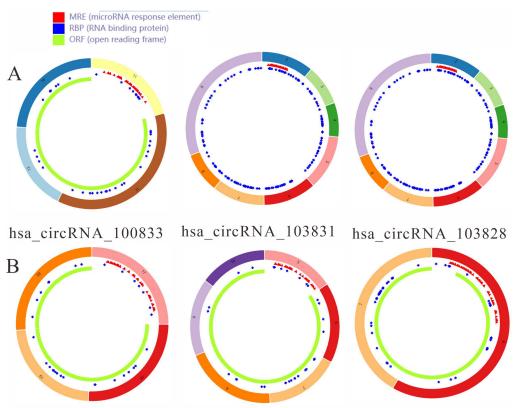


Figure S1 Boxplot represents the data quality of each chip is reliable after data standardization





hsa\_circRNA\_103752 hsa\_circRNA\_071106 hsa\_circRNA\_102293

Figure S2 The basic structural patterns of 3 up-regulated circRNAs and 3 down-regulated circRNAs predicted by CSCD. (A) hsa\_circRNA\_100833, hsa\_circRNA\_103831, hsa\_circRNA\_103828. (B) hsa\_circRNA\_103752, hsa\_circRNA\_071106, hsa\_circRNA\_102293. MicroRNA response element (MRE) is represented in red. The RNA binding protein (RBP) is represented in blue. The open reading frame (ORF) is represented in green.

Figure 3	S3
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hsa_circRNA_100833 vs. hsa 2D Structure	a_miR_765	Position	Conconvotion	Predicted By
183 7mer-m8 203 5'-cgtgtTCTTCCTCCTCCT-3' UTR :             3'-guaguGGAAGGAAGGAGGAGGA-5' miRNA Busket 3'pairing Seed			X	MT
hsa_circRNA_103831 vs. hsa	a_miR_411_5p	Position	Conservation	Predicted By
700 Tmer-m8 720 5'-ccgcTGCTATTCTGTCTACTg-3' UTR ::::::::::::::::::::::::::::::::::::	GTCTACT		×	MT
Imperfect 1179 match 1202 5'-aagATGCTACACCGGGGTCTGCTc -3' UTR ::!!!! 3'-gcaUGCGAUAUGCCAGAUGAu-5' miRNA maxim 3'pairing Seed			×	M
hsa_circRNA_103828 vs. hsa		Desition	0	Desisted Dec
2D Structure 53 <u>8mer</u> 74 5'-gctatctGAATATCCTATAGTa-3' UTR	Local AU	Position		Predicted By
	8mer	_	×	MT
293 5'-agataaaATAGTATCTATAGTg-3' UTR IIIIIIIII 3'-acucccccUUUCA-AGAUAUCAg-5' miRNA 2'pairing Seed		!_	×	MT
hsa_circRNA_103752 vs. hsa				
2D Structure Imperfect 98 match 121 5'-agATCTITATGGCAAACAGAGTg -3' UTR 3'-ggUAGA_AUGGULUGUCACAAu-5' miRNA asymptic Seed	Local AU	Position	Conservation	Predicted By
357 5'-aaATCAGTATCCAGTGTT-3' UTR 	CAGTGTT	- !-	×	MT
hsa_circRNA_071106 vs. hsa_miR_1206				
2D Structure    126  6mer  146    5'-ccggcAACACTTCTATGAACt-3'  UTR    3'-cgaauUd0XAGAUGUACAUGACUUGu-5'  miRNA    3'-cgaaiuda  25441    3'-pairing  Seed		Position	Conservation	M
243 5'-cttctATCATCAGGGCCATGAACt-3' UTR         : 3'-cgaauUUGUAGAUGUACUUGu-5' miRNA <u>Auxu</u> 3'pairing Seed		- 1		MT
351  8mer  370    5'-agTGGAAGAGCT-CATGAACa-3' UTR				MT
hsa_circRNA_102293 vs. hsa				
2D Structure    158  7mer-m8  179    5'-gcctgAAAGTG6CTGAGACGGg-3'  UTR  111111111111111111111111111111111111	GAGACGG 7mcr-m8	Position	Conservation X	Predicted By

Figure S3 The details of circRNA-miRNA potential interaction sites. MiRNA Binding Sites, circRNA and miRNA Binding secondary structure.

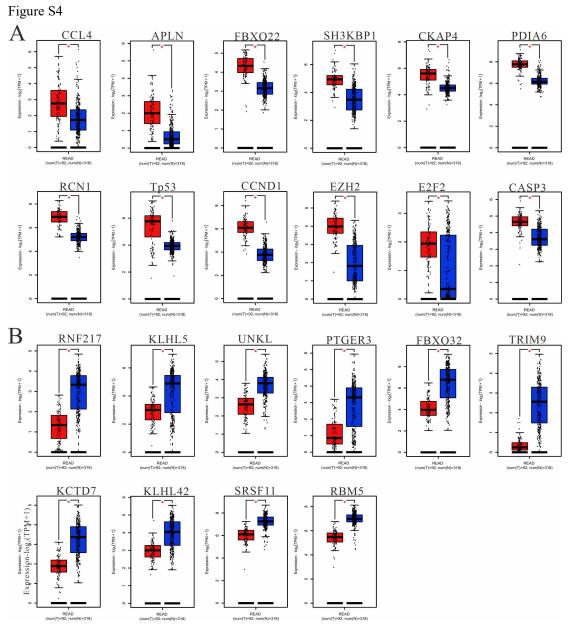


Figure S4 Hub gene expression. (A) Up-regulated hub genes via GEPIA analysis in READ tissues. (B) Down-regulated hub genes via GEPIA analysis in READ tissues. "\*" represent P<0.05, P<0.05 indicated a difference in comparison between the two groups.

## Figure S5

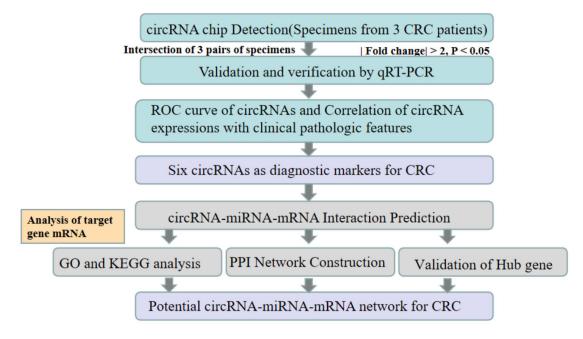


Figure S5 Flow Chart of this study