Boldmann	hsa_circRN	A_101062 vs hsa-miR		Conservation	Prodicted By
Alight of the second of the	87 7mer-m8 110 5'-caaGGTTTTACCAG-TGTGCCCAGc-3' UTR 3'-uucCUCGAGUCUUCGGGACGGGUCg-5' miRNA				
IntercretAl_101062 vs hsa-miRNA-212-5p Variable intercentant intercentan	162 5'-tatacaCTCTGTGAG-TTTGCCCAGe-3' UTR 3'-uuccucGAGUC-UUCGGGACGGGUCg-5' miRNA	TGCCCAG 7mer-m8		×	MT
3) 20 State of the second	hsa_circRN 2D Structure		NA-212-5p Position	Conservation	Predicted By
9 ² /2	3'-ucAUUCGUCAGAUCUCGGUUCCa-5' miRNA	7mer-m8	!	×	MT
hsa_circRNA_101062 vs hsa-miRNA-764	92 5'-ttTTACCAGTGTGCCCAGCCAGGGt-3' UTR 3'-ucAUUCGUCAGAUCUCGGUUCGa-5' miRNA	Imperfect	!	x	M
287 - space to conservation for a 228 units and the conservation for a conservation f	hsa_circRN	A_101062 vs hsa-miR	NA-764	Concernation	Producted Ry
hsa_circRNA_101062 vs hsa-let-7f-2-30 ************************************	207 <u>Smer</u> 228 5'-gagattctgcGTGGGCACCTGa-3' UTR 3'-uccuccuguuCACUCGUGGACg-5' miRNA			X	
⁴⁹ - getting control of the rest of	hsa_circRN				
hsa_circRNA_101062 vs hsa-miRNA-660-3p ***********************************	49 7mer-m8 71 5'-gctttGACCAGGTGACTGTATAc-3' UTR 3'-ccuuucu-GUCAUCUGACAUAUc-5' miRNA				
178	hsa_circRN			onconstion	Prodicted Ry
Iss_circRNA_100332 vs hsa-miRNA-892a Political Conservation Predicted BY 3'	178 7mer-m8 196 5'-ttgcCCA-GGA-ACAGGAGGt-3' UTR 3'-auuaGGACGUGUGUCCUCCa-5' miRNA				
20 Structure 198 379					
3*pairing Seed Main 3*starting Seed Position 3*starting Seed Conservation Predicted By 3*starting Seed Main Main Main 3*starting Seed Seed Main Main 3*starting Seed Seed Main Main 3*starting Seed Seed Seed Main Main 3*starting Seed	2D Structure	A_100332 vs hsa-miRN	A-892a Position	Conservation	Predicted By
arrest Seed bas_circRNA_100332 vs hsa-miRNA-216a-3p Conservation Predicted By 3 ³ -tatATTC14166ACT017Ct-3 ⁵ UTR 3 ³ -uauUAdscinctUCG010004Ct-1 ⁵ UTR 3 ³ -uauUAdscinctUCG01004Ct-1 ⁵ UTR 3 ³ -tacATGACGAGAGACC01 ² Ct-3 ³ UTR 3 ³ -balang Seed Matcata Do Structure Conservation Predicted By Offset 6 ² 2 ³ -tacATGACGAGAGACC01 ² Ct-3 ³ UTR 3 ³ -galang Seed Conservation Predicted By Solution Conser	3'pairing Seed	ACACAGTA III	- ' -	×	MT
20 Structure Local AU Postion Conservation Predicted By 3 ³ - taAATTC1ATGGACTGTACTGTG- 5 ³ UTR 3 ³ - subUAGGGUTUUG- duiAACu-5 ³ niRNA	688, <u>sker</u> 768 5'-cgcttcatgtgcACAGTa-3' UTR 3'-gaugcgucucUGGGUCA-5' miRNA 3'pairing Seed	ACACAGTA IIm	L	x	MT
33	hsa_circRN			Conservation	Predicted By
629 - tracATRACGGARA CARTGETER 549 3'- usual cartering 549 3'- usual cartering 549 3'- tracATRACGGARA CARTGETER 59 3'- tracATRACGGARA CARTGETER 59 5'- tracATRACGARA CARTGETER 50 5'- tracATRACGARA 50 5'- tracATRACGARA 50 5'- tracATRACGARA 50 5'- tracATRACGARA 50 5'- tracATRACGARA 50 5'- tracATRACGARA 50	3'-uaUUAGGGUCUCUGGUGACACu-5' miRNA	ACTGTG	-		_
hsa_circRNA_100332 vs hsa-miRNA-302c-3p Souther for the set of th	Offset 629 5'-tacATGACGGAGA-CACTGTCt-3'UTR 3'-uauUAGGUUCUGUUACACu-5' miRNA			x	
593		Offset omer			M
3' palling ised 3' palling ised 671. ascfcfAAC60TrCc43' CT - 3' UTR 3' - gguonumeration - 5' minNA magnetic - 1' X M hsa_circRNA_100332 vs hsa-miRNA-493-5p Conservation Predicted By 246 S'-ttr66A16-CT6AC4 TOTACA - 3' UTR 3' - gguonumeration	hsa_circRN				
3' parting Seed hsa_circRNA_100332 vs hsa-miRNA-493-5p 265 3' - tutGGAIG-CTGACAIGTACAA-3' UTR 3' - uuAcUULGGALGGGUACADGUU-5' mIRNA 3' parting Seed hsa_circRNA_100332 vs hsa-miRNA-200c-5p Conservation Predicted By 262 5' - tacAACCT - CTCTGTAACA-2' UTR 3' - sguudguagaGACCCULCucc-5' mIRNA	hsa_circRN/ 2D Structure 593 Offset 615 5'-ttgTTAAGAACTTGGAACTTCG-1' UTR	A_100332 vs hsa-miRN	Position	Conservation X	Predicted By
20 Structure Local AU Postion Conservation Predicted By 246 5' - ttrGGATG-CTGACATGTACAa-3' UTR	Los Structure 593 5°- ctigo Tadacado Tigo Angelo 3°- geigo da culori, cta 3° una 3°- geigo da culori, cta 3° una 3° paleing Expertert	A_100332 vs hsa-miRN	Position	×	Predicted By
3'pairing Seed Anti- hsa_circRNA_100332 vs hsa-miRNA-200c-5p 20Structure Cocal AU Position Conservation Predicted By 5'-tacAAGCCT-CTCTGTAGAC-3' UT AT AGAC Conservation Conser	20 Structure Offset 593 5 * Structure 5 * Structure 1 * Seguedander Callet - Structure 3 * Seguedander Structure 5 * Structure 615 5 * Seguedander Structure 615 616 617 618 619 619 610 610 610 611 611 612 613 614 615 616 617 618 619 621 610 611 611 612 613 614 614 615 616 617 618 619 619 619 610 610 6111 6111 612 613 <	A_100332 vs hsa-miRN Local AU Citist fine Citist fine Imperfect	Position	×	Predicted By
2D Structure Local AU Position Conservation Predicted By 262 TetracAACGT-CTCTGTARGAC-3' UTR 3'- tgguodocascGACCAUCUCC-5' mIRNA	hsa_circRN.	A_100332 vs hsa-miRN	Position	×	Predicted By
262 - Techano Carto Cart	bsa_circRNA	A_100332 vs hsa-miRN	Position	X X Conservation	Predicted By
	Biggeric Systemer	A_100332 vs hsa-miRN Local AU 	Position	X X Conservation X	Predicted By (f) (h) President By (f) T

Supplementary Fig. 3. Detailed annotation of circular RNA (circRNA)/microRNA (miRNA) interaction for hsa_circRNA_101062 and hsa_circRNA_100332. For each circRNA, five predicted miRNA response elements are included: (A) hsa_circRNA_101062, (B) hsa_circRNA_100332.