Additional file

Title: Mechanism of piR-DQ590027/MIR17HG Regulation of Permeability across the glioma conditioned normal BBB

Additional file Summary

-- Figure Legends

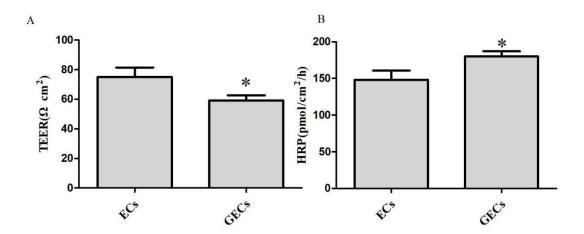
- Figures

Figure.S1 The permeability of glioma-conditioned normal BBB was increased. "ECs" represents co-cultured ECs (hCMEC/D3) with human astrocytes; "GECs" represents co-cultured ECs (hCMEC/D3) with glioma cells. (A) TEER values in the *in vitro* glioma-conditioned normal BBB model. Data represent the mean \pm SD (n = 5, each). *P < 0.05 vs. the ECs group. (B) HRP flux in the *in vitro* glioma-conditioned normal BBB model. Data represent the mean \pm SD (n=5, each). *P < 0.05 vs. the ECs group. (B) HRP flux in the *in vitro* stronglioma-conditioned normal BBB model. Data represent the mean \pm SD (n=5, each).

Figure.S2 The prediction results of Bioinformatics software. (A) The predicted binding site for piR-DQ590027 in the base sequence of MIR17HG. (B) The predicted binding sites of MIR17HG and miR-153/miR-377. (C) The predicted binding sites of miR-153 and miR-377 in 3'UTR of FOXR2. (D) The predicted binding sites of FOXR2 and the promoter regions of ZO-1, claudin-5 and occludin respectively ("yeloow" represents the binding sites; "red" represents transcription start site).

Figure.S3 The schematic cartoon underlying the mechanism of piR-DQ590027 /MIR17HG regulating the permeability of glioma conditioned normal BBB.







2. piR_N	lame: hsa_piR_014633								
Accessio	on: DQ590027								
	26 bases								
FASTA Se	somal position: <u>13:92005142-9200</u>	05167 [Minus]	(NCBI:	37)					
)hsa_i	01R_014633 gb DQ590027 Homo_sapiens:	:13:92005142:92	2005167:M	inus					
UGGUCI	ICGAACUCCUGACCUCAGGUA			8740 TA					
BDeveload - Graphy	18 245137 Longth: 20 Number of Matches: 1					A Descript			
Range 1: 1 to 30 Qr	achics v		a matata		Rickated Inform	mation			
50.5 bits(30)	Expect Identifies Gaps 28-12 30/30(100%) 0/30(0%)	Strand Phys/Phys							
Guery 3814 TAAODOCK	International and and the state of the state								
Ibjet I Tanoitoca	CladesCateFatPinasta 30								
niRNA-Target Inf	ormation								
(1) IncRNA:miRNA	MIR17HG:hsa-miR-377-3p								
Target Location	chr13:92003466-92003491[+]								
Target Name	MIR17HG								
Target Transcripts	MIR17HG-003 MIR17HG-002								
ClipSeq peakCluster	HPKMA 4052/AGO2 PAR-CLIP HEK293) HPSLC								
	HPC01 11440(AGO2 FAR-CLIP BC-1) HPRTA 16859(AGO2 FAR-CLIP HEX283) HPRO7 050(AGO1 FAR-CLIP HEX283) HPRT3 7555(AGO2 FAR-CLIP HEX283) HPTA3 5559(AGO3 FAR-CLIP HEX283)								
	HETA4 1036/AGO4 RAR-CLIP HEK293) HPTK1 9850/AGO2 RAR-CLIP HEK293) HPROB 4350/AGO1 RAR-CLIP HEK293) HPROB 22699/AGO1 RAR-CLIP HEK293) HPTA1 3414/AGO1 RAR-CLIP HEK293) HPRMB 2169/AGO2 RAR-CLIP HEK293)								
	HPRO6 22099(AGO1 PAR-CLIP HER292) HPTA HPRO6 22700(AGO1 PAR-CLIP HER293) HPSL			HPKMB_2169(AGOJ	PAR-CLIP HEK293	D			
ClipSeq ReadNum	2380170	Contraction of the local data							
miRIGA-target									
	niRNA 3'-tgtTTTCAACGGAAACACACTa-S'								
	ncRNA 5'-tgcAGGTTTGCATCCAGCTGTGTGAt-3'								
alignScore	142								
miRNA-Target In	formation								
(1) IncRNA:miRNA	MIR1216G:https://miR-153-2p								
Target Location	chi13:92023186:92003209[+]								
Target Name	MIRAZHG								
Target Transcripts	MIRLING-002 HIRLING-002								
ClipSeq peakCluster	HPROB 22097(AGO1 PAS.CLIP HER283) HPKR HPKMB 2107(AGO2 PAS.CLIP HER283) HHRT	A 15409(AG02 HITS	-CLIP HEK291	HPCB1 11437(AG	O2 PAR-CLIP BC-1	1			
	HPHES 2228/AGO2 FAR-CLP RESCIPA-001) HPSEF 6439(AGO2 FAR-CLP RE3D-AGO2) HPSEB 2136(AGO2 FAR-CLP LCL-BAC) HPSEB 6348(AGO2 FAR-CLP RC-2) HPRTE 3024(AGO2 FAR-CLP REX230) HPRO7 655(AGO1 FAR-CLP REX230)								
	HPROB AJMRAADI MANCUM HELIDI HPRIJ ZASKADU PARCUM HELIDI HELIDI HPROJ ZANADU PARCUM HELIDI HPROJ JUJZADU MACUM HULIBACOJI HPRUC JANKADU PARCUM LUUJI HPTAL JALZADU MARCUM HEKIDI								
	HPTA3 5556(AGO2 PAR-CLIP HEX293) HPTA4	1033/AG04 PAR-CL	IP HEK293)	HPTK1 0050(AG02 6	AR-CLIP HEK293)				
ClipSeq Readlium	HPTK7 2252/AGO2 PAR-CLIP HEK292] HPTA7 4.14700#+00	510(AGO2 PAR-CLIP	P. HEK293)						
milluiA-target									
100000000	#1998 3'-ctxGTGAAAGACACTGATACGTt-5' -								
	ecRob 5" - atgTAGTTGTGCGAATCTATGCAp-3"								
alignocore	146								
	Predicted consequential pairing of larget is and miRNA (bottom)	egion (top) Site type	Context++	Context++ score	Weighted	Conserved bras			
ation 1181-1188 of FOXR	and miRNA (bottom)		score	percentile	context++ score	length			
-miR-153-3p	2 3 UTR 8' 00000ACA0000000A06CAA 1111 11111 3' 00606AAAACA00CA00CA00000	8mar		99	-0.48	1.059			
ation 1438-1444 of FOXR		7mer-A1		85	-0.17	0.499			
-miR-193-3p	3' CURFUGAMACACUGAINCSUU	Indicat .			2011	D and			
Participation and and a	And the second descent of the second s	H.							
hsa-miR-3	77/FOXR2 Alignment								
				1					
Sector Constant		3' ugUUUUCAACGGAAACAC-ACUa 5' hsa-miR-377				mirSVR score: -1.0706			
		-m1R-377		mirSVR sc	ore: -1.	0706			
	JUCAACGGAAACAC-ACUa 5' hsa 	-m1R-377			ore: -1. s score: 0.6				

D

AGICTAGAGGCTEGGAGGCCAGGAGTACCAAGGAGGAGGAGCAGCCCCTGGAGAGTIGA



