

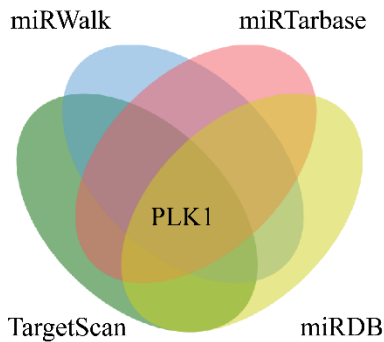
A

CircRNA Mirbase ID	CircRNA (Top) - miRNA (Bottom) pairing	Site Type	CircRNA Start	CircRNA End	3' pairing	local AU	position	TA	SPS	context+ score	context+ score percentile
hsa_circ_0000615 (5' ... 3')	GAGCCUUGAAUCUUGAGGUGGGA GACUCCUCUCUCCUCCACCCC	8mer-1a	107	114	0.003	0.057	-0.087	0.038	-0.137	-0.373	99
hsa-miR-1224-3p (3' ... 5')											

B

circ-ZNF609 wt 5'-GAGCCUUGAAUCUUGAGGUGGGA-3'
 miR-1224-3p 3'-GACUCCUCUCUCCUCCACCCC-5'
 circ-ZNF609 mut 5'-GAGCCUUGAAUCUUGUCCACCCA-3'

C



D

PLK1 wt 5'-CUGCAUCAUCCUUGCAGGUGGG-3'
 miR-1224-3p 3'-GACUCCUCUCUCCUCCACCCC-5'
 PLK1 mut 5'-CUGCAUCAUCCUUGC UCCACCCG-3'

Fig S1: Circ-ZNF609 might act as a ceRNA to bind to miR-1224-3p with PLK1

(A) Bioinformatics websites (cirinteractome: <https://circinteractome.nia.nih.gov/>) was used to predict miRNAs that could bind to circ-ZNF609. (B) The bioinformatics website predicted the binding sites of circ-ZNF609 and miR-1224-3p, and constructed circ-ZNF609 wild-type plasmids and mutant plasmids. (C) Possible targets of miR-1224-3p were predicted through the bioinformatics website (miRWalk, miRTarbase, TargetScan and miRDB) and PLK1 may be a potential target through the intersection. (D) The bioinformatics website predicted the binding sites of PLK1 and miR-1224-3p, and constructed PLK1 wild-type plasmids and mutant plasmids.