

Table SI. Primers and siRNAs

Primers and siRNAs	Sequence
GAPDH	F: CTCTCTGCTCCTCCTGTTCG R: TGACTCCGACCTTCACCTTC
circ72309	F: TAAAGTGG AACGACAGGGGT R: CATCTGTGCAATGCAGTCAGTC
SLC29A1	F: GTGCCTTCGGCTACTTTATCAC R: GCTAATGAGGTCCA ACTTGGTCT
CDA	F: AAGTCAGCCTACTGCCCTAC R: GATAGCGGTCCGTT CAGCAC
miR-1225-3p	TGAGCCCCTGTGCCGCCCCCAG
miR-1234	TCGGCCTGACCACCCACCCAC
si_circ72309	Sense: 5'-CTCGTAAAATTAGACTGACTG dTdT-3' Antisense: 5'-CAGTCAGTCTAATTTTACGAG dTdT-3'

circRNA, circular RNA; miR, microRNA; si, small interfering.

Table SII. Sequencing coverage and quality statistics for each sample

Sample ID	Status	Total number of sequenced reads	Total number of uniquely mapped reads (mapping rate based on hg19)	RIN	rRNA rate	Total number of detected transcripts with reads ≥ 1
GA69617	GR3_circ72309OE	30,050,782	94.9%	>7	NA	9,959/26,255
GA69618	GR3_circ72309OE	26,439,586	95.1%	>7	NA	10,314/26,255
GA69619	GR3_circ72309OE	40,165,973	95.0%	>7	NA	9,716/26,255
GA69620	GR3_NC	28,185,480	91.4%	>7	NA	9,951/26,255
GA69621	GR3_NC	24,407,074	91.8%	>7	NA	10,112/26,255
GA69622	GR3_NC	24,572,356	91.5%	>7	NA	10,052/26,255

Table SIII. Target miRNAs of circ72309 predicted by CircInteractome

Target miRNAs of circ72309 predicted by CircInteractome

hsa-miR1206	hsa-miR149	hsa-miR518a-5p
hsa-miR1225-3p	hsa-miR326	hsa-miR527
hsa-miR1234	hsa-miR330-5p	hsa-miR543
hsa-miR1257	hsa-miR331-5p	hsa-miR579
hsa-miR127-5p	hsa-miR375	hsa-miR580
hsa-miR1276	hsa-miR409-3p	hsa-miR607
hsa-miR1277	hsa-miR492	hsa-miR648
hsa-miR1299	hsa-miR515-5p	hsa-miR665
hsa-miR1305	hsa-miR516b	

Bold entries represent miRNAs identified by TargetScan as having putative binding sites with *SLC29A1*.

Table SV. Primer–target overlap within the circ72309 back-splice junction sequence.

Primer–target overlap within the circ72309 back-splice junction sequence

5'-

CCTAAAGTGGAAACGACAGGGGTCAGGTTTTCCACACCCGCTCAAATGTTTATCTGGGAAATTAAGTTCTACGTAAAGAGAGTATGG
AGCTCGTAAAATTA|GACTGACTGCATTGCACAGATGATGAGATATTTACGTATGTTGAAACGACCATCCTGGATGTGGACAATAAAA
AAGATGAGGACTGCTCAAATTCCAG -3'

The full circ72309 back-splice junction sequence (5'→3') is shown, with the forward primer sequence highlighted in red and the reverse-primer binding region highlighted in blue. The vertical bar (|) indicates the precise back-splice junction.
