

Supplementary Table S1 RNA Primer sequences

Gene	Primer Sequence
hsa_circ_0000118	Forward-TTGCAAGGAAAGGACACTCC Reverse-CGTTCTTCCTCTTCCCTCCT
hsa_circ_0000284	Forward-TCGGCCAGTCATGTATCAA Reverse-CCCTTAGTGGGAGGATGAGA
hsa_circ_0000567	Forward-CAAACCCTCCCCAGTGAATA Reverse-TCCTTTGGTGACACAGTTGC
hsa_circ_0000119	Forward-GGAGGCCTACTTGCAGCATA Reverse-GCTTCTTCCAAGGCCTTCTC
hsa_circ_0000847	Forward-TATTCCAGAAACGCCACCTC Reverse-TTCCATCCCAGCAGTCTCTT
hsa_circ_0000117	Forward-GGGCAAAGATGGATTGAAGA Reverse-AATAGGGACTGGTGGCAGTG
hsa_circ_0001829	Forward-GTGATGTTTGGCAGGGAGTT Reverse-TGGCTTGCTGGTTTACTGTG
hsa_circ_0002484	Forward- AAGTGTCCCAGCCTGTCACT Reverse- AGCTTTCCAAGCATTTCTG
hsa_circ_0000620	Forward- CTGAATGCCAATGTGTGGTC Reverse- CTATCAAGGCCCGATTTTTG
hsa_circ_0000592	Forward- CATGCAGTTGATGGGACAAC Reverse- TGAAGCTTCCGTTCTGGTCT
hsa_circ_0003221	Forward- GGGGCAATGCACTAGAAAAG Reverse- CCAGGTGGTTGGCTCACTAT
hsa_circ_0000268	Forward- TTGGCTCTTCCCTCAATGCTT Reverse- TCTTTGGGCACGACACATAG
hsa_circ_0074990	Forward- ATCTTCGAGGGATTGCCTTT Reverse- GACACCTGAAGTCGCTGAGA
hsa_circ_0004594	Forward- GCGAGAAGCTCACCTTCAAC Reverse- CCAGAAGACCACCTTCTCCA
hsa_circ_0004873	Forward- ATGGTGACCTGGCTAACTGG Reverse- CTTCCCATCTCCCTCTTTC
GAPDH	Forward-CAATGACCCCTTCATTGACC Reverse-GACAAGCTTCCCGTTCTCAG
U6	Forward -CTCGCTTCGGCAGCACA Reverse-AACGCTTCACGAATTTGCGT

Supplementary Table S2 siRNA sequences

siRNA	sequences
si-hsa_circ_0000592-1	sense 5'-AAUAAGACUUCUUGAAGAC-3', antisense 5'-GUCUUCAAGAAGUCUUUU-3'
si-hsa_circ_0000592-2	sense 5'-AGAAGUCUUUUUGCCAGCA-3', antisense 5'-UGCUGGCAAUAAGACUUCU-3'
negative control siRNA	sense 5'-UUCUCCGAACGUGUCACGU-3', antisense 5'-ACGUGACACGUUCGGAGAA-3'

Supplementary Table S3

circRNA hsa_circ_0000592	oligonucleotide probe sequence
	TCTTATTGCCAGCAGTTTTGAAGATGACTCCCCTGTAGCCTCA CCGTTAGACCAGAACGGAAGCTTCAATGTTGTTATTAAGAG GAACCTCTAGATGATTATGACTACGAACTTGGTGAGTGCCCAG AAGGGTCACTGTGAAACAGGAAGAGACAGATGAAGAGACG GATGTATACTCAAACAGTGATGATGATCCTATACTAGAGAAAC AGCTAAAGAGGCACAATAAAGTTGACAACCCAGAAGCTGAC CATCTATCTTCTAAATGGCTTCCAAGCAGCCATCAGGTGTTG CTAAAGCTAAAATGTTCAAATTAGACACTGGAAAGATGCCAGT AGTCTATCTGGAGCCCTGTGCTGTCACCAGAAGCACAGTTAA GATTTCTGAACTCCCCGATAACATGCTTCCACATCTCGAAAG GATAAATCTTCTATGTTGGCAGAATTGGAATATTTGCCTACATA CATTGAAAATCCAATGAGACTGCCTTCTGCTTAGGCAAGGAA TCAGAAAATGGTCTTAGAAAACATTCACCAGATCTCAGAGTG GTACAAAAATATCCCTTACTGAAAGAGCCTCAGTGGAATATC CTGATATATCTGACAGCATTAGCACAGAAAGAATACTCGACGA TTCAAAGGATTCAGTTGGAGACTCACTTTCAGGAAAAGAGGA CTTGGGCAGAAAGAGAACAACACTATGCTTAAGATTGCAACAGC CGCAAAGGTAGTGAATGCTAATCAGAATGCCTCTCCAAATGTC CCTGGAAAAAGAGGAAGGCCACGAAAATTGAACTCTGTAA GGCAGGACGACCACCTAAGAACACAGGAAAGTCTTTAATTTT TACAAAGAATACACCTGTAAGCCCTGGGAGTACCTTTCAGAT GTGAAGCCTGATCTGGAAGATGTGGATGGTGTCTCTTTGTTT CCTTTGAATCAAAGGAAGCTCTAGACATTCATGCAGTTGATGG GACAACAGAAGAATCTTCTAGTCTCCAGGCATCAACCACAAA TGAATCAGGTTACAGAGCAAGAATTTCCAGTTGGAAAAGGA ATTGATAGAAGATTTGAAGACTTTGCGGCACAAGCAGGTGAT ACATCCTGGTCTTCAAGAAG