


Supplemental Table 1. Candidate *hsa-miR-206-3p* binding circRNA divergent primer sequences.

Candidate circRNA	Forward	Reverse	Host Gene	Host gene Accession #
<i>hsa_circ_0000199</i>	ATCATTGCTTTCAGGGCTCT	CACCCGCTCTCTCGACAAAT	<i>AKT3</i>	NM_181690
<i>hsa_circ_0001264</i>	CAGCTCATTAAAAGGCACCA	GGAAGAAGCAGGAGATTTGG	<i>RAD18</i>	NM_020165
<i>hsa_circ_0001982</i>	CAATCCAGCTGTTCCCTCAG	TGGTGCATCAGAAGGAATCTC	<i>RNF111</i>	NM_017610
<i>hsa_circ_0004662</i>	GTGTGGGAGCACGCTTACTA	CGTTAGGGCTGAGGTTTGTC	<i>SOD2</i>	NM_001024465
<i>hsa_circ_0007428</i>	GCAGGAGAGGGTAGTTGTGC	TCCCCAAGTACCAAGTGCAT	<i>SH3BP4</i>	NM_014521
<i>hsa_circ_0008726</i>	GGTGGAAGGGACCCATTTTC	TGCCTCCGCTACTTGCTTG	<i>DNAJB6</i>	NM_058246
<i>hsa_circ_0056618</i>	GAACCCACCCACCTCTAC	CTTCCCCGGGATAAACAAACC	<i>SPOPL</i>	NM_001001664
<i>hsa_circ_0057558</i>	AGTCACTGCAGGCATGTTC	TGCAACAAGGAATGTAAGA	<i>SLC39A10</i>	NM_001127257
<i>hsa_circ_0058141</i>	GCCCTCAATTCATTCCAATG	TGAGGCTCTCTTCTTCATCA	<i>FN1</i>	NM_212482
<i>hsa_circ_0072088</i>	ACGCATTCTTCGAGACCTCT	TGCCTGTAACTCCTCTTCAGT	<i>ZFR</i>	NM_016107


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miRNA ID:

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

circBase ID:

circRNA conservation ☐

circRNA m6A ☐

Protein coding potentation coding_prob >=

Search

circBank ID	circbase ID	length	miRNA ID (miR_ID)	miRanda binding site (positions)	targetscan binding site (positions)
No matching records found					

Figure S1. Screenshot from CircBank (<http://www.circbank.cn/searchMiRNA.html>; accessed July 8th, 2024), showing no predicted binding between *hsa-miR-381-3p* and *hsa_circ_0008726*.