

Table SI. Primer sequences used for reverse transcription-quantitative PCR.

Primer name	Sequences (5'-3')
lncKRT16P6	F: CGAGGATGCCCAATGAGTCT R: GAGGAGGAGAGGCTGTGAAG
miR-3180	F: ATATCGTGGGGCGGAGCTT R: AGTGCAGGGTCCGAGGTATT RT: GTCGTATCCAGTGCAGGGTCCGAGGTA TTCGCACTGGATACGACCTCCGG
miR-mimics NC	F: UUCUCCGAACGUGUCACGUTT R: ACGUGACACGUUCGGAGAATT
hsa-miR-3180 mimics	F: UGGGGCGGAGCUUCCGGAG R: CCGGAAGCUCCGCCCAU
miR-inhibitor NC	CAGUACUUUUGUGUAGUACAA
hsa-miR-3180 inhibitor	CUCCGGAAGCUCCGCCCA
GATAD2A	F: AATCCACAGCATTAGGCAACATT R: GATGATCCTCTGTCCCTGAATCT
GAPDH	F: CACCCACTCCTCCACCTTTGA R: TCTCTCTTCCTCTTGTGCTCTTGC
U6	F: CTCGCTTCGGCAGCACA R: AACGCTTCACGAATTTGCGT

lnc, long noncoding; miR, microRNA; NC, negative control; F, forward; R, reverse.

Table SII. Sequences of the si/shRNAs.

siRNAs	Sequences (5'-3')
si-NC	F: UUCUCCGAACGUGUCACGUTT R: ACGUGACACGUUCGGAGAATT
lncKRT16P6-si-1	F: CCAGCUCAGCAUAAAGCAUTT R: AUGCUUUAUGCUGAGCUGGGA
lncKRT16P6-si-2	F: GCAAUCAAUACAGCUUCAUTT R: AUGAAGCUGUAUUGAUUGCCA
sh-NC	F: GATCCGTTCTCCGAACGTGTCACGTTT CAAGAGAACGTGACACGTTCCGGAGAA CTTTTTTG R: AATTCAAAAAAGTTCTCCGAACGTGTC ACGTTCTCTTGAAACGTGACACGTTTCG GAGAACG
sh-lncKRT16P6	F: GATCCGCAATCAATACAGCTTCATTTC AGAGAATGAAGCTGTATTGATTGCTTTT TTG R: AATTCAAAAAAGCAATCAATACAGCTT CATTCTCTTGAAATGAAGCTGTATTGAT TGCG
GATAD2A-si-1	F: CCACAGCAUUAGGCAACAUTT R: AUGUUGCCUAAUGCUGUGGTT
GATAD2A-si-2	F: GGCAGACAUUCUGAGAGAATT R: UUCUCUCAGAAUGCUGCCTT

si, small interfering; sh short hairpin; NC, negative control; lnc, long noncoding; F, forward; R, reverse.

Table SIII. Sequence information of the fluorescence *in situ* hybridization probes.

Probe	Sequences (5'-3')	Modification
lncKRT16P6 probe	GT+TGT+TGG+TGCGAAGGACC+T	5'CY3
lncKRT16P6 probe-1	GAAG+TGCT+TAGGCGGCAGG+AGA	5'CY3
18S	CTGCCTTCCTTGGATGTGGTAGCCGTTTC	5'CY3
NC	TGCTTTGCACGGTAACGCCTGTTTT	5'CY3

lnc, long noncoding; NC, negative control.