

Figure S1. Bioinformatics analysis of HAND2-AS1-related genes. (A) Using GSE15709, Pearson's correlation coefficient analysis was performed by a Psych toolkit with R language to identify genes positively correlated with HAND2-AS1. A total of 124 genes were positively correlated ($r>0.95$, $\text{adj.P}<0.01$) and 78 were negatively correlated with HAND2-AS1 ($r<-0.95$, $\text{adj.P}<0.01$). (B) Co-expressed genes were analyzed by Gene Set Enrichment Analysis based on the tumor marker pathway gene set (Hall mark genesets: h.aLL.v7.2.entrez. GMT) from msigdb. (C) 'hallmark_Pi3K_AKT_MTOR_signaling' was found to be negatively associated with HAND2-AS1 ($P=0.0074$, $\text{adj.P}=0.0168$).

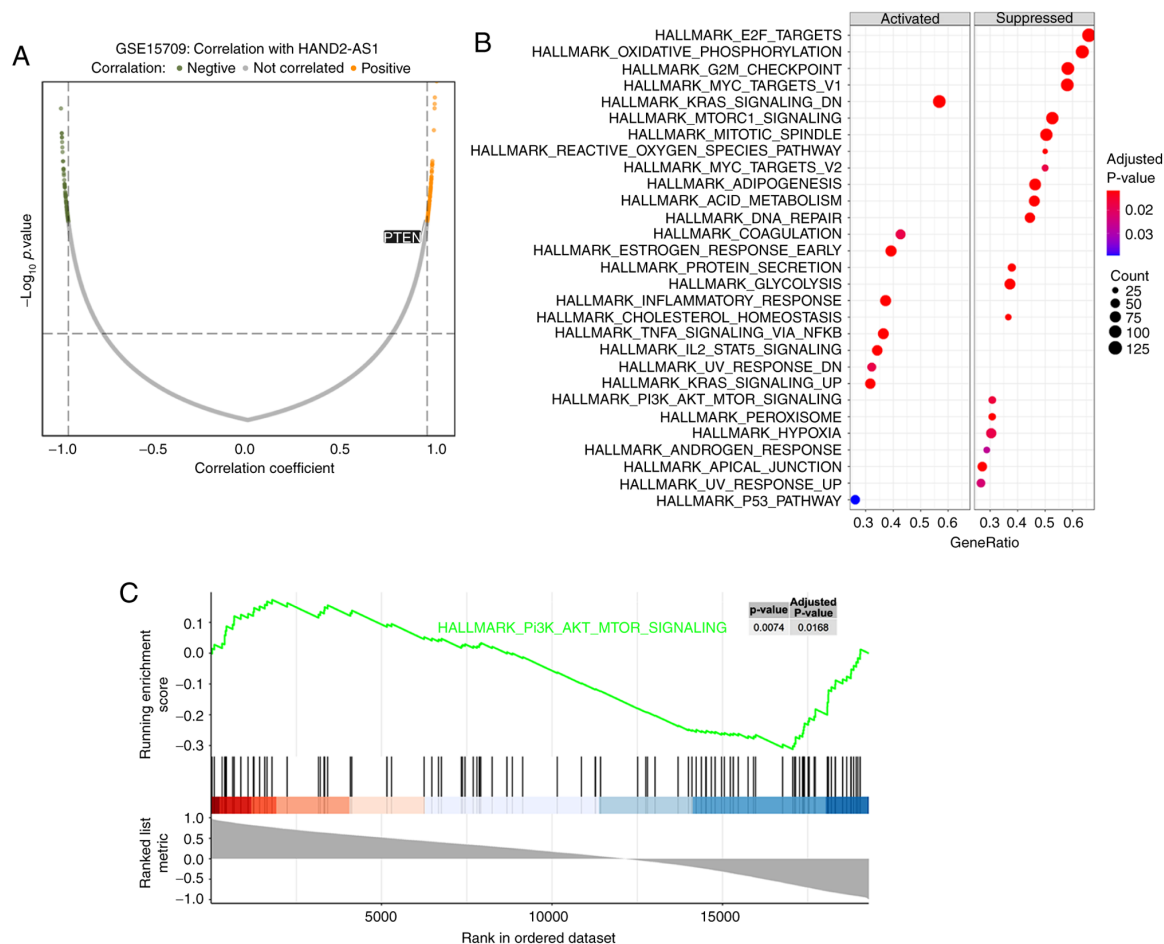


Table SI. Primer sequences used in the present study.

A, Primer sequences for RT-qPCR

Gene	Forward primer sequences (5'→3')	Reverse primer sequences (5'→3')
HAND2-AS1	GTAGTGTGGCTGGTATCGGTGTTT	TTCTGGAGTCACAGGCAGTCGT
GAPDH	ACAGCCTCAAGATCATCAGC	GGTCATGAGTCCTTCCACGAT
PTEN	TGAAGACCATAACCCACCACAGC	TACACCAGTTCGTCCCTTTCCAG
miR-106a-5p	GCAAAAGTGCTTACAGTGC	CAGTGCGTGTCGTGGA
miR-106a-5p RT	GTCGTATCCAGTGC GTGTCGTGGAGTC	
	GGCAATTGCACTGGATACGACCTACCT	
U6	CTCGCTTCGGCAGCACA	AACGCTTCACGAATTTGCGT

B, Primer sequences for transfection

Gene	Forward primer sequences (5'→3')	Reverse primer sequences (5'→3')
miR-NC	UUCUCCGAACGUGUCACGUTT	ACGUGACACGUUCGGAGAATT
Anti-NC	CAGUACUUUUGUGUAGUACAA	
miR-106a-5p mimics	AAAAGUGCUUACAGUGCAGGUAG	ACCUGCACUGUAAGCACUUUUUU
miR-106a-5p inhibitor	CUACCUGCACUGUAAGCACUUUU	
wt-HAND2-AS1	AATTCTAGGCGATCGCTCGAGAGGC	ATTTTATTGCGGCCAGCGGCCGCAG
	CAGCCTAGTTTGTATCAGC	TATCTGTATCACTTCAGCTGTGTCTG
mut-HAND2-AS1	CGAGATCGTGAAATAAAGTAAAAA	CTTTATTTACGATCTCGGTATA
	AGAAAAAACCATACT	GAACAAAGTAAATATTACAGTTT
wt-PTEN-3'UTR	AATTCTAGGCGATCGCTCGAGATCT	ATTTTATTGCGGCCAGCGGCCGCAA
	TGTTTTACCCTATACATCCACAG	CTTATCTGTTGCCACAAGTGCA
mut-PTEN-3'UTR	AGATGGGTGAATCCCGTTTTATTC	ACGGGATTCACCCATCTTTATTA
	CAGTTTTATAAAAA	ATCCTAATTGAATTTTAAATG
HAND2-AS1	CTAGCGTTTAACTTAAGCTTGA	TGCTGGATATCTGCAGAATTCTTTT
overexpression vector	TTGGCTACCTCCTCATAACCA	TTTTTTTTTTTTTAGATTCTGTAATTT
sh-NC vector	GATCCACACAGCAGGTCAAGAGG	AATTCAAAAAACACAGCAGGTC
	AGTCTCGAGACTCCTCTTG	AAGAGGAGTCTCGAGACTCC
	ACCTGCTGTGTTTTTTG	TCTTGACCTGCTGTGTG
sh-HAND2-AS1 vector	GATCCGCCGATTGTAAATGCT	AATTCAAAAAGCCGATTGTAAATG
	GTTATCTCGAGATAACAGCA	CTGTTATCTCGAGATAACAGC
	TTTACAATCGGCTTTTTTG	ATTTACAATCGGCG

RT-qPCR, reverse transcription-quantitative PCR; miR, microRNA; NC, negative control; wt, wild-type; mut, mutant type; sh, short hairpin.