

Supplementary Table and Figures

Table S1. PCR primer sequence, siRNA sequence, Agomirs and Antagomirs sequence

Name	Sequences (5'-3')
p66Shc mRNA for mouse	Forward: GTCCGACTACCTGTGTTTCCT Reverse: CAGCAGGATTGGCCAGCTT
p66Shc mRNA for human	Forward: GAGGCCATCAGTCTGGTGTGT Reverse: GCTGGTGGAGACGGTGAGA
PRKCB mRNA for mouse	Forward/convergent F: GCCATGAGTTCGTACCGTTC Reverse/convergent R: TGAGAACCTCTCTGTCTGATGTG
PRKCB mRNA for human	Forward: ATCGCCCCGAGATAATTGC Reverse: GGATGGCGGGTGAAAAATCG
β -actin mRNA for mouse	Forward/convergent F: AGAGGGAAATCGTGCGTGAC Reverse/convergent R: CAATAGTGATGACCTGGCCGT
β -actin mRNA for mouse	Forward/ divergent F: ACGGCCAGGTCATCACTATTG Reverse/ divergent R: GTCACGCACGATTTCCCTCT
β -actin mRNA for human	Forward: ACCCTGAAGTACCCCATCGAG Reverse: ACATGATCTGGGTCATCTTCTCG
circ-PRKCB for mouse	Forward/ divergent F: CACATCGACAGAGAGGTTCTCA Reverse/ divergent R: GAACGTGACGAACTCATGGC
circ-WDR37 for mouse	Forward: GACAGAACTGCCAACCTGTATG Reverse: GGAAAACATTCACGGAGTGG
circ-MGA for mouse	Forward: CCAAAATCAAGGGATGGAGAG Reverse: TTAAGATCAATGCTCACTGTTGG
circ-PRKCB for human	Forward: GCCGCATCTACATCCAGG Reverse: TGCACCACAAAGCAGCAA
p66Shc siRNA	AUGAGUCUCUGUCAUCGCUTT AGCGAUGACAGAGACUCAUTT
negative control siRNA	UUCUCCGAACGUGUCACGUTT ACGUGACACGUUCGGAGAATT
circ-PRKCB siRNAs	Provided by Ribobio
miR-339-5p agomir	UCCCUGUCCUCCAGGAGCUCACG UGAGCUCCUGGAGGACAGGGAAU
negative control agomir	UUCUCCGAACGUGUCACGUTT ACGUGACACGUUCGGAGAATT
miR-339-5p antagomir	CGUGAGCUCCUGGAGGACAGGGA
negative control antagomir	CAGUACUUUUGUGUAGUACAA

mmu_circ_0013842|ENSMUST00000143692|Prkcb
 Sequence ID: Query_54737 Length: 324 Number of Matches: 1

Range 1: 3 to 319

Score	Expect	Identities	Gaps
398 bits(215)	1e-115	283/317(89%)	0/317(0%)
Mouse 3	TGCTGCTTTGTGGTGCACAAGCGGTGCCATGAATTTGTCACATTCTCCTGCCCTGGCGCT	62	
Human 3	TGCTGCTTTGTTGTACACAAGCGCTGCCATGAGTTTCGTACGTTCTCCTGCCCGGTGGCG	62	
Mouse 63	GACAAGGGTCCAGCCTCCGATGACCCCGCAGCAAACACAAGTTAAGATCCACACGTAC	122	
Human 63	GACAAGGGCCCGCCTCTGATGACCCCGGAGCAAACACAAGTTAAGATCCACACGTAC	122	
Mouse 123	TCCAGCCCCACGTTTTGTGACCACTGTGGGTCACTGCTGTATGGACTCATCCACCAGGGG	182	
Human 123	TCCAGTCTTACCTTCTGTGACCACTGTGGATCGCTGCTGTATGGACTTATCACCAGGGG	182	
Mouse 183	ATGAAATGTGACACCTGCATGATGAATGTGCACAAGCGCTGCGTGATGAATGTTCCACGC	242	
Human 183	ATGAAATGCGACACCTGTATGATGAACGTGCACAAGCGCTGCGTGATGAACGTCCACGC	242	
Mouse 243	CTGTGTGGCACGGACCACACGGAGCGCCGCGCCGCATCTACATCCAGGCCACATCGAC	302	
Human 243	CTCTGCGGCACTGACCACACGGAACGCGCCGCGCCGCATCTATATCCAGGCCACATCGAC	302	
Mouse 303	AGGGACGTCTCATTGT	319	
Human 303	AGAGAGGTTCTCATTGT	319	

Figure S1. circ-PRKCB gene homology comparison.

circ-PRKCB homology between the human and mouse genomes was analyzed using the BLAST.

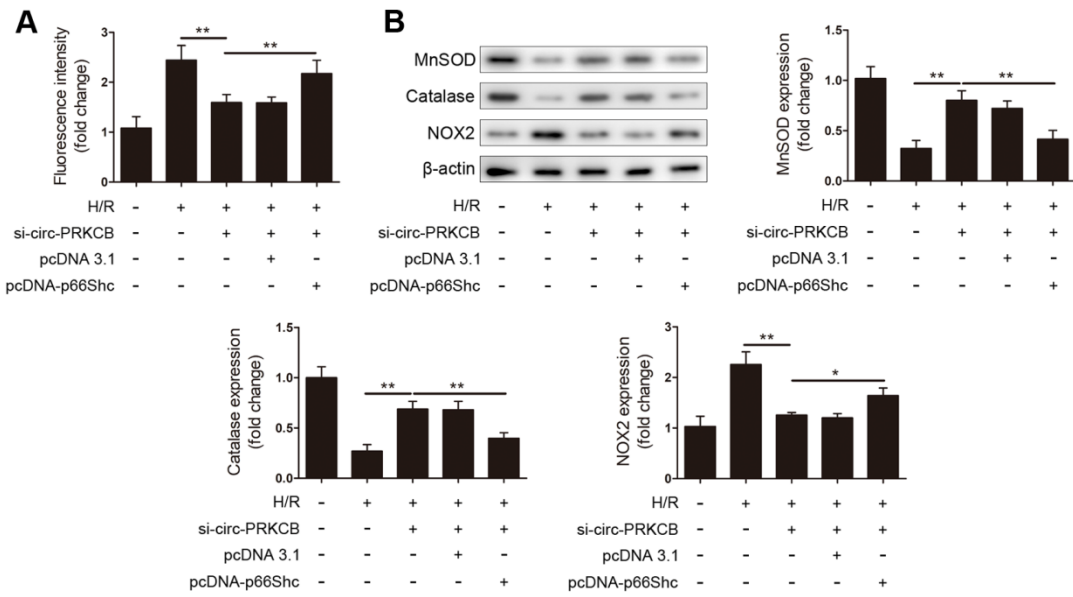


Figure S2. circ-PRKCB regulates H/R-induced oxidative stress through targeting p66Shc.

Caco-2 cells were cotransfected with circ-PRKCB siRNA or pcDNA-p66Shc and then exposed to H/R. **(A)** Fluorescence quantification of MitoSOX-stained cells. **(B)** MnSOD, catalase and NOX2 protein expression (n=3). * $P < 0.05$, ** $P < 0.01$. The values represent the mean \pm SD.