

Supplementary table 2. The list of primers used in the study.

Primer name	Sequence
PKN3 T639G F	TTTGTGGGTGAGTTTGTGCC
PKN3 T639G R	GCAGGCATGGCTGGAGGT
ARHGAP18 N200 F	TAGGATCCATGAGCTGGCTCTCCAGT
ARHGAP18 N200 R	TAGAATTCTCATTTGTTTTCATTTGTTCT
ARHGAP18 N50 R	TAGAATTCTCAGCTTTCCTGGTTCATAGT
ARHGAP18 Iso2 F	ACAAGTCCGGACTCAGATCTATGAACCAGGAAAGCACCACCA
ARHGAP18 Iso2 R	TGGTGGTGCTTTCCTGGTTCATAGATCTGAGTCCGGACTTGT
ARHGAP18 ΔN200 F	ATCTATGAGCTGGTACCAAGGAAGAGA
ARHGAP18 ΔN200 R	TCTCTTCCTTGGTACCAGCTCATAGAT
ARHGAP18 Δ201-323 F	CAAATGAAAACAAAGTTCCATTGACAGC
ARHGAP18 Δ201-323 R	GCTGTCAATGGAACTTTGTTTTCATTTG
ARHGAP18 ΔGAP F	CTGGTCTTTTTTGCCCCAAGTTTATTGT
ARHGAP18 ΔGAP R	ACAATAAACTTGGGGCAAAAAAGACCAG
ARHGAP18 ΔC525 F	AACTTCTGTGGACATAGAAGTCGAGAATTC
ARHGAP18 ΔC525 R	GAATTCTCGAGTTCTATGTCCACAGAAGTT
ARHGAP18 N200 Δ1-50 F	CGGACTCAGATCCATGACCACCATCAAAGTTA
ARHGAP18 N200 Δ1-50 R	TAACTTTGATGGTGGTCATGGATCTGAGTCCG
ARHGAP18 N200 Δ51-100 F	TATGAACCAGGAAAGCGTCAAAGAGCCTGATG
ARHGAP18 N200 Δ51-100 R	CATCAGGCTCTTTGACGCTTTCCTGGTTCATA
ARHGAP18 N200 Δ101-150 F	TCAAGAGGTGGTTGTTTCGAGTAGAGACGGTCT
ARHGAP18 N200 Δ101-150 R	AGACCGTCTCTACTCGAACAACCACCTCTTGA
ARHGAP18 N200 Δ151-200 F	AGCAGCAGTTCAGAAAGTGAGAATTCTGCAGTC
ARHGAP18 N200 Δ151-200 R	GACTGCAGAATTCTCACTTCTGAACTGCTGCT
ARHGAP18 N200 Δ1-12 F	CGGACTCAGATCCATGACAGCCTACCACCCCA
ARHGAP18 N200 Δ1-12 R	TGGGGTGGTAGGCTGTCATGGATCTGAGTCCG
ARHGAP18 N200 Δ13-25 F	CCAGGGAGTGGTACTAAACAGCCATGCAAAG
ARHGAP18 N200 Δ13-25 R	CTTTCATGGCTGTTTAGTACCACTCCCTGG
ARHGAP18 N200 Δ26-37 F	GGACCAGACCGTCGGGAGTCGCAGATATGGCC
ARHGAP18 N200 Δ26-37 R	GGCCATATCTGCGACTCCCGACGGTCTGGTCC
ARHGAP18 N200 Δ38-50 F	GGAGGAAGCCACGTCGACCACCATCAAAGTTA
ARHGAP18 N200 Δ38-50 R	TAACTTTGATGGTGGTCGACGTGGCTTCCTCC

Supplementary table 3. The sequence of synthesized ARHGAP18. Silent mutations were introduced in the design of ARHGAP18 cDNA in order to disrupt *XhoI*, *SacI*, *BamHI* and *NcoI* restriction sites.

ARHGAP18
TACAGATCTATGAGCTGGCTCTCCAGTTCCCAGGGAGTGGTACTAACAGCCTACCACCCCAGCGGCAAGGACC AGACCGTCGGGAACAGCCATGCAAAGGCAGGGGAGGAAGCCACGTCGAGTCGCAGATATGGCCAGTACACTAT GAACCAGGAAAGCACCACCATCAAAGTTATGGAGAAGCCTCCATTTGATCGATCAATTTCCCAGGATTCTTTG GATGAACTATCTATGGAAGACTATTGGATAGAACTAGAAAACATCAAGAAATCTAGTGAAAACAGCCAAGAAG ATCAAGAGGTGGTTGTTGTCAAAGAGCCTGATGAGGGAGAATTGGAAGAAGAGTGGCTTAAAGAGGCCGGTTT ATCCAATCTCTTCGGAGAGTCTGCTGGAGATCCACAGGAAAGCATTGTGTTTTTATCAACATTGACGCGGACC CAGGCAGCAGCAGTTCAGAAGCGAGTAGAGACGGTCTCCCAGACCTTGAGGAAAAAAAAACAAACAGTACCAGA TTCCTGACGTCAGAGACATATTTGCTCAACAGAGAGAATCAAAAGAAACAGCTCCAGGTGGCACTGAATCGCA GTCACTTAGAACAAATGAAAACAAATACCAAGGAAGAGATGACGAGGCATCTAACCTTGTTGGTGAAGAGAAG CTGATCCACCTGAGGAGACGCCTGCCCCTGAAACAGACATCAACCTGGAGGTATCATTTGCCGAGCAAGCAC TCAATCAGAAAGAGAGTTCCAAGGAGAAAATCCAGAAGAGCAAAGGCGATGATGCCACATTACCTAGTTTCAG ATTGCCAAAAGACAAAACGGGTACCACAAGGATTGGTGACCTCGCACCCCAGGACATGAAGAAAGTTTGCCAT TTAGCCCTAATTGAGCTGACTGCCCTCTATGATGTATTGGGTATTGAGCTGAAACAACAAAAAGCTGTGAAAA TCAAAACAAAAGATTCTGGTCTTTTTTTCGCTTCCATTGACAGCGCTATTAGAACAAGATCAGAGGAAAGTACC AGGAATGCGAATACCCTTGATCTTTCAAAAACCTGATTTCTCGAATTGAAGAGAGAGGTTTGAAAACAGAAGGC CTCTTACGAATCCCTGGAGCTGCCATTAGAATCAAGAATCTTTGCCAAGAAGCTAGAAGCAAAGTTTTATGAAG GGACTTTTAATTGGGAAAGTGTCAAACAGCATGATGCCGCCAGCCTGCTGAAGCTCTTCATTTCGGGAGTTGCC CCAGCCACTGCTCAGTGTGGAGTATCTCAAAGCCTTTTCAGGCTGTCCAGAATCTTCCAACCAAGAAGCAGCAA CTACAGGCTTTGAACCTTCTTGTCATCCTCCTACCTGATGCAAACAGGGACACACTGAAGGCCCTTCTTGAAT TTCTCCAAAGAGTAATAGATAATAAAGAAAAAAATAAAATGACAGTCATGAATGTAGCAATGGTCATGGCCCC GAATCTCTTTATGTGTCATGCATTGGGATTGAAGTCCAGTGAACAGCGAGAATTTGTAATGGCAGCTGGGACA GCAAATACCATGCACTTATTGATTAAGTACCAAAAACCTTCTGTGGACAATTCCCAAGTTTATTGTAAACCAAG TGAGGAAGCAAAACACGGAAAATCATAAAAAGGATAAAAAGAGCCATGAAGAAATTGCTGAAGAAAATGGCTTA TGACCGAGAAAAATATGAAAAGCAAGATAAGAGTACAAATGATGCTGACGTTTCCTCAGGGAGTGATTTCGAGTG CAAGCTCCCCATCTTTCGAAAGTTTCAATGGCAATACAGCTAACTGAAGAACTAAAAGCCAGTGATGTACTTG CCAGGTTTCTCAGCCAAGAAAGTGGGGTTGCCCAGACTCTCAAGAAAGGAGAAGTTTTTTTTGTATGAAATTGG AGGAAATATTGGGGAACGCTGCCTTGATGATGACACTTACATGAAGGATTTATATCAGCTTAACCCAAATGCT GAGTGGGTTATAAAGTCAAAGCCATTGTAGAACTCGAGAATTCTGA