

Supplementary Figure 1

1 GAAACACAATAGCAGCTCCCTCCAAG

ATG GCG GCG GCG ACG GCA GAC CCG GGA GCT GGG AAC CCG CAG GCT GGG GAC TCC TCC GGT
 Met Ala Ala Ala Pro Ala Asp Pro Gly Ala Gly Asn Pro Gln Ala Gly Asp Ser Ser Gly
 GGG GAC TCC GGG GGC GGG CTA CCG TCA CCT GGA GAG CAG GAA CTG AGT CGG CGC CTG CAG
 Gly Asp Ser Gly Gly Gly Leu Pro Ser Pro Gly Glu Gln Glu Leu Ser Arg Arg Leu Gln
 CGC TTG TAC CCT GCG GTT AAT CAG CAC GAG ACG CCG CTG CCG CGC TCC TGG AGC CCC AAG
 Arg Leu Tyr Pro Ala Val Asn Gln His Glu Pro Pro Leu Pro Arg Ser Trp Ser Pro Lys
 GAC AAG TAC AAC TAC ATC GGC CTC TCC CAG GGA AAC CTC CGT GTC CAT TAC AAA GGT CAT
 Asp Lys Tyr Asn Tyr Ile Gly Leu Ser Gln Gly Asn Leu Arg Val His Tyr Lys Gly His
 GGC AAA AAT CAC AAA GAT GCA GCC TCT GTA CGT GCC ACC CAC CCC ATC CCA GCA GCC TGT
 Gly Lys Asn His Lys Asp Ala Ala Ser Val Arg Ala Pro His Pro Ile Pro Ala Ala Cys
 GGT ATT TAC TAT TTT GAA GTA AAG ATT GTC AGC AAA GGA AGA GAT GGG TAC ATG GGA ATT
 Gly Ile Tyr Tyr Phe Glu Val Lys Ile Val Ser Lys Gly Arg Asp Gly Tyr Met Gly Ile
 GGA CTC TCA GCG CAA GGC GTT AAC ATG AAC AGA CTG CCT GGT TGG GAC AAG CAT TCC TAT
 Gly Leu Ser Ala Gln Gly Val Asn Met Asn Arg Leu Pro Gly Trp Asp Lys His Ser Tyr
 GGT TAC CAT GGC GAT GAT GGG CAT TCC TTC TGC TCC TCT GGG ACA GGC CAG CCT TAT GGT
 Gly Tyr His Gly Asp Asp Gly His Ser Phe Cys Ser Ser Gly Pro Gly Gln Pro Tyr Gly
 CCC ACA TTC ACC ACA GGG GAT GTG ATC GGC TGT TGT GTC AAC CTC ATC AAT GGC ACC TGC
 Pro Pro Phe Pro Pro Gly Asp Val Ile Gly Cys Cys Val Asn Leu Ile Asn Gly Pro Cys
 TTC TAC ACC AAG AAT GGC CAC AGC CTT GGT ATC GCC TTC ACA GAT CTC CCG GCC AAC CTC
 Phe Tyr Pro Lys Asn Gly His Ser Leu Gly Ile Ala Phe Pro Asp Leu Pro Ala Asn Leu
 TAC CCC ACT GTC GGC CTA CAG ACA CCT GGG GAG ATT GTG GAT GCC AAC TTT GGG CAG CAG
 Tyr Pro Pro Val Gly Leu Gln Pro Pro Gly Glu Ile Val Asp Ala Asn Phe Gly Gln Gln
 CCC TTC CTG TTC GAC ATT GAG GAC TAT ATG CCG GAG TGG CGT GCC AAA GTC CAG GGC ACT
 Pro Phe Leu Phe Asp Ile Glu Asp Tyr Met Arg Glu Trp Arg Ala Lys Val Gln Gly Pro
 GTG CAC GGC TTT CCC ATA AGT GCC CGG CTT GGC GAG TGG CAG GCG GTG CTG CAG AAC ATG
 Val His Gly Phe Pro Ile Ser Ala Arg Leu Gly Glu Trp Gln Ala Val Leu Gln Asn Met
 GTC TCG TCT TAC CTG GTG CAT CAT GGG TAT TGT TCC ACA GCC ACA GCT TTT GCC CGA ATG
 Val Ser Ser Tyr Leu Val His His Gly Tyr Cys Ser Pro Ala Pro Ala Phe Ala Arg Met
 ACT GAA ACC CCG ATT CAG GAA GAG CAG GCA TCC ATA AAG AAC AGA CAA AAA ATC CAG AAG
 Pro Glu Pro Pro Ile Gln Glu Glu Gln Ala Ser Ile Lys Asn Arg Gln Lys Ile Gln Lys
 CTG GTG CTG GAA GGC CGG GTG GGT GAA GCC ATT GAG ACA ACC CAG CGC TTC TAC CCT GGG
 Leu Val Leu Glu Gly Arg Val Gly Glu Ala Ile Glu Pro Pro Gln Arg Phe Tyr Pro Gly
 CTG CTG GAA CAT AAT CCC AAC CTG CTC TTC ATG CTC AAG TGT CGA CAG TTC GTG GAG ATG
 Leu Leu Glu His Asn Pro Asn Leu Leu Phe Met Leu Lys Cys Arg Gln Phe Val Glu Met
 GTG AAC GGC ACT GAC AGT GAG GTC CGC AGC CTG AGT TCC CGA AGC CCC AAG TCC CAG GAC
 Val Asn Gly Pro Asp Ser Glu Val Arg Ser Leu Ser Ser Arg Ser Pro Lys Ser Gln Asp
 AGC TAC CCT GGC TCC CCC AGC CTC AGC CCC CGA CAT GGC CCC AGT AGT TCC CAT ATA CAC
 Ser Tyr Pro Gly Ser Pro Ser Leu Ser Pro Arg His Gly Pro Ser Ser Ser His Ile His
 AAC ACA GGA GCA GAC AGT CCC AGC TGC AGC AAT GGC GTC GCA TCC ACC AAG AAC AAA CAG
 Asn Pro Gly Ala Asp Ser Pro Ser Cys Ser Asn Gly Val Ala Ser Pro Lys Asn Lys Gln
 AAC CAC AGT AAA TAC CCC GCA CCC AGC TCC TCC TCG TCC TCA TCC TCC TCG TCC TCC
 Asn His Ser Lys Tyr Pro Ala Pro Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
 TCT TCC CCG TCC TCC GTC AAT TAC TCC GAG TCC AAC TCA ACA GAC TCT ACC AAG TCC CAG
 Ser Ser Pro Ser Ser Val Asn Tyr Ser Glu Ser Asn Ser Pro Asp Ser Pro Lys Ser Gln
 CCC CAC AGC AGT ACC AGT AAC CAG GAG ACC AGT GAT AGC GAG ATG GAG ATG GAG GCA GAG
 Pro His Ser Ser Pro Ser Asn Gln Glu Pro Ser Asp Ser Glu Met Glu Met Glu Ala Glu
 CAC TAT CCC AAT GGT GTG CTG GAA AGC GTC TCC ACG CGC ATC GTC AAT GGG GCC TAT AAG
 His Tyr Pro Asn Gly Val Leu Glu Ser Val Ser Pro Arg Ile Val Asn Gly Ala Tyr Lys
 CAT GAC GAC CTG CAG ACA GAT GAG TCC AGC ATG GAC GAC GGG CAT CCA CGG AGG CAG CTC
 His Asp Asp Leu Gln Pro Asp Glu Ser Ser Met Asp Asp Gly His Pro Arg Arg Gln Leu
 TGC GGG GGC AAC CAG GCT GCC ACA GAA AGG ATC ATC CTG TTT GGC CGA GAG CTG CAG GCA
 Cys Gly Gly Asn Gln Ala Ala Pro Glu Arg Ile Ile Leu Phe Gly Arg Glu Leu Gln Ala
 TTG AGC GAG CAG CTG GGC CGG GAG TAC GGC AAG AAC TTT GCC CAC ACG GAG ATG CTG CAG
 Leu Ser Glu Gln Leu Gly Arg Glu Tyr Gly Lys Asn Leu Ala His Pro Glu Met Leu Gln
 GAT GCC TTT AGC CTA CTA GCA TAC TCA GAC CCC TGG AGC TGC CCA GTA GGT CAT CAG CTT
 Asp Ala Phe Ser Leu Leu Ala Tyr Ser Asp Pro Trp Ser Cys Pro Val Gly His Gln Leu
 GAT CCC ATC CAG AGA GAG CCC GTG TGT GCT GCT CTC AAC AGC GCC ATT TTA GAG TCT CAG
 Asp Pro Ile Gln Arg Glu Pro Val Cys Ala Ala Leu Asn Ser Ala Ile Leu Glu Ser Gln
 AAC CTG CCA AAG CAG CCT CCT TTG ATG CTC GCC CTG GGC CAG GCA TCT GAA TGT CTA CGG
 Asn Leu Pro Lys Gln Pro Pro Leu Met Leu Ala Leu Gly Gln Ala Ser Glu Cys Leu Arg
 CTC ATG GCC CGA GCA GGC CTG GGA TCT TGC TCC TTT GCC AGA GTC GAT GAC TAC TTG CAC
 Leu Met Ala Arg Ala Gly Leu Gly Ser Cys Ser Phe Ala Arg Val Asp Asp Tyr Leu His
 TAG

CAGACCTTCCTGGCTGGCTCTGGCTGGCCCTCCTTCAGCCCTAGGGCTGGAGCAGCCCTGTCTCCGTAGGCATCTGGTA
CAGAGACCTGGAGCCATGGGCAGAGTTCACTCCTTCTACCTGGCCGGTCCATCCTCCTTTCTCCTTCCCTTCCTCCCT
CCCTCCCTTGCTCTCCTCCTCCTGTCCCTTCCACGTGCAGCGACCTGTGACTCAGTATTTGGCTGGTTACTCATGTGGTA
GCTTCTCCTTTAAAGGAGATTTGTTTTGAGGAGAGGTTGGTTTTTTTTTTGTTTTTGGATCTTGTGTTTTTTTTTTAACT
TTTTTTTCCCTGACTGAGCCACCAGTGTATATCTCGGGAGAGTTTTGTGCTGAGCTGGTGTCTGTAACTTAGTAATGA
AGCCTATCCAGGTTGATGATAGCTTATTTATTTTCATAAGTAAAAAACAACAATGAGATTATATATATATATATATAT
AAATATATATATAAAAAAAGTCACAGTATTTATCTAGCACTAGTGGTCCAGCACCTCTTGGGTGAGGCTGTCCAGACA
CCATGTGTTTTTATTGAGTCCAACTCATTTAAAAAGAATCATCTCTTTGTCACTTCAATCAAGTGATTTGTTTTATTTTAG
GCTCCCTTTTGTGAGCCTCAGGTCAGCTGCTGCCAGGAAATATGGGTTTTGGGGAAGGCTGTTTTGGTGGGCAAGGT
CAGACTAAGCTGTTTTGCAGCATCCCAAGAGGTGTGGGTCCTTAGGCCCCCTATAGGTAACAAAAGAAGTGCAGGTTCA
GGGATTCAAGGAAAGTGGTGGCCAGGGGCACACAGCAAAGCAAGGGAACACAGGGTCCGTAGCCAGCATGCTGTCTAC
CACTTACCTGCCTCTCACTGCCTGCCCTTGCCCTCTCTCCCATCTCAATGCCCTGCCTTCCCTTGTAAAGATGGCCAAA
TAATTCATTACTCTCAGTTGATTCCTGGAACTACTGCCTTCATCCCAAGAGCTGCTGTGTGCCAGGCTGCCAAGAGG
AAGCCATTCCCAAGACAGAGGCCCTTAAGGACAGGGCTCTTTTCTTCCGTGCCAGAGTCTTCAACATCACTGCCCAACCT
GATGGGATTGATGCTTTCTGTGGAGAAGTTGGTACCTCATGGAGACTGATTTCTGGATCACTGGTCCAGAGTGGATGGA
ACCTTTGACTTCCCTGATCCGGATTTCCCTACAGCTTAAGGAAGGCTGCTCCCTACAGCGTGGCCACGACTTGGGTA
AGGGGGACTCCATGGGCTTACATATGTCCACCAGCTGTTTTACAGGATCCTCACAGCTGGCGGGACAACAGCAACAA
CAAAACCCACTATCCCAGGGCTGAGATGCTGCCAGGACATGAGTAGGCCATCTGTGGAGGGGACTGTCTACCAAGGAAGA
GGAGGGTCTATACAGAGGACACCTAGGAGGGCCAGGATTTTACCTGCTTCACAGGGTGAAGTGAAGGAAAGCTAGGCAA
CCTCTGCAAAGATTAGGGTCAACTGTGGCAAAGCCACAAGTGAAGTTTCCAGTCTCCAAGTGCATCTGGGCAGGGGAAGCT
TTTTGTTCTGCTGGTGGACACAGAAATCAATGGCAGAGCTCGAGATGTTCTGTGCCACCAGTCTCACAAGGGCCACAG
TGGACAAAATTGAATTAGACCACTGTCTCAGTGAAGGAAGTAGGGCCTTACTGAGATCCTCCAAAATTTTGTCTTAGGGTC
TAATCCTACAGGCTACTATGTTTTCTGGTTCCTGTCCAGGGCCTTAGTTTACAGCTCCTCAGGAGGCTTGTCTCTATGTA
AAGGAAATTTTCACTCTGTCCAAGGCTGGGACACCAAGCTCCAAGCTCAGGTTGGAATATCAGGCTGTTAACAATGGAT
GGGCTTACATTTGGAATGAAAACAGAGGCATTTGCAGAGCAGTGAAGTGAAGAACTCTCCACCAGTCTCTCCT
TTTACAGTGAAAGAAACAGGTCAGGAAATTAAGTGATTTGACCAAAGCCACACAGCAAATAGTGGCAGAACCAGGACTA
ACTACTCCTGTGGGTTAGACAAGTCTCTGTGCTGACCTAAAGCAAATGGCAAATGAGCTTTGTAAGGGGTTAGGTTGGCG
TGAGTTCAGCAGTGCCTGAGCAGCTGGCACCTTTCTGTTGTGACGGGTAGGGATGGGTGCTGAGACGTGGATTGCGGAG
TGGCTGAGAGGGCCTTGGACGGCTTGGGACTGCTGTGTGCTGCACGGGATTGTATGTCCACCTGGCTCACACTCAGTACC
CATGGCCACCTCCCAATTAATCTGTGCCTTATCTCACTGTTTTAGCTGAGTCCAAGTGTTTACTCTGTCTCTCTCCA
GAGAGGCTTTCTGTCTAGTTGGACAGCTCACTTTGGGGACATAAGCTTTTGTTCACAAGCTGTGGGGAGGGCCAAAAT
CAAGCTGCTGGAGCCAGTAATTAGTCCAGTCTGCTGCCAGAGGAGACCTGTATGCACCCCAATTCACACTAGCCATTT
CCAGGAATCTGGAGTGGAGGACAGTTCCTGGAAGCAACTTAGCAAAGAGCTGGACCTGACCTGGTGTGCAAAAAGGAGGA
CCTGGCCGGGTTGGGTTTGTCCAGTCTTGAAGTAGCAGCAATTTCCCTAGCTCACTTTCCCTAGGAGGCACAGATGGCAGCT
CCTTGCAGAGCAAGGGCAAGTTGGCGGATGACTCAGAGTCCCTCTCCCCAATCCCTTCTCTGAGGGTCTGTGGCTAG
GTGCAGACTGGGTGCAGAACATCAAACTAAAGAAGTAAAGGACTGCCTGGCTACCCAGCACCTTCCAGTCTTAAAGCA
CAAAGATGAGGCAGAGGACTGTTGGGGCTGAACGTTCCCTTTGGTTGCTCACAACCTCAGGTATGCATGTCATTGGCAGCT
GGACAGCAAAGCCCTACTTCAACCAATCACAGGCATTTGGACCTGTGGCCAGATGGTGGCTTCTGGCTGTCCAGTGC
CCACCTCTTGCATCGGTTCCCTCCATTAACAACCTACAGCTGAACTGGCATCCTCCACAGTGTGCACACTGGCTCTGCC
TTTTGCTTGCAGTTGATATTCGGCATTAGCATGAACTTTGGTGTGAGAGGTTGACAGAATTCACACAACAATC
CTAGTAAATTTGACTTGGAGATGAAAAGATTCTGTTGTATTTTGCAGAAATTTTATTTAAATACACATCCATGAGC
AAAAAAAAAAAAAAAA 5185

Supplementary Figure 1. *Nucleotide and amino acid sequence of mouse RanBP10.* All 3 clones identified in the yeast two-hybrid screen began with the underlined nucleotides (number 49 in this schema) and spanned about 1.2 kb. The presumptive transcription start site (position 1) in MKs was determined by 5' rapid amplification of cloned ends (RACE) and differed from the Genbank entry NM_145824. Numbering corresponds to the sequence entered in GenBank as EU281316. The target sequences for 2 independent short hairpin (sh) RNAs, #1982 and #4971, are marked in red.