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1 - TTCGGATCCTTGCGCCACTCGCACTGTTCCCCCTCCTTACCCCGAGAGGCCCATGAGTCC
61 - GAACCCCTCCCGCCAGCCTCCACGTGCGCCGACCCGCAATGGCCAAGCGAGTTCGCTGT
      M A K R S S L S 8
121 - CCATCCGAATCGTAGAAGGAAAAATCTGCCGCCAAGGACATCACGGCAGCAGCGACC
      I R I V E G K N L P A K D I T G S S D P 28
181 - CCTACTGCATCGTAGAGTGGACAATGAACCCATCATCAGGACAGCCACTGTGTGGAAGA
      Y C I V K V D N E P I I R T A T V W K T 48
241 - CCCTGTGCCCTTCTGGGGTGAAGACTACCAAGTACACTTGCCCCCAGTTCACACCGG
      L C P F W G E D Y Q V H L P P T F H T V 68
301 - TGGCCTTCTATGTATGGATGAGGATGCCCTTAGCCGGGACGATGTGATCGGGAAGTCT
      A F Y V M D E D A L S R D D V I G K V C 88
361 - GCCTCAGAGGACGCGTAGCCTCTACCCAAAGGATTACAGTGGATGGACCCACCTGG
      L T R D A L A S H P K G F S G W T H L V 108
421 - TGGAGGTGGACCCGAACGAGGAGTGCAGGTGAGATCCACCTGCGCTGGAGGTGGTGC
      E V D P N E E V Q G E I H L R L E V V P 128
481 - CAGGGTCCATGCCAGCCGCTGCGCTGCGGGTGTGAGGCGAGGACTTAGCACCAA
      G V H A S R L R C A V L E A R D L A P K 148
541 - AAGATCGAATGGGCATCTGACCCCTTTGTCCGAGTGCATCAATGGCCGACCCAGG
      D R N G A S D P F V R V H Y N G R T Q E 168
601 - AGACCTCGTGGTGAAGAAATCTGCTACCCACGCTGGAATGAGACTTTGATTTTGAC
      T S V V K K S C Y P R W N E T F D F E L 188
661 - TGGAAAAAGGACCTCAGAAGCACTGTGGTGGAGCCTGGGACTGGGATCTTGTTAGCC
      E K G A S E A L L V E A W D W D L V S R 208
721 - GGAATGACTTCTAGGCAAGTGGCGTCAATGCCAGAGACTTTGTCAGCCAGCAGG
      N D F L G K V A V N V Q R L C S A Q Q E 228
781 - AAGAGGCTGGTTCGGCTGACGCTGACCAAGTCCAAAAGCCGTCAGGCAAGGCAACC
      E G W F R L Q P D Q S K S R Q G K G N L 248
841 - TGGGCTCCTTGAGTGGAGTGGCGTGCAGGACGAGAGTGTGCTGCGCTCCGCTCGT
      G S L Q L E V R L R D E T V L P S V C Y 268
901 - ACCAGCCCTGGTCAACTGTTGTCAGGAGTGAAGTGGGCACTCAGGCCCAGGAC
      Q P L V Q L L C Q E V K L G T Q G P G R 288
961 - GGCTGATTCCTGTATTGAGGAGACAAGTGTGCCGAGTGTGCCAGGAGTGGCCACCA
      L I P V I E E T T S A E C R Q E V A T T 308
1021 - CCCTGCTCAAACCTTCTGGGGCAGGGCTGGCCAAGGACTTTCTGGATCTGCTTTTTC
      L L K L F L G Q G L A K D F L D L L F Q 328
1081 - AGTGGAGTGGGCGCAGCAGTGAAGCAACACCCTTTCGGGAGCAATCTCTGGCCT
      L E L G R T S E A N T L F R S N S L A S 348
1141 - CAAAGTCCATGGAGTCTTCTGAAGTGGCAGGATGCGCTATCTGCATGGCCTCGG
      K S M E S F L K V A G M R Y L H G I L G 368
1201 - GCCCATCATTGACAGAGTGTTCGAGGAGAAGAAGTACGTGGAGTGGACCCAGCAAG
      P I I D R V F E E K K Y V E L D P S K V 388
1261 - TGAAGTTAAGGATGATGGTGTCTGGCTGCACGCCACAGCCGAAAGTGAAGT
      E V K D V G C S G L H R P Q T E A E V L 408
1321 - TAGAGCAGAGTGCACAGCCTGCGTGCCTACTAGTGGCGTGTGAGCCCATATGCC
      E Q S A Q T L R A H L V A L L S A I C R 428
1381 - GCTCGGTTGCGCAGTGCAGCCATCATCCGCGCCATTCGCGAGTGTTCAGGCGCG
      S V R T C P A I I R A T F R Q L F R R V 448
1441 - TGCGCAGCGCTTCCGAAAGCCAGCAGCAGAGTACCATTATCGCGTCCAGCAGT
      R E R F P N A Q H Q N V P P I A V T S F 468
1501 - TCCTGTGCTGCGCTTCTCTCCGCCATCCTGTGCGCCAAAGCTTCTCCACTGCGAG
      L C L R F F S P A I L S P K L F H L R E 488
1561 - AGCGGCATCGAGTGCAGCCAGCCAGCCAGCAGTCTGCTGCTGCGCCAGGCGTCCAGA
      R H A D A R T S R T L L L A K A V Q N 508
1621 - ACATAGGCAATATGGACACACCGGTCTTAGGGCCAAAGTGCATGGATGGAAACCCTCC
      I G N M D T P V S R A K E S W M E P L Q 528
1681 - AGCCTACCGTGCAGGCGTGGCGCAGTGAAGACTTCAATATGAAGCTTGTGGACA
      P T V R Q G V A Q L K D F I M K L V D I 548
1741 - TAGAAGAAAAGGAGAGTGGACTGACGCGGCTTTGAACTCACAGCCACCACTGTGA
      E E K E E L D L Q R A L N S Q A P P V K 568
1801 - AGGAGGACCAATGTTTATCCACAGGACCAAGGCAAGGCGCTTGTGATCCTCCTCGT
      E G P L F I H R T K G K G P L A S S S F 588
1861 - TCAAGAACTCTACTTCTCCCTTACCACTGAAGCCCTCAGCTTGCAGCAAGCTGCGAG
      K K L Y F S L T T E A L S F A K T S S S 608
1921 - CCAAGAAAAGCACCTTATCAAGCTGGCCAGCATCGGGCTGCGGAGAAGGTGGAGGAAA
      K K S T F I K L A S I R A A E K V E E K 628
1981 - AGAGCTTCGGCAGTCCACATCATGAGGTATCTATGCAGATGATGTGGCCGTGCC
      S F G S S H I M Q V I Y A D D V G R A Q 648
2041 - AGACTGTACTCTGAGTCAAGTGTGAAACGAGTTGAACCAAGTGGTGTCTGATTGC
      T V Y L Q C K C V N E L N Q W L S A L R 668
2101 - GCAAAGCAGCACCAACAGGGGCTCCTACGGTATACCATCCTGGCATCTCCGCTG
      K A S T N N R G L L R S Y H P G I F R G 688
2161 - GGGCAAAGTGGAGTGTGTACCAGAAGCAAGACAGATCAGGATGTGACAAAGACCC
      D K W S C C H Q K D K T D Q G C D K T H 708
2221 - ACTCTCGGTTGACCTGCAGGAATGGAATGACCCACTGGATCATGACCTTGGAGCTCAGC
      S R V T L Q E W N D P L D H D L E A Q L 728
2281 - TCATCTACAGGCACCTGATAGGCTGGAGCTGCTCTGCGGGAAGATACCAGCTCCTGC
      I Y R H L L G V E A A L R E R Y Q L L R 748
2341 - GTGGGGCAGAGAAGCAGGTGTCTACCCAGGGCTGTGATGGAGTCCCGAGGACTCGC
      G A T E A G V S P T G C D G A P E D S L 768
2401 - TGGCCAGCTGCTTCTGTGTGCAAGACTTCGAGAAGCCAGGCTCCAGCTGGCCA
      A Q L L R V L Q D L R E A H G S S L A S 788
2461 - GCCCAGCCAGAGAGCCCATCACCTTCTAGAGCTACAGAGTGAAGTGTCCGTGAGG
      P A A R E P H H L G L E L Q T * 802
2521 - TGTCCATCAAGCCCTGTAGGTGTTGAGATCCGAGCTCGGG - 2564

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**Supplemental Figure 1** cDNA sequence of mouse CAPRI and its protein translation. Mouse CAPRI cDNA was isolated by RT-PCR of C57BL/6 mouse thymus mRNA based on sequences from a gene product obtained in a differential analysis. The gene bank accession number for mouse CAPRI is AY591339.