

Due to an error in production, on pages 82 and 83, the nucleotide sequence in Fig. 2 appeared out of order. The correct sequence appears below.

AGAAGACACACCAAGGACGACGCAAAACAAACAAACAAACAAACAGAGTCTCTCTCTTATGATGATCTCTCTACCTCTGTTTATATATATACAAACAAAGGTTAACTGAGTGCTCTCTGCTTCA - 5
 -124
 MDP SGV KVL ETA EDI QERR QQV LDR YHR FKE LSS LRR QK 39
 GAAATGGATCCAGTGGGGTAAAGTGTGTTGAACACGAGAGATATCCAGAACGGGTCAGCAGGTTTTCAGCGGTTACACACAGGTTCCAGGAGCTGTCTCTCTGAGGCGCCAAA +116
 +1
 L E D S Y R Q F F Q F Q R D A D E L G K G W I Q E K L Q I A S D N E Y K D P S N L Q 79
 ACTGAGAGATTCCTATCGGTTCCAGTCTTCCAGCGTGATCCAGTAGCTGGGAAATGGATCCAGAGAACTCCAGATAGCATGTGATGAAATTCACAAAGACCAAGCAATTTCAG 236
 G K L Q K H Q A F E A E V Q A N S G A I V K L D E T G N Q M I N E G B F A S E T 119
 GGGGAGCTGCAAGACACAGGCGTTTGAAGCTGAGGTGAGGCAATTGAGGCGTATCGTTAAGCTGGATGAGACTGGAAATCAGATGATCAATGAAGGCGATTTTGACATCGAAAC 356
 I R T R L Q E L H R L M W E L L E K M R E K G V K L L Q A Q N L V Q F L R E C E 159
 CATAAGACTGTCTACAGGAGCTGCACCGACTATGGGATGTACTGCTGGAAAAATGAGAGAGAGGAGTGAAGCTGTTCAGACACAGAGCTGGTGCATTTCTACGGGATGTGA 476
 D V M D W I N D K E A I V T S E E L G Q D L E H V E V L Q K K F E E F Q T D L A 199
 AGATGTGAGCTGGATCAATGACAGGAGCAATGAGTACCTCAGAGAGCTTGACAGGAGCTTGAGAGCTTTGAGGTTTGCAGAGAAATTTAGAGAGTTCCAAACAGATCGG 596
 A H E E R V N E V N Q F A G R L I Q E Q R P E E E L I K S Q D E V N A S W Q R 239
 AGCTCATGAGGAGAGGTGAATGAAGTGAACAGTGTGCTGGGAACTTATCCAGAACACAGCCTTGAGGAGGAACTTATAAGTCCAAACAGAGTGAAGTAAATCAAGCTGGCAGG 716
 L K G L A Q Q R Q G K L F G A A E V Q R F N R D V D E T I S W I K E K G Q L M A 279
 TCTTAAAGGCTTGCCACACAGAGCCAGGAAACTCTTGGGCGAGCTGAAGTTCAGCGCTTCAACAGGAGTGTGATGAACATACAGCTGGATTAAGAGAGAGGCGAGTGTATGGC 836
 S D D F G R D L A S V Q A L L R K H E G L E R D L A A F H K V K A L C A E A D 319
 CTCAGATGAGTTGGCAGAGCTGGCCAGGTCCAGGTTTACTACTGATGACAGGCGCTGGAAGAGAGATCTTCAGCTTTCCACATAGAGTTAGGCGCCTCTGTGCGAGAGCTGA 956
 R L Q Q S H P I N A S Q I Q V K R E E L I A N W E Q I R T L A A E R H A R L N D 359
 CGGTTTGACGAATCTCACCTATAAATGCTTCTCAATTCAGATGAACGGGAGGAACTGATGCCAATCGGAGCAGATCCGAACTCTGGCAGCAGAGAGGCAATGCTGCTTAAATGA 1076
 S Y R L Q R F L A D F R D L T S W V T E M K A L I N A D E L A N D V A G A G A E A L 399
 CTCCTACAGTTTGCAGCGCTTCTTTCGAGATTTCCGGGACTACTAGCTGGGTAACTGAGATGAAGCGTGTGATAAGTGTGATGAGCTTGCCAAATGTGGCTGGAGCGAGCGCT 1296
 I D R H Q E K G E I D A H E D S F R S A D E S G Q A L L A A G H Y A S D E V K 439
 TCTAGATAGACCTCAGGACATAGGGAGAAATGATGCTCATGAGGATAGCTTCAGATCTGTCTGATGAGTCTGGGCGAGCTTTGCTTCGAGCTGGGCACTATGCTTCTGATGAAGTAA 1216
 E K L T I L S D E R S A L L E L W E L R Q R Q Q Y E Q C M D L Q L F Y R T D E T Q V 479
 AGAAAGCTGACTATCTCTCAGATGAAGATCTGCTTCTGCGAATCTGAGGAGCTTGCGAGCGCAACAGTATGAGCAGTGCATGGATGGATCGAGCTTTCTACAGAGATCTAGCAAGT 1436
 D N W M S G E Q A E A L L I N E D L G D S L T G S A V E A L L K K B E D D F E K S L A Q 519
 TGAACACTGGATGAGCAACAGGAAGTTTCTGCTGAACGAAGCACTTGGTGAATCTTGAGTATGAGTGTGGAGCTTCTTAAGAGAGCATGAAGATTTGAGAAATCCCTAAGTGTCT 569
 E E K I T A L D E F A T K L I Q N N H Y A M D D V A T R R D A L L S R R N A L H 559
 AGAGGAGAAATCAGACGACTGATGAGTTTCTACTAACTGATCAAAATACCAATTTATGCCATGGATGAGTGTGCTACGCGCAGAGATGCTCTTCTGAGTGGCCGAATGTCTCTTCA 1676
 E R A M K R R A Q L A D S F H L Q Q F F R D S D E L K S W V N E K M K T A T D E 599
 TGAAGAGCCATGAGAGCGCTTGCCCACTGGCAGAGCTTTCACACTCCAGCAGTTTTTCAGGAGCTCTGATGAATGAAGAGTGGGTTAATGAAAAATGAAGTCTGCAACGATGA 1796
 Y A K D P S N L Q G K V Q K H Q A F E A E L S A N Q S R I D A L E K A G Q K L I 639
 GGCTTACAGAGTCCATCCAACTTGCAAGGTAAAGTTCAGAGAGCACTCAGGCTTTGAGAGCAGAGCTTCTGCTTAATCAGAGTGTATGATGACACTGGAGAGACTGGCCAGAGTGTAT 1936
 D V N H Y A S D E V A A R M N E V I S L W K K L L E A T E L K G I K L R E A N Q 679
 TGATGTCAATCACTATGATCTGATGAGGTGGCAGCTGCGATGAATGAAGTCAATCAGCTTGTGGAGAAACTCTGGAAGCCACCGAGCTCAAGAGTATAAGCTGCGTGAAGCAATCA 2036
 Q Q Q F N R N V E D I E L W L Y E V E G H L A S D D Y G K D L T S V Q N L Q K K 719
 ACAGCAGCAATTAATGCCAATGTGAAGACATGAGTTGTGGCTGTATGAAGTGAAGGCTCACTGGCTTCTGATGATTAAGAAAGATTTACACAGCTTCAGAGATCTTCAGAGAA 2156
 H A L L E A D V A A H G G C C A G G A T P I D G I T I Q A R Q F D A G H F D A D N I K K K Q 759
 ACATGGCTGCTAGAGCAGATGTTCGCGCCATCAGGATCCGATAGGATTTACCATCAGGACCGAGTTCAGAGTCTGGGCACTTTGATGCTGACAATATCAAGAGAAACA 1226
 E A L V A R Y E A L K K D P M V A R K Q K L A D S L R L Q L F R D I E D E E T W 799
 AGAAGCTTTAGTACGTGTGATGAAGCTTGAGAGATCCATAGTGGCTGCGAGCAGAACTTGCAAGATCTCTCTGCGCTCGAGCAGCTTTTCGCTGACATGAGGATGAAGAGACCTG 2396
 I R E K E P I A A S T N R G K D L I G V Q N L L K K H Q A L Q A E I A G H E P R 839
 GATCAGGGAAGAGAACTTATTCAGGCTCAACAAACGAGGCAAGCACTTAAATGGTTCAGATCTCTGTAAGAGAGCAGAGCTTTGAGGAGAAATGAGGCGCATGAGGCTCG 2516
 I K A V T Q K G N A M G V E E G H F A E G K I K L N E A Q K Q W D S L K A K A 879
 CATTAAGAGCTCACAACAAAGAAATGAGATGAGGAGAGGCAATTTGCTGCTAGAGATGTGAAGATCAATTAATGAATCAACAAATGAGGACTTCTGAAGAGAGAGG 2636
 S Q R R Q D L E D S L Q A Q Q Y F A D A N E A Q S W M R E K E P I V G S T D Y G 919
 ATCTCAAGCGGACAGAGCTAGAGATTTCTCGAAGCTCAGCAGTATTTGCTGATGCTAATGAGGCGCAATCATGATGAGGGAAGAGAGGCCATTTGTAGGACGACAGGATATGG 2756
 K D E D S A E A L L K K E A L M S D L T G T S G T A G G C A G S S I A Q G A L R E A Q Q A S C R Q Q 959
 AAAGATGAAGACTTCTGAGGCTCTCTGGAAGAGCAATGAAGCTTGTATGCTGATCTTTCTGCTTACGCGAGTASCATACGAGTATAGGGAACAGGCGGAGCTCTCGAGGCAACA 2876
 V A P T D D E T G K E L V L A L Y D Y O E K S P R E V T M K F G D I L T L L N S 999
 AGTTGCTCCACTGATGATGAACCTGGAAGAGAGCTTGTGCTAGCCTATGATTTACCAAGAGAGAGTCTCGGGAGGCTGACTATGAAGAAAGGAGATATTCTAACCTGCTCAACAG 2996
 T N K E D W N R V E V N D R Q G F V P A A Y V K K L D P A Q S A S R E N L L E E Q 1039
 CACCAACAGGAGCTGTGGAGGTTGAGTTAAGCATGCTCGAGGCTTTGTACAGCTGCTATGTGAAGAAATAGATCTCGCCAGCTGCTCATCCGAGAGAGATCTTCTGGAAGAGCA 3116
 G S I A L R Q E Q I D N Q T L I T K E V G S V S L R M K Q V E E L Y H S L L E L 1079
 AGGCAAGATAGCATTTGCAAGAGCAAAATGACAACAGCTCTCAATTACGAAGAGTGGCAGTGATCTGCGATGAACACAGCTCGAAGAGCTGTATCATTCCTTCTGAGCT 3236
 G E K R K G M L E K S C K K F M L F R E A N E L Q Q W I N E K E A A L T N E E V 1119
 GGGAGAAACAGCTAAAGGACTGTGAGAAAGAGCTGCAAGAGTTTATGCTTTTCGAGAGCTAATGAGCTTCAACAGTGAATCAATGAGAAGAGAGCTGCACTCACTAACAGAGAGT 3356
 G A D L E Q V E V L Q K K F G D D F Q K D L K A N E S R L K D I N K V A N D L E S 1159
 GGGTGTGATTTGAGCAGGTGGAGGTCTACAGAGAGTTGATGATTTTCAGAGAGATTAAGAGCTAATGAGCAGACTGAGGACATTAACAGAGTGTCAATGATCTGAGTGT 3456

[illegible]