KanMX4 sequence used in serial or block PCR method

```
        UP TAG PRIMER (70 bp)
    Gene seq.-UPtag-AATCGAACGGAGCAGGGG
                    ||||||||||||||||||                 BstXI
                 1  TTAGCTTGCCTCGTCCCCGCCGGGTCACCCGGCCAGCGACATGGAGGCCCAGAATACCCT
                    ---------+---------+---------+---------+---------+---------+


                61  CCTTGACAGTCTTGACGTGCGCAGCTCAGGGGCATGATGTGACTGTCGCCCGTACATTTA
                    ---------+---------+---------+---------+---------+---------+


               121  GCCCATACATCCCCATGTATAATCATTTGCATCCATACATTTTGATGGCCGCACGGCGCG
                    ---------+---------+---------+---------+---------+---------+

                                            PstI
               181  AAGCAAAAATTACGGCTCCTCGCTGCAGACCTGCGAGCAGGGAAACGCTCCCCTCACAGA
                    ---------+---------+---------+---------+---------+---------+
                                                              TTTGCGAGGGGAGTGTCT
                                                                       cp-N1

               241  CGCGTTGAATTGTCCCCACGCCGCGCCCCTGTAGAGAAATATAAAAGGTTAGGATTTGCC
                    ---------+---------+---------+---------+---------+---------+
                    GC

                                                 DraI
               301  ACTGAGGTTCTTCTTTCATATACTTCCTTTTAAAATCTTGCTAGGATACAGTTCTCACAT
                    ---------+---------+---------+---------+---------+---------+
                                                        GAACGATCCTATGTCAAGAGTGTA
                                                               cp-N10
                                         NcoI
                                          M  G  K  E  K  T  H  V  S  R  P  R  L
               361  CACATCCGAACATAAACAACCATGGGTAAGGAAAAGACTCACGTTTCGAGGCCGCGATTA
                    ---------+---------+---------+---------+---------+---------+
                    G

                                                              NruI
                     N  S  N  M  D  A  D  L  Y  G  Y  K  W  A  R  D  N  V  G  Q
               421  AATTCCAACATGGATGCTGATTTATATGGGTATAAATGGGCTCGCGATAATGTCGGGCAA
                    ---------+---------+---------+---------+---------+---------+

                                     ClaI
                     S  G  A  T  I  Y  R  L  Y  G  K  P  D  A  P  E  L  F  L  K
               481  TCAGGTGCGACAATCTATCGATTGTATGGGAAGCCCGATGCGCCAGAGTTGTTTCTGAAA
                    ---------+---------+---------+---------+---------+---------+


                     H  G  K  G  S  V  A  N  D  V  T  D  E  M  V  R  L  N  W  L
               541  CATGGCAAAGGTAGCGTTGCCAATGATGTTACAGATGAGATGGTCAGACTAAACTGGCTG
                    ---------+---------+---------+---------+---------+---------+


                     T  E  F  M  P  L  P  T  I  K  H  F  I  R  T  P  D  D  A  W
               601  ACGGAATTTATGCCTCTTCCGACCATCAAGCATTTTATCCGTACTCCTGATGATGCATGG
                    ---------+---------+---------+---------+---------+---------+

                                                                           EcoNI
                     L  L  T  T  A  I  P  G  K  T  A  F  Q  V  L  E  E  Y  P  D
               661  TTACTCACCACTGCGATCCCCGGCAAAACAGCATTCCAGGTATTAGAAGAATATCCTGAT
                    ---------+---------+---------+---------+---------+---------+

                              SspI
                     S  G  E  N  I  V  D  A  L  A  V  F  L  R  R  L  H  S  I  P
               721  TCAGGTGAAAATATTGTTGATGCGCTGGCAGTGTTCCTGCGCCGGTTGCATTCGATTCCT
                    ---------+---------+---------+---------+---------+---------+


                                            PvuI
                     V  C  N  C  P  F  N  S  D  R  V  F  R  L  A  Q  A  Q  S  R
               781  GTTTGTAATTGTCCTTTTAACAGCGATCGCGTATTTCGTCTCGCTCAGGCGCAATCACGA
                    ---------+---------+---------+---------+---------+---------+
```

```
       M  N  N  G  L  V  D  A  S  D  F  D  D  E  R  N  G  W  P  V
 841  ATGAATAACGGTTTGGTTGATGCGAGTGATTTTGATGACGAGCGTAATGGCTGGCCTGTT
      ---------+---------+---------+---------+---------+---------+
                                ACTAAAACTACTGCTCGCATTACCGACCGGACAA
                                          cp-C1

                              HindIII
       E  Q  V  W  K  E  M  H  K  L  L  P  F  S  P  D  S  V  V  T
 901  GAACAAGTCTGGAAAGAAATGCATAAGCTTTTGCCATTCTCACCGGATTCAGTCGTCACT
      ---------+---------+---------+---------+---------+---------+
      CTTGTTCAGACCT
         cp-C3

       H  G  D  F  S  L  D  N  L  I  F  D  E  G  K  L  I  G  C  I
 961  CATGGTGATTTCTCACTTGATAACCTTATTTTTGACGAGGGGAAATTAATAGGTTGTATT
      ---------+---------+---------+---------+---------+---------+

                                                   PflMI
       D  V  G  R  V  G  I  A  D  R  Y  Q  D  L  A  I  L  W  N  C
1021  GATGTTGGACGAGTCGGAATCGCAGACCGATACCAGGATCTTGCCATCCTATGGAACTGC
      ---------+---------+---------+---------+---------+---------+

       L  G  E  F  S  P  S  L  Q  K  R  L  F  Q  K  Y  G  I  D  N
1081  CTCGGTGAGTTTTCTCCTTCATTACAGAAACGGCTTTTTCAAAAATATGGTATTGATAAT
      ---------+---------+---------+---------+---------+---------+

                                                           ScaI
       P  D  M  N  K  L  Q  F  H  L  M  L  D  E  F  F  *
1141  CCTGATATGAATAAATTGCAGTTTCATTTGATGCTCGATGAGTTTTTCTAATCAGTACTG
      ---------+---------+---------+---------+---------+---------+

1201  ACAATAAAAAGATTCTTGTTTTCAAGAACTTGTCATTTGTATAGTTTTTTTATATTGTAG
      ---------+---------+---------+---------+---------+---------+

1261  TTGTTCTATTTTAATCAAATGTTAGCGTGATTTATATTTTTTTTCGCCTCGACATCATCT
      ---------+---------+---------+---------+---------+---------+

1321  GCCCAGATGCGAAGTTAAGTGCGCAGAAAGTAATATCATGCGTCAATCGTATGTGAATGC
      ---------+---------+---------+---------+---------+---------+

1381  TGGTCGCTATACTGCTGTCGATTCGATACTAACGCCGCCATCCAGTGTCGAAA 1433
      ---------+---------+---------+---------+---------+---
                                         ||||||||||||||||||
                                         GCGGTAGGTCACAGCTTT-DNtag-Gene seq.
                                            DOWN TAG PRIMER (70 bp)
```

KanMX4 sequence used in gene synthesis method

```
                       BstXI
   1  GCCGGGTCACCCGGCCAGCGACATGGAGGCCCAGAATACCCTCCTTGACAGTCTTGACGT
      ---------+---------+---------+---------+---------+---------+


  61  GCGCAGCTCAGGGGCATGATGTGACTGTCGCCCGTACATTTAGCCCATACATCCCCATGT
      ---------+---------+---------+---------+---------+---------+


 121  ATAATCATTTGCATCCATACATTTTGATGGCCGCACGGCGCGAAGCAAAAATTACGGCTC
      ---------+---------+---------+---------+---------+---------+

           PstI
 181  CTCGCTGCAGACCTGCGAGCAGGGAAACGCTCCCCTCACAGACGCGTTGAATTGTCCCCA
      ---------+---------+---------+---------+---------+---------+
                            < TTTGCGAGGGGAGTGTCTGC
                                    cp-N1

 241  CGCCGCGCCCCTGTAGAGAAATATAAAAGGTTAGGATTTGCCACTGAGGTTCTTCTTTCA
      ---------+---------+---------+---------+---------+---------+

                 DraI
 301  TATACTTCCTTTTAAAATCTTGCTAGGATACAGTTCTCACATCACATCCGAACATAAACA
      ---------+---------+---------+---------+---------+---------+
                      < GAACGATCCTATGTCAAGAGTGTAG
                                  cp-N10
        NcoI
          M  G  K  E  K  T  H  V  S  R  P  R  L  N  S  N  M  D  A
 361  ACCATGGGTAAGGAAAAGACTCACGTTTCGAGGCCGCGATTAAATTCCAACATGGATGCT
      ---------+---------+---------+---------+---------+---------+

                              NruI
       D  L  Y  G  Y  K  W  A  R  D  N  V  G  Q  S  G  A  T  I  Y
 421  GATTTATATGGGTATAAATGGGCTCGCGATAATGTCGGGCAATCAGGTGCGACAATCTAT
      ---------+---------+---------+---------+---------+---------+

      ClaI
       R  L  Y  G  K  P  D  A  P  E  L  F  L  K  H  G  K  G  S  V
 481  CGATTGTATGGGAAGCCCGATGCGCCAGAGTTGTTTCTGAAACATGGCAAAGGTAGCGTT
      ---------+---------+---------+---------+---------+---------+


       A  N  D  V  T  D  E  M  V  R  L  N  W  L  T  E  F  M  P  L
 541  GCCAATGATGTTACAGATGAGATGGTCAGACTAAACTGGCTGACGGAATTTATGCCTCTT
      ---------+---------+---------+---------+---------+---------+


       P  T  I  K  H  F  I  R  T  P  D  D  A  W  L  L  T  T  A  I
 601  CCGACCATCAAGCATTTTATCCGTACTCCTGATGATGCATGGTTACTCACCACTGCGATC
      ---------+---------+---------+---------+---------+---------+

                                            EcoNI        SspI
       P  G  K  T  A  F  Q  V  L  E  E  Y  P  D  S  G  E  N  I  V
 661  CCCGGCAAAACAGCATTCCAGGTATTAGAAGAATATCCTGATTCAGGTGAAAATATTGTT
      ---------+---------+---------+---------+---------+---------+


       D  A  L  A  V  F  L  R  R  L  H  S  I  P  V  C  N  C  P  F
 721  GATGCGCTGGCAGTGTTCCTGCGCCGGTTGCATTCGATTCCTGTTTGTAATTGTCCTTTT
      ---------+---------+---------+---------+---------+---------+

            PvuI
       N  S  D  R  V  F  R  L  A  Q  A  Q  S  R  M  N  N  G  L  V
 781  AACAGCGATCGCGTATTTCGTCTCGCTCAGGCGCAATCACGAATGAATAACGGTTTGGTT
      ---------+---------+---------+---------+---------+---------+
```

```
       D  A  S  D  F  D  D  E  R  N  G  W  P  V  E  Q  V  W  K  E 
 841  GATGCGAGTGATTTTGATGACGAGCGTAATGGCTGGCCTGTTGAACAAGTCTGGAAAGAA
      ---------+---------+---------+---------+---------+---------+
              ACTAAAACTACTGCTCGCATTACCGACCGGACAACTTGTTCAGACCT
                     cp-C1                   cp-C3

            HindIII
       M  H  K  L  L  P  F  S  P  D  S  V  V  T  H  G  D  F  S  L 
 901  ATGCATAAGCTTTTGCCATTCTCACCGGATTCAGTCGTCACTCATGGTGATTTCTCACTT
      ---------+---------+---------+---------+---------+---------+


       D  N  L  I  F  D  E  G  K  L  I  G  C  I  D  V  G  R  V  G 
 961  GATAACCTTATTTTTGACGAGGGGAAATTAATAGGTTGTATTGATGTTGGACGAGTCGGA
      ---------+---------+---------+---------+---------+---------+

                               pflMI
       I  A  D  R  Y  Q  D  L  A  I  L  W  N  C  L  G  E  F  S  P 
1021  ATCGCAGACCGATACCAGGATCTTGCCATCCTATGGAACTGCCTCGGTGAGTTTTCTCCT
      ---------+---------+---------+---------+---------+---------+


       S  L  Q  K  R  L  F  Q  K  Y  G  I  D  N  P  D  M  N  K  L 
1081  TCATTACAGAAACGGCTTTTTCAAAAATATGGTATTGATAATCCTGATATGAATAAATTG
      ---------+---------+---------+---------+---------+---------+

                                         ScaI
       Q  F  H  L  M  L  D  E  F  F  *
1141  CAGTTTCATTTGATGCTCGATGAGTTTTTCTAATCAGTACTGACAATAAAAAGATTCTTG
      ---------+---------+---------+---------+---------+---------+


1201  TTTTCAAGAACTTGTCATTTGTATAGTTTTTTTATATTGTAGTTGTTCTATTTTAATCAA
      ---------+---------+---------+---------+---------+---------+


1261  ATGTTAGCGTGATTTATATTTTTTTTCGCCTCGACATCATCTGCCCAGATGCGAAGTTAA
      ---------+---------+---------+---------+---------+---------+


1321  GTGCGCAGAAAGTAATATCATGCGTCAATCGTATGTGAATGCTGGTCGCTATACTGCTGT
      ---------+---------+---------+---------+---------+---------+


1381  CGATTCGATACTAACGC 1397
      ---------+-------
```