**(A)**

*Sal*I    *Bam*HI    *Xmn*I    *Bgl*I    *Pst*I
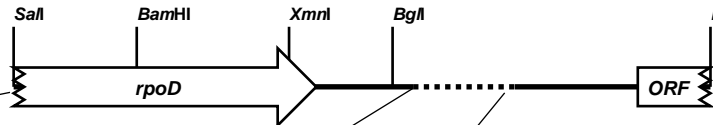
|—| 100 bp    *rpoD*    ORF    p4A4 insert (~2000 bp)

**(B)**

```
1    gtcgacgaaagctggagcgacgcgctggccaaaggcaaaagcaaatacgctgaagccatt  60
     V  D  E  S  W  S  D  A  L  A  K  G  K  S  K  Y  A  E  A  I
61   ggtcgcctgcaaccggacatcatccgttgccagcagaagctgtctgcactggaagctgaa  120
     G  R  L  Q  P  D  I  I  R  C  Q  Q  K  L  S  A  L  E  A  E
121  accggcttgaagattgccgagatcaaggacatcaaccgtcgcatgtccgatcggtgaggcc  180
     T  G  L  K  I  A  E  I  K  D  I  N  R  R  M  S  I  G  E  A
181  aaggcccgccgcgcgaaagagatggttgaagccaacttgcgtctggtgatctccatc  240
     K  A  R  R  A  K  K  E  M  V  E  A  N  L  R  L  V  I  S  I
241  gccaagaagtacaccaaccgtggcttgcagttcctcgacttgatccaggaaggcaacatc  300
     A  K  K  Y  T  N  R  G  L  Q  F  L  D  L  I  Q  E  G  N  I
301  ggcttgatgaaagcggtagacaagtttgaataccgccgcggctacaaattctcgacttat  360
     G  L  M  K  A  V  D  K  F  E  Y  R  R  G  Y  K  F  S  T  Y
361  gccacctggtggatccgtcaggcgatcactcgctcgatcgccgaccaggccgcaccatc  420
     A  T  W  W  I  R  Q  A  I  T  R  S  I  A  D  Q  A  R  T  I
421  cgtattccggtgcacatgatcgagacgatcaacaagctcaaccgcatttcccgccagatg  480
     R  I  P  V  H  M  I  E  T  I  N  K  L  N  R  I  S  R  Q  M
481  ttgcaggaaatgggtcgtgaaccgaccccggaagagctgggcgaacgcatggaaatgcct  540
     L  Q  E  M  G  R  E  P  T  P  E  E  L  G  E  R  M  E  M  P
541  gaggataaaatccgcaaggtattgaagatcgctaaagagccgatctccatggaaacccg  600
     E  D  K  I  R  K  V  L  K  I  A  K  E  P  I  S  M  E  P
601  atcggtgatgacgaagactcccatctgggcgacttcatcgaagactcgaccatgcagtcg  660
     I  G  D  D  E  D  S  H  L  G  D  F  I  E  D  S  T  M  Q  S
661  ccaatcgatgtagccaccgttgagagccttaaagaagcgacacgcgacgtactctccggc  720
     P  I  D  V  A  T  V  E  S  L  K  E  A  T  R  D  V  L  S  G
721  ctcaccgcacgtgaagccaaagtactgcgcatgcgcttcggcatcgataatgataataccgac  780
     L  T  A  R  E  A  K  V  L  R  M  R  F  G  I  D  M  N  T  D
781  cacacccttgaggaggttggtaagcagttcgacgttacccgtgaacggattcgtcagatc  840
     H  T  L  E  E  V  G  K  Q  F  D  V  T  R  E  R  I  R  Q  I
841  gaagccaaggcgttgcgcaagctcgcgcacccgacgagaagcgagcatctcgctcctttc  900
     E  A  K  A  L  R  K  L  R  H  P  T  R  S  E  H  L  R  S  F
901  ctcgacgagtgaTACCAAAAACCCCCGGCCCTGCCGGGGGTTTTGCTTTATAGCAACCTGC  960
     L  D  E  *
961  CCTCCCCGTTCTTTCGCCTGCCAGGCGCATGTCACGTCCGCAGACCACTCCATGACTGCA  1020
1021 ACCTCTTGCCCCCTGCTGCGAAGAAACCCCCGACAAAACCATCATTAGCGACGAGTGCC  1080
1081 GAGACCTGGCTCGACAGGATTTTCTTGCCGCACAAGCTGCGAACGGATACAGACCCGCAT  1140
1141 CGCCCAGCACGGCGCAAACCGC 1161
```

**(C)**

```
1    TCGCAGAGACCATTGTTCACGCCTCTATTTCAGACTTTTCGGATAGCACTCACGAGAAAC  60
61   CATCGTTATAATCCNCGACCTACTGAGGGCCTATAGCTCAGTTGGTTAGAGCAGGGGACT  120
121  CATAATCCCTTGGTCGTAGGTTCGAGTCCTACTGGGCCCACCATACTCAAAGCCGCGCAC  180
181  TGCGCGGCTTTCGTGTTTCTGGCTCCAGCGCAGCAGCGCTGGCTCGCCTGCGGCCGACAC  240
241  TTCTTCCGCCATCTGAAAGTCCCGGGCGCTTAAAACAACAGGCTGATCTATTGCACCTGC  300
301  AACCACGAGCCGTCAGGCCatgtaccatgaccaccgcgtcaccaatgccacaggagccc  360
                        M  Y  H  D  H  P  R  H  Q  C  H  R  S  P
361  tcccttgtctgatgcccaccgcccgcgctggatgaaaccgaccgccaattgatcggggc  420
     P  L  S  D  A  H  P  P  A  L  D  E  T  D  R  Q  L  I  G  A
421  cctgcaactcaatgcccgcgaaagcgttgcaatgctggctcgccagctggggatcgcgcg  480
     L  Q  L  N  A  R  E  S  V  A  M  L  A  R  Q  L  I  A  R
481  caccacggtgaccttgcggctggcacgactggagaaaaccggagtgattaccggctatgg  540
     T  T  V  T  L  R  L  A  R  L  E  K  T  G  V  I  T  G  Y  G
541  cgttcgcctgggccagcgactgattgatggcggactgcag  580
     V  R  L  G  Q  R  L  I  D  G  G  L  Q
```

**(D)**

```
                        c
                       c   t
                       c - g
                       g - c
                       g - c
                       c - g
                       c - g
                       c - g
                       c - g
                       c - g
                       a - t
                       a - t
                       a - t
     L   D   E   *     a - t
5' ctc gac gag tga tacc-gctttatagcaacctgc 3'
```