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peTurboYFP-dest1 vector restriction map

The data has not been verified by restriction digestion with each enzyme listed and does not take into account possible methylation sites. Enzymes that recognize unambiguous sequences less than 6 basepairs long are not included – for the more complete enzyme list please refer to the Table of restriction sites.

Unique sites shown in bold blue. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site).

MCS sequence shown in frame, amino acids coded by MCS and MODC amino acids are shown in bold black.

```
         Ase1                                                                               Bgl1
            |                                                                                  |
      TAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCG
   1  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 100
      ATCAATAATTATCATTAGTTAATGCCCCAGTAATCAAGTATCGGGTATATACCTCAAGGCGCAATGTATTGAATGCCATTTACCGGGCGGACCGACTGGC

                           Aat2                   SpAcc                         Aat2
                              |                       |                            |
      CCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGT
 101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 200
      GGGTTGCTGGGGGCGGGTAACTGCAGTTATTACTGCATACAAGGGTATCATTGCGGTTATCCCTGAAAGGTAACTGCAGTTACCCACCTCATAAATGCCA

              Bgl1                  Nde1                       Aat2                  Bgl1  Bmr1
                 |                     |                          |                     |     |
      AAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTA
 201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 300
      TTTGACGGGTGAACCGTCATGTAGTTCACATAGTATACGGTTCATGCGGGGGATAACTGCAGTTACTGCCATTTACCGGGCGGACCGTAATACGGGTCAT

                                   BtgZ1 SnaB1                Nco1
                                       |     |                   |
      CATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGA
 301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 400
      GTACTGGAATACCCTGAAAGGATGAACCGTCATGTAGATGCATAATCAGTAGCGATAATGGTACCACTACGCCAAAACCGTCATGTAGTTACCCGCACCT
```

```
                                                          Aat2                                             Eci1
                                                             |                                                |
               TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
          401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 500
               ATCGCCAAACTGAGTGCCCCTAAAGGTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT


                                                                                                      Nhe1 Afe1
                                                                                                         |    |
               ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCGCTA
          501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
               TGTTGAGGCGGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT
MCS          >                                                                                            L  A  L

                                                                      BamH1
                                                                     Sma1 |
                                                                    Apa1| |
                                                               PspOM   || |
                                Hind3                          Sac2|   || |
                        Xho1   Sac1 |  EcoR1      Sal1      Kpn1  ||   || |                         Nar1
              BpuE1 Bgl2   | Ecl2 | |BstB1 |     Pst1| Acc65   |  ||   || |  Age1                  Kas1|
                  |    |   |    | | |    | |        ||     |   |  ||   || |     |                     ||
               CCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCTGCAGTCGACGGTACCGCGGGCCCGGGATCCACCGGTCGCCACCATGAGCAGCGGCGCCCTGCTGT
          601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
               GGCCTGAGTCTAGAGCTCGAGTTCGAAGCTTAAGACGTCAGCTGCCATGGCGCCCGGGCCCTAGGTGGCCAGCGGTGGTACTCGTCGCCGCGGGACGACA
MCS/TurboYFP > P  D  S  D  L  E  L  K  L  R  I  L  Q  S  T  V  P  R  A  R  D  P  P  V  A  T  M  S  S  G  A  L  L  F


                                                      BsrD1
                                                   Eco57  | Msc1               Sac2                        BtgZ1
                                                       |  |    |                  |                            |
               TCCACGGCAAGATCCCCTACGTGGTGGAGATGGAGGGCAATGTGGATGGCCACACCTTCAGCATCCGCGGCAAGGGCTACGGCGATGCCAGCGTGGGCAA
          701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
               AGGTGCCGTTCTAGGGGATGCACCACCTCTACCTCCCGTTACACCTACCGGTGTGGAAGTCGTAGGCGCCGTTCCCGATGCCGCTACGGTCGCACCCGTT
TurboYFP     >   H  G  K  I  P  Y  V  V  E  M  E  G  N  V  D  G  H  T  F  S  I  R  G  K  G  Y  G  D  A  S  V  G  K
```

```
                                                                                         Nar1
               Bsg1                                             BstE2               Kas1|
               Bmr1                 SgrA1              BtgZ1       Ale1 |     Bpm1     Bmr1||
                  |                     |                  |          | |        |        |||
               GGTGGATGCCCAGTTCATCTGCACCACCGGCGATGTGCCCGTGCCCTGGAGCACCCTGGTGACCACCCTGACCTACGGCGCCCAGTGCTTCGCCAAGTAC
          801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
               CCACCTACGGGTCAAGTAGACGTGGTGGCCGCTACACGGGCACGGGACCTCGTGGGACCACTGGTGGGACTGGATGCCGCGGGTCACGAAGCGGTTCATG
TurboYFP     >  V  D  A  Q  F  I  C  T  T  G  D  V  P  V  P  W  S  T  L  V  T  T  L  T  Y  G  A  Q  C  F  A  K  Y


                              SpAcc
                           Xmn1   |      Eco57 Sph1                              Bsg1                 BtgZ1
                              |   |          |    |                                 |                     |
               GGCCCCGAGCTGAAGGATTTCTACAAGAGCTGCATGCCCGATGGCTACGTGCAGGAGCGCACCATCACCTTCGAGGGCGATGGCAATTTCAAGACCCGCG
          901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
               CCGGGGCTCGACTTCCTAAAGATGTTCTCGACGTACGGGCTACCGATGCACGTCCTCGCGTGGTAGTGGAAGCTCCCGCTACCGTTAAAGTTCTGGGCGC
TurboYFP     > G  P  E  L  K  D  F  Y  K  S  C  M  P  D  G  Y  V  Q  E  R  T  I  T  F  E  G  D  G  N  F  K  T  R  A


                                                                                          PflM1
                                                                                          BseY1
                                                                                        Pml1  |
               BstE2                  BsrG1                    Msc1                 Msc1   |  |
                   |                      |                       |                    |   |  |
               CCGAGGTGACCTTCGAGAATGGCAGCGTGTACAATCGCGTGAAGCTGAATGGCCAGGGCTTCAAGAAGGATGGCCACGTGCTGGGCAAGAATCTGGAGTT
         1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
               GGCTCCACTGGAAGCTCTTACCGTCGCACATGTTAGCGCACTTCGACTTACCGGTCCCGAAGTTCTTCCTACCGGTGCACGACCCGTTCTTAGACCTCAA
TurboYFP     >   E  V  T  F  E  N  G  S  V  Y  N  R  V  K  L  N  G  Q  G  F  K  K  D  G  H  V  L  G  K  N  L  E  F


                         Bpm1                            Sap1                      BssS1
                        Bts1|  BsrG1                     Ear1                   Eco57  |
                           ||      |                        |                       |  |
               CAATTTCACCCCCCACTGCCTGTACATCTGGGGCGATCAGGCCAATCACGGCCTGAAGAGCGCCTTCAAAATCTGCCACGAGATCACCGGCAGCAAGGGC
         1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
               GTTAAAGTGGGGGGTGACGGACATGTAGACCCCGCTAGTCCGGTTAGTGCCGGACTTCTCGCGGAAGTTTTAGACGGTGCTCTAGTGGCCGTCGTTCCCG
TurboYFP     >  N  F  T  P  H  C  L  Y  I  W  G  D  Q  A  N  H  G  L  K  S  A  F  K  I  C  H  E  I  T  G  S  K  G
```

```
                                                                  ApaL1 Pml1                          Pml1   Blp1
                                                                      |    |                             |      |
                GATTTCATCGTGGCCGATCACACCCAGATGAATACCCCCATCGGCGGCGGCCCCGTGCACGTGCCCGAGTACCACCACATGAGCTACCACGTGAAGCTGA
          1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
                CTAAAGTAGCACCGGCTAGTGTGGGTCTACTTATGGGGGTAGCCGCCGCCGGGGCACGTGCACGGGCTCATGGTGGTGTACTCGATGGTGCACTTCGACT
TurboYFP      > D  F  I  V  A  D  H  T  Q  M  N  T  P  I  G  G  G  P  V  H  V  P  E  Y  H  H  M  S  Y  H  V  K  L  S

                                                Bsa1
                                              SpAcc|         BssH2  Eco57                               BspE1
                                                  ||             |      |                                   |
                GCAAGGATGTGACCGATCACCGCGATAATATGAGCCTGAAGGAGACCGTGCGCGCCGTGGATTGCCGCAAGACCTACGACTTCGACGCCGGTTCCGGAGA
          1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
                CGTTCCTACACTGGCTAGTGGCGCTATTATACTCGGACTTCCTCTGGCACGCGCGGCACCTAACGGCGTTCTGGATGCTGAAGCTGCGGCCAAGGCCTCT
TurboYFP      >   K  D  V  T  D  H  R  D  N  M  S  L  K  E  T  V  R  A  V  D  C  R  K  T  Y  D  F  D  A  G  S  G  D

                                                         Nae1
                             Bsa1                     SgrA1 |
                             Bgl2          Nco1       NgoM4 |                                                 BsrB1
                                |             |           | |                                                     |
                TACAAGCTCCGGTCTCAGATCTCGAATCAGCCATGGCTTCCCGCCGGCGGTGGCGGCGCAGGATGATGGCACGCTGCCCATGTCTTGTGCCCAGGAGAGC
          1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
                ATGTTCGAGGCCAGAGTCTAGAGCTTAGTCGGTACCGAAGGGCGGCCGCCACCGCCGCGTCCTACTACCGTGCGACGGGTACAGAACACGGGTCCTCTCG
TurboYFP/MODC>   T  S  S  G  L  R  S  R  I  S  H  G  F  P  P  A  V  A  A  Q  D  D  G  T  L  P  M  S  C  A  Q  E  S

                                                                 Not1                  BamH1
                                    BstAP                        Eag1                Pml1  |
                                 Pst1   |                        Bsg1               Eco57  |
                                    |   |                           |                   |  |
                GGGATGGACCGTCACCCTGCAGCCTGTGCTTCTGCTAGGATCAATGTGTAGGCGGCCGCGTGACAAGCTGCACGTGGATCCTGAGAACTTCAGGGTGAGT
          1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
                CCCTACCTGGCAGTGGGACGTCGGACACGAAGACGATCCTAGTTACACATCCGCCGGCGCACTGTTCGACGTGCACCTAGGACTCTTGAAGTCCCACTCA
MODC          > G  M  D  R  H  P  A  A  C  A  S  A  R  I  N  V  *

                 SanD1
                     |
                CTATGGGACCCTTGATGTTTTCTTTCCCCTTCTTTTCTATGGTTAAGTTCATGTCATAGGAAGGGGATAAGTAACAGGGTACAGTTTAGAATGGGAAACA
          1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
                GATACCCTGGGAACTACAAAAGAAAGGGGAAGAAAAGATACCAATTCAAGTACAGTATCCTTCCCCTATTCATTGTCCCATGTCAAATCTTACCCTTTGT
```

```
                                                       polyA         Mfe1
                                                           |            |
      GACGAATGATTGCATCAGTGTGGAAGTCTCAGGATCGTTTTAGTTTCTTTTATTTGCTGTTCATAACAATTGTTTTCTTTTGTTTAATTCTTGCTTTCTT
1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
      CTGCTTACTAACGTAGTCACACCTTCAGAGTCCTAGCAAAATCAAAGAAAATAAACGACAAGTATTGTTAACAAAAGAAAACAAATTAAGAACGAAAGAA

                          SpDon
                              |
      TTTTTTTCTTCTCCGCAATTTTTACTATTATACTTAATGCCTTAACATTGTGTATAACAAAAGGAAATATCTCTGAGATACATTAAGTAACTTAAAAAAA
1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
      AAAAAAAGAAGAGGCGTTAAAAATGATAATATGAATTACGGAATTGTAACACATATTGTTTTCCTTTATAGAGACTCTATGTAATTCATTGAATTTTTTT

                                                                                   polyA     polyA
                                                                                       |         |
      AACTTTACACAGTCTGCCTAGTACATTACTATTTGGAATATATGTGTGCTTATTTGCATATTCATAATCTCCCTACTTTATTTTCTTTTATTTTTAATTG
1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
      TTGAAATGTGTCAGACGGATCATGTAATGATAAACCTTATATACACACGAATAAACGTATAAGTATTAGAGGGATGAAATAAAAGAAAATAAAAATTAAC

                                                     BsrG1                                         Dra1
                                                         |                                            |
      ATACATAATCATTATACATATTTATGGGTTAAAGTGTAATGTTTTAATATGTGTACACATATTGACCAAATCAGGGTAATTTTGCATTTGTAATTTTAAA
2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
      TATGTATTAGTAATATGTATAAATACCCAATTTCACATTACAAAATTATACACATGTGTATAACTGGTTTAGTCCCATTAAAACGTAAACATTAAAATTT

                                                                          SpAcc
                                                                              |
      AAATGCTTTCTTCTTTTAATATACTTTTTTGTTTATCTTATTTCTAATACTTTCCCTAATCTCTTTCTTTCAGGGCAATAATGATACAATGTATCATGCC
2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
      TTTACGAAAGAAGAAAATTATATGAAAAAACAAATAGAATAAAGATTATGAAAGGGATTAGAGAAAGAAAGTCCCGTTATTACTATGTTACATAGTACGG

                                                           Ssp1            Ssp1                     SpDon
                                                              |               |                         |
      TCTTTGCACCATTCTAAAGAATAACAGTGATAATTTCTGGGTTAAGGCAATAGCAATATTTCTGCATATAAATATTTCTGCATATAAATTGTAACTGATG
2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
      AGAAACGTGGTAAGATTTCTTATTGTCACTATTAAAGACCCAATTCCGTTATCGTTATAAAGACGTATATTTATAAAGACGTATATTTAACATTGACTAC
```

```
                                                          polyA
                                                              |
      TAAGAGGTTTCATATTGCTAATAGCAGCTACAATCCAGCTACCATTCTGCTTTTATTTTATGGTTGGGATAAGGCTGGATTATTCTGAGTCCAAGCTAGG
2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
      ATTCTCCAAAGTATAACGATTATCGTCGATGTTAGGTCGATGGTAAGACGAAAATAAAATACCAACCCTATTCCGACCTAATAAGACTCAGGTTCGATCC

                                                AlwN1
                                             SpAcc  |                                BstX1    EcoR1
                                                 |  |                                    |        |
      CCCTTTTGCTAATCATGTTCATACTTCTTATCTTCCTCCCACAGCTCCTGGGCAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCAC
2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
      GGGAAAACGATTAGTACAAGTATGAAGAATAGAAGGAGGGTGTCGAGGACCCGTTGCACGACCAGACACACGACCGGGTAGTGAAACCGTTTCTTAAGTG

                               Bsg1
                                  |
      CCCACCAGTGCAGGCTGCCTATCAGAAAGTGGTGGCTGGTGTGGCTAATGCCCTGGCCCACAAGTATCACTAAGCTCGCTTTCTTGCTGTCCAATTTCTA
2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
      GGGTGGTCACGTCCGACGGATAGTCTTTCACCACCGACCACACCGATTACGGGACCGGGTGTTCATAGTGATTCGAGCGAAAGAACGACAGGTTAAAGAT

                                                                                 BpuE1
                                                 Bmr1                            Xba1|  BsaB1
                                                    |                               ||      |
      TTAAAGGTTCCTTTGTTCCCTAAGTCCAACTACTAAACTGGGGGATATTATGAAGGGCCTTGAGCATTGGATTCTGCCTCTAGATCATAATCAGCCATAC
2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
      AATTTCCAAGGAAACAAGGGATTCAGGTTGATGATTTGACCCCCTATAATACTTCCCGGAACTCGTAACCTAAGACGGAGATCTAGTATTAGTCGGTATG

                                                                              Bsm1
                     SpDon   Dra1                                            Mfe1|        Hpa1
                         |      |                                               ||           |
      CACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATT
2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
      GTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAA

 polyA    Psi1      polyA                        polyA            Bts1 Bsm1
     |       |          |                            |               |    |
      GCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCA
2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
      CGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGT
```

```
         Afl2         SpDon        Ssp1
            |             |           |
      ATGTATCTTAAGGCGTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCG
2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
      TACATAGAATTCCGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGC

               Psi1                                                         BsaXb                 Drd1
                  |                                                             |                    |
      GCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGT
3001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
      CGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCA

                                           BtgZ1
      BsaXa                                Dra3|
          |                                   ||
      CAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGG
3101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
      GTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCC

                                              Nae1
     SpAcc                                 NgoM4 |                                    BsrB1
         |                                     | |                                        |
      AACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGC
3201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
      TTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCG

      TGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCG
3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
      ACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGC

                                                       BciV1
                                                    BspH1  |
                      polyA                       BsrB1 |  |                            Ssp1  Ear1
                          |                           | |  |                               |     |
      CGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAG
3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
      GCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCCTTC
```

```
                                                                                                   Nsi1
                                                                                                 Sph1 |
                           Eci1                                                                 BfrB1 |
      Bsu36              Pvu2 |                                      BseY1                   BstAP  | |
          |                 | |                                          |                       |  | |
      AGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCT
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      TCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGA

                                                                       Nsi1
                                                                     Sph1 |
                                                                    BfrB1 |
               SexA1                     BseY1                   BstAP  | |                       Eci1
                   |                         |                       |  | |                          |
      CAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCC
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      GTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGG

                             Eci1
                   Eci1     Bmr1|       Eci1            Nco1                   polyA
                      |        ||          |               |                       |
      CTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCT
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      GATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGA

                                                 Avr2
  Sfi1                                          Stu1|
  Bgl1                    SpDon             BseR1  ||              Cla1              BsaB1
     |                        |                 |  ||                 |                  |
      CGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGA
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      GCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACT

             BspM1               Eag1                                       Bmr1
                 |                  |                                          |
      TTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGC
3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
      AACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCG
```

```
                           Nar1
                          Kas1|                       Drd1
                             ||                          |
      CGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCG
4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
      GCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGC

                                 Pvu2
         Msc1                Fsp1   |       PflF1                       Eco57
            |                   |   |           |                           |
      TGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATC
4101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
      ACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAG

                                                                                                 BtgZ1
               SpDon                         BciV1         BsrD1                              BspM1  |
                   |                             |             |                                  |  |
      TCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCA
4201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
      AGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGT

                                                                       Sap1
                                                                       Ear1
                                                                          |
      CCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCC
4301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
      GGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGG

  BpuE1                         Sph1                       Nco1               BtgZ1
      |                            |                          |                   |
      GAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCC
4401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
      CTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGG
```

```
                              BseY1
                             Nae1 |                                              Sap1
                          NgoM4 | |        Rsr2         Eci1                     Ear1
                              | | |           |            |                        |
      GCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGA
4501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
      CGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCT
```

```
                                         BtgZ1
    Eco57         BssS1                BsrB1 |                                               BsrB1
        |             |                    | |                                                   |
      ATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTC
4601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
      TACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAG
```

```
                                            BssS1
        BstB1                               BspM1                      SpAcc
            |                                   |                          |
      TGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTT
4701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
      ACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAA
```

```
            Nae1                                                   Bpm1
         NgoM4 |                                               SpAcc  |
          Bpm1 |                                                Avr2  |
             | |                                                   |  |
      CCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATA
4801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
      GGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTAT
```

```
                           polyA        polyA
                               |            |
      CCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGC
4901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
      GGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCG
```

```
                Bsa1
                   |
      ACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCT
5001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
      TGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGA

                           BstAP
                           AlwN1      Bsu36                            Dra1               Dra1
                               |          |                               |                  |
      CGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAG
5101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
      GCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATC


                        BspH1
                            |
      GTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTT
5201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
      CACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAA


                    BpuE1
                        |
      GAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTT
5301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5400
      CTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAA


  Eco57                                               SpAcc
      |                                                   |
      TCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCT
5401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5500
      AGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGA


                                   AlwN1                BpuE1
                                       |                    |
      ACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGG
5501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5600
      TGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCC
```

```
                              ApaL1     BseY1                                             SpAcc
                                  |         |                                                 |
      CGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAG
5601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5700
      GCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTC

                                              BciV1
                                           Eci1   |                    BssS1
                                              |   |                        |
      CGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGG
5701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5800
      GCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACC

            SpAcc                          Drd1            BpuE1               SpAcc     Eci1
                |                             |                |                   |        |
      TATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACG
5801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5900
      ATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGC

                                             SpDon
                                            BspLU|                                                 BfrB1
                                                ||                                                     |
      CGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCA
5901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6000
      GCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGT

  Nsi1
     |
      T
6001  | 6001
      A
```

Found:

Aat2 **Acc65** **Afe1** **Afl2** **Age1** **Ale1** AlwN1 **Apa1** ApaL1 **Ase1** Avr2 BamH1 BciV1 BfrB1
Bgl1 Bgl2 **Blp1** Bmr1 Bpm1 BpuE1 Bsa1 BsaB1 **BsaXa** **BsaXb** **BseR1** BseY1 Bsg1 Bsm1
BspE1 BspH1 **BspLU** BspM1 BsrB1 BsrD1 BsrG1 **BssH2** BssS1 BstAP BstB1 BstE2 **BstX1** Bsu36
BtgZ1 Bts1 **Cla1** Dra1 **Dra3** Drd1 Eag1 Ear1 Eci1 **Ecl2** Eco57 EcoR1 **Fsp1** **Hind3**
Hpa1 Kas1 **Kpn1** Mfe1 Msc1 Nae1 Nar1 Nco1 **Nde1** NgoM4 **Nhe1** **Not1** Nsi1 **PflF1**
PflM1 Pml1 polyA Psi1 **PspOM** Pst1 Pvu2 **Rsr2** **Sac1** Sac2 **Sal1** **SanD1** Sap1 **SexA1**
Sfi1 SgrA1 **Sma1** **SnaB1** SpAcc SpDon Sph1 Ssp1 **Stu1** **Xba1** **Xho1** **Xmn1**

Unique:

Acc65 **Afe1** **Afl2** **Age1** **Ale1** **Apa1** **Ase1** **Blp1** **BsaXa** **BsaXb** **BseR1** **BspE1** **BspLU** **BssH2**
BstX1 **Cla1** **Dra3** **Ecl2** **Fsp1** **Hind3** **Hpa1** **Kpn1** **Nde1** **Nhe1** **Not1** **PflF1** **PflM1** **PspOM**
Rsr2 **Sac1** **Sal1** **SanD1** **SexA1** **Sfi1** **Sma1** **SnaB1** **Stu1** **Xba1** **Xho1** **Xmn1**

Not found:

Aar1 Acl1 Ahd1 Asc1 AsiS1 Bae1a Bae1b Bbs1 BbvC1 Bcg1a Bcg1b Bcl1 BmgB1 Bpu10
BsiW1 BsmB1 BstZ1 BxatB BxatL BxatR BxatP _Chi EcoK EcoN1 EcoRV FCatB FCatL FCatR
FCatP ScFRT Fse1 FspA1 I_Ceu loxP Mlu1 Nru1 Pac1 Pme1 PshA1 Pvu1 R4atB R4atL
R4atP R4atR Sbf1 Sca1 Sgf1 Spe1 Srf1 Swa1 T3RNA T7RNA T7Ter PISce Xcm1

Excluded by site complexity:

Acc1 Aci1 Afl3 Alu1 Alw1 Apo1 Ava1 Ava2 Ban1 Ban2 Bbv1 BceA1 Bfa1 Bme15
BsaA1 BsaH1 BsaJ1 BsaW1 BseM2 BsiE1 BsiH1 Bsl1 BsmA1 BsmF1 Bsp12 BspCa BspCb Bsr1
BsrF1 BssK1 BstF5 BstN1 BstU1 BstY1 Btg1 Cac8 CviJ1 Dde1 Eae1 EcoO1 Fau1 Fnu4H
Fok1 Hae2 Hae3 Hga1 Hha1 Hinc2 Hinf1 HinP1 Hpa2 Hph1 Hpy99 Hpy1 Hpy3 HpyC3
HpyC4 HpyC5 Mae3 Mbo2 Mnl1 Mse1 Msl1 MspA1 Mwo1 Nci1 Nla3 Nla4 Nsp1 Ple1
PpuM1 Rsa1 Sau3A Sau96 SfaN1 Sfc1 Sml1 Sty1 Taq1 Tat1 Tfi1 Tse1 Tsp45 Tsp50
TspR1