pTurboGFP-mito 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). Mitochondrial targeting sequence (MTS) shown in bold black.

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

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

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

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

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

                                                                                                      Nhe1
                                                                                                         |
               ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCATGT
          501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
               TGTTGAGGCGGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGTACA
MTS         >                                                                                                  M

                                                           Bmr1         BssH2             PflM1 BamH1  Age1
                                                              |             |                 |     |     |
               CCGTCCTGACGCCGCTGCTGCTGCGGGGCTTGACAGGCTCGGCCCGGCGGCTCCCAGTGCCGCGCGCCAAGATCCATTCGTTGGGGGATCCACCGGTCGC
          601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
               GGCAGGACTGCGGCGACGACGACGCCCCGAACTGTCCGAGCCGGGCCGCCGAGGGTCACGGCGCGCGGTTCTAGGTAAGCAACCCCCTAGGTGGCCAGCG
MTS         > S  V  L  T  P  L  L  L  R  G  L  T  G  S  A  R  R  L  P  V  P  R  A  K  I  H  S  L  G  D  P  P  V  A

                                            Nco1
              Nco1             BsrB1   BsaXa   |                     BsaXb                             _Chi
                 |                 |       |   |                         |                                |
               CACCATGGAGAGCGACGAGAGCGGCCTGCCCGCCATGGAGATCGAGTGCCGCATCACCGGCACCCTGAACGGCGTGGAGTTCGAGCTGGTGGGCGGCGGA
          701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
               GTGGTACCTCTCGCTGCTCTCGCCGGACGGGCGGTACCTCTAGCTCACGGCGTAGTGGCCGTGGGACTTGCCGCACCTCAAGCTCGACCACCCGCCGCCT
TurboGFP    >   T  M  E  S  D  E  S  G  L  P  A  M  E  I  E  C  R  I  T  G  T  L  N  G  V  E  F  E  L  V  G  G  G

                                                                                                    PflM1
                                                                                                  Pml1  |
                                                                Nar1                         BspM1   |  |
                                             Sap1              Kas1|                         BfuA1   |  |
                      Eci1                   Ear1         Eco57   ||                     Blp1   |    |  |
                         |                      |             |   ||                         |   |   |  |
               GAGGGCACCCCCGAGCAGGGCCGCATGACCAACAAGATGAAGAGCACCAAAGGCGCCCTGACCTTCAGCCCCTACCTGCTGAGCCACGTGATGGGCTACG
          801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
               CTCCCGTGGGGGCTCGTCCCGGCGTACTGGTTGTTCTACTTCTCGTGGTTTCCGCGGGACTGGAAGTCGGGGATGGACGACTCGGTGCACTACCCGATGC
TurboGFP    >  E  G  T  P  E  Q  G  R  M  T  N  K  M  K  S  T  K  G  A  L  T  F  S  P  Y  L  L  S  H  V  M  G  Y
```

```
                                  BseY1     Bsg1     Xmn1                                                     Bsg1
                                      |        |        |                                                        |
               GCTTCTACCACTTCGGCACCTACCCCAGCGGCTACGAGAACCCCTTCCTGCACGCCATCAACAACGGCGGCTACACCAACACCCGCATCGAGAAGTACGA
          901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
               CGAAGATGGTGAAGCCGTGGATGGGGTCGCCGATGCTCTTGGGGAAGGACGTGCGGTAGTTGTTGCCGCCGATGTGGTTGTGGGCGTAGCTCTTCATGCT
TurboGFP    > G  F  Y  H  F  G  T  Y  P  S  G  Y  E  N  P  F  L  H  A  I  N  N  G  G  Y  T  N  T  R  I  E  K  Y  E

                                                           Fse1
                                                         Nae1 |
                                                         Eag1 |
                    Eco57     Pml1                    NgoM4 | |
                        |        |                        | | |
               GGACGGCGGCGTGCTGCACGTGAGCTTCAGCTACCGCTACGAGGCCGGCCGCGTGATCGGCGACTTCAAGGTGATGGGCACCGGCTTCCCCGAGGACAGC
         1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
               CCTGCCGCCGCACGACGTGCACTCGAAGTCGATGGCGATGCTCCGGCCGGCGCACTAGCCGCTGAAGTTCCACTACCCGTGGCCGAAGGGGCTCCTGTCG
TurboGFP    >   D  G  G  V  L  H  V  S  F  S  Y  R  Y  E  A  G  R  V  I  G  D  F  K  V  M  G  T  G  F  P  E  D  S

                                                                   Nco1
                                                                  BspM1
                                                                  BfuA1
                                             Bsg1                  Aar1       BsaB1        Eco57
                                                |                     |           |            |
               GTGATCTTCACCGACAAGATCATCCGCAGCAACGCCACCGTGGAGCACCTGCACCCCATGGGCGATAACGATCTGGATGGCAGCTTCACCCGCACCTTCA
         1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
               CACTAGAAGTGGCTGTTCTAGTAGGCGTCGTTGCGGTGGCACCTCGTGGACGTGGGGTACCCGCTATTGCTAGACCTACCGTCGAAGTGGGCGTGGAAGT
TurboGFP    >  V  I  F  T  D  K  I  I  R  S  N  A  T  V  E  H  L  H  P  M  G  D  N  D  L  D  G  S  F  T  R  T  F

                                                                                                           Eci1
                                                                                                        Apa1  |
                   BsaXb                         BsaXa                         BseY1         Pst1  PspOM   |  |
                       |                             |                             |            |      |   |  |
               GCCTGCGCGACGGCGGCTACTACAGCTCCGTGGTGGACAGCCACATGCACTTCAAGAGCGCCATCCACCCCAGCATCCTGCAGAACGGGGGCCCCATGTT
         1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
               CGGACGCGCTGCCGCCGATGATGTCGAGGCACCACCTGTCGGTGTACGTGAAGTTCTCGCGGTAGGTGGGGTCGTAGGACGTCTTGCCCCCGGGGTACAA
TurboGFP    > S  L  R  D  G  G  Y  Y  S  S  V  V  D  S  H  M  H  F  K  S  A  I  H  P  S  I  L  Q  N  G  G  P  M  F
```

```
                                          BseR1   BseY1
                                              |       |
               CGCCTTCCGCCGCGTGGAGGAGGATCACAGCAACACCGAGCTGGGCATCGTGGAGTACCAGCACGCCTTCAAGACCCCGGATGCAGATGCCGGTGAAGAA
         1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
               GCGGAAGGCGGCGCACCTCCTCCTAGTGTCGTTGTGGCTCGACCCGTAGCACCTCATGGTCGTGCGGAAGTTCTGGGGCCTACGTCTACGGCCACTTCTT
TurboGFP    >   A  F  R  R  V  E  E  D  H  S  N  T  E  L  G  I  V  E  Y  Q  H  A  F  K  T  P  D  A  D  A  G  E  E

                 Not1
                 Eag1      Xba1   BsaB1                                    Dra1
                    |         |       |                                       |
               TAAAGCGGCCGCGACTCTAGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACA
         1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
               ATTTCGCCGGCGCTGAGATCTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGT
TurboGFP    >  *

                        Bsm1
                       Mfe1|        Hpa1                Psi1
                          ||           |                   |
               TAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTT
         1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
               ATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAA

            Bts1 Bsm1                                  Afl2                      Ssp1
               |    |                                     |                         |
               TCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGT
         1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
               AGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTCCGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACA

                                                             Psi1
                                                                |
               TAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGA
         1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
               ATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCT

                      BsaXb                 Drd1    BsaXa                                Dra3
                          |                    |        |                                   |
               ACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAG
         1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
               TGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTC
```

```
                                                                                   Nae1
                                                                                NgoM4 |
                                                                                    | |
      TTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAG
1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
      AAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTC

                       BsrB1
                           |
      GAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTAC
2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
      CTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATG

                                                                                            BciV1
                                                                                         BspH1  |
                                                                                       BsrB1 |  |
                                                                                           | |  |
      AGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATA
2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
      TCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTAT

                                                                Eci1
                         Ssp1  Ear1        Bsu36              Pvu2 |
                            |     |            |                 | |
      ACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAG
2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
      TGGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTC

                                    Nsi1
                                  Sph1 |
                                 BfrB1 |
      BseY1                   BstAP  | |            SexA1                     BseY1
          |                       |  | |                |                        |
      GCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAG
2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
      CGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTC
```

```
        Nsi1
      Sph1 |
     BfrB1 |                                                      Eci1
  BstAP  | |                       Eci1                 Eci1     Bmr1|       Eci1            Nco1
      |  | |                          |                    |        ||          |               |
      CATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGA
2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
      GTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACT

                                                                                      Avr2
                                       Sfi1                                          Stu1|
                                       Bgl1                                      BseR1  ||
                                          |                                          |  ||
      CTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAG
2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
      GATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTC

                                                  BspM1
    Cla1              BsaB1                       BfuA1               Eag1
       |                  |                           |                  |
      ATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATG
2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
      TAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATAC

                                                                Nar1
             Bmr1                                              Kas1|                       Drd1
                |                                                 ||                          |
      ACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGC
2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
      TGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACG

                                                                      Pvu2
                                              Msc1                Fsp1   |       PflF1
                                                 |                   |   |           |
      CCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGG
2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
      GGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCC
```

```
         Eco57                                                                    BciV1         BsrD1
             |                                                                        |             |
      GACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGC
2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
      CTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCG

                               BspM1
                               BfuA1
                                   |
      TGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGA
3001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
      ACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCT

        Sap1
        Ear1                           BpuE1                         Sph1                       Nco1
           |                               |                            |                          |
      TGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGC
3101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
      ACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCG

                                                                   BseY1
                                                                  Nae1 |
                                                               NgoM4 | |        Rsr2         Eci1
                                                                   | | |           |            |
      GATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGT
3201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
      CTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCA

                  Sap1
                  Ear1                   Eco57         BssS1                BsrB1
                     |                       |             |                   |
      TGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTT
3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
      ACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAA
```

```
                                                                                 BssS1
                                                                                 BspM1
                              BsrB1          BstB1                               BfuA1
                                  |              |                                   |
      CTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCG
3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
      GATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGC

                                                 Nae1
                                              NgoM4 |
                                               Bpm1 |                                                Avr2
                                                  | |                                                   |
      CCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCC
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      GGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGG

    Bpm1
       |
      TAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCG
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      ATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGC

                                                     Bsa1
                                                        |
      TTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCC
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      AAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGG

                                                                BstAP
                                                                AlwN1      Bsu36
                                                                    |         |
      CACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGAT
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      GTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTA

        Dra1               Dra1                              BspH1
           |                  |                                  |
      TGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGA
3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
      ACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACT
```

```
                                                         BpuE1
                                                             |
      GCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGG
4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
      CGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCC

                                       Eco57
                                           |
      TGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTA
4101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
      ACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCAT

                                                                        AlwN1                     BpuE1
                                                                            |                         |
      GTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTT
4201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
      CAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAA

                                                                   ApaL1     BseY1
                                                                       |         |
      ACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACA
4301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
      TGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGT

                                                                                   BciV1
                                                                                Eci1   |
                                                                                   |   |
      CCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGG
4401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
      GGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCC

        BssS1                                                                   Drd1            BpuE1
            |                                                                      |                |
      AGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCG
4501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
      TCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGC
```

```
                          Eci1                                                   BspLU
                             |                                                       |
      TCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTAT
4601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
      AGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATA

                                       Nsi1
                                    BfrB1 |
                                        | |
      CCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
4701  |||||||||*|||||||||*|||||||||*|||||||| 4738
      GGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aar1 Aat2 **Afl2** **Age1** AlwN1 **Apa1** **ApaL1** **Ase1** Avr2 **BamH1** BciV1 BfrB1 BfuA1 Bgl1

Blp1 Bmr1 Bpm1 BpuE1 **Bsa1** BsaB1 BsaXa BsaXb BseR1 BseY1 Bsg1 Bsm1 BspH1 **BspLU**

BspM1 BsrB1 **BsrD1** **BssH2** BssS1 BstAP **BstB1** Bsu36 **Bts1** **_Chi** **Cla1** Dra1 **Dra3** Drd1

Eag1 Ear1 Eci1 Eco57 **Fse1** **Fsp1** **Hpa1** Kas1 **Mfe1** **Msc1** Nae1 Nar1 Nco1 **Nde1**

NgoM4 **Nhe1** **Not1** Nsi1 **PflF1** PflM1 Pml1 Psi1 **PspOM** **Pst1** Pvu2 **Rsr2** Sap1 **SexA1**

Sfi1 **SnaB1** Sph1 Ssp1 **Stu1** **Xba1** **Xmn1**

```
Unique:


    Aar1    Afl2    Age1    Apa1   ApaL1    Ase1   BamH1    Blp1    Bsa1   BspLU   BsrD1   BssH2   BstB1    Bts1

    _Chi    Cla1    Dra3    Fse1    Fsp1    Hpa1    Mfe1    Msc1    Nde1    Nhe1    Not1   PflF1   PspOM    Pst1

    Rsr2   SexA1    Sfi1   SnaB1    Stu1    Xba1    Xmn1

Not found:

   Acc65    Acl1    Afe1    Ahd1    Ale1    Asc1   AsiS1   Bae1a   Bae1b    Bbs1   BbvC1   Bcg1a   Bcg1b    Bcl1
    Bgl2   BmgB1   Bpu10   BsiW1   BsmB1   BspE1   BsrG1   BstE2   BstX1   BstZ1    EcoK   EcoN1   EcoR1   EcoRV
   ScFRT   FspA1   Hind3   I_Ceu    Kpn1    loxP    Mlu1    Nru1    Pac1    Pme1   PshA1    Pvu1    Sac1    Sac2
    Sal1   SanD1    Sbf1    Sca1    Sgf1   SgrA1    Sma1    Spe1    Srf1    Swa1   PISce    Xcm1    Xho1

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
```