pTagGFP2-tubulin 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 are shown in bold blue. The location given specifies the 3’ end of the cut DNA (the base to the left of the cut site). TagGFP2 amino acids are shown in green, Tubulin amino acids are shown in red, linker amino acids are shown in 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
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                                                           Aat2                                             Eci1
                                                              |                                                |
                TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
           401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 500
                ATCGCCAAACTGAGTGCCCCTAAAGGTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT


                                                                                                       Nhe1
                                                                                                          |
                ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCGGTC
           501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
                TGTTGAGGCGGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCCAG


                                             BseR1
                                             Nae1|                               ApaL1
                      BsrB1               NgoM4 ||                              BmgB1|
                          |                   | ||                                  ||
                GCCACCATGAGCGGGGGCGAGGAGCTGTTCGCCGGCATCGTGCCCGTGCTGATCGAGCTGGACGGCGACGTGCACGGCCACAAGTTCAGCGTGCGCGGCG
           601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
                CGGTGGTACTCGCCCCCGCTCCTCGACAAGCGGCCGTAGCACGGGCACGACTAGCTCGACCTGCCGCTGCACGTGCCGGTGTTCAAGTCGCACGCGCCGC
TagGFP2       >       M  S  G  G  E  E  L  F  A  G  I  V  P  V  L  I  E  L  D  G  D  V  H  G  H  K  F  S  V  R  G  E

                                                                 BsaXb                           BstE2
                                   BsaXa    Bsg1               Bpm1  |                          Ale1 |
                                       |       |                  |  |                             | |
                AGGGCGAGGGCGACGCCGACTACGGCAAGCTGGAGATCAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTGGTGACCACCCTCTG
           701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
                TCCCGCTCCCGCTGCGGCTGATGCCGTTCGACCTCTAGTTCAAGTAGACGTGGTGGCCGTTCGACGGGCACGGGACCGGGTGGGACCACTGGTGGGAGAC
TagGFP2       >   G  E  G  D  A  D  Y  G  K  L  E  I  K  F  I  C  T  T  G  K  L  P  V  P  W  P  T  L  V  T  T  L  C

                       BstAP                                  Xmn1                                      EcoK
                           |                                     |                                         |
                CTACGGCATCCAGTGCTTCGCCCGCTACCCCGAGCACATGAAGATGAACGACTTCTTCAAGAGCGCCATGCCCGAGGGCTACATCCAGGAGCGCACCATC
           801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
                GATGCCGTAGGTCACGAAGCGGGCGATGGGGCTCGTGTACTTCTACTTGCTGAAGAAGTTCTCGCGGTACGGGCTCCCGATGTAGGTCCTCGCGTGGTAG
TagGFP2       >  Y  G  I  Q  C  F  A  R  Y  P  E  H  M  K  M  N  D  F  F  K  S  A  M  P  E  G  Y  I  Q  E  R  T  I
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                                                                          SpDon
                                            Sac2 SpDon                  Ale1 |
                                               |     |                     | |
               CAGTTCCAGGACGACGGCAAGTACAAGACCCGCGGCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCAAGGACTTCAAGG
          901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
               GTCAAGGTCCTGCTGCCGTTCATGTTCTGGGCGCCGCTCCACTTCAAGCTCCCGCTGTGGGACCACTTGGCGTAGCTCGACTTCCCGTTCCTGAAGTTCC
TagGFP2      > Q  F  Q  D  D  G  K  Y  K  T  R  G  E  V  K  F  E  G  D  T  L  V  N  R  I  E  L  K  G  K  D  F  K  E

                                                                 BsrG1
                                                                Dra3 |
                                                              Eci1 | |
          Eco57                     PflM1                  Bpm1  | | |                        Xcm1
              |                         |                     |  | | |                           |
               AGGACGGCAACATCCTGGGCCACAAGCTGGAGTACAGCTTCAACAGCCACAACGTGTACATCCGCCCCGACAAGGCCAACAACGGCCTGGAGGCTAACTT
         1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
               TCCTGCCGTTGTAGGACCCGGTGTTCGACCTCATGTCGAAGTTGTCGGTGTTGCACATGTAGGCGGGGCTGTTCCGGTTGTTGCCGGACCTCCGATTGAA
TagGFP2      >   D  G  N  I  L  G  H  K  L  E  Y  S  F  N  S  H  N  V  Y  I  R  P  D  K  A  N  N  G  L  E  A  N  F

                   Bpm1                         Pvu2            Bsg1       Xcm1                       BsaB1
                      |                            |               |          |                           |
               CAAGACCCGCCACAACATCGAGGGCGGCGGCGTGCAGCTGGCCGACCACTACCAGACCAACGTGCCCCTGGGCGACGGCCCCGTGCTGATCCCCATCAAC
         1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
               GTTCTGGGCGGTGTTGTAGCTCCCGCCGCCGCACGTCGACCGGCTGGTGATGGTCTGGTTGCACGGGGACCCGCTGCCGGGGCACGACTAGGGGTAGTTG
TagGFP2      >  K  T  R  H  N  I  E  G  G  G  V  Q  L  A  D  H  Y  Q  T  N  V  P  L  G  D  G  P  V  L  I  P  I  N

                                                                      Eco57
                 Bpu10                                                 Dra3                  AlwN1 Bpm1
                     |                                                    |                      |    |
               CACTACCTGAGCACTCAGACCAAGATCAGCAAGGACCGCAACGAGGCCCGCGACCACATGGTGCTCCTGGAGTCCTTCAGCGCCTGCTGCCACACCCACG
         1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
               GTGATGGACTCGTGAGTCTGGTTCTAGTCGTTCCTGGCGTTGCTCCGGGCGCTGGTGTACCACGAGGACCTCAGGAAGTCGCGGACGACGGTGTGGGTGC
TagGFP2      > H  Y  L  S  T  Q  T  K  I  S  K  D  R  N  E  A  R  D  H  M  V  L  L  E  S  F  S  A  C  C  H  T  H  G
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                                                                                                           BseY1
                                             Xho1                                                        BsrD1 |
            PflM1      BsrG1   BspE1     Bgl2   |                             Msc1                      BstAP| |
                |          |       |        |   |                                |                          || |
               GCATGGACGAGCTGTACAGGTCCGGACTCAGATCTCGAGTGCGTGAGTGCATCTCCATCCACGTTGGCCAGGCTGGTGTCCAGATTGGCAATGCCTGCTG
         1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
               CGTACCTGCTCGACATGTCCAGGCCTGAGTCTAGAGCTCACGCACTCACGTAGAGGTAGGTGCAACCGGTCCGACCACAGGTCTAACCGTTACGGACGAC
TagGFP2/tubulin  M  D  E  L  Y  R  S  G  L  R  S  R  V  R  E  C  I  S  I  H  V  G  Q  A  G  V  Q  I  G  N  A  C  W

                 Sac1                             Msc1                                                       SpAcc
               Ecl2 |                        BstX1   |                                   Eco57BseR1      BsmB1   |
                  | |                            |   |                                       |    |          |   |
               GGAGCTCTACTGCCTGGAACACGGCATCCAGCCCGATGGCCAGATGCCAAGTGACAAGACCATTGGGGGAGGAGATGACTCCTTCAACACCTTCTTCAGT
         1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
               CCTCGAGATGACGGACCTTGTGCCGTAGGTCGGGCTACCGGTCTACGGTTCACTGTTCTGGTAACCCCCTCCTCTACTGAGGAAGTTGTGGAAGAAGTCA
Tubulin      >  E  L  Y  C  L  E  H  G  I  Q  P  D  G  Q  M  P  S  D  K  T  I  G  G  G  D  D  S  F  N  T  F  F  S

                                Pml1   Sma1
                                   |      |
               GAGACGGGCGCTGGCAAGCACGTGCCCCGGGCTGTGTTTGTAGACTTGGAACCCACAGTCATTGATGAAGTTCGCACTGGCACCTACCGCCAGCTCTTCC
         1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
               CTCTGCCCGCGACCGTTCGTGCACGGGGCCCGACACAAACATCTGAACCTTGGGTGTCAGTAACTACTTCAAGCGTGACCGTGGATGGCGGTCGAGAAGG
Tubulin      > E  T  G  A  G  K  H  V  P  R  A  V  F  V  D  L  E  P  T  V  I  D  E  V  R  T  G  T  Y  R  Q  L  F  H

              Bpu10
           Sap1   |
           Ear1   |
              |   |
               ACCCTGAGCAGCTCATCACAGGCAAGGAAGATGCTGCCAATAACTATGCCCGAGGGCACTACACCATTGGCAAGGAGATCATTGACCTTGTGTTGGACCG
         1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
               TGGGACTCGTCGAGTAGTGTCCGTTCCTTCTACGACGGTTATTGATACGGGCTCCCGTGATGTGGTAACCGTTCCTCTAGTAACTGGAACACAACCTGGC
Tubulin      >   P  E  Q  L  I  T  G  K  E  D  A  A  N  N  Y  A  R  G  H  Y  T  I  G  K  E  I  I  D  L  V  L  D  R
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                                     Age1                             Xcm1
                                  Bbs1  |                            BstX1
          EcoR1            Eco57ApaL1|  |                          SpAcc |          Xmn1         SpDon
              |                |    ||  |                              | |             |             |
               AATTCGCAAGCTGGCTGACCAGTGCACCGGTCTTCAGGGCTTCTTGGTTTTCCACAGCTTTGGTGGGGGAACTGGTTCTGGGTTCACCTCCCTGCTCATG
         1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
               TTAAGCGTTCGACCGACTGGTCACGTGGCCAGAAGTCCCGAAGAACCAAAAGGTGTCGAAACCACCCCCTTGACCAAGACCCAAGTGGAGGGACGAGTAC
Tubulin      >  I  R  K  L  A  D  Q  C  T  G  L  Q  G  F  L  V  F  H  S  F  G  G  G  T  G  S  G  F  T  S  L  L  M

                                                                     Bpm1             SpAcc
                    BsmB1                                       BseY1   |              Pvu2
                        |                                           |   |                 |
               GAACGTCTCTCAGTTGATTATGGCAAGAAGTCCAAGCTGGAGTTCTCCATTTACCCAGCACCCCAGGTTTCCACAGCTGTAGTTGAGCCCTACAACTCCA
         1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
               CTTGCAGAGAGTCAACTAATACCGTTCTTCAGGTTCGACCTCAAGAGGTAAATGGGTCGTGGGGTCCAAAGGTGTCGACATCAACTCGGGATGTTGAGGT
Tubulin      > E  R  L  S  V  D  Y  G  K  K  S  K  L  E  F  S  I  Y  P  A  P  Q  V  S  T  A  V  V  E  P  Y  N  S  I

                 SpDon                               Bpm1                          PshA1              EcoRV
                     |                                  |                              |                  |
               TCCTCACCACCCACACCACCCTGGAGCACTCTGATTGTGCCTTCATGGTAGACAATGAGGCCATCTATGACATCTGTCGTAGAAACCTCGATATCGAGCG
         1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
               AGGAGTGGTGGGTGTGGTGGGACCTCGTGAGACTAACACGGAAGTACCATCTGTTACTCCGGTAGATACTGTAGACAGCATCTTTGGAGCTATAGCTCGC
Tubulin      >   L  T  T  H  T  T  L  E  H  S  D  C  A  F  M  V  D  N  E  A  I  Y  D  I  C  R  R  N  L  D  I  E  R

                                                              Bts1                                          EcoR1
                                                                 |                                              |
               CCCAACCTACACTAACCTTAACCGCCTTATTAGCCAGATTGTGTCCTCCATCACTGCTTCCCTGAGATTTGATGGAGCCCTGAATGTTGACCTGACAGAA
         2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
               GGGTTGGATGTGATTGGAATTGGCGGAATAATCGGTCTAACACAGGAGGTAGTGACGAAGGGACTCTAAACTACCTCGGGACTTACAACTGGACTGTCTT
Tubulin      >  P  T  Y  T  N  L  N  R  L  I  S  Q  I  V  S  S  I  T  A  S  L  R  F  D  G  A  L  N  V  D  L  T  E

                     SexA1                               Msc1 Nde1              SpAcc
                         |                                  |    |                  |
               TTCCAGACCAACCTGGTGCCCTACCCCCGCATCCACTTCCCTCTGGCCACATATGCCCCTGTCATCTCTGCTGAGAAAGCCTACCATGAACAGCTTTCTG
         2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
               AAGGTCTGGTTGGACCACGGGATGGGGGCGTAGGTGAAGGGAGACCGGTGTATACGGGGACAGTAGAGACGACTCTTTCGGATGGTACTTGTCGAAAGAC
Tubulin      > F  Q  T  N  L  V  P  Y  P  R  I  H  F  P  L  A  T  Y  A  P  V  I  S  A  E  K  A  Y  H  E  Q  L  S  V
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                                                      SpDon                 SpDon
             SpAcc                                 BstX1  |              Nco1   |
                 |                                     |  |                 |   |
               TAGCAGAGATCACCAATGCTTGCTTTGAGCCAGCCAACCAGATGGTGAAATGTGACCCTCGCCATGGTAAATACATGGCTTGCTGCCTGTTGTACCGTGG
         2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
               ATCGTCTCTAGTGGTTACGAACGAAACTCGGTCGGTTGGTCTACCACTTTACACTGGGAGCGGTACCATTTATGTACCGAACGACGGACAACATGGCACC
Tubulin      >   A  E  I  T  N  A  C  F  E  P  A  N  Q  M  V  K  C  D  P  R  H  G  K  Y  M  A  C  C  L  L  Y  R  G

              BmgB1                     BsrD1                                PflM1             Bgl1
                  |                         |                                    |                |
               TGACGTGGTTCCCAAAGATGTCAATGCTGCCATTGCCACCATCAAAACCAAGCGCAGCATCCAGTTTGTGGATTGGTGCCCCACTGGCTTCAAGGTTGGC
         2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
               ACTGCACCAAGGGTTTCTACAGTTACGACGGTAACGGTGGTAGTTTTGGTTCGCGTCGTAGGTCAAACACCTAACCACGGGGTGACCGAAGTTCCAACCG
Tubulin      >  D  V  V  P  K  D  V  N  A  A  I  A  T  I  K  T  K  R  S  I  Q  F  V  D  W  C  P  T  G  F  K  V  G

                                                      Msc1                       Blp1                 Bpu10
                                 Ale1   Bsa1         EcoN1                      Sph1|           BsrD1 BbvC1 Stu1
                                    |      |             |                         ||               |     |    |
               ATCAACTACCAGCCTCCCACTGTGGTGCCTGGTGGAGACCTGGCCAAGGTACAGAGAGCTGTGTGCATGCTGAGCAACACCACAGCCATTGCTGAGGCCT
         2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
               TAGTTGATGGTCGGAGGGTGACACCACGGACCACCTCTGGACCGGTTCCATGTCTCTCGACACACGTACGACTCGTTGTGGTGTCGGTAACGACTCCGGA
Tubulin      > I  N  Y  Q  P  P  T  V  V  P  G  G  D  L  A  K  V  Q  R  A  V  C  M  L  S  N  T  T  A  I  A  E  A  W

                                                            Bae1b                            Bae1a
                                                                |                                |
               GGGCTCGCCTGGACCACAAGTTTGACCTGATGTATGCCAAGCGTGCCTTTGTTCACTGGTACGTGGGTGAGGGGATGGAGGAAGGCGAGTTTTCAGAGGC
         2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
               CCCGAGCGGACCTGGTGTTCAAACTGGACTACATACGGTTCGCACGGAAACAAGTGACCATGCACCCACTCCCCTACCTCCTTCCGCTCAAAAGTCTCCG
Tubulin      >   A  R  L  D  H  K  F  D  L  M  Y  A  K  R  A  F  V  H  W  Y  V  G  E  G  M  E  E  G  E  F  S  E  A

                                 EcoN1             BpuE1    BseR1                                        BamH1
                                     |                 |        |                                            |
               CCGTGAAGATATGGCTGCCCTTGAGAAGGATTATGAGGAGGTTGGTGTGGATTCTGTTGAAGGAGAGGGTGAGGAAGAAGGAGAGGAATACTAAGGATCC
         2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
               GGCACTTCTATACCGACGGGAACTCTTCCTAATACTCCTCCAACCACACCTAAGACAACTTCCTCTCCCACTCCTTCTTCCTCTCCTTATGATTCCTAGG
Tubulin      >  R  E  D  M  A  A  L  E  K  D  Y  E  E  V  G  V  D  S  V  E  G  E  G  E  E  E  G  E  E  Y  *
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         Xba1      Bcl1BsaB1                            SpDon   Dra1
            |         |    |                                |      |
      ACCGGATCTAGATAACTGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATA
2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
      TGGCCTAGATCTATTGACTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTAT

             Bsm1
            Mfe1|        Hpa1       polyA    Psi1      polyA                        polyA            Bts1
               ||           |           |       |          |                            |               |
      AAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTC
2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
      TTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAG

      Bsm1                                      Mlu1     SpDon        Ssp1
         |                                         |         |           |
      ACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAACGCGTAAATTGTAAGCGTTAATATTTGTTAAAATTCGCGTTAAATTTTTGTTA
2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
      TGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTGCGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAAT

                                                  Psi1
                                                     |
      AATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAAC
3001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
      TTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTG

                                                                              BtgZ1
           BsaXb                 Drd1    BsaXa                                Dra3|
               |                    |        |                                   ||
      AAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTT
3101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
      TTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAA

                                                                                 Nae1
                                        SpAcc                                 NgoM4 |
                                            |                                     | |
      TTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGA
3201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
      AAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCT
```

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                     BsrB1
                         |
      AGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAG
3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
      TCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTC

                                                                                          BciV1
                                                                                       BspH1  |
                                                         polyA                       BsrB1 |  |
                                                             |                           | |  |
      GGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAAC
3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
      CCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTG

                                                              Eci1
                       Ssp1  Ear1        Bsu36              Pvu2 |
                          |     |            |                 | |
      CCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGC
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      GGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCG

                                  Nsi1
                                Sph1 |
                               BfrB1 |
    BseY1                   BstAP  | |            SexA1                     BseY1                   BstAP
        |                       |  | |                |                         |                       |
      TCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCA
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      AGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGT

      Nsi1
    Sph1 |                                                      Eci1
   BfrB1 |                       Eci1                 Eci1     Bmr1|       Eci1            Nco1
       | |                          |                    |        ||          |               |
      TGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACT
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      ACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGA
```

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                                                                                    Avr2
                                     Sfi1                                          Stu1|
              polyA                  Bgl1                    SpDon             BseR1  ||
                  |                     |                        |                 |  ||
      AATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGAT
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      TTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTCTA

                                                BspM1
  Cla1              BsaB1                       BfuA1               Eag1
     |                  |                           |                  |
      CGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGAC
3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
      GCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTG

                                                              Nar1
           Bmr1                                              Kas1|                       Drd1
              |                                                 ||                          |
      TGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCC
4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
      ACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGG

                                                                    Pvu2
                                            Msc1                Fsp1   |       PflF1
                                               |                   |   |           |
      TGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGA
4101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
      ACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCT

       Eco57                                      SpDon                         BciV1         BsrD1
           |                                          |                             |             |
      CTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTG
4201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
      GACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGAC
```

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                                BtgZ1
                             BspM1  |
                             BfuA1  |
                                 |  |
      CATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATG
4301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
      GTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTAC

      Sap1
      Ear1                           BpuE1                         Sph1                       Nco1
         |                               |                            |                          |
      ATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGA
4401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
      TAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCT

                                                                 BseY1
                                                                Nae1 |
             BtgZ1                                           NgoM4 | |        Rsr2         Eci1
                 |                                               | | |           |            |
      TGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTG
4501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
      ACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAAC

                Sap1                                                        BtgZ1
                Ear1                   Eco57         BssS1                BsrB1 |
                   |                       |             |                    | |
      GCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCT
4601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
      CGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGA

                                                                               BssS1
                                                                               BspM1
                            BsrB1          BstB1                               BfuA1
                                |              |                                  |
      ATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCGCC
4701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
      TAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGG
```

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                                               Nae1
                                            NgoM4 |                                               SpAcc
      SpAcc                                  Bpm1 |                                                Avr2
          |                                     | |                                                   |
      GCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTA
4801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
      CGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGAT

  Bpm1                                                        polyA        polyA
     |                                                            |            |
      GGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTT
4901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
      CCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAA

                                                   Bsa1
                                                      |
      TGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCA
5001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
      ACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGT

                                                              BstAP
                                                              AlwN1      Bsu36
                                                                  |          |
      CCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTG
5101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
      GGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAAC

      Dra1               Dra1                              BspH1
         |                  |                                  |
      ATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGC
5201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
      TAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCG

                                                       BpuE1
                                                           |
      GTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTG
5301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5400
      CAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCAC
```

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                                     Eco57                                               SpAcc
                                         |                                                   |
      GTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGT
5401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5500
      CAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCA

                                                                      AlwN1                     BpuE1
                                                                          |                         |
      TAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTAC
5501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5600
      ATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATG

                                                                 ApaL1     BseY1
                                                                     |         |
      CGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACC
5601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5700
      GCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGG

                                                                                 BciV1
                         SpAcc                                          Eci1   |
                             |                                                   |   |
      GAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAG
5701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5800
      CTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTC

      BssS1                                    SpAcc                          Drd1            BpuE1
          |                                        |                             |                |
      AGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTC
5801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5900
      TCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAG

                                                                                SpDon
              SpAcc     Eci1                                                   BspLU|
                  |        |                                                       ||
      AGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCC
5901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6000
      TCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGG
```

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                                              Nsi1
                                           BfrB1 |
                                               | |
               CCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
         6001  |||||||||*|||||||||*|||||||||*|||||| 6036
               GGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

```
Found:

Aat2    Age1    Ale1   AlwN1   ApaL1    Ase1    Avr2   Bae1a   Bae1b   BamH1    Bbs1   BbvC1   BciV1    Bcl1   BfrB1
BfuA1   Bgl1    Bgl2    Blp1   BmgB1    Bmr1    Bpm1   Bpu10   BpuE1    Bsa1   BsaB1   BsaXa   BsaXb   BseR1   BseY1
Bsg1    Bsm1   BsmB1   BspE1   BspH1   BspLU   BspM1   BsrB1   BsrD1   BsrG1   BssS1   BstAP   BstB1   BstE2   BstX1
Bsu36  BtgZ1    Bts1    Cla1    Dra1    Dra3    Drd1    Eag1    Ear1    Eci1    Ecl2   Eco57    EcoK   EcoN1   EcoR1
EcoRV   Fsp1    Hpa1    Kas1    Mfe1    Mlu1    Msc1    Nae1    Nar1    Nco1    Nde1   NgoM4    Nhe1    Nsi1   PflF1
PflM1   Pml1   polyA   PshA1    Psi1    Pvu2    Rsr2    Sac1    Sac2    Sap1   SexA1    Sfi1    Sma1   SnaB1   SpAcc
SpDon   Sph1    Ssp1    Stu1    Xba1    Xcm1    Xho1    Xmn1
Unique:

Age1    Ase1   Bae1a   Bae1b   BamH1    Bbs1   BbvC1    Bcl1    Bgl2    Blp1   BspE1   BspLU   BstB1   BstE2    Cla1
Eag1    Ecl2    EcoK   EcoRV    Fsp1    Hpa1    Kas1    Mfe1    Mlu1    Nar1    Nhe1   PflF1    Pml1   PshA1    Rsr2
Sac1    Sac2    Sfi1    Sma1   SnaB1    Xba1    Xho1


Not found:

Aar1   Acc65    Acl1    Afe1    Afl2    Ahd1    Apa1    Asc1   AsiS1   Bcg1a   Bcg1b   BsiW1   BssH2   BstZ1   BxatB
BxatL  BxatR   BxatP    _Chi   FCatB   FCatL   FCatR   FCatP   ScFRT    Fse1   FspA1   Hind3   I_Ceu    Kpn1    loxP
Not1    Nru1    Pac1    Pme1   PspOM    Pst1    Pvu1   R4atB   R4atL   R4atP   R4atR    Sal1   SanD1    Sbf1    Sca1
Sgf1   SgrA1    Spe1    Srf1    Swa1   T3RNA   T7RNA   T7Ter   PISce

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
```