pTagGFP-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). TagGFP 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

                                                Aat2                                             Eci1
                                                   |                                                |
     TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 500
     ATCGCCAAACTGAGTGCCCCTAAAGGTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT
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                                                                                                      Nhe1 Afe1
                                                                                                         |    |
               ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCGCTA
          501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
               TGTTGAGGCGGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT

                                                  BseR1
                                                  Nae1|                               ApaL1
           Age1            BsrB1               NgoM4 ||                              BmgB1|
              |                |                   | ||                                  ||
               CCGGTCGCCACCATGAGCGGGGGCGAGGAGCTGTTCGCCGGCATCGTGCCCGTGCTGATCGAGCTGGACGGCGACGTGCACGGCCACAAGTTCAGCGTGC
          601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
               GGCCAGCGGTGGTACTCGCCCCCGCTCCTCGACAAGCGGCCGTAGCACGGGCACGACTAGCTCGACCTGCCGCTGCACGTGCCGGTGTTCAAGTCGCACG
TagGFP       >             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

                                                                      BsaXb                           BstE2
                                        BsaXa    Bsg1               Bpm1  |                          Ale1 |
                                            |       |                  |  |                             | |
               GCGGCGAGGGCGAGGGCGACGCCGACTACGGCAAGCTGGAGATCAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTGGTGACCAC
          701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
               CGCCGCTCCCGCTCCCGCTGCGGCTGATGCCGTTCGACCTCTAGTTCAAGTAGACGTGGTGGCCGTTCGACGGGCACGGGACCGGGTGGGACCACTGGTG
TagGFP       >   G  E  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

                            BstAP                                  Xmn1
                                |                                     |
               CCTCTGCTACGGCATCCAGTGCTTCGCCCGCTACCCCGAGCACATGAAGATGAACGACTTCTTCAAGAGCGCCATGCCCGAGGGCTACATCCAGGAGCGC
          801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
               GGAGACGATGCCGTAGGTCACGAAGCGGGCGATGGGGCTCGTGTACTTCTACTTGCTGAAGAAGTTCTCGCGGTACGGGCTCCCGATGTAGGTCCTCGCG
TagGFP       >  L  C  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

                         SpAcc
                        Ear1 |                                                 SpDon
                    EcoN1  | |                    Sac2 SpDon                  Ale1 |
                        |  | |                       |     |                     | |
               ACCATCCTCTTCCAGGACGACGGCAAGTACAAGACCCGCGGCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCAAGGACT
          901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
               TGGTAGGAGAAGGTCCTGCTGCCGTTCATGTTCTGGGCGCCGCTCCACTTCAAGCTCCCGCTGTGGGACCACTTGGCGTAGCTCGACTTCCCGTTCCTGA
TagGFP       > T  I  L  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
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                                                                       BsrG1
                Eco57                     PflM1                  Bpm1 Dra3 |                        Xcm1    SpDon
                    |                         |                     |    | |                           |        |
               TCAAGGAGGACGGCAACATCCTGGGCCACAAGCTGGAGTACAGCTTCAACAGCCACAACGTGTACATCATGCCCGACAAGGCCAACAACGGCCTGGAGGT
         1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
               AGTTCCTCCTGCCGTTGTAGGACCCGGTGTTCGACCTCATGTCGAAGTTGTCGGTGTTGCACATGTAGTACGGGCTGTTCCGGTTGTTGCCGGACCTCCA
TagGFP       >   K  E  D  G  N  I  L  G  H  K  L  E  Y  S  F  N  S  H  N  V  Y  I  M  P  D  K  A  N  N  G  L  E  V

                                                      Pvu2            Bsg1       Xcm1
                                                         |               |          |
               GAACTTCAAGACCCGCCACAACATCGAGGGCGGCGGCGTGCAGCTGGCCGACCACTACCAGACCAACGTGCCCCTGGGCGACGGCCCCGTGCTGATCCCC
         1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
               CTTGAAGTTCTGGGCGGTGTTGTAGCTCCCGCCGCCGCACGTCGACCGGCTGGTGATGGTCTGGTTGCACGGGGACCCGCTGCCGGGGCACGACTAGGGG
TagGFP       >  N  F  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

                                                                            Eco57
                       Bpu10                                                 Dra3                  AlwN1
                           |                                                    |                      |
               ATCAACCACTACCTGAGCACTCAGACCGCCATCAGCAAGGACCGCAACGAGGCCCGCGACCACATGGTGCTCCTGGAGTCCTTCAGCGCCTGCTGCCACA
         1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
               TAGTTGGTGATGGACTCGTGAGTCTGGCGGTAGTCGTTCCTGGCGTTGCTCCGGGCGCTGGTGTACCACGAGGACCTCAGGAAGTCGCGGACGACGGTGT
TagGFP       > I  N  H  Y  L  S  T  Q  T  A  I  S  K  D  R  N  E  A  R  D  H  M  V  L  L  E  S  F  S  A  C  C  H  T

                                                   Xho1
                  PflM1      BsrG1   BspE1     Bgl2   |
                      |          |       |        |   |
               CCCACGGCATGGACGAGCTGTACAGGTCCGGACTCAGATCTCGAGTGCGTGAGTGCATCTCCATCCACGTTGGCCAGGCTGGTGTCCAGATTGGCAATGC
         1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
               GGGTGCCGTACCTGCTCGACATGTCCAGGCCTGAGTCTAGAGCTCACGCACTCACGTAGAGGTAGGTGCAACCGGTCCGACCACAGGTCTAACCGTTACG
TagGFP/Tubulin   H  G  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

             BseY1
           BsrD1 |                                      Msc1
          BstAP| |     Sac1                        BstX1   |                                   Eco57BseR1
              || |        |                            |   |                                       |    |
               CTGCTGGGAGCTCTACTGCCTGGAACACGGCATCCAGCCCGATGGCCAGATGCCAAGTGACAAGACCATTGGGGGAGGAGATGACTCCTTCAACACCTTC
         1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
               GACGACCCTCGAGATGACGGACCTTGTGCCGTAGGTCGGGCTACCGGTCTACGGTTCACTGTTCTGGTAACCCCCTCCTCTACTGAGGAAGTTGTGGAAG
Tubulin      >  C  W  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
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               SpAcc
           BsmB1   |                  Pml1   Sma1
               |   |                     |      |
               TTCAGTGAGACGGGCGCTGGCAAGCACGTGCCCCGGGCTGTGTTTGTAGACTTGGAACCCACAGTCATTGATGAAGTTCGCACTGGCACCTACCGCCAGC
         1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
               AAGTCACTCTGCCCGCGACCGTTCGTGCACGGGGCCCGACACAAACATCTGAACCTTGGGTGTCAGTAACTACTTCAAGCGTGACCGTGGATGGCGGTCG
Tubulin      > F  S  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

                    Bpu10
                 Sap1   |
                 Ear1   |
                    |   |
               TCTTCCACCCTGAGCAGCTCATCACAGGCAAGGAAGATGCTGCCAATAACTATGCCCGAGGGCACTACACCATTGGCAAGGAGATCATTGACCTTGTGTT
         1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
               AGAAGGTGGGACTCGTCGAGTAGTGTCCGTTCCTTCTACGACGGTTATTGATACGGGCTCCCGTGATGTGGTAACCGTTCCTCTAGTAACTGGAACACAA
Tubulin      >   F  H  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

                                           Age1                             Xcm1
                                        Bbs1  |                            BstX1
                EcoR1            Eco57ApaL1|  |                          SpAcc |          Xmn1         SpDon
                    |                |    ||  |                              | |             |             |
               GGACCGAATTCGCAAGCTGGCTGACCAGTGCACCGGTCTTCAGGGCTTCTTGGTTTTCCACAGCTTTGGTGGGGGAACTGGTTCTGGGTTCACCTCCCTG
         1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
               CCTGGCTTAAGCGTTCGACCGACTGGTCACGTGGCCAGAAGTCCCGAAGAACCAAAAGGTGTCGAAACCACCCCCTTGACCAAGACCCAAGTGGAGGGAC
Tubulin      >  D  R  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

                                                                           Bpm1             SpAcc
                          BsmB1                                       BseY1   |              Pvu2
                              |                                           |   |                 |
               CTCATGGAACGTCTCTCAGTTGATTATGGCAAGAAGTCCAAGCTGGAGTTCTCCATTTACCCAGCACCCCAGGTTTCCACAGCTGTAGTTGAGCCCTACA
         1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
               GAGTACCTTGCAGAGAGTCAACTAATACCGTTCTTCAGGTTCGACCTCAAGAGGTAAATGGGTCGTGGGGTCCAAAGGTGTCGACATCAACTCGGGATGT
Tubulin      > L  M  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

                       SpDon                                                             PshA1              EcoRV
                           |                                                                 |                  |
               ACTCCATCCTCACCACCCACACCACCCTGGAGCACTCTGATTGTGCCTTCATGGTAGACAATGAGGCCATCTATGACATCTGTCGTAGAAACCTCGATAT
         1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
               TGAGGTAGGAGTGGTGGGTGTGGTGGGACCTCGTGAGACTAACACGGAAGTACCATCTGTTACTCCGGTAGATACTGTAGACAGCATCTTTGGAGCTATA
Tubulin      >   S  I  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
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                                                                    Bts1
                                                                       |
               CGAGCGCCCAACCTACACTAACCTTAACCGCCTTATTAGCCAGATTGTGTCCTCCATCACTGCTTCCCTGAGATTTGATGGAGCCCTGAATGTTGACCTG
         2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
               GCTCGCGGGTTGGATGTGATTGGAATTGGCGGAATAATCGGTCTAACACAGGAGGTAGTGACGAAGGGACTCTAAACTACCTCGGGACTTACAACTGGAC
Tubulin      >  E  R  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

              EcoR1                                            Msc1 Nde1              SpAcc
                  |                                               |    |                  |
               ACAGAATTCCAGACCAACCTGGTGCCCTACCCCCGCATCCACTTCCCTCTGGCCACATATGCCCCTGTCATCTCTGCTGAGAAAGCCTACCATGAACAGC
         2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
               TGTCTTAAGGTCTGGTTGGACCACGGGATGGGGGCGTAGGTGAAGGGAGACCGGTGTATACGGGGACAGTAGAGACGACTCTTTCGGATGGTACTTGTCG
Tubulin      > T  E  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

                                                            SpDon                 SpDon
                   SpAcc                                 BstX1  |              Nco1   |
                       |                                     |  |                 |   |
               TTTCTGTAGCAGAGATCACCAATGCTTGCTTTGAGCCAGCCAACCAGATGGTGAAATGTGACCCTCGCCATGGTAAATACATGGCTTGCTGCCTGTTGTA
         2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
               AAAGACATCGTCTCTAGTGGTTACGAACGAAACTCGGTCGGTTGGTCTACCACTTTACACTGGGAGCGGTACCATTTATGTACCGAACGACGGACAACAT
Tubulin      >   S  V  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

                    BmgB1                     BsrD1                                PflM1            Bgl1
                        |                         |                                    |                |
               CCGTGGTGACGTGGTTCCCAAAGATGTCAATGCTGCCATTGCCACCATCAAAACCAAGCGCAGCATCCAGTTTGTGGATTGGTGCCCCACTGGCTTCAAG
         2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
               GGCACCACTGCACCAAGGGTTTCTACAGTTACGACGGTAACGGTGGTAGTTTTGGTTCGCGTCGTAGGTCAAACACCTAACCACGGGGTGACCGAAGTTC
Tubulin      >  R  G  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

                                                                                       Blp1                 Bpu10
                                       Ale1                EcoN1                      Sph1|           BsrD1 BbvC1
                                          |                    |                         ||               |     |
               GTTGGCATCAACTACCAGCCTCCCACTGTGGTGCCTGGTGGAGACCTGGCCAAGGTACAGAGAGCTGTGTGCATGCTGAGCAACACCACAGCCATTGCTG
         2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
               CAACCGTAGTTGATGGTCGGAGGGTGACACCACGGACCACCTCTGGACCGGTTCCATGTCTCTCGACACACGTACGACTCGTTGTGGTGTCGGTAACGAC
Tubulin      > V  G  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
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                                                                  Bae1b                            Bae1a
                                                                      |                                |
               AGGCCTGGGCTCGCCTGGACCACAAGTTTGACCTGATGTATGCCAAGCGTGCCTTTGTTCACTGGTACGTGGGTGAGGGGATGGAGGAAGGCGAGTTTTC
         2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
               TCCGGACCCGAGCGGACCTGGTGTTCAAACTGGACTACATACGGTTCGCACGGAAACAAGTGACCATGCACCCACTCCCCTACCTCCTTCCGCTCAAAAG
Tubulin      >   A  W  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

                                       EcoN1             BpuE1    BseR1             SpDon
                                           |                 |        |                 |
               AGAGGCCCGTGAAGATATGGCTGCCCTTGAGAAGGATTATGAGGAGGTTGGTGTGGATTCTGTTGAAGGAGAGGGTGAGGAAGAAGGAGAGGAATACTAA
         2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
               TCTCCGGGCACTTCTATACCGACGGGAACTCTTCCTAATACTCCTCCAACCACACCTAAGACAACTTCCTCTCCCACTCCTTCTTCCTCTCCTTATGATT
Tubulin      >  E  A  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  *

           BamH1                                                       SpDon   Dra1
               |                                                           |      |
               GGATCCACCGGATCTAGATAACTGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGA
         2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
               CCTAGGTGGCCTAGATCTATTGACTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACT

                            Bsm1
                           Mfe1|        Hpa1       polyA    Psi1      polyA                        polyA
                              ||           |           |       |          |                            |
               AACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATT
         2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
               TTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAA

                Bts1 Bsm1                                      Mlu1     SpDon        Ssp1
                   |    |                                         |         |           |
               TTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAACGCGTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTT
         2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
               AAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTGCGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAA

                                                                 Psi1
                                                                    |
               TTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTT
         3001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
               AACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAA
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                                                                                    BtgZ1
                 BsaXb                 Drd1    BsaXa                                Dra3|
                     |                    |        |                                   ||
      TGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAAT
3101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
      ACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTA

                                                                                       Nae1
                                              SpAcc                                 NgoM4 |
                                                  |                                     | |
      CAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAG
3201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
      GTTCAAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTC

                           BsrB1
                               |
      AAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCG
3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
      TTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGC

                                                                                                BciV1
                                                                                             BspH1  |
                                                               polyA                     BsrB1 |  |
                                                                   |                           | |  |
      CTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGAC
3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
      GATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTG

                                                                    Eci1
                             Ssp1  Ear1        Bsu36              Pvu2 |
                                |     |            |                 | |
      AATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCC
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      TTATTGGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGG
```

```
                                        Nsi1
                                      Sph1 |
                                     BfrB1 |
          BseY1                   BstAP  | |                                      BseY1
              |                       |  | |                                          |
      CCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGC
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      GGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACG

            Nsi1
          Sph1 |
         BfrB1 |                                                      Eci1
      BstAP  | |                       Eci1                 Eci1     Bmr1|       Eci1            Nco1
          |  | |                          |                    |        ||          |               |
      AAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGG
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      TTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACC

                                                                                          Avr2
                                           Sfi1                                          Stu1|
                    polyA                  Bgl1                    SpDon             BseR1  ||
                        |                     |                        |                 |  ||
      CTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGC
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      GACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACG

                                                      BspM1
                                                      BfuA1               Eag1
                                                          |                   |
      AAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGC
3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
      TTTCTAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCG

                                                                    Nar1
                 Bmr1                                              Kas1|                       Drd1
                    |                                                 ||                          |
      TATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCG
4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
      ATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGC
```

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                                                                          Pvu2
                                                  Msc1                Fsp1   |       PflF1
                                                     |                   |   |           |
      GTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGG
4101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
      CACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCC

             Eco57                                      SpDon                         BciV1         BsrD1
                 |                                          |                             |             |
      AAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGG
4201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
      TTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCC

                                      BtgZ1
                                   BspM1  |
                                   BfuA1  |
                                       |  |
      CGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATC
4301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
      GCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAG

            Sap1
            Ear1                           BpuE1                    Sph1                       Nco1
               |                               |                       |                          |
      AGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCA
4401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
      TCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGT

                                                                       BseY1
                                                                      Nae1 |
                   BtgZ1                                           NgoM4 | |        Rsr2         Eci1
                       |                                               | | |          |            |
      TGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATA
4501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
      ACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTAT
```

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                      Sap1                                                        BtgZ1
                      Ear1                   Eco57         BssS1                BsrB1 |
                         |                       |             |                    | |
      GCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCG
4601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
      CGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGC

                                                                                     BssS1
                                                                                     BspM1
                                  BsrB1          BstB1                               BfuA1
                                      |              |                                   |
      CCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCC
4701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
      GGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGG

                                                     Nae1
                                                  NgoM4 |
            SpAcc                                  Bpm1 |
                |                                     | |
      ACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCC
4801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
      TGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGG

        Bpm1
    SpAcc  |
     Avr2  |                                                        polyA        polyA
        |  |                                                            |            |
      ACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGG
4901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
      TGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACC

                                                         Bsa1
                                                            |
      GTCGTTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTT
5001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
      CAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAA
```

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                                                                    BstAP
                          SpDon                                     AlwN1      Bsu36
                              |                                         |          |
      TCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTT
5101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
      AGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAA

            Dra1               Dra1                              BspH1
               |                  |                                  |
      AGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCA
5201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
      TCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGT

                                                             BpuE1
                                                                 |
      CTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCA
5301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5400
      GACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGT

                                           Eco57                                              SpAcc
                                               |                                                  |
      GCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGC
5401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5500
      CGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCG

                                                                            AlwN1
                                                                                |
      CGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTG
5501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5600
      GCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCAC

  BpuE1                                                                ApaL1     BseY1
      |                                                                    |         |
      TCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACC
5601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5700
      AGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGG

                                                                                       BciV1
                               SpAcc                                            Eci1   |
                                   |                                                   |   |
```

```
      TACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAA
5701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5800
      ATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTT

            BssS1                                    SpAcc                          Drd1            BpuE1
                |                                        |                             |                |
      CAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATG
5801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5900
      GTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTAC

                                                                                      SpDon
                    SpAcc     Eci1                                                   BspLU|
                        |        |                                                       ||
      CTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCG
5901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6000
      GAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGC

                                           Nsi1
                                        BfrB1 |
                                            | |
      TTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
6001  |||||||||*|||||||||*|||||||||*|||||||||*|| 6042
      AATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

```
    Aat2    Afe1    Age1    Ale1   AlwN1   ApaL1    Ase1    Avr2   Bae1a   Bae1b   BamH1    Bbs1   BbvC1   BciV1
   BfrB1   BfuA1    Bgl1    Bgl2    Blp1   BmgB1    Bmr1    Bpm1   Bpu10   BpuE1    Bsa1   BsaXa   BsaXb   BseR1
   BseY1    Bsg1    Bsm1   BsmB1   BspE1   BspH1   BspLU   BspM1   BsrB1   BsrD1   BsrG1   BssS1   BstAP   BstB1
   BstE2   BstX1   Bsu36   BtgZ1    Bts1    Dra1    Dra3    Drd1    Eag1    Ear1    Eci1   Eco57   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    Sfi1    Sma1   SnaB1
   SpAcc   SpDon    Sph1    Ssp1    Stu1    Xcm1    Xho1    Xmn1
```

Unique:

```
    Afe1    Ase1   Bae1a   Bae1b   BamH1    Bbs1   BbvC1    Bgl2    Blp1    Bsa1   BspE1   BspLU   BstB1   BstE2
    Eag1   EcoRV    Fsp1    Hpa1    Kas1    Mfe1    Mlu1    Nar1    Nhe1   PflF1    Pml1   PshA1    Rsr2    Sac1
    Sac2    Sfi1    Sma1   SnaB1    Stu1    Xho1
```

Not found:

```
    Aar1   Acc65    Acl1    Afl2    Ahd1    Apa1    Asc1   AsiS1   Bcg1a   Bcg1b    Bcl1   BsaB1   BsiW1   BssH2
   BstZ1    _Chi    Cla1    EcoK   ScFRT    Fse1   FspA1   Hind3   I_Ceu    Kpn1    loxP    Not1    Nru1    Pac1
    Pme1   PspOM    Pst1    Pvu1    Sal1   SanD1    Sbf1    Sca1   SexA1    Sgf1   SgrA1    Spe1    Srf1    Swa1
   T3RNA   T7RNA   T7Ter   PISce    Xba1
```

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   Eco01    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
```