pTagGFP2-H2B 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 base pairs 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, H2B 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

                                                                                                Nhe1 Afe1
                                                                                                  |    |
     ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCGCTA
501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
     TGTTGAGGCGGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT

                          Hind3
                 Xho1    Sac1 |  EcoR1       Sal1       Kpn1
        BpuE1 Bgl2    | Ecl2 | |BstB1 |      Pst1| Acc65    |
            |    |    |    | | |    | |         ||      |    |
     CCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCTGCAGTCGACGGTACCGCCACCATGCCAGAGCCAGCGAAGTCTGCTCCCGCCCCGAAAAAGGGCTC
601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
     GGCCTGAGTCTAGAGCTCGAGTTCGAAGCTTAAGACGTCAGCTGCCATGGCGGTGGTACGGTCTCGGTCGCTTCAGACGAGGGCGGGGCTTTTTCCCGAG
H2B     >                                                M  P  E  P  A  K  S  A  P  A  P  K  K  G  S

                                                                                      BspM1
                                                                                BsrG1  BfuA1
                                                                                  |      |
     CAAGAAGGCGGTGACTAAGGCGCAGAAGAAAGGCGGCAAGAAGCGCAAGCGCAGCCGCAAGGAGAGCTATTCCATCTATGTGTACAAGGTTCTGAAGCAG
701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
     GTTCTTCCGCCACTGATTCCGCGTCTTCTTTCCGCCGTTCTTCGCGTTCGCGTCGGCGTTCCTCTCGATAAGGTAGATACACATGTTCCAAGACTTCGTC
H2B     >  K  K  A  V  T  K  A  Q  K  K  G  G  K  K  R  K  R  S  R  K  E  S  Y  S  I  Y  V  Y  K  V  L  K  Q

                                                                    BspM1
                                  BstX1       EcoR1                 BfuA1
                 Eco57            Nco1|   BspH1   |          BtgZ1    Aar1       SpDon
                     |                ||       |   |              |         |           |
     GTCCACCCTGACACCGGCATTTCGTCCAAGGCCATGGGCATCATGAATTCGTTTGTGAACGACATTTTCGAGCGCATCGCAGGTGAGGCTTCCCGCCTGG
801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
     CAGGTGGGACTGTGGCCGTAAAGCAGGTTCCGGTACCCGTAGTACTTAAGCAAACACTTGCTGTAAAAGCTCGCGTAGCGTCCACTCCGAAGGGCGGACC
H2B     > V  H  P  D  T  G  I  S  S  K  A  M  G  I  M  N  S  F  V  N  D  I  F  E  R  I  A  G  E  A  S  R  L  A
```

```
                        Afe1
                       Bpm1|                          Eag1                          Msc1       Dra3
                          ||                            |                             |          |
            CGCATTACAACAAGCGCTCGACCATCACCTCCAGGGAGATCCAGACGGCCGTGCGCCTGCTGCTGCCTGGGGAGTTGGCCAAGCACGCCGTGTCCGAGGG
       901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
            GCGTAATGTTGTTCGCGAGCTGGTAGTGGAGGTCCCTCTAGGTCTGCCGGCACGCGGACGACGACGGACCCCTCAACCGGTTCGTGCGGCACAGGCTCCC
H2B       >  H  Y  N  K  R  S  T  I  T  S  R  E  I  Q  T  A  V  R  L  L  L  P  G  E  L  A  K  H  A  V  S  E  G

                                      BamH1                                       BseR1
                                  Bpu10   |                                       Nae1|
                                 Afe1 |   |  Age1            BsrB1               NgoM4 ||
                                    | |   |     |                |                   | ||
            TACTAAGGCCATCACCAAGTACACCAGCGCTAAGGATCCACCGGTCGCCACCATGAGCGGGGGCGAGGAGCTGTTCGCCGGCATCGTGCCCGTGCTGATC
      1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
            ATGATTCCGGTAGTGGTTCATGTGGTCGCGATTCCTAGGTGGCCAGCGGTGGTACTCGCCCCCGCTCCTCGACAAGCGGCCGTAGCACGGGCACGACTAG
H2B/TagGFP2 > T  K  A  I  T  K  Y  T  S  A  K  D  P  P  V  A  T  M  S  G  G  E  E  L  F  A  G  I  V  P  V  L  I

                        ApaL1
                       BmgB1|                                                BsaXa    Bsg1                Bpm1
                           ||                                                   |       |                   |
            GAGCTGGACGGCGACGTGCACGGCCACAAGTTCAGCGTGCGCGGCGAGGGCGAGGGCGACGCCGACTACGGCAAGCTGGAGATCAAGTTCATCTGCACCA
      1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
            CTCGACCTGCCGCTGCACGTGCCGGTGTTCAAGTCGCACGCGCCGCTCCCGCTCCCGCTGCGGCTGATGCCGTTCGACCTCTAGTTCAAGTAGACGTGGT
TagGFP2   > E  L  D  G  D  V  H  G  H  K  F  S  V  R  G  E  G  E  G  D  A  D  Y  G  K  L  E  I  K  F  I  C  T  T

                                  BstE2
       BsaXb                     Ale1 |                     BstAP                                  Xmn1
          |                         | |                       |                                      |
            CCGGCAAGCTGCCCGTGCCCTGGCCCACCCTGGTGACCACCCTCTGCTACGGCATCCAGTGCTTCGCCCGCTACCCCGAGCACATGAAGATGAACGACTT
      1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
            GGCCGTTCGACGGGCACGGGACCGGGTGGGACCACTGGTGGGAGACGATGCCGTAGGTCACGAAGCGGGCGATGGGGCTCGTGTACTTCTACTTGCTGAA
TagGFP2   >  G  K  L  P  V  P  W  P  T  L  V  T  T  L  C  Y  G  I  Q  C  F  A  R  Y  P  E  H  M  K  M  N  D  F

                                         EcoK                                     Sac2 SpDon
                                            |                                        |     |
            CTTCAAGAGCGCCATGCCCGAGGGCTACATCCAGGAGCGCACCATCCAGTTCCAGGACGACGGCAAGTACAAGACCCGCGGCGAGGTGAAGTTCGAGGGC
      1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
            GAAGTTCTCGCGGTACGGGCTCCCGATGTAGGTCCTCGCGTGGTAGGTCAAGGTCCTGCTGCCGTTCATGTTCTGGGCGCCGCTCCACTTCAAGCTCCCG
TagGFP2   > F  K  S  A  M  P  E  G  Y  I  Q  E  R  T  I  Q  F  Q  D  D  G  K  Y  K  T  R  G  E  V  K  F  E  G
```

```
                                                                                                                                Dra3
                 SpDon                                                                                                        Eci1 |
                Ale1 |                                Eco57                      PflM1                   Bpm1  | |
                   | |                                   |                          |                       |  | |
            GACACCCTGGTGAACCGCATCGAGCTGAAGGGCAAGGACTTCAAGGAGGACGGCAACATCCTGGGCCACAAGCTGGAGTACAGCTTCAACAGCCACAACG
      1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
            CTGTGGGACCACTTGGCGTAGCTCGACTTCCCGTTCCTGAAGTTCCTCCTGCCGTTGTAGGACCCGGTGTTCGACCTCATGTCGAAGTTGTCGGTGTTGC
TagGFP2       > D  T  L  V  N  R  I  E  L  K  G  K  D  F  K  E  D  G  N  I  L  G  H  K  L  E  Y  S  F  N  S  H  N  V

          BsrG1                       Xcm1                     Bpm1                        Pvu2            Bsg1
            |                           |                        |                           |               |
            TGTACATCCGCCCCGACAAGGCCAACAACGGCCTGGAGGCTAACTTCAAGACCCGCCACAACATCGAGGGCGGCGGCGTGCAGCTGGCCGACCACTACCA
      1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
            ACATGTAGGCGGGGCTGTTCCGGTTGTTGCCGGACCTCCGATTGAAGTTCTGGGCGGTGTTGTAGCTCCCGCCGCCGCACGTCGACCGGCTGGTGATGGT
TagGFP2       >   Y  I  R  P  D  K  A  N  N  G  L  E  A  N  F  K  T  R  H  N  I  E  G  G  G  V  Q  L  A  D  H  Y  Q

                 Xcm1                      BsaB1          Bpu10
                    |                         |              |
            GACCAACGTGCCCCTGGGCGACGGCCCCGTGCTGATCCCCATCAACCACTACCTGAGCACTCAGACCAAGATCAGCAAGGACCGCAACGAGGCCCGCGAC
      1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
            CTGGTTGCACGGGGACCCGCTGCCGGGGCACGACTAGGGGTAGTTGGTGATGGACTCGTGAGTCTGGTTCTAGTCGTTCCTGGCGTTGCTCCGGGCGCTG
TagGFP2       >  T  N  V  P  L  G  D  G  P  V  L  I  P  I  N  H  Y  L  S  T  Q  T  K  I  S  K  D  R  N  E  A  R  D

                Eco57                                                          Not1
                 Dra3                  AlwN1 Bpm1         PflM1      BsrG1 SpDon  Eag1      Xba1   BsaB1
                    |                      |    |             |          |     |     |         |       |
            CACATGGTGCTCCTGGAGTCCTTCAGCGCCTGCTGCCACACCCACGGCATGGACGAGCTGTACAGGTAAGCGGCCGCGACTCTAGATCATAATCAGCCAT
      1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
            GTGTACCACGAGGACCTCAGGAAGTCGCGGACGACGGTGTGGGTGCCGTACCTGCTCGACATGTCCATTCGCCGGCGCTGAGATCTAGTATTAGTCGGTA
TagGFP2       > H  M  V  L  L  E  S  F  S  A  C  C  H  T  H  G  M  D  E  L  Y  R  *

                                                                                   Bsm1
                                SpDon   Dra1                                      Mfe1|        Hpa1
                                   |      |                                          ||           |
            ACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTA
      1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
            TGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAAT
```

```
   polyA    Psi1      polyA                        polyA            Bts1 Bsm1
      |       |          |                            |                |    |
     TTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCAT
1901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
     AACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTA

          Afl2         SpDon        Ssp1
            |             |           |
     CAATGTATCTTAAGGCGTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAAT
2001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
     GTTACATAGAATTCCGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTA

                Psi1                                                          BsaXb                 Drd1
                  |                                                             |                     |
     CGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAAC
2101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
     GCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTG

                                          BtgZ1
       BsaXa                              Dra3|
          |                                  ||
     GTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATC
2201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
     CAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCCAGCTCCACGGCATTTCGTGATTTAG

                                             Nae1
      SpAcc                               NgoM4 |                                     BsrB1
         |                                    | |                                       |
     GGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGC
2301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
     CCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCG

     GCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTG
2401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
     CGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACAC
```

```
                                                   BciV1
                                                 BspH1  |
                          polyA                 BsrB1 |  |                          Ssp1  Ear1
                              |                     | |  |                             |     |
     CGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGA
2501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
     GCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCCT

                                                                                                   Nsi1
                                                                                                 Sph1 |
                            Eci1                                                               BfrB1 |
       Bsu36              Pvu2 |                                       BseY1                 BstAP  | |
           |                  | |                                         |                       |  | |
     AGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCAT
2601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
     TCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTA

                                                                  Nsi1
                                                                Sph1 |
                                                               BfrB1 |
                 SexA1                      BseY1                BstAP  | |                        Eci1
                    |                          |                   |  | |                           |
     CTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGC
2701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
     GAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCG

                             Eci1
                    Eci1     Bmr1|       Eci1            Nco1                   polyA
                       |        ||          |               |                      |
     CCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGC
2801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
     GGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCG

                                                 Avr2
    Sfi1                                        Stu1|
    Bgl1                     SpDon             BseR1  ||              Cla1              BsaB1
      |                         |                 |  ||                 |                  |
     CTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCAT
2901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
     GAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTA
```

```
                BspM1
                BfuA1                Eag1                                        Bmr1
                    |                  |                                           |
     GATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCC
3001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
     CTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGG

                            Nar1
                           Kas1|                        Drd1
                               ||                          |
     GCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTAT
3101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
     CGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATA

                                 Pvu2
          Msc1                Fsp1   |       PflF1                        Eco57
             |                   |   |           |                          |
     CGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGA
3201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
     GCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCT

                                                                                                  BtgZ1
                                                                                             BspM1  |
                SpDon                          BciV1         BsrD1                         BfuA1  |
                    |                            |             |                                |  |
     TCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGAC
3301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
     AGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTG

                                                                    Sap1
                                                                    Ear1
                                                                      |
     CACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAG
3401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
     GTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTC
```

```
    BpuE1                         Sph1                        Nco1               BtgZ1
       |                             |                           |                  |
      CCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGG
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      GGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACC

                                BseY1
                               Nae1 |                                                  Sap1
                            NgoM4 | |        Rsr2         Eci1                       Ear1
                                | | |           |            |                           |
      CCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGC
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      GGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCG

                                          BtgZ1
      Eco57         BssS1                BsrB1 |                                                BsrB1
        |             |                    | |                                                  |
      GAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGAC
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      CTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTG

                                          BssS1
                                          BspM1
          BstB1                           BfuA1                       SpAcc
            |                                |                          |
      TCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTT
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      AGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAA

              Nae1                                                  Bpm1
           NgoM4 |                                              SpAcc  |
            Bpm1 |                                               Avr2  |
              | |                                                  |  |
      TTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAA
3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
      AAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTT
```

```
                          polyA        polyA
                              |            |
     TACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTG
4001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
     ATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGAC

                 Bsa1
                    |
     GCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGG
4101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
     CGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCC

                          BstAP
                          AlwN1      Bsu36                            Dra1               Dra1
                              |          |                               |                  |
     CTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCT
4201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
     GAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGA

                        BspH1
                            |
     AGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTC
4301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
     TCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAG

                      BpuE1
                          |
     TTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTT
4401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
     AACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAA

    Eco57                                                 SpAcc
       |                                                    |
     TTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGC
4501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
     AAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCG
```

```
                                  AlwN1                     BpuE1
                                      |                         |
      CTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAA
4601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
      GATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATT

                             ApaL1     BseY1                                                SpAcc
                                 |         |                                                    |
      GGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAA
4701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
      CCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTT

                                          BciV1
                                       Eci1   |                    BssS1
                                          |   |                        |
      AGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCT
4801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
      TCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGA

              SpAcc                           Drd1            BpuE1               SpAcc     Eci1
                  |                              |                |                   |        |
      GGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAA
4901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
      CCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTT


                                          SpDon
                                         BspLU|
                                             ||
      CGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATG
5001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
      GCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTAC


    Nsi1
 BfrB1 |
     | |
      CAT
5101  ||| 5103
      GTA
```

Found:

Aar1	Aat2	**Acc65**	Afe1	**Afl2**	**Age1**	Ale1	AlwN1	ApaL1	**Ase1**	Avr2	**BamH1**	BciV1	BfrB1
BfuA1	Bgl1	**Bgl2**	**BmgB1**	Bmr1	Bpm1	Bpu10	BpuE1	**Bsa1**	BsaB1	BsaXa	BsaXb	BseR1	BseY1
Bsg1	Bsm1	BspH1	**BspLU**	BspM1	BsrB1	**BsrD1**	BsrG1	BssS1	BstAP	BstB1	**BstE2**	**BstX1**	Bsu36
BtgZ1	**Bts1**	**Cla1**	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	**Ecl2**	Eco57	**EcoK**	EcoR1	**Fsp1**
Hind3	**Hpa1**	**Kas1**	**Kpn1**	**Mfe1**	Msc1	Nae1	**Nar1**	Nco1	**Nde1**	NgoM4	**Nhe1**	**Not1**	Nsi1
PflF1	PflM1	polyA	Psi1	**Pst1**	Pvu2	**Rsr2**	**Sac1**	**Sac2**	**Sal1**	Sap1	**SexA1**	**Sfi1**	**SnaB1**
SpAcc	SpDon	Sph1	Ssp1	**Stu1**	**Xba1**	Xcm1	**Xho1**	**Xmn1**					

Unique:

Aar1	**Acc65**	**Afl2**	**Age1**	**Ase1**	**BamH1**	**Bgl2**	**BmgB1**	**Bsa1**	**BspLU**	**BsrD1**	**BstE2**	**BstX1**	**Bts1**
Cla1	**Ecl2**	**EcoK**	**Fsp1**	**Hind3**	**Hpa1**	**Kas1**	**Kpn1**	**Mfe1**	**Nar1**	**Nde1**	**Nhe1**	**Not1**	**PflF1**
Pst1	**Rsr2**	**Sac1**	**Sac2**	**Sal1**	**SexA1**	**Sfi1**	**SnaB1**	**Stu1**	**Xba1**	**Xho1**	**Xmn1**		

Not found:

Acl1	Ahd1	Apa1	Asc1	AsiS1	Bae1a	Bae1b	Bbs1	BbvC1	Bcg1a	Bcg1b	Bcl1	Blp1	BsiW1
BsmB1	BspE1	BssH2	BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	EcoN1	EcoRV	FCatB	FCatL	FCatR
FCatP	ScFRT	Fse1	FspA1	I_Ceu	loxP	Mlu1	Nru1	Pac1	Pme1	Pml1	PshA1	PspOM	Pvu1
R4atB	R4atL	R4atP	R4atR	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Sma1	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													