pTagRFP-zyxin 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). TagRFP amino acids are shown in red, Zyxin amino acids are shown in green, 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 Afe1
                                                                                            |    |
     ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCGCTA
501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
     TGTTGAGGCGGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT

                 Xho1    Hind3  EcoR1
    BpuE1 Bgl2    |    Sac1 |BstB1 | Nco1                  BsmB1                  Bsa1
        |     |    |       | |     | |     |                     |                     |
     CCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCCATGGCGGCCCCCCGCCCGTCTCCCGCGATCCCCGTTTCGGTCTCGGCTCCGGCTTTTTACGCCCC
601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
     GGCCTGAGTCTAGAGCTCGAGTTCGAAGCTTAAGGTACCGCCGGGGGGCGGGCAGAGGGCGCTAGGGGCAAAGCCAGAGCCGAGGCCGAAAAATGCGGGG
Zyxin        >                                M  A  A  P  R  P  S  P  A  I  P  V  S  V  S  A  P  A  F  Y  A  P

                                                                                                  BssH2
                                                                                                 Apa1  |
                                                                                                BseY1|  |
                                                                                              PspOM  ||  |
         Xmn1                            SpDon   Xmn1                                        Sma1 |  ||  |
            |                                |      |                                          | |  ||  |
     GCAGAAGAAGTTCGGCCCTGTGGTGGCCCCAAAGCCCAAAGTGAATCCCTTCCGGCCCAGGGACAGCGAGCCTCCCCCGGCACCCGGGGCCCAGCGCGCA
701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
     CGTCTTCTTCAAGCCGGGACACCACCGGGGTTTCGGGTTTCACTTAGGGAAGGCCGGGTCCCTGTCGCTCGGAGGGGGCCGTGGGCCCCGGGTCGCGCGT
Zyxin        >  Q  K  K  F  G  P  V  V  A  P  K  P  K  V  N  P  F  R  P  R  D  S  E  P  P  P  A  P  G  A  Q  R  A

                                                Bbs1
                  Bgl1                         Xmn1  |                  BseY1                   BstAP
                     |                            |  |                     |                       |
     CAGATGGGCCGGGTGGGCGATATTCCCCCGCCGCCCCCGGAAGACTTTCCCCTGCCTCCACCTCCCCTTGCTGGGGATGGCGACGATGCAGAGGGTGCTC
801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
     GTCTACCCGGCCCACCCGCTATAAGGGGGCGGCGGGGGCCTTCTGAAAGGGGACGGAGGTGGAGGGGAACGACCCCTACCGCTGCTACGTCTCCCACGAG
Zyxin        > Q  M  G  R  V  G  D  I  P  P  P  P  P  E  D  F  P  L  P  P  P  P  L  A  G  D  G  D  D  A  E  G  A  L
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                                                                                                BseR1
                                                                                               BseR1|
                                                                                                Bpm1|
                                                Pvu1     Xmn1           SpAcc       Bgl2   BseR1  ||        BspE1
                                                   |        |               |          |       |  ||            |
            TGGGAGGTGCCTTCCCGCCGCCCCCTCCCCCGATCGAGGAATCATTTCCCCCTGCGCCTCTGGAGGAGGAGATCTTCCCTTCCCCGCCGCCTCCTCCGGA
        901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
            ACCCTCCACGGAAGGGCGGCGGGGGAGGGGGCTAGCTCCTTAGTAAAGGGGGACGCGGAGACCTCCTCCTCTAGAAGGGAAGGGGCGGCGGAGGAGGCCT
Zyxin          >   G  G  A  F  P  P  P  P  P  P  I  E  E  S  F  P  P  A  P  L  E  E  E  I  F  P  S  P  P  P  P  P  E

                          BseR1
                        Bsu36 |
                       BseR1| |                                  SpDon                          Ahd1   Bts1
                           || |                                     |                              |      |
            GGAGGAGGGAGGGCCTGAGGCCCCCATACCGCCCCCACCACAGCCCAGGGAGAAGGTGAGCAGTATTGATTTGGAGATCGACTCTCTGTCCTCACTGCTG
       1001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
            CCTCCTCCCTCCCGGACTCCGGGGGTATGGCGGGGGTGGTGTCGGGTCCCTCTTCCACTCGTCATAACTAAACCTCTAGCTGAGAGACAGGAGTGACGAC
Zyxin          >  E  E  G  G  P  E  A  P  I  P  P  P  P  Q  P  R  E  K  V  S  S  I  D  L  E  I  D  S  L  S  S  L  L

                                                Sma1                            Msc1
                                                   |                               |
            GATGACATGACCAAGAATGATCCTTTCAAAGCCCGGGTGTCATCTGGATATGTGCCCCCACCAGTGGCCACTCCATTCAGTTCCAAGTCCAGTACCAAGC
       1101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
            CTACTGTACTGGTTCTTACTAGGAAAGTTTCGGGCCCACAGTAGACCTATACACGGGGGTGGTCACCGGTGAGGTAAGTCAAGGTTCAGGTCATGGTTCG
Zyxin          > D  D  M  T  K  N  D  P  F  K  A  R  V  S  S  G  Y  V  P  P  P  V  A  T  P  F  S  S  K  S  S  T  K  P

                                                                   BseY1
                 Pst1                                           SpAcc  |  AlwN1
                    |                                              |  |      |
            CTGCAGCCGGGGGCACAGCACCCCTGCCTCCTTGGAAGTCCCCTTCCAGCTCCCAGCCTCTGCCCCAGGTTCCGGCTCCGGCTCAGAGCCAGACACAGTT
       1201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
            GACGTCGGCCCCCGTGTCGTGGGGACGGAGGAACCTTCAGGGGAAGGTCGAGGGTCGGAGACGGGGTCCAAGGCCGAGGCCGAGTCTCGGTCTGTGTCAA
Zyxin          >   A  A  G  G  T  A  P  L  P  P  W  K  S  P  S  S  S  Q  P  L  P  Q  V  P  A  P  A  Q  S  Q  T  Q  F
```

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                                                                                                              Apa1
                                                                                                         PspOM    |
                      BseY1 BseY1       Bsu36                         BseY1                   BseY1       Bgl1|   |
                           |     |           |                             |                       |         ||   |
               CCATGTTCAGCCCCAGCCCCAGCCCAAGCCTCAGGTCCAACTCCATGTCCAGTCCCAGACCCAGCCTGTGTCTTTGGCTAACACCCAGCCCCGAGGGCCC
         1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
               GGTACAAGTCGGGGTCGGGGTCGGGTTCGGAGTCCAGGTTGAGGTACAGGTCAGGGTCTGGGTCGGACACAGAAACCGATTGTGGGTCGGGGCTCCCGGG
Zyxin        >  H  V  Q  P  Q  P  Q  P  K  P  Q  V  Q  L  H  V  Q  S  Q  T  Q  P  V  S  L  A  N  T  Q  P  R  G  P

             Bpm1
          BseY1 |               Bpm1               SpAcc
              | |                  |                   |
               CCAGCCTCATCTCCGGCTCCAGCCCCTAAGTTTTCTCCAGTGACTCCTAAGTTTACTCCTGTGGCTTCCAAGTTCAGTCCTGGAGCCCCAGGTGGATCTG
         1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
               GGTCGGAGTAGAGGCCGAGGTCGGGGATTCAAAAGAGGTCACTGAGGATTCAAATGAGGACACCGAAGGTTCAAGTCAGGACCTCGGGGTCCACCTAGAC
Zyxin        > P  A  S  S  P  A  P  A  P  K  F  S  P  V  T  P  K  F  T  P  V  A  S  K  F  S  P  G  A  P  G  G  S  G

            Bpm1                                                               BseY1           BseY1
               |                                                                    |               |
               GGTCACAACCAAATCAAAAATTGGGGCACCCCGAAGCTCTTTCTGCTGGCACAGGCTCCCCTCAACCTCCCAGCTTCACCTATGCCCAGCAGAGGGAGAA
         1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
               CCAGTGTTGGTTTAGTTTTTAACCCCGTGGGGCTTCGAGAAAGACGACCGTGTCCGAGGGGAGTTGGAGGGTCGAAGTGGATACGGGTCGTCTCCCTCTT
Zyxin        >   S  Q  P  N  Q  K  L  G  H  P  E  A  L  S  A  G  T  G  S  P  Q  P  P  S  F  T  Y  A  Q  Q  R  E  K

                                                                                               Apa1
                                        Bsg1                                              PspOM    |
                                        Dra3|                                          Apa1    |   |
                                       BstAP|                   SexA1             PspOM    |   |   | SpAcc
                                           ||                        |                 |   |   |   |      |
               GCCCCGAGTGCAGGAGAAGCAGCACCCCGTGCCCCCACCGGCTCAGAACCAAAACCAGGTGCGCTCCCCTGGGGCCCCAGGGCCCCTGACTCTGAAGGAG
         1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
               CGGGGCTCACGTCCTCTTCGTCGTGGGGCACGGGGGTGGCCGAGTCTTGGTTTTGGTCCACGCGAGGGGACCCCGGGGTCCCGGGGACTGAGACTTCCTC
Zyxin        >  P  R  V  Q  E  K  Q  H  P  V  P  P  P  A  Q  N  Q  N  Q  V  R  S  P  G  A  P  G  P  L  T  L  K  E
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                                BseY1
                          BseR1   |     BstAP
                   Eco57 Pvu2|    |    Bpm1 |                                                Eag1
                       |    ||    |       | |                                                  |
            GTGGAGGAGCTGGAGCAGCTGACCCAGCAGCTAATGCAGGACATGGAGCATCCTCAGAGGCAGAATGTGGCTGTCAACGAACTCTGCGGCCGATGCCATC
      1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
            CACCTCCTCGACCTCGTCGACTGGGTCGTCGATTACGTCCTGTACCTCGTAGGAGTCTCCGTCTTACACCGACAGTTGCTTGAGACGCCGGCTACGGTAG
Zyxin          > V  E  E  L  E  Q  L  T  Q  Q  L  M  Q  D  M  E  H  P  Q  R  Q  N  V  A  V  N  E  L  C  G  R  C  H  Q

                                                                                   Ale1
                                                                                 BspM1|
                                                                                  Bpm1|
                   Srf1                                                          BfuA1|
                   Sma1                      BtgZ1  Pvu2                  SpDon    Aar1|  Fsp1
                     |                          |     |                       |       ||     |
            AACCCCTGGCCCGGGCGCAGCCAGCCGTCCGCGCTCTAGGGCAGCTGTTCCACATCGCCTGCTTCACCTGCCACCAGTGTGCGCAGCAGCTCCAGGGCCA
      1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
            TTGGGGACCGGGCCCGCGTCGGTCGGCAGGCGCGAGATCCCGTCGACAAGGTGTAGCGGACGAAGTGGACGGTGGTCACACGCGTCGTCGAGGTCCCGGT
Zyxin          >   P  L  A  R  A  Q  P  A  V  R  A  L  G  Q  L  F  H  I  A  C  F  T  C  H  Q  C  A  Q  Q  L  Q  G  Q

                                                                                      BspM1
                                                                                      BfuA1
                                 Nar1                                                  Aar1
                   SpAcc        Kas1|  SpAcc Bpm1                SpAcc            SpAcc Bpm1  |
                     |            ||      |    |                  |                |    |  |
            GCAGTTCTACAGTCTGGAGGGGGCGCCGTACTGCGAGGGCTGTTACACTGACACCCTGGAGAAGTGTAACACCTGCGGGGAGCCCATCACTGACCGCATG
      1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
            CGTCAAGATGTCAGACCTCCCCCGCGGCATGACGCTCCCGACAATGTGACTGTGGGACCTCTTCACATTGTGGACGCCCCTCGGGTAGTGACTGGCGTAC
Zyxin          >  Q  F  Y  S  L  E  G  A  P  Y  C  E  G  C  Y  T  D  T  L  E  K  C  N  T  C  G  E  P  I  T  D  R  M

              Bpu10
              BbvC1                                   Ale1
              Sph1|              Stu1       Bts1      SpDon |                                    Bpm1
                 ||                |          |          | |                                      |
            CTGAGGGCCACGGGCAAGGCCTATCACCCGCACTGCTTCACCTGTGTGGTCTGCGCCCGCCCCCTGGAGGGCACCTCCTTCATCGTGGACCAGGCCAACC
      2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
            GACTCCCGGTGCCCGTTCCGGATAGTGGGCGTGACGAAGTGGACACACCAGACGCGGGCGGGGGACCTCCCGTGGAGGAAGTAGCACCTGGTCCGGTTGG
Zyxin          > L  R  A  T  G  K  A  Y  H  P  H  C  F  T  C  V  V  C  A  R  P  L  E  G  T  S  F  I  V  D  Q  A  N  R
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                                                                                Bpu10
                                                                                  |
            GGCCCCACTGTGTCCCCGACTACCACAAGCAGTACGCCCCGAGGTGCTCCGTCTGCTCTGAGCCCATCATGCCTGAGCCTGGCCGAGATGAGACTGTGCG
      2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
            CCGGGGTGACACAGGGGCTGATGGTGTTCGTCATGCGGGGCTCCACGAGGCAGACGAGACTCGGGTAGTACGGACTCGGACCGGCTCTACTCTGACACGC
Zyxin     >   P  H  C  V  P  D  Y  H  K  Q  Y  A  P  R  C  S  V  C  S  E  P  I  M  P  E  P  G  R  D  E  T  V  R

                                                  SpAcc
                                                    |
            AGTGGTCGCCCTGGACAAGAACTTCCACATGAAGTGTTACAAGTGTGAGGACTGCGGGAAGCCCCTGTCGATTGAGGCAGATGACAATGGCTGCTTCCCC
      2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
            TCACCAGCGGGACCTGTTCTTGAAGGTGTACTTCACAATGTTCACACTCCTGACGCCCTTCGGGGACAGCTAACTCCGTCTACTGTTACCGACGAAGGGG
Zyxin     >  V  V  A  L  D  K  N  F  H  M  K  C  Y  K  C  E  D  C  G  K  P  L  S  I  E  A  D  D  N  G  C  F  P

                                                                                Ale1      Sap1
                     Pml1                Bts1                BamH1  Age1       Nco1 |      Ear1
                       |                   |                   |     |          | |         |
            CTGGACGGTCACGTGCTCTGTCGGAAGTGCCACACTGCTAGAGCCCAGACGGATCCACCGGTCGCCACCATGGTGTCTAAGGGCGAAGAGCTGATTAAGG
      2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
            GACCTGCCAGTGCACGAGACAGCCTTCACGGTGTGACGATCTCGGGTCTGCCTAGGTGGCCAGCGGTGGTACCACAGATTCCCGCTTCTCGACTAATTCC
Zyxin/TagRFP > L  D  G  H  V  L  C  R  K  C  H  T  A  R  A  Q  T  D  P  P  V  A  T  M  V  S  K  G  E  E  L  I  K  E

                          BsrG1                                ApaL1                     SpAcc
                            |                                    |                         |
            AGAACATGCACATGAAGCTGTACATGGAGGGCACCGTGAACAACCACCACTTCAAGTGCACATCCGAGGGCGAAGGCAAGCCCTACGAGGGCACCCAGAC
      2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
            TCTTGTACGTGTACTTCGACATGTACCTCCCGTGGCACTTGTTGGTGGTGAAGTTCACGTGTAGGCTCCCGCTTCCGTTCGGGATGCTCCCGTGGGTCTG
TagRFP    >   N  M  H  M  K  L  Y  M  E  G  T  V  N  N  H  H  F  K  C  T  S  E  G  E  G  K  P  Y  E  G  T  Q  T

            CATGAGAATCAAGGTGGTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGCTACCAGCTTCATGTACGGCAGCAGAACCTTCATCAACCACACC
      2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
            GTACTCTTAGTTCCACCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTCGAAGTACATGCCGTCGTCTTGGAAGTAGTTGGTGTGG
TagRFP    >  M  R  I  K  V  V  E  G  G  P  L  P  F  A  F  D  I  L  A  T  S  F  M  Y  G  S  R  T  F  I  N  H  T

                                      Bsu36       SpDon                         Bbs1              Bpm1
                                        |           |                             |                 |
            CAGGGCATCCCCGACTTCTTTAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACATACGAAGACGGGGGCGTGCTGACCGCTACCCAGG
      2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
            GTCCCGTAGGGGCTGAAGAAATTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGGTGTATGCTTCTGCCCCCGCACGACTGGCGATGGGTCC
TagRFP    > Q  G  I  P  D  F  F  K  Q  S  F  P  E  G  F  T  W  E  R  V  T  T  Y  E  D  G  G  V  L  T  A  T  Q  D
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                                                                                                                BseY1
                                                                                                                  |
            ACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACTTCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTG
      2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
            TGTGGTCGGAGGTCCTGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCCACTTGAAGGGTAGGTTGCCGGGACACTACGTCTTCTTTTGTGAGCCGAC
TagRFP      >  T  S  L  Q  D  G  C  L  I  Y  N  V  K  I  R  G  V  N  F  P  S  N  G  P  V  M  Q  K  K  T  L  G  W

                                                Bgl1                    BssS1          Eco57
                                                  |                       |              |
            GGAGGCCAACACCGAGATGCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAAGCGACATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAAC
      2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
            CCTCCGGTTGTGGCTCTACGACATGGGGCGACTGCCGCCGGACCTTCCGTCTTCGCTGTACCGGGACTTCGAGCACCCGCCCCCGGTGGACTAGACGTTG
TagRFP      > E  A  N  T  E  M  L  Y  P  A  D  G  G  L  E  G  R  S  D  M  A  L  K  L  V  G  G  G  H  L  I  C  N

                                                                                SpAcc
                                BpuE1                                           PflM1                   Bsa1
                                   |                                               |                       |
            TTCAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGCGTCTACTATGTGGACCACAGACTGGAAAGAATCAAGGAGGCCGACA
      2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
            AAGTTCTGGTGTATGTCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCGCAGATGATACACCTGGTGTCTGACCTTTCTTAGTTCCTCCGGCTGT
TagRFP      > F  K  T  T  Y  R  S  K  K  P  A  K  N  L  K  M  P  G  V  Y  Y  V  D  H  R  L  E  R  I  K  E  A  D  K

                                                                                                   Not1
                                                                                                   Eag1
                PshA1       BssS1 Dra3      Msc1  AlwN1          SpAcc          Bmr1       BsrB1|      Xba1
                   |           |    |         |      |              |             |           ||         |
            AAGAGACCTACGTCGAGCAGCACGAGGTGGCTGTGGCCAGATACTGCGACCTCCCTAGCAAACTGGGGCACAAACTTAATTGAGCGGCCGCGACTCTAGA
      3001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
            TTCTCTGGATGCAGCTCGTCGTGCTCCACCGACACCGGTCTATGACGCTGGAGGGATCGTTTGACCCCGTGTTTGAATTAACTCGCCGGCGCTGAGATCT
TagRFP      >  E  T  Y  V  E  Q  H  E  V  A  V  A  R  Y  C  D  L  P  S  K  L  G  H  K  L  N  *

                                                                                                      Bsm1
    BsaB1                           SpDon   Dra1                                                     Mfe1|
      |                                |      |                                                        ||
            TCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGT
      3101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
            AGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACA
```

```
      Hpa1       polyA    Psi1      polyA                        polyA            Bts1 Bsm1
        |          |       |          |                            |                |    |
      TGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGT
3201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
      ACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGACGTAAGATCAACACCA

                        Afl2         SpDon        Ssp1
                          |            |           |
      TTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAAC
3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
      AACAGGTTTGAGTAGTTACATAGAATTCCGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTG

                            Psi1                                                          BsaXb
                              |                                                             |
      CAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGA
3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
      GTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCT

                                                        BtgZ1
              Drd1    BsaXa                             Dra3|
                 |        |                                ||
      ACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCG
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      TGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCCAGCTCCACGGC

                                                           Nae1
                     SpAcc                              NgoM4 |
                        |                                  | |
      TAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGA
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      ATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCT

  BsrB1
      |
      GCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTT
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      CGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAA
```

```
                                                                  BciV1
                                                               BspH1  |
                                     polyA                   BsrB1 |  |
                                         |                       | |  |
      TTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATA
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      AAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTAT

                                          Eci1
    Ssp1  Ear1        Bsu36              Pvu2 |                                   BseY1
       |     |            |                 | |                                      |
      ATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTA
3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
      TATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCAT

              Nsi1                                                                  Nsi1
            Sph1 |                                                               Sph1 |
           BfrB1 |                                                              BfrB1 |
        BstAP  | |            SexA1                     BseY1                  BstAP  | |
            |  | |               |                       |                       |  | |
      TGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGC
4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
      ACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCG

                                          Eci1
              Eci1                 Eci1     Bmr1|       Eci1            Nco1                   polyA
                 |                    |        ||          |               |                       |
      AACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCA
4101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
      TTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAAATAAATACGT

                                                        Avr2
                 Sfi1                                  Stu1|
                 Bgl1                     SpDon             BseR1  ||              Cla1
                    |                        |                 |  ||                 |
      GAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGA
4201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
      CTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCTACT
```

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                                BspM1
 BsaB1                          BfuA1                Eag1                                        Bmr1
     |                             |                   |                                           |
      GGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCG
4301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
      CCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGC

                                          Nar1
                                         Kas1|                        Drd1
                                            ||                          |
      GCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGA
4401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
      CGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCT

                                              Pvu2
                        Msc1                Fsp1   |       PflF1                        Eco57
                           |                   |   |           |                           |
      GGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAA
4501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
      CCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTT

                              SpDon                          BciV1         BsrD1
                                 |                              |             |
      GTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTA
4601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
      CACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGAT

             BtgZ1
         BspM1  |                                                                  Sap1
         BfuA1  |                                                                  Ear1
             |  |                                                                     |
      CCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCA
4701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
      GGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGT

                  BpuE1                          Sph1                          Nco1                BtgZ1
                     |                              |                             |                   |
      GGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATC
4801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
      CCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAG
```

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                                        BseY1
                                       Nae1 |                                          Sap1
                                     NgoM4 | |        Rsr2         Eci1                Ear1
                                         | | |           |            |                    |
     ATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTG
4901 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 5000
     TACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAACGAC

                                                   BtgZ1
                  Eco57         BssS1                BsrB1 |
                      |             |                    | |
     AAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTT
5001 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 5100
     TTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAA

                                                      BssS1
                                                      BspM1
        BsrB1          BstB1                         BfuA1                      SpAcc
           |              |                             |                          |
     CTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGG
5101 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 5200
     GAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACC

                          Nae1                                                   Bpm1
                        NgoM4 |                                              SpAcc  |
                         Bpm1 |                                               Avr2  |
                            | |                                                  |  |
     GCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAAC
5201 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 5300
     CGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTG

                                         polyA        polyA
                                            |            |
     ACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTT
5301 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 5400
     TGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAA
```

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                                Bsa1
                                  |
      CGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGG
5401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5500
      GCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCC

                                          BstAP
                                          AlwN1      Bsu36                            Dra1
                                              |          |                               |
      GTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTA
5501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5600
      CACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAAT

      Dra1                              BspH1
         |                                 |
      ATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAG
5601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5700
      TAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTC

                                    BpuE1
                                      |
      ATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAG
5701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5800
      TAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTC

                 Eco57                                                  SpAcc
                    |                                                     |
      AGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAA
5801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5900
      TCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTT

                                                  AlwN1                     BpuE1
                                                      |                         |
      CTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGA
5901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6000
      GAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCT
```

```
                                                ApaL1     BseY1
                                                   |         |
      TAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGC
6001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6100
      ATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCG

                                                                   BciV1
      SpAcc                                                      Eci1   |                    BssS1
          |                                                         |   |                        |
      GTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCC
6101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6200
      CACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGG

                              SpAcc                          Drd1            BpuE1               SpAcc
                                  |                             |                |                   |
      AGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGG
6201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6300
      TCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCCGCCTCGGATACC

                                                                 SpDon
     Eci1                                                       BspLU|
        |                                                          ||
      AAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACC
6301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6400
      TTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGG

                 Nsi1
              BfrB1 |
                  | |
      GTATTACCGCCATGCAT
6401  |||||||||*||||||| 6417
      CATAATGGCGGTACGTA
```

Found:

Aar1	Aat2	**Afe1**	**Afl2**	**Age1**	**Ahd1**	Ale1	AlwN1	Apa1	ApaL1	**Ase1**	Avr2	**BamH1**	Bbs1
BbvC1	BciV1	BfrB1	BfuA1	Bgl1	Bgl2	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	**BsaXa**	**BsaXb**
BseR1	BseY1	**Bsg1**	Bsm1	**BsmB1**	**BspE1**	BspH1	**BspLU**	BspM1	BsrB1	**BsrD1**	**BsrG1**	**BssH2**	BssS1
BstAP	BstB1	Bsu36	BtgZ1	Bts1	**Cla1**	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	**EcoR1**
Fsp1	**Hind3**	**Hpa1**	Kas1	**Mfe1**	Msc1	Nae1	Nar1	Nco1	**Nde1**	NgoM4	**Nhe1**	**Not1**	Nsi1
PflF1	**PflM1**	**Pml1**	polyA	**PshA1**	Psi1	PspOM	**Pst1**	**Pvu1**	Pvu2	**Rsr2**	**Sac1**	Sap1	SexA1
Sfi1	Sma1	**SnaB1**	SpAcc	SpDon	Sph1	**Srf1**	Ssp1	Stu1	**Xba1**	**Xho1**	Xmn1		

Unique:

Afe1	**Afl2**	**Age1**	**Ahd1**	**Ase1**	**BamH1**	**BbvC1**	**BsaXa**	**BsaXb**	**Bsg1**	**BsmB1**	**BspE1**	**BspLU**	**BsrD1**
BsrG1	**BssH2**	**Cla1**	**EcoR1**	**Hind3**	**Hpa1**	**Mfe1**	**Nde1**	**Nhe1**	**Not1**	**PflF1**	**PflM1**	**Pml1**	**PshA1**
Pst1	**Pvu1**	**Rsr2**	**Sac1**	**Sfi1**	**SnaB1**	**Srf1**	**Xba1**	**Xho1**					

Not found:

Acc65	Acl1	Asc1	AsiS1	Bae1a	Bae1b	Bcg1a	Bcg1b	Bcl1	Blp1	BmgB1	BsiW1	BstE2	BstX1
BstZ1	_Chi	EcoK	EcoN1	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	I_Ceu	Kpn1
loxP	Mlu1	Nru1	Pac1	Pme1	R4atB	R4atL	R4atP	R4atR	Sac2	Sal1	SanD1	Sbf1	Sca1
Sgf1	SgrA1	Spe1	Swa1	T3RNA	T7RNA	T7Ter	PISce	Xcm1					

Excluded by site complexity:

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