pTagGFP2-laminB1 vector restriction map

The data has not been verified by restriction digestion with each enzyme listed and does not take into account possible methylation sites. Enzymes that recognize unambiguous sequences less than 6 basepairs long are not included – for the more complete enzyme list please refer to the Table of restriction sites.

Unique sites are shown in bold blue. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site). TagGFP2 amino acids are shown in green, Lamin B1 amino acids are shown in red, linker amino acids are shown in black.

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

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

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

                                  BtgZ1 SnaB1                 Nco1
                                      |     |                   |
      CATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGA
  301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 400
      GTACTGGAATACCCTGAAAGGATGAACCGTCATGTAGATGCATAATCAGTAGCGATAATGGTACCACTACGCCAAAACCGTCATGTAGTTACCCGCACCT
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                                                Aat2                                                Eci1
                                                  |                                                   |
        TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
    401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 500
        ATCGCCAAACTGAGTGCCCCTAAAGGTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT

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

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

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

                BstAP                                Xmn1                                          EcoK
                   |                                   |                                             |
        CTACGGCATCCAGTGCTTCGCCCGCTACCCCGAGCACATGAAGATGAACGACTTCTTCAAGAGCGCCATGCCCGAGGGCTACATCCAGGAGCGCACCATC
    801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
        GATGCCGTAGGTCACGAAGCGGGCGATGGGGCTCGTGTACTTCTACTTGCTGAAGAAGTTCTCGCGGTACGGGCTCCCGATGTAGGTCCTCGCGTGGTAG
TagGFP2   >  Y  G  I  Q  C  F  A  R  Y  P  E  H  M  K  M  N  D  F  F  K  S  A  M  P  E  G  Y  I  Q  E  R  T  I
```

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                                                                  SpDon
                                          Sac2 SpDon             Ale1 |
                                             |     |                 | |
            CAGTTCCAGGACGACGGCAAGTACAAGACCCGCGGCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCAAGGACTTCAAGG
       901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
            GTCAAGGTCCTGCTGCCGTTCATGTTCTGGGCGCCGCTCCACTTCAAGCTCCCGCTGTGGGACCACTTGGCGTAGCTCGACTTCCCGTTCCTGAAGTTCC
TagGFP2       > Q  F  Q  D  D  G  K  Y  K  T  R  G  E  V  K  F  E  G  D  T  L  V  N  R  I  E  L  K  G  K  D  F  K  E

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

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

                                                                 Eco57
                Bpu10                                             Dra3                  AlwN1 Bpm1
                    |                                               |                       |    |
            CACTACCTGAGCACTCAGACCAAGATCAGCAAGGACCGCAACGAGGCCCGCGACCACATGGTGCTCCTGGAGTCCTTCAGCGCCTGCTGCCACACCCACG
      1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
            GTGATGGACTCGTGAGTCTGGTTCTAGTCGTTCCTGGCGTTGCTCCGGGCGCTGGTGTACCACGAGGACCTCAGGAAGTCGCGGACGACGGTGTGGGTGC
TagGFP2       > H  Y  L  S  T  Q  T  K  I  S  K  D  R  N  E  A  R  D  H  M  V  L  L  E  S  F  S  A  C  C  H  T  H  G
```

```
                                                Hind3
                                 BpuE1     Xho1   Sac1 |
          PflM1      BsrG1   BspE1   | Bgl2   | Ecl2 | |  Bcg1a                        Sac2 Bcg1b      Bgl1
              |          |       |   |    |   |    | | |      |                           |     |         |
             GCATGGACGAGCTGTACAGGTCCGGACTCAGATCTCGAGCTCAAGCTTCGATGGCGACTGCGACCCCCGTGCCGCCGCGGATGGGCAGCCGCGCTGGCGG
        1301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
             CGTACCTGCTCGACATGTCCAGGCCTGAGTCTAGAGCTCGAGTTCGAAGCTACCGCTGACGCTGGGGGCACGGCGGCGCCTACCCGTCGGCGCGACCGCC
TagGFP2/Lamin>   M  D  E  L  Y  R  S  G  L  R  S  R  A  Q  A  S  M  A  T  A  T  P  V  P  P  R  M  G  S  R  A  G  G
```

```
                                                                   Sac1
                                                                 BseR1|
                       Blp1     Bpm1                             Ecl2||             BsrG1
                          |        |                               |||                |
             CCCCACCACGCCGCTGAGCCCCACGCGCCTGTCGCGGCTCCAGGAGAAGGAGGAGCTGCGCGAGCTCAATGACCGGCTGGCGGTGTACATCGACAAGGTG
        1401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
             GGGGTGGTGCGGCGACTCGGGGTGCGCGGACAGCGCCGAGGTCCTCTTCCTCCTCGACGCGCTCGAGTTACTGGCCGACCGCCACATGTAGCTGTTCCAC
Lamin        >  P  T  T  P  L  S  P  T  R  L  S  R  L  Q  E  K  E  E  L  R  E  L  N  D  R  L  A  V  Y  I  D  K  V
```

```
                                     Pvu2
                                    Pst1|
                                 Bpm1   ||
                               BspM1|   ||                          BseR1
           BsmB1                Aar1|   ||                          BpuE1   Sac1
          Fsp1  |              BssH2   ||   || Pst1                Eag1   | Ecl2 |             Bsa1
             |  |                 |   ||   ||    |                   |   |    | |                |
             CGCAGCCTGGAGACGGAGAACAGCGCGCTGCAGCTGCAGGTGACGGAGCGCGAGGAGGTGCGCGGCCGTGAGCTCACCGGCCTCAAGGCGCTCTACGAGA
        1501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
             GCGTCGGACCTCTGCCTCTTGTCGCGCGACGTCGACGTCCACTGCCTCGCGCTCCTCCACGCGCCGGCACTCGAGTGGCCGGAGTTCCGCGAGATGCTCT
Lamin        > R  S  L  E  T  E  N  S  A  L  Q  L  Q  V  T  E  R  E  E  V  R  G  R  E  L  T  G  L  K  A  L  Y  E  T
```

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                                                                                                   Eci1
                          BssH2                     BssH2          Pst1  BseY1                  BseR1 Pvu2|
                              |                         |             |      |                        |    ||
             CCGAGCTGGCCGACGCGCGACGCGCGCTCGACGACACGGCCCGCGAGCGCGCCAAGCTGCAGATCGAGCTGGGCAAGTGCAAGGCGGAACACGACCAGCT
        1601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
             GGCTCGACCGGCTGCGCGCTGCGCGCGAGCTGCTGTGCCGGGCGCTCGCGCGGTTCGACGTCTAGCTCGACCCGTTCACGTTCCGCCTTGTGCTGGTCGA
Lamin        >  E  L  A  D  A  R  R  A  L  D  D  T  A  R  E  R  A  K  L  Q  I  E  L  G  K  C  K  A  E  H  D  Q  L
```

```
                                                Nar1                                                    BstAP
                        SpAcc                  Kas1|      Hind3     Bcg1b               BstB1   Bsg1  Bcg1a|
                          |                      ||          |         |                   |      |      ||
            GCTCCTCAACTATGCTAAGAAGGAATCTGATCTTAATGGCGCCCAGATCAAGCTTCGAGAATATGAAGCAGCACTCAATTCGAAAGATGCAGCTCTTGCT
      1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
            CGAGGAGTTGATACGATTCTTCCTTAGACTAGAATTACCGCGGGTCTAGTTCGAAGCTCTTATACTTCGTCGTGAGTTAAGCTTTCTACGTCGAGAACGA
Lamin     >  L  L  N  Y  A  K  K  E  S  D  L  N  G  A  Q  I  K  L  R  E  Y  E  A  A  L  N  S  K  D  A  A  L  A

                                                                                          SpAcc
                      Dra3                                                  Bmr1     Eco57      Bpu10   | Pst1
                        |                                                     |         |          |   |    |
            ACTGCACTTGGTGACAAAAAAAGTTTAGAGGGAGATTTGGAGGATCTGAAGGATCAGATTGCCCAGTTGGAAGCCTCCTTAGCTGCAGCCAAAAAACAGT
      1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
            TGACGTGAACCACTGTTTTTTTCAAATCTCCCTCTAAACCTCCTAGACTTCCTAGTCTAACGGGTCAACCTTCGGAGGAATCGACGTCGGTTTTTTGTCA
Lamin     > T  A  L  G  D  K  K  S  L  E  G  D  L  E  D  L  K  D  Q  I  A  Q  L  E  A  S  L  A  A  A  K  K  Q  L

                                                                EcoN1                          Ear1          Bsa1
                                                                  |                              |             |
            TAGCAGATGAAACTTTACTTAAAGTAGATTTGGAGAATCGTTGTCAGAGCCTTACTGAGGACTTGGAGTTTCGCAAAAGCATGTATGAAGAGGAGATTAA
      1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
            ATCGTCTACTTTGAAATGAATTTCATCTAAACCTCTTAGCAACAGTCTCGGAATGACTCCTGAACCTCAAAGCGTTTTCGTACATACTTCTCCTCTAATT
Lamin     >   A  D  E  T  L  L  K  V  D  L  E  N  R  C  Q  S  L  T  E  D  L  E  F  R  K  S  M  Y  E  E  E  I  N

            BseR1                                                                                   BspH1
                |                                                                                     |
            CGAGACCAGAAGGAAGCATGAAACGCGCTTGGTAGAGGTGGATTCTGGGCGTCAAATTGAGTATGAGTACAAGCTGGCGCAAGCCCTTCATGAGATGAGA
      2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
            GCTCTGGTCTTCCTTCGTACTTTGCGCGAACCATCTCCACCTAAGACCCGCAGTTTAACTCATACTCATGTTCGACCGCGTTCGGGAAGTACTCTACTCT
Lamin     >  E  T  R  R  K  H  E  T  R  L  V  E  V  D  S  G  R  Q  I  E  Y  E  Y  K  L  A  Q  A  L  H  E  M  R

                          SpDon                                 BseR1SpDon   Bpm1          Bsm1     BpuE1
                            |                                       |    |      |             |         |
            GAGCAACATGATGCCCAAGTGAGGCTGTATAAGGAGGAGCTGGAGCAGACTTACCATGCCAAACTTGAGAATGCCAGACTGTCATCAGAGATGAATACTT
      2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
            CTCGTTGTACTACGGGTTCACTCCGACATATTCCTCCTCGACCTCGTCTGAATGGTACGGTTTGAACTCTTACGGTCTGACAGTAGTCTCTACTTATGAA
Lamin     > E  Q  H  D  A  Q  V  R  L  Y  K  E  E  L  E  Q  T  Y  H  A  K  L  E  N  A  R  L  S  S  E  M  N  T  S
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                                                                BseY1        SpAcc         Xba1
                                                                  |            |             |
            CTACTGTCAACAGTGCCAGGGAAGAACTGATGGAAAGCCGCATGAGAATTGAGAGCCTTTCATCCCAGCTTTCTAATCTACAGAAAGAGTCTAGAGCATG
      2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
            GATGACAGTTGTCACGGTCCCTTCTTGACTACCTTTCGGCGTACTCTTAACTCTCGGAAAGTAGGGTCGAAAGATTAGATGTCTTTCTCAGATCTCGTAC
Lamin     >  T  V  N  S  A  R  E  E  L  M  E  S  R  M  R  I  E  S  L  S  S  Q  L  S  N  L  Q  K  E  S  R  A  C

                 Xmn1                     SpAcc                        Sph1
                   |                        |                            |
            TTTGGAAAGGATTCAAGAATTAGAGGACTTGCTTGCTAAAGAAAAAGACAACTCTCGTCGCATGCTGACAGACAAAGAGAGAGAGATGGCGGAAATAAGG
      2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
            AAACCTTTCCTAAGTTCTTAATCTCCTGAACGAACGATTTCTTTTTCTGTTGAGAGCAGCGTACGACTGTCTGTTTCTCTCTCTACCGCCTTTATTCC
Lamin     >  L  E  R  I  Q  E  L  E  D  L  L  A  K  E  K  D  N  S  R  R  M  L  T  D  K  E  R  E  M  A  E  I  R

            Eci1          Pvu2             Xmn1     SpDon                                                Ear1
              |             |                |         |                                                    |
            GATCAAATGCAGCAACAGCTGAATGACTATGAACAGCTTCTTGATGTAAAGTTAGCCCTGGACATGGAAATCAGTGCTTACAGGAAACTCTTAGAAGGCG
      2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
            CTAGTTTACGTCGTTGTCGACTTACTGATACTTGTCGAAGAACTACATTTCAATCGGGACCTGTACCTTTAGTCACGAATGTCCTTTGAGAATCTTCCGC
Lamin     > D  Q  M  Q  Q  Q  L  N  D  Y  E  Q  L  L  D  V  K  L  A  L  D  M  E  I  S  A  Y  R  K  L  L  E  G  E

                                                BpuE1       BciV1              SnaB1 SpAcc     Ear1
                                                  |           |                  |     |        |
            AAGAAGAGAGGTTGAAGCTGTCTCCAAGCCCTTCTTCCCGTGTGACAGTATCCCGAGCATCCTCAAGTCGTAGTGTACGTACAACTAGAGGAAAGCGGAA
      2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
            TTCTTCTCTCCAACTTCGACAGAGGTTCGGGAAGAAGGGCACACTGTCATAGGGCTCGTAGGAGTTCAGCATCACATGCATGTTGATCTCCTTTCGCCTT
Lamin     >  E  E  R  L  K  L  S  P  S  P  S  S  R  V  T  V  S  R  A  S  S  S  R  S  V  R  T  T  R  G  K  R  K

                                                                Bpu10
                                                Eci1            BbvC1  AlwN1
                                                  |               |      |
            GAGGGTTGATGTGGAAGAATCAGAGGCGAGTAGTAGTGTTAGCATCTCTCATTCCGCCTCAGCCACTGGAAATGTTTGCATCGAAGAAATTGATGTTGAT
      2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
            CTCCCAACTACACCTTCTTAGTCTCCGCTCATCATCACAATCGTAGAGAGTAAGGCGGAGTCGGTGACCTTTACAAACGTAGCTTCTTTAACTACAACTA
Lamin     >  R  V  D  V  E  E  S  E  A  S  S  S  V  S  I  S  H  S  A  S  A  T  G  N  V  C  I  E  E  I  D  V  D
```

```
                                                   BseY1
                                                 Xcm1  |     Bcl1                   Drd1BpuE1 Psi1
                                                    |  |        |                      |    |    |
            GGGAAATTTATCCGCTTGAAGAACACTTCTGAACAGGATCAACCAATGGGAGGCTGGGAGATGATCAGAAAAATTGGAGACACATCAGTCAGTTATAAAT
      2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
            CCCTTTAAATAGGCGAACTTCTTGTGAAGACTTGTCCTAGTTGGTTACCCTCCGACCCTCTACTAGTCTTTTTAACCTCTGTGTAGTCAGTCAATATTTA
Lamin       > G  K  F  I  R  L  K  N  T  S  E  Q  D  Q  P  M  G  G  W  E  M  I  R  K  I  G  D  T  S  V  S  Y  K  Y
```

```
                                        Eco57                                                 SpAcc
                                           |                                                    |
            ATACCTCAAGATATGTGCTGAAGGCAGGCCAGACTGTTACAATTTGGGCTGCAAACGCTGGTGTCACAGCCAGCCCCCCAACTGACCTCATCTGGAAGAA
      2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
            TATGGAGTTCTATACACGACTTCCGTCCGGTCTGACAATGTTAAACCCGACGTTTGCGACCACAGTGTCGGTCGGGGGGTTGACTGGAGTAGACCTTCTT
Lamin       >   T  S  R  Y  V  L  K  A  G  Q  T  V  T  I  W  A  A  N  A  G  V  T  A  S  P  P  T  D  L  I  W  K  N
```

```
                                                                                  BsaXb
                 BssS1                SpDon                BsaXa                BseR1   |      Dra1
                     |                    |                    |                    |   |         |
            CCAGAACTCGTGGGGCACTGGCGAAGATGTGAAGGTTATATTGAAAAATTCTCAGGGAGAGGAGGTTGCTCAAAGAAGTACAGTCTTTAAAACAACCATA
      2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
            GGTCTTGAGCACCCCGTGACCGCTTCTACACTTCCAATATAACTTTTTAAGAGTCCCTCTCCTCCAACGAGTTTCTTCATGTCAGAAATTTTGTTGGTAT
Lamin       >  Q  N  S  W  G  T  G  E  D  V  K  V  I  L  K  N  S  Q  G  E  E  V  A  Q  R  S  T  V  F  K  T  T  I
```

```
                                  Pvu2
                                 BseR1
                               BseR1  |
                              BsaXa |  |                        _Chi
                   Ear1      BseR1| |  |                    BsaXb  |
                 SpAcc|     Eco57 || |  |                  Bpm1  |  |
                     ||          | || |  |                     |  |  |
            CCTGAAGAAGAGGAGGAGGAGGAAGAAGCAGCTGGAGTGGTTGTTGAGGAAGAACTTTTCCACCAGCAGGGAACCCCAAGAGCATCCAATAGAAGCTGTG
      3001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
            GGACTTCTTCTCCTCCTCCTCCTTCTTCGTCGACCTCACCAACAACTCCTTCTTGAAAAGGTGGTCGTCCCTTGGGGTTCTCGTAGGTTATCTTCGACAC
Lamin       > P  E  E  E  E  E  E  E  E  A  A  G  V  V  V  E  E  E  L  F  H  Q  Q  G  T  P  R  A  S  N  R  S  C  A
```

```
                 BamH1        Xba1      Bcl1BsaB1                           SpDon   Dra1
                    |            |          |    |                              |      |
      CAATTATGTAGGGATCCACCGGATCTAGATAACTGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCC
3101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
      GTTAATACATCCCTAGGTGGCCTAGATCTATTGACTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGG
Lamin        >   I  M  *

                                Bsm1
                               Mfe1|        Hpa1       polyA    Psi1      polyA
                                  ||           |           |       |          |
      CCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACA
3201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
      GGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGT

 polyA            Bts1 Bsm1                                        Mlu1     SpDon        Ssp1
     |                |    |                                          |         |           |
      AATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAACGCGTAAATTGTAAGCGTTAATATTTTGTTAAAATTC
3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
      TTATTTCGTAAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTGCGCATTTAACATTCGCAATTATAAAACAATTTTAAG

                                                                  Psi1
                                                                    |
      GCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTG
3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
      CGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCAC

                                                                                          BtgZ1
                          BsaXb                 Drd1    BsaXa                           Dra3|
                              |                    |        |                                ||
      TTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACC
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      AACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGG

                                                                                            Nae1
                                                        SpAcc                           NgoM4 |
                                                           |                                | |
      ATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCG
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      TAGTGGGATTAGTTCAAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGC
```

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                                    BsrB1
                                       |
      AACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGC
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      TTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCG

                                                                                polyA
                                                                                  |
      TTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCC
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      AATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGG


       BciV1
    BspH1  |                                                                  Eci1
  BsrB1 |  |                            Ssp1  Ear1        Bsu36              Pvu2 |
      | |  |                               |     |           |                 | |
      GCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGT
3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
      CGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCA


                                                Nsi1
                                              Sph1 |
                                             BfrB1 |
                     BseY1                  BstAP  | |            SexA1                    BseY1
                        |                      |  | |                |                        |
      GTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGG
4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
      CACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCC


                       Nsi1
                     Sph1 |
                    BfrB1 |                                                      Eci1
                BstAP  | |                        Eci1                  Eci1     Bmr1|        Eci1
                    |  | |                          |                     |        ||           |
      CAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCT
4101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
      GTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGA
```

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                                                                                                                Avr2
                                                                  Sfi1                                         Stu1|
        Nco1                    polyA                   Bgl1                    SpDon             BseR1  ||
           |                        |                      |                        |                 |  ||
     CCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCC
4201 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 4300
     GGCGGGGTACCGACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGG

                 Cla1               BsaB1                       BspM1                Eag1
                    |                  |                           |                    |
     TAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGA
4301 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 4400
     ATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCT

                                                                                   Nar1
                         Bmr1                                                     Kas1|
                            |                                                        ||
     GGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGAC
4401 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 4500
     CCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTG

                                                                                                Pvu2
     Drd1                                                          Msc1                  Fsp1   |       PflF1
        |                                                            |                      |   |           |
     CGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTC
4501 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 4600
     GCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAG

                        Eco57                                           SpDon                        BciV1
                           |                                              |                            |
     ACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTG
4601 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 4700
     TGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGAC

                                                 BtgZ1
          BsrD1                                BspM1  |
             |                                    |   |
     ATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGG
4701 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 4800
     TACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCC
```

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                  Sap1
                  Ear1                          BpuE1                       Sph1
                     |                             |                           |
     TCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTC
4801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
     AGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAG

                                                                                  BseY1
                                                                                 Nae1 |
          Nco1              BtgZ1                                            NgoM4 | |        Rsr2
             |                 |                                                 | | |           |
     GTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCT
4901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
     CAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGA

                                Sap1                                                        BtgZ1
       Eci1                     Ear1                   Eco57         BssS1                BsrB1 |
          |                        |                      |             |                    | |
     ATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTC
5001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
     TAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAG

                                                                                                BssS1
                                          BsrB1          BstB1                                BspM1
                                             |              |                                     |
     GCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAG
5101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
     CGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTC

                                                      Nae1
                                                    NgoM4 |
                  SpAcc                              Bpm1 |
                     |                                 | |
     ATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGA
5201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
     TAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCT
```

```
                 Bpm1
             SpAcc  |
              Avr2  |                                                        polyA        polyA
                 |  |                                                           |            |
      GTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACG
5301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5400
      CAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGC

                                                                  Bsa1
                                                                    |
      CACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCG
5401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5500
      GTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGC

                                                                        BstAP
                                                                        AlwN1      Bsu36
                                                                           |          |
      TTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTC
5501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5600
      AAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAG

                      Dra1               Dra1                                BspH1
                         |                  |                                   |
      ATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAG
5601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5700
      TATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTC

                                                                     BpuE1
                                                                       |
      TTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAAC
5701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5800
      AAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTG

                                                  Eco57
                                                    |
      CACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCT
5801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5900
      GTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGA
```

```
      SpAcc                                                                  AlwN1
          |                                                                    |
      TCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGC
5901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6000
      AGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCG

             BpuE1                                                       ApaL1     BseY1
                 |                                                          |         |
      GATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGG
6001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6100
      CTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACC

                                                                                                  BciV1
                                        SpAcc                                               Eci1   |
                                            |                                                  |   |
      AGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGG
6101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6200
      TCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCC

                      BssS1                                   SpAcc                           Drd1
                          |                                       |                               |
      CAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGA
6201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6300
      GTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCT


                                                                                                 SpDon
           BpuE1                SpAcc     Eci1                                                 BspLU|
               |                    |        |                                                     ||
      TTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGT
6301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6400
      AAAAACACTACGAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACA


                                                   Nsi1
                                                BfrB1 |
                                                    | |
      TCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
6401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*||| 6453
      AGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aar1	Aat2	Ale1	AlwN1	ApaL1	**Ase1**	Avr2	**BamH1**	**BbvC1**	Bcg1a	Bcg1b	BciV1	Bcl1	BfrB1
Bgl1	**Bgl2**	**Blp1**	**BmgB1**	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1
Bsg1	Bsm1	**BsmB1**	**BspE1**	BspH1	**BspLU**	BspM1	BsrB1	**BsrD1**	BsrG1	BssH2	BssS1	BstAP	BstB1
BstE2	Bsu36	BtgZ1	**Bts1**	**_Chi**	**Cla1**	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Ecl2	Eco57
EcoK	**EcoN1**	Fsp1	Hind3	**Hpa1**	Kas1	**Mfe1**	**Mlu1**	**Msc1**	Nae1	Nar1	Nco1	**Nde1**	NgoM4
Nhe1	Nsi1	**PflF1**	PflM1	polyA	Psi1	Pst1	Pvu2	**Rsr2**	Sac1	Sac2	Sap1	**SexA1**	**Sfi1**
SnaB1	SpAcc	SpDon	Sph1	Ssp1	**Stu1**	Xba1	Xcm1	**Xho1**	Xmn1				

Unique:

Aar1	**Ase1**	**BamH1**	**BbvC1**	**Bgl2**	**Blp1**	**BmgB1**	**BsmB1**	**BspE1**	**BspLU**	**BsrD1**	**BstE2**	**Bts1**	**_Chi**
Cla1	**EcoK**	**EcoN1**	**Hpa1**	**Mfe1**	**Mlu1**	**Msc1**	**Nde1**	**Nhe1**	**PflF1**	**Rsr2**	**SexA1**	**Sfi1**	**Stu1**
Xho1													

Not found:

Acc65	Acl1	Afe1	Afl2	Age1	Ahd1	Apa1	Asc1	AsiS1	Bae1a	Bae1b	Bbs1	BsiW1	BstX1
BstZ1	BxatB	BxatL	BxatR	BxatP	EcoR1	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1
I_Ceu	Kpn1	loxP	Not1	Nru1	Pac1	Pme1	Pml1	PshA1	PspOM	Pvu1	R4atB	R4atL	R4atP
R4atR	Sal1	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													