pmKate2-lamin 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). mKate2 amino acids are shown in red, Lamin B1 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

                    SpDon
                   Ale1 |
         Age1       Nco1 | |                                BsrG1                                ApaL1
            |          | | |                                   |                                    |
        CCGGTAGCCACCATGGTGAGCGAGCTGATTAAGGAGAACATGCACATGAAGCTGTACATGGAGGGCACCGTGAACAACCACCACTTCAAGTGCACATCCG
    601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
        GGCCATCGGTGGTACCACTCGCTCGACTAATTCCTCTTGTACGTGTACTTCGACATGTACCTCCCGTGGCACTTGTTGGTGGTGAAGTTCACGTGTAGGC
mKate2     >            M  V  S  E  L  I  K  E  N  M  H  M  K  L  Y  M  E  G  T  V  N  N  H  H  F  K  C  T  S  E

                     SpAcc
                        |
        AGGGCGAAGGCAAGCCCTACGAGGGCACCCAGACCATGAGAATCAAGGCGGTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGCTACCAGCTT
    701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
        TCCCGCTTCCGTTCGGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCCGCCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTCGAA
mKate2     >  G  E  G  K  P  Y  E  G  T  Q  T  M  R  I  K  A  V  E  G  G  P  L  P  F  A  F  D  I  L  A  T  S  F

                                                                                Bsu36       SpDon
                                                                                  |           |
        CATGTACGGCAGCAAAACCTTCATCAACCACACCCAGGGCATCCCCGACTTCTTTAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACA
    801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
        GTACATGCCGTCGTTTTGGAAGTAGTTGGTGTGGGTCCCGTAGGGGCTGAAGAAATTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGGTGT
mKate2     >  M  Y  G  S  K  T  F  I  N  H  T  Q  G  I  P  D  F  F  K  Q  S  F  P  E  G  F  T  W  E  R  V  T  T
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                    Bbs1              Bpm1
                      |                 |
            TACGAAGACGGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACTTCCCATCCA
       901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
            ATGCTTCTGCCCCCGCACGACTGGCGATGGGTCCTGTGGTCGGAGGTCCTGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCCACTTGAAGGGTAGGT
mKate2      > Y  E  D  G  G  V  L  T  A  T  Q  D  T  S  L  Q  D  G  C  L  I  Y  N  V  K  I  R  G  V  N  F  P  S  N

                                                Bsa1
                                  BseY1    Stu1  |                                Bgl1          Bgl1
                                      |        |  |                                   |             |
            ACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCTCCACCGAGACCCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAGCCGACATGGCCCT
      1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
            TGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCTCCGGAGGTGGCTCTGGGACATGGGGCGACTGCCGCCGGACCTTCCGTCTCGGCTGTACCGGGA
mKate2      >   G  P  V  M  Q  K  K  T  L  G  W  E  A  S  T  E  T  L  Y  P  A  D  G  G  L  E  G  R  A  D  M  A  L

            BssS1          Eco57                    Bbs1          BpuE1
                |              |                       |             |
            GAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACTTGAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGCGTCTACTATGTG
      1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
            CTTCGAGCACCCGCCCCCGGTGGACTAGACGTTGAACTTCTGGTGTATGTCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCGCAGATGATACAC
mKate2      >  K  L  V  G  G  G  H  L  I  C  N  L  K  T  T  Y  R  S  K  K  P  A  K  N  L  K  M  P  G  V  Y  Y  V

                    Bbs1
                SpAcc  |                Bsa1       PshA1       BssS1 Dra3      Msc1  AlwN1          SpAcc
                    |  |                  |           |           |    |         |      |              |
            GACAGAAGACTGGAAAGAATCAAGGAGGCCGACAAAGAGACCTACGTCGAGCAGCACGAGGTGGCTGTGGCCAGATACTGCGACCTCCCTAGCAAACTGG
      1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
            CTGTCTTCTGACCTTTCTTAGTTCCTCCGGCTGTTTCTCTGGATGCAGCTCGTCGTGCTCCACCGACACCGGTCTATGACGCTGGAGGGATCGTTTGACC
mKate2      > D  R  R  L  E  R  I  K  E  A  D  K  E  T  Y  V  E  Q  H  E  V  A  V  A  R  Y  C  D  L  P  S  K  L  G

                                        Hind3
                        BpuE1     Xho1   Sac1 |
                Bmr1    BspE1   | Bgl2   | Ecl2 | |  Bcg1a                        Sac2 Bcg1b      Bgl1
                    |        |   |    |   |    | | |      |                           |     |         |
            GGCACAAACTTAATTCCGGACTCAGATCTCGAGCTCAAGCTTCGATGGCGACTGCGACCCCCGTGCCGCCGCGGATGGGCAGCCGCGCTGGCGGCCCCAC
      1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
            CCGTGTTTGAATTAAGGCCTGAGTCTAGAGCTCGAGTTCGAAGCTACCGCTGACGCTGGGGGCACGGCGGCGCCTACCCGTCGGCGCGACCGCCGGGGTG
mKate2/Lamin >  H  K  L  N  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  P  T
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                                                        Sac1
                                                      BseR1|                                BsmB1
                 Blp1     Bpm1                        Ecl2||             BsrG1             Fsp1  |
                    |        |                          |||                 |                 |  |
            CACGCCGCTGAGCCCCACGCGCCTGTCGCGGCTCCAGGAGAAGGAGGAGCTGCGCGAGCTCAATGACCGGCTGGCGGTGTACATCGACAAGGTGCGCAGC
      1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
            GTGCGGCGACTCGGGGTGCGCGGACAGCGCCGAGGTCCTCTTCCTCCTCGACGCGCTCGAGTTACTGGCCGACCGCCACATGTAGCTGTTCCACGCGTCG
LaminB1     > 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  R  S

                                  Pvu2
                                 Pst1|
                            Bpm1   ||
                          BspM1|   ||
                          BfuA1|   ||                          BseR1
                           Aar1|   ||                          BpuE1   Sac1
                       BssH2   ||   || Pst1                  Eag1   | Ecl2 |             Bsa1
                           |   ||   ||    |                     |   |    | |                |
            CTGGAGACGGAGAACAGCGCGCTGCAGCTGCAGGTGACGGAGCGCGAGGAGGTGCGCGGCCGTGAGCTCACCGGCCTCAAGGCGCTCTACGAGACCGAGC
      1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
            GACCTCTGCCTCTTGTCGCGCGACGTCGACGTCCACTGCCTCGCGCTCCTCCACGCGCCGGCACTCGAGTGGCCGGAGTTCCGCGAGATGCTCTGGCTCG
LaminB1     > 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  E  L

                                                                                                      Eci1
                       BssH2                    BssH2          Pst1  BseY1                    BseR1 Pvu2|
                          |                        |             |      |                          |    ||
            TGGCCGACGCGCGACGCGCGCTCGACGACACGGCCCGCGAGCGCGCCAAGCTGCAGATCGAGCTGGGCAAGTGCAAGGCGGAACACGACCAGCTGCTCCT
      1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
            ACCGGCTGCGCGCTGCGCGCGAGCTGCTGTGCCGGGCGCTCGCGCGGTTCGACGTCTAGCTCGACCCGTTCACGTTCCGCCTTGTGCTGGTCGACGAGGA
LaminB1     >  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  L  L

                                 Nar1                                                   BstAP
                SpAcc           Kas1|      Hind3     Bcg1b              BstB1   Bsg1  Bcg1a|
                   |               ||          |         |                  |      |      ||
            CAACTATGCTAAGAAGGAATCTGATCTTAATGGCGCCCAGATCAAGCTTCGAGAATATGAAGCAGCACTCAATTCGAAAGATGCAGCTCTTGCTACTGCA
      1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
            GTTGATACGATTCTTCCTTAGACTAGAATTACCGCGGGTCTAGTTCGAAGCTCTTATACTTCGTCGTGAGTTAAGCTTTCTACGTCGAGAACGATGACGT
LaminB1     > 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  T  A
```

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                                                                                SpAcc
            Dra3                                          Bmr1     Eco57      Bpu10   | Pst1
              |                                             |         |          |   |    |
            CTTGGTGACAAAAAAAGTTTAGAGGGAGATTTGGAGGATCTGAAGGATCAGATTGCCCAGTTGGAAGCCTCCTTAGCTGCAGCCAAAAAACAGTTAGCAG
      1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
            GAACCACTGTTTTTTTCAAATCTCCCTCTAAACCTCCTAGACTTCCTAGTCTAACGGGTCAACCTTCGGAGGAATCGACGTCGGTTTTTTGTCAATCGTC
LaminB1   > 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  A  D

                                                EcoN1                          Ear1          Bsa1    BseR1
                                                  |                              |             |        |
            ATGAAACTTTACTTAAAGTAGATTTGGAGAATCGTTGTCAGAGCCTTACTGAGGACTTGGAGTTTCGCAAAAGCATGTATGAAGAGGAGATTAACGAGAC
      1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
            TACTTTGAAATGAATTTCATCTAAACCTCTTAGCAACAGTCTCGGAATGACTCCTGAACCTCAAAGCGTTTTCGTACATACTTCTCCTCTAATTGCTCTG
LaminB1   >   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  E  T

                                                                                                BspH1
                                                                                                  |
            CAGAAGGAAGCATGAAACGCGCTTGGTAGAGGTGGATTCTGGGCGTCAAATTGAGTATGAGTACAAGCTGGCGCAAGCCCTTCATGAGATGAGAGAGCAA
      2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
            GTCTTCCTTCGTACTTTGCGCGAACCATCTCCACCTAAGACCCGCAGTTTAACTCATACTCATGTTCGACCGCGTTCGGGAAGTACTCTACTCTCTCGTT
LaminB1   >  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  E  Q

                   SpDon                          BseR1SpDon   Bpm1          Bsm1     BpuE1
                     |                                |    |      |             |         |
            CATGATGCCCAAGTGAGGCTGTATAAGGAGGAGCTGGAGCAGACTTACCATGCCAAACTTGAGAATGCCAGACTGTCATCAGAGATGAATACTTCTACTG
      2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
            GTACTACGGGTTCACTCCGACATATTCCTCCTCGACCTCGTCTGAATGGTACGGTTTGAACTCTTACGGTCTGACAGTAGTCTCTACTTATGAAGATGAC
LaminB1   > 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  T  V

                                                                BseY1        SpAcc         Xba1
                                                                  |            |             |
            TCAACAGTGCCAGGGAAGAACTGATGGAAAGCCGCATGAGAATTGAGAGCCTTTCATCCCAGCTTTCTAATCTACAGAAAGAGTCTAGAGCATGTTTGGA
      2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
            AGTTGTCACGGTCCCTTCTTGACTACCTTTCGGCGTACTCTTAACTCTCGGAAAGTAGGGTCGAAAGATTAGATGTCTTTCTCAGATCTCGTACAAACCT
LaminB1   >   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  L  E
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                Xmn1                    SpAcc                        Sph1                                    Eci1
                  |                       |                           |                                       |
            AAGGATTCAAGAATTAGAGGACTTGCTTGCTAAAGAAAAAGACAACTCTCGTCGCATGCTGACAGACAAAGAGAGAGAGATGGCGGAAATAAGGGATCAA
      2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
            TTCCTAAGTTCTTAATCTCCTGAACGAACGATTTCTTTTTCTGTTGAGAGCAGCGTACGACTGTCTGTTTCTCTCTCTCTACCGCCTTTATTCCCTAGTT
LaminB1     > 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  D  Q

                      Pvu2             Xmn1     SpDon                                                  Ear1
                        |                |         |                                                      |
            ATGCAGCAACAGCTGAATGACTATGAACAGCTTCTTGATGTAAAGTTAGCCCTGGACATGGAAATCAGTGCTTACAGGAAACTCTTAGAAGGCGAAGAAG
      2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
            TACGTCGTTGTCGACTTACTGATACTTGTCGAAGAACTACATTTCAATCGGGACCTGTACCTTTAGTCACGAATGTCCTTTGAGAATCTTCCGCTTCTTC
LaminB1     > 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  E  E

                                                BpuE1       BciV1              SnaB1 SpAcc     Ear1
                                                  |           |                  |     |        |
            AGAGGTTGAAGCTGTCTCCAAGCCCTTCTTCCCGTGTGACAGTATCCCGAGCATCCTCAAGTCGTAGTGTACGTACAACTAGAGGAAAGCGGAAGAGGGT
      2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
            TCTCCAACTTCGACAGAGGTTCGGGAAGAAGGGCACACTGTCATAGGGCTCGTAGGAGTTCAGCATCACATGCATGTTGATCTCCTTTCGCCTTCTCCCA
LaminB1     >  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  R  V

                                                          Bpu10
                                            Eci1          BbvC1  AlwN1
                                              |              |      |
            TGATGTGGAAGAATCAGAGGCGAGTAGTAGTGTTAGCATCTCTCATTCCGCCTCAGCCACTGGAAATGTTTGCATCGAAGAAATTGATGTTGATGGGAAA
      2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
            ACTACACCTTCTTAGTCTCCGCTCATCATCACAATCGTAGAGAGTAAGGCGGAGTCGGTGACCTTTACAAACGTAGCTTCTTTAACTACAACTACCCTTT
LaminB1     > 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  G  K

                                                      BseY1
                                                     Xcm1  |     Bcl1                    Drd1BpuE1 Psi1
                                                        |  |       |                       |    |    |
            TTTATCCGCTTGAAGAACACTTCTGAACAGGATCAACCAATGGGAGGCTGGGAGATGATCAGAAAAATTGGAGACACATCAGTCAGTTATAAATATACCT
      2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
            AAATAGGCGAACTTCTTGTGAAGACTTGTCCTAGTTGGTTACCCTCCGACCCTCTACTAGTCTTTTTAACCTCTGTGTAGTCAGTCAATATTTATATGGA
LaminB1     > 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  T  S
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                                   Eco57                                                SpAcc
                                     |                                                    |
            CAAGATATGTGCTGAAGGCAGGCCAGACTGTTACAATTTGGGCTGCAAACGCTGGTGTCACAGCCAGCCCCCCAACTGACCTCATCTGGAAGAACCAGAA
      2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
            GTTCTATACACGACTTCCGTCCGGTCTGACAATGTTAAACCCGACGTTTGCGACCACAGTGTCGGTCGGGGGGTTGACTGGAGTAGACCTTCTTGGTCTT
LaminB1       >  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  Q  N

                                                                                  BsaXb                    Ear1
          BssS1                 SpDon                BsaXa                     BseR1   |      Dra1        SpAcc|
            |                     |                    |                          |   |         |             ||
            CTCGTGGGGCACTGGCGAAGATGTGAAGGTTATATTGAAAAATTCTCAGGGAGAGGAGGTTGCTCAAAGAAGTACAGTCTTTAAAACAACCATACCTGAA
      2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
            GAGCACCCCGTGACCGCTTCTACACTTCCAATATAACTTTTTAAGAGTCCCTCTCCTCCAACGAGTTTCTTCATGTCAGAAATTTTGTTGGTATGGACTT
LaminB1       > 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  P  E

                                 Pvu2
                                BseR1
                              BseR1  |
                             BsaXa |  |                        _Chi
                            BseR1| |  |                     BsaXb  |
                         Eco57 || |  |                   Bpm1  |  |
                             | || |  |                      |  |  |
            GAAGAGGAGGAGGAGGAAGAAGCAGCTGGAGTGGTTGTTGAGGAAGAACTTTTCCACCAGCAGGGAACCCCAAGAGCATCCAATAGAAGCTGTGCAATTA
      3001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
            CTTCTCCTCCTCCTCCTTCTTCGTCGACCTCACCAACAACTCCTTCTTGAAAAGGTGGTCGTCCCTTGGGGTTCTCGTAGGTTATCTTCGACACGTTAAT
LaminB1       > 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  I  M

             BamH1        Xba1      Bcl1BsaB1                                SpDon   Dra1
                |           |         |    |                                  |      |
            TGTAGGGATCCACCGGATCTAGATAACTGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAA
      3101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
            ACATCCCTAGGTGGCCTAGATCTATTGACTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTT
LaminB1       >   *

                              Bsm1
                             Mfe1|        Hpa1       polyA    Psi1      polyA                        polyA
                                ||           |           |       |          |                            |
            CCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAA
      3201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
            GGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTT
```

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            Bts1 Bsm1                                        Mlu1     SpDon        Ssp1
                |    |                                          |         |           |
     GCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAACGCGTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTA
3301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
     CGTAAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTGCGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAAT

                                                          Psi1
                                                            |
     AATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTC
3401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
     TTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAG

                                                                                          BtgZ1
                    BsaXb                 Drd1    BsaXa                                   Dra3|
                        |                    |        |                                      ||
     CAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACC
3501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
     GTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGG

                                                                                             Nae1
                                                SpAcc                                   NgoM4 |
                                                    |                                       | |
     CTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTG
3601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
     GATTAGTTCAAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCAC

                            BsrB1
                                |
     GCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATG
3701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
     CGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTAC

                                                                                                  BspH1
                                                                        polyA                   BsrB1 |
                                                                            |                         | |
     CGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCAT
3801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
     GCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTA
```

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                                                                  Eci1
 BciV1                          Ssp1  Ear1        Bsu36          Pvu2 |
     |                             |     |            |              | |
      GAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAA
3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
      CTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTT

                                        Nsi1
                                      Sph1 |
                                     BfrB1 |
             BseY1                  BstAP  | |            SexA1                    BseY1
                 |                     |  | |               |                        |
      AGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAG
4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
      TCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTC

                Nsi1
              Sph1 |
             BfrB1 |                                                      Eci1
         BstAP  | |                       Eci1                 Eci1     Bmr1|       Eci1
             |  | |                          |                    |        ||          |
      TATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCC
4101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
      ATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGG

                                                                                                  Avr2
                                                 Sfi1                                            Stu1|
  Nco1                   polyA                  Bgl1                      SpDon             BseR1  ||
     |                      |                     |                          |                 |  ||
      CATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCT
4201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
      GTACCGACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGA

                                                        BspM1
             Cla1                BsaB1                  BfuA1                Eag1
                |                    |                      |                   |
      TTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTAT
4301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
      AAACGTTTCTAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATA
```

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                                                                  Nar1
                    Bmr1                                         Kas1|                        Drd1
                       |                                           ||                          |
     TCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCT
4401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
     AGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGA

                                                                          Pvu2
                                                   Msc1                Fsp1   |       PflF1
                                                      |                   |   |           |
     GTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAA
4501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
     CAGGCCACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTT

                 Eco57                                      SpDon                        BciV1
                    |                                          |                            |
     GCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAA
4601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
     CGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTT

                                        BtgZ1
                                     BspM1  |
     BsrD1                           BfuA1  |
        |                                |  |
     TGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGT
4701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
     ACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACA

                Sap1
                Ear1                            BpuE1                        Sph1
                   |                               |                            |
     CGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTG
4801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
     GCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCAC
```

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                                                                  BseY1
                                                                 Nae1 |
     Nco1               BtgZ1                                 NgoM4 | |        Rsr2
       |                  |                                       | | |           |
      ACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGG
4901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
      TGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCC

                          Sap1                                                          BtgZ1
  Eci1                    Ear1                    Eco57         BssS1                 BsrB1 |
     |                       |                       |             |                     | |
      ACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCG
5001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
      TGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGC

                                                                                          BssS1
                                                                                          BspM1
                                  BsrB1          BstB1                                   BfuA1
                                     |              |                                        |
      CATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCG
5101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
      GTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGC

                                                   Nae1
                                                 NgoM4 |
                SpAcc                             Bpm1 |
                   |                                 | |
      ATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTT
5201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
      TAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAA

            Bpm1
         SpAcc  |
          Avr2  |                                                        polyA        polyA
            |   |                                                          |            |
      CGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGT
5301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5400
      GCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCA
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                                                        Bsa1
                                                          |
     GTTGGGTCGTTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTT
5401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5500
     CAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAA

                                                                  BstAP
                                                                  AlwN1      Bsu36
                                                                     |          |
     CCTTTTCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATAT
5501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5600
     GGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATA

               Dra1               Dra1                              BspH1
                  |                  |                                 |
     ACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCG
5601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5700
     TGAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGC

                                                                 BpuE1
                                                                   |
     TTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGC
5701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5800
     AAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCG

                                            Eco57                                                  SpAcc
                                              |                                                      |
     TACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGT
5801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5900
     ATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCA

                                                                                AlwN1
                                                                                  |
     GTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAG
5901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6000
     CATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTC
```

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       BpuE1                                                          ApaL1     BseY1
           |                                                              |         |
      TCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAA
6001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6100
      AGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTT

                                                                                                  BciV1
                                 SpAcc                                                         Eci1   |
                                     |                                                            |   |
      CGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGT
6101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6200
      GCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCA

                BssS1                                      SpAcc                          Drd1
                    |                                          |                              |
      CGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTG
6201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6300
      GCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAC

                                                                                                SpDon
     BpuE1                SpAcc     Eci1                                                      BspLU|
        |                    |        |                                                          ||
      TGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTC
6301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6400
      ACTACGAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAG

                                                Nsi1
                                             BfrB1 |
                                                 | |
      CTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
6401  |||||||||*|||||||||*|||||||||*|||||||||*||||||| 6447
      GACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aar1	Aat2	**Afe1**	**Age1**	**Ale1**	AlwN1	ApaL1	**Ase1**	Avr2	**BamH1**	Bbs1	**BbvC1**	Bcg1a	Bcg1b
BciV1	Bcl1	BfrB1	BfuA1	Bgl1	**Bgl2**	**Blp1**	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**	**_Chi**	**Cla1**	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1
Ecl2	Eco57	**EcoN1**	Fsp1	Hind3	**Hpa1**	Kas1	**Mfe1**	**Mlu1**	Msc1	Nae1	Nar1	Nco1	**Nde1**
NgoM4	**Nhe1**	Nsi1	**PflF1**	polyA	**PshA1**	Psi1	Pst1	Pvu2	**Rsr2**	Sac1	**Sac2**	Sap1	**SexA1**
Sfi1	SnaB1	SpAcc	SpDon	Sph1	Ssp1	Stu1	Xba1	**Xcm1**	**Xho1**	Xmn1			

Unique:

Aar1	**Afe1**	**Age1**	**Ale1**	**Ase1**	**BamH1**	**BbvC1**	**Bgl2**	**Blp1**	**Bsg1**	**BsmB1**	**BspE1**	**BspLU**	**BsrD1**
Bts1	**_Chi**	**Cla1**	**EcoN1**	**Hpa1**	**Mfe1**	**Mlu1**	**Nde1**	**Nhe1**	**PflF1**	**PshA1**	**Rsr2**	**Sac2**	**SexA1**
Sfi1	**Xcm1**	**Xho1**											

Not found:

Acc65	Acl1	Afl2	Ahd1	Apa1	Asc1	AsiS1	Bae1a	Bae1b	BmgB1	BsiW1	BstE2	BstX1	BstZ1
BxatB	BxatL	BxatR	BxatP	EcoK	EcoR1	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1
I_Ceu	Kpn1	loxP	Not1	Nru1	Pac1	PflM1	Pme1	Pml1	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													