pTagRFP-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 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, 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

                 Ale1      Sap1
 Age1        Nco1 |      Ear1                                BsrG1                                ApaL1
    |           | |         |                                   |                                    |
     CCGGTCGCCACCATGGTGTCTAAGGGCGAAGAGCTGATTAAGGAGAACATGCACATGAAGCTGTACATGGAGGGCACCGTGAACAACCACCACTTCAAGT
601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
     GGCCAGCGGTGGTACCACAGATTCCCGCTTCTCGACTAATTCCTCTTGTACGTGTACTTCGACATGTACCTCCCGTGGCACTTGTTGGTGGTGAAGTTCA
TagRFP     >            M  V  S  K  G  E  E  L  I  K  E  N  M  H  M  K  L  Y  M  E  G  T  V  N  N  H  H  F  K  C

                          SpAcc
                             |
     GCACATCCGAGGGCGAAGGCAAGCCCTACGAGGGCACCCAGACCATGAGAATCAAGGTGGTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGC
701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
     CGTGTAGGCTCCCGCTTCCGTTCGGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCCACCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCG
TagRFP     >  T  S  E  G  E  G  K  P  Y  E  G  T  Q  T  M  R  I  K  V  V  E  G  G  P  L  P  F  A  F  D  I  L  A

                                                                                Bsu36       SpDon
                                                                                  |           |
     TACCAGCTTCATGTACGGCAGCAGAACCTTCATCAACCACACCCAGGGCATCCCCGACTTCTTTAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGA
801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
     ATGGTCGAAGTACATGCCGTCGTCTTGGAAGTAGTTGGTGTGGGTCCCGTAGGGGCTGAAGAAATTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCT
TagRFP     >  T  S  F  M  Y  G  S  R  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

                         Bbs1             Bpm1
                           |                |
     GTCACCACATACGAAGACGGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACT
901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
     CAGTGGTGTATGCTTCTGCCCCCGCACGACTGGCGATGGGTCCTGTGGTCGGAGGTCCTGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCCACTTGA
TagRFP     > V  T  T  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
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                                                BseY1                                                Bgl1
                                                  |                                                    |
            TCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCAACACCGAGATGCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAAGCGA
      1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
            AGGGTAGGTTGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCTCCGGTTGTGGCTCTACGACATGGGGCGACTGCCGCCGGACCTTCCGTCTTCGCT
TagRFP        >   P  S  N  G  P  V  M  Q  K  K  T  L  G  W  E  A  N  T  E  M  L  Y  P  A  D  G  G  L  E  G  R  S  D

                      BssS1          Eco57                                  BpuE1
                        |              |                                      |
            CATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACTTCAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGCGTC
      1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
            GTACCGGGACTTCGAGCACCCGCCCCCGGTGGACTAGACGTTGAAGTTCTGGTGTATGTCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCGCAG
TagRFP        >  M  A  L  K  L  V  G  G  G  H  L  I  C  N  F  K  T  T  Y  R  S  K  K  P  A  K  N  L  K  M  P  G  V

                         SpAcc
                         PflM1                  Bsa1       PshA1       BssS1 Dra3      Msc1  AlwN1
                           |                      |           |           |    |         |      |
            TACTATGTGGACCACAGACTGGAAAGAATCAAGGAGGCCGACAAAGAGACCTACGTCGAGCAGCACGAGGTGGCTGTGGCCAGATACTGCGACCTCCCTA
      1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
            ATGATACACCTGGTGTCTGACCTTTCTTAGTTCCTCCGGCTGTTTCTCTGGATGCAGCTCGTCGTGCTCCACCGACACCGGTCTATGACGCTGGAGGGAT
TagRFP        > Y  Y  V  D  H  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

                                  BpuE1     Xho1    Hind3
          SpAcc          Bmr1    BspE1   | Bgl2   |   Sac1 |  Bcg1a                        Sac2 Bcg1b      Bgl1
            |              |        |    |    |    |      | |      |                          |     |         |
            GCAAACTGGGGCACAAACTTAATTCCGGACTCAGATCTCGAGCTCAAGCTTCGATGGCGACTGCGACCCCCGTGCCGCCGCGGATGGGCAGCCGCGCTGG
      1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
            CGTTTGACCCCGTGTTTGAATTAAGGCCTGAGTCTAGAGCTCGAGTTCGAAGCTACCGCTGACGCTGGGGGCACGGCGGCGCCTACCCGTCGGCGCGACC
TagRFP/Lamin >   K  L  G  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

                                                                                  Sac1
                         Blp1     Bpm1                                          BseR1|             BsrG1
                           |        |                                              ||                |
            CGGCCCCACCACGCCGCTGAGCCCCACGCGCCTGTCGCGGCTCCAGGAGAAGGAGGAGCTGCGCGAGCTCAATGACCGGCTGGCGGTGTACATCGACAAG
      1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
            GCCGGGGTGGTGCGGCGACTCGGGGTGCGCGGACAGCGCCGAGGTCCTCTTCCTCCTCGACGCGCTCGAGTTACTGGCCGACCGCCACATGTAGCTGTTC
Lamin         >  G  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
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                                        Pvu2
                                       Pst1|
                                  Bpm1   ||
                                BspM1|   ||
                                BfuA1|   ||                              BseR1
          BsmB1                  Aar1|   ||                              BpuE1
        Fsp1  |              BssH2   ||   || Pst1                     Eag1   |   Sac1             Bsa1
           |  |                 |   ||   ||    |                        |   |      |                |
        GTGCGCAGCCTGGAGACGGAGAACAGCGCGCTGCAGCTGCAGGTGACGGAGCGCGAGGAGGTGCGCGGCCGTGAGCTCACCGGCCTCAAGGCGCTCTACG
1501    |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 1600
        CACGCGTCGGACCTCTGCCTCTTGTCGCGCGACGTCGACGTCCACTGCCTCGCGCTCCTCCACGCGCCGGCACTCGAGTGGCCGGAGTTCCGCGAGATGC
Lamin     > V  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

                                BssH2                    BssH2          Pst1  BseY1                    BseR1
                                   |                        |             |      |                        |
        AGACCGAGCTGGCCGACGCGCGACGCGCGCTCGACGACACGGCCCGCGAGCGCGCCAAGCTGCAGATCGAGCTGGGCAAGTGCAAGGCGGAACACGACCA
1601    |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 1700
        TCTGGCTCGACCGGCTGCGCGCTGCGCGCGAGCTGCTGTGCCGGGCGCTCGCGCGGTTCGACGTCTAGCTCGACCCGTTCACGTTCCGCCTTGTGCTGGT
Lamin     >   T  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

            Eci1                                  Nar1                                                  BstAP
           Pvu2|          SpAcc                   Kas1|      Hind3     Bcg1b               BstB1   Bsg1  Bcg1a|
        ||              |                       ||          |         |                   |      |      ||
        GCTGCTCCTCAACTATGCTAAGAAGGAATCTGATCTTAATGGCGCCCAGATCAAGCTTCGAGAATATGAAGCAGCACTCAATTCGAAAGATGCAGCTCTT
1701    |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 1800
        CGACGAGGAGTTGATACGATTCTTCCTTAGACTAGAATTACCGCGGGTCTAGTTCGAAGCTCTTATACTTCGTCGTGAGTTAAGCTTTCTACGTCGAGAA
Lamin     >  L  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

                                                                                                SpAcc
                     Dra3                                          Bmr1     Eco57      Bpu10   | Pst1
                        |                                             |         |          |   |    |
        GCTACTGCACTTGGTGACAAAAAAAGTTTAGAGGGAGATTTGGAGGATCTGAAGGATCAGATTGCCCAGTTGGAAGCCTCCTTAGCTGCAGCCAAAAAAC
1801    |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 1900
        CGATGACGTGAACCACTGTTTTTTTCAAATCTCCCTCTAAACCTCCTAGACTTCCTAGTCTAACGGGTCAACCTTCGGAGGAATCGACGTCGGTTTTTTG
Lamin     > A  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
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                                                          EcoN1                        Ear1          Bsa1
                                                            |                            |             |
            AGTTAGCAGATGAAACTTTACTTAAAGTAGATTTGGAGAATCGTTGTCAGAGCCTTACTGAGGACTTGGAGTTTCGCAAAAGCATGTATGAAGAGGAGAT
      1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
            TCAATCGTCTACTTTGAAATGAATTTCATCTAAACCTCTTAGCAACAGTCTCGGAATGACTCCTGAACCTCAAAGCGTTTTCGTACATACTTCTCCTCTA
Lamin     >  L  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

               BseR1                                                                                  BspH1
                  |                                                                                      |
            TAACGAGACCAGAAGGAAGCATGAAACGCGCTTGGTAGAGGTGGATTCTGGGCGTCAAATTGAGTATGAGTACAAGCTGGCGCAAGCCCTTCATGAGATG
      2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
            ATTGCTCTGGTCTTCCTTCGTACTTTGCGCGAACCATCTCCACCTAAGACCCGCAGTTTAACTCATACTCATGTTCGACCGCGTTCGGGAAGTACTCTAC
Lamin     >  N  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

                                SpDon                          BseR1SpDon   Bpm1          Bsm1     BpuE1
                                   |                               |    |      |             |         |
            AGAGAGCAACATGATGCCCAAGTGAGGCTGTATAAGGAGGAGCTGGAGCAGACTTACCATGCCAAACTTGAGAATGCCAGACTGTCATCAGAGATGAATA
      2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
            TCTCTCGTTGTACTACGGGTTCACTCCGACATATTCCTCCTCGACCTCGTCTGAATGGTACGGTTTGAACTCTTACGGTCTGACAGTAGTCTCTACTTAT
Lamin     > R  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

                                                                                  BseY1        SpAcc         Xba1
                                                                                    |            |             |
            CTTCTACTGTCAACAGTGCCAGGGAAGAACTGATGGAAAGCCGCATGAGAATTGAGAGCCTTTCATCCCAGCTTTCTAATCTACAGAAAGAGTCTAGAGC
      2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
            GAAGATGACAGTTGTCACGGTCCCTTCTTGACTACCTTTCGGCGTACTCTTAACTCTCGGAAAGTAGGGTCGAAAGATTAGATGTCTTTCTCAGATCTCG
Lamin     >  S  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

                        Xmn1                      SpAcc                          Sph1
                           |                         |                              |
            ATGTTTGGAAAGGATTCAAGAATTAGAGGACTTGCTTGCTAAAGAAAAAGACAACTCTCGTCGCATGCTGACAGACAAAGAGAGAGAGATGGCGGAAATA
      2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
            TACAAACCTTTCCTAAGTTCTTAATCTCCTGAACGAACGATTTCTTTTTCTGTTGAGAGCAGCGTACGACTGTCTGTTTCTCTCTCTACCGCCTTTAT
Lamin     >  C  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
```

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                Eci1          Pvu2             Xmn1     SpDon
                  |             |                |         |
           AGGGATCAAATGCAGCAACAGCTGAATGACTATGAACAGCTTCTTGATGTAAAGTTAGCCCTGGACATGGAAATCAGTGCTTACAGGAAACTCTTAGAAG
      2401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
           TCCCTAGTTTACGTCGTTGTCGACTTACTGATACTTGTCGAAGAACTACATTTCAATCGGGACCTGTACCTTTAGTCACGAATGTCCTTTGAGAATCTTC
Lamin      > R  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

           Ear1                                          BpuE1       BciV1              SnaB1 SpAcc     Ear1
           |                                                |           |                  |     |        |
           GCGAAGAAGAGAGGTTGAAGCTGTCTCCAAGCCCTTCTTCCCGTGTGACAGTATCCCGAGCATCCTCAAGTCGTAGTGTACGTACAACTAGAGGAAAGCG
      2501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
           CGCTTCTTCTCTCCAACTTCGACAGAGGTTCGGGAAGAAGGGCACACTGTCATAGGGCTCGTAGGAGTTCAGCATCACATGCATGTTGATCTCCTTTCGC
Lamin      >   E  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

                                                                                Bpu10
                                                        Eci1                    BbvC1  AlwN1
                                                          |                       |      |
           GAAGAGGGTTGATGTGGAAGAATCAGAGGCGAGTAGTAGTGTTAGCATCTCTCATTCCGCCTCAGCCACTGGAAATGTTTGCATCGAAGAAATTGATGTT
      2601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
           CTTCTCCCAACTACACCTTCTTAGTCTCCGCTCATCATCACAATCGTAGAGAGTAAGGCGGAGTCGGTGACCTTTACAAACGTAGCTTCTTTAACTACAA
Lamin      > K  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

                                                                  BseY1
                                                                 Xcm1  |     Bcl1                   Drd1BpuE1 Psi1
                                                                   |   |       |                      |    |    |
           GATGGGAAATTTATCCGCTTGAAGAACACTTCTGAACAGGATCAACCAATGGGAGGCTGGGAGATGATCAGAAAAATTGGAGACACATCAGTCAGTTATA
      2701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
           CTACCCTTTAAATAGGCGAACTTCTTGTGAAGACTTGTCCTAGTTGGTTACCCTCCGACCCTCTACTAGTCTTTTTAACCTCTGTGTAGTCAGTCAATAT
Lamin      > D  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

                                                  Eco57                                                SpAcc
                                                    |                                                    |
           AATATACCTCAAGATATGTGCTGAAGGCAGGCCAGACTGTTACAATTTGGGCTGCAAACGCTGGTGTCACAGCCAGCCCCCCAACTGACCTCATCTGGAA
      2801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
           TTATATGGAGTTCTATACACGACTTCCGTCCGGTCTGACAATGTTAAACCCGACGTTTGCGACCACAGTGTCGGTCGGGGGGTTGACTGGAGTAGACCTT
Lamin      >   Y  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
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                                                                                BsaXb
                 BssS1                SpDon                BsaXa                BseR1   |      Dra1
                     |                    |                    |                    |   |         |
           GAACCAGAACTCGTGGGGCACTGGCGAAGATGTGAAGGTTATATTGAAAAATTCTCAGGGAGAGGAGGTTGCTCAAAGAAGTACAGTCTTTAAAACAACC
      2901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
           CTTGGTCTTGAGCACCCCGTGACCGCTTCTACACTTCCAATATAACTTTTTAAGAGTCCCTCTCCTCCAACGAGTTTCTTCATGTCAGAAATTTTGTTGG
Lamin        >  N  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

                                   Pvu2
                                  BseR1
                              BseR1  |
                             BsaXa |  |                      _Chi
            Ear1            BseR1| |  |                   BsaXb  |
          SpAcc|           Eco57 || |  |                 Bpm1  |  |
              ||                | || |  |                   |  |  |
           ATACCTGAAGAAGAGGAGGAGGAGGAAGAAGCAGCTGGAGTGGTTGTTGAGGAAGAACTTTTCCACCAGCAGGGAACCCCAAGAGCATCCAATAGAAGCT
      3001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
           TATGGACTTCTTCTCCTCCTCCTCCTTCTTCGTCGACCTCACCAACAACTCCTTCTTGAAAAGGTGGTCGTCCCTTGGGGTTCTCGTAGGTTATCTTCGA
Lamin        > I  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

                     BamH1        Xba1      Bcl1BsaB1                            SpDon   Dra1
                         |           |         |    |                               |      |
           GTGCAATTATGTAGGGATCCACCGGATCTAGATAACTGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCT
      3101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
           CACGTTAATACATCCCTAGGTGGCCTAGATCTATTGACTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGA
Lamin        >   A  I  M  *

                                  Bsm1
                                 Mfe1|        Hpa1       polyA    Psi1      polyA
                                    ||           |           |       |          |
           CCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTC
      3201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
           GGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAG


               polyA            Bts1 Bsm1                                      Mlu1     SpDon        Ssp1
                   |               |    |                                        |         |           |
           ACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAACGCGTAAATTGTAAGCGTTAATATTTTGTTAAAA
      3301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
           TGTTTATTTCGTAAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTGCGCATTTAACATTCGCAATTATAAAACAATTTT
```

```
                                                                Psi1
                                                                  |
     TTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGA
3401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
     AAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACT

                                                                                                  BtgZ1
                              BsaXb                 Drd1    BsaXa                                 Dra3|
                                  |                   |        |                                     ||
     GTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGA
3501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
     CACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACT

                                                                                                     Nae1
                                                          SpAcc                                 NgoM4 |
                                                              |                                     | |
     ACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCG
3601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
     TGGTAGTGGGATTAGTTCAAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGC

                                      BsrB1
                                        |
     GCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCG
3701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
     CGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGC

                                                                          polyA
                                                                            |
     CGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTA
3801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
     GCGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACAT


         BciV1
      BspH1  |                                                                  Eci1
    BsrB1 |  |                            Ssp1  Ear1        Bsu36              Pvu2 |
        | |  |                               |     |            |                 | |
     TCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAG
3901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
     AGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATC
```

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                                                Nsi1
                                              Sph1 |
                                             BfrB1 |
                        BseY1              BstAP  | |          SexA1                BseY1
                            |                 |  | |             |                    |
     GGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGC
4001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
     CCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCG

                          Nsi1
                        Sph1 |
                       BfrB1 |                                                   Eci1
                     BstAP  | |                      Eci1                Eci1     Bmr1|       Eci1
                        |  | |                        |                   |        ||          |
     AGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCAT
4101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
     TCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTA

                                                      Sfi1
          Nco1                    polyA               Bgl1                    SpDon             BseR1
            |                        |                  |                        |                 |
     TCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAG
4201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
     AGAGGCGGGGTACCGACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTC

    Avr2                                                          BspM1
   Stu1|              Cla1              BsaB1                      BfuA1               Eag1
     ||                 |                 |                          |                  |
     GCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGG
4301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
     CGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACC

                                                                                  Nar1
                            Bmr1                                                 Kas1|
                              |                                                     ||
     AGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAA
4401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
     TCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTT
```

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                                                                                  Pvu2
         Drd1                                                Msc1                Fsp1   |       PflF1
           |                                                   |                   |   |           |
     GACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTT
4501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
     CTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAA

                        Eco57                                       SpDon                        BciV1
                            |                                           |                            |
     GTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGG
4601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
     CAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACC

                                                BtgZ1
                                             BspM1  |
             BsrD1                           BfuA1  |
                |                                |  |
     CTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGC
4701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
     GACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCG

                        Sap1
                        Ear1                          BpuE1                        Sph1
                          |                             |                            |
     CGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGAT
4801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
     GCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTA

                                                                                  BseY1
                                                                                 Nae1 |
             Nco1                BtgZ1                                       NgoM4 | |        Rsr2
               |                   |                                           | | |           |
     CTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACC
4901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
     GAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGG
```

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                                Sap1                                                        BtgZ1
     Eci1                       Ear1                    Eco57         BssS1               BsrB1 |
        |                          |                       |             |                   | |
GCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGA
5001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
CGATAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCT

                                                                                                BssS1
                                                                                                BspM1
                                          BsrB1          BstB1                                 BfuA1
                                             |              |                                      |
TTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCAC
5101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
AAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTG

                                                          Nae1
                                                       NgoM4 |
                      SpAcc                             Bpm1 |
                         |                                 | |
GAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCT
5201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
CTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGA

                   Bpm1
             SpAcc  |
              Avr2  |                                                        polyA        polyA
                 |  |                                                           |            |
GGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAA
5301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5400
CCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTT

                                                                  Bsa1
                                                                    |
ACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCC
5401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5500
TGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGG
```

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                                                                                BstAP
                                                                                AlwN1      Bsu36
                                                                                    |          |
     GCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTA
5501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5600
     CGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAAT

                        Dra1               Dra1                             BspH1
                          |                  |                                |
     CTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGT
5601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5700
     GAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCA

                                                                          BpuE1
                                                                            |
     GAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAA
5701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5800
     CTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTT


                                                      Eco57
                                                        |
     AACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGT
5801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5900
     TTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACA


        SpAcc                                                                           AlwN1
            |                                                                               |
     CCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGT
5901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6000
     GGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCA


                 BpuE1                                                                ApaL1     BseY1
                    |                                                                     |          |
     GGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCT
6001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6100
     CCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGA
```

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                                          SpAcc                                                   Eci1
                                             |                                                      |
      TGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAG
6101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6200
      ACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTC

 BciV1                    BssS1                                   SpAcc                          Drd1
     |                       |                                       |                              |
      CGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGT
6201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6300
      GCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCA

                                                                                                  SpDon
              BpuE1                SpAcc     Eci1                                                BspLU|
                  |                    |        |                                                     ||
      CGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACA
6301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6400
      GCTAAAAACACTACGAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGT

                                                   Nsi1
                                                BfrB1 |
                                                    | |
      TGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
6401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||| 6456
      ACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

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
Eco57	**EcoN1**	Fsp1	Hind3	**Hpa1**	Kas1	**Mfe1**	**Mlu1**	Msc1	Nae1	Nar1	Nco1	**Nde1**	NgoM4
Nhe1	Nsi1	**PflF1**	**PflM1**	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**	**Bbs1**	**BbvC1**	**Bgl2**	**Blp1**	**Bsg1**	**BsmB1**	**BspE1**	**BspLU**
BsrD1	**Bts1**	**_Chi**	**Cla1**	**EcoN1**	**Hpa1**	**Mfe1**	**Mlu1**	**Nde1**	**Nhe1**	**PflF1**	**PflM1**	**PshA1**	**Rsr2**
Sac2	**SexA1**	**Sfi1**	**Stu1**	**Xcm1**	**Xho1**								

Not found:

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