pTagFP635-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). TagFP635 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

                          Sap1
 Age1         Ale1        Ear1                                BsrG1                                ApaL1
   |            |          |                                    |                                    |
     CCGGTCGCCACAATGGTGTCTAAGGGCGAAGAGCTGATTAAGGAGAACATGCACATGAAGCTGTACATGGAGGGCACCGTGAACAACCACCACTTCAAGT
601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
     GGCCAGCGGTGTTACCACAGATTCCCGCTTCTCGACTAATTCCTCTTGTACGTGTACTTCGACATGTACCTCCCGTGGCACTTGTTGGTGGTGAAGTTCA
TagFP635   >            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
TagFP635   >  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
                                                                                  |           |
     TACCAGCTTCATGTACGGCAGCAAAACCTTCATCAACCACACCCAGGGCATCCCCGACTTCTTTAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGA
801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
     ATGGTCGAAGTACATGCCGTCGTTTTGGAAGTAGTTGGTGTGGGTCCCGTAGGGGCTGAAGAAATTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCT
TagFP635   >  T  S  F  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

                        Bbs1            Bpm1
                          |                |
     GTCACCACATACGAAGACGGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACT
901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
     CAGTGGTGTATGCTTCTGCCCCCGCACGACTGGCGATGGGTCCTGTGGTCGGAGGTCCTGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCCACTTGA
TagFP635   > 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    Stu1                                    Bgl1
                                                   |       |                                       |
            TCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCTCCACCGAGATGCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAAGCGA
      1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
            AGGGTAGGTTGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCTCCGGAGGTGGCTCTACGACATGGGGCGACTGCCGCCGGACCTTCCGTCTTCGCT
TagFP635     >  P  S  N  G  P  V  M  Q  K  K  T  L  G  W  E  A  S  T  E  M  L  Y  P  A  D  G  G  L  E  G  R  S  D

                     BssS1          Eco57                    Bbs1          BpuE1
                        |              |                        |              |
            CATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACTTGAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGCGTC
      1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
            GTACCGGGACTTCGAGCACCCGCCCCCGGTGGACTAGACGTTGAACTTCTGGTGTATGTCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCGCAG
TagFP635     >  M  A  L  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

                          Bbs1
                     SpAcc  |                Bsa1       PshA1       BssS1 Dra3      Msc1  AlwN1
                        |  |                   |           |           |    |         |      |
            TACTATGTGGACAGAAGACTGGAAAGAATCAAGGAGGCCGACAAAGAGACCTACGTCGAGCAGCACGAGGTGGCTGTGGCCAGATACTGCGACCTCCCTA
      1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
            ATGATACACCTGTCTTCTGACCTTTCTTAGTTCCTCCGGCTGTTTCTCTGGATGCAGCTCGTCGTGCTCCACCGACACCGGTCTATGACGCTGGAGGGAT
TagFP635     > Y  Y  V  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

                                 BpuE1     Xho1    Hind3
          SpAcc          Bmr1    BspE1   | Bgl2   |   Sac1 |  Bcg1a                        Sac2 Bcg1b      Bgl1
            |             |        |   |    |   |      | |      |                           |     |         |
            GCAAACTGGGGCACAAACTTAATTCCGGACTCAGATCTCGAGCTCAAGCTTCGATGGCGACTGCGACCCCCGTGCCGCCGCGGATGGGCAGCCGCGCTGG
      1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
            CGTTTGACCCCGTGTTTGAATTAAGGCCTGAGTCTAGAGCTCGAGTTCGAAGCTACCGCTGACGCTGGGGGCACGGCGGCGCCTACCCGTCGGCGCGACC
TagFP635/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
LaminB1      >  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
LaminB1     > 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
LaminB1     >  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
LaminB1     >  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
LaminB1     > 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
LaminB1      >  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
LaminB1      >  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
LaminB1      > 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
LaminB1      >  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
LaminB1      >  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
LaminB1     > 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
LaminB1     >   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
LaminB1     >  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
LaminB1     > 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
LaminB1     >   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
LaminB1      >  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
LaminB1      > 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
LaminB1      >   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**	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
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													