pCase12-Mito 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).

Mitochondrial targeting sequence (MTS) are shown in bold blue, linker amino acids are shown in black, Case12 amino acids are shown in bold-green.

```
        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
                                                                                                        |
            ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCATGT
        501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
            TGTTGAGGCGGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGTACA
MTS       >                                                                                                 M  S

                                                   Bmr1        BssH2             PflM1 BamH1  Age1
                                                     |            |                 |     |     |
            CCGTCCTGACGCCGCTGCTGCTGCGGGGCTTGACAGGCTCGGCCCGGCGGCTCCCAGTGCCGCGCGCCAAGATCCATTCGTTGGGGGATCCACCGGTCGC
        601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
            GGCAGGACTGCGGCGACGACGACGCCCCGAACTGTCCGAGCCGGGCCGCCGAGGGTCACGGCGCGCGGTTCTAGGTAAGCAACCCCCTAGGTGGCCAGCG
MTS/linker  >  V  L  T  P  L  L  L  R  G  L  T  G  S  A  R  R  L  P  V  P  R  A  K  I  H  S  L  G  D  P  P  V  A

                                                                                 Xho1
                                                                              Sac1  |
                                                                            Ecl2 |  |
                     BmgB1                                                Blp1   | |  |
                       |                                                    |   | |  |
            CACCATGTCATCACGTCGTAAGTGGAATAAGACAGGTCACGCAGTCAGAGCTATAGGTCGGCTGAGCTCACTCGAGAACGTCTATATCATGGCCGACAAG
        701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
            GTGGTACAGTAGTGCAGCATTCACCTTATTCTGTCCAGTGCGTCAGTCTCGATATCCAGCCGACTCGAGTGAGCTCTTGCAGATATAGTACCGGCTGTTC
linker/Case12> T  M  S  S  R  R  K  W  N  K  T  G  H  A  V  R  A  I  G  R  L  S  S  L  E  N  V  Y  I  M  A  D  K

                                 Eci1                                                  Bsg1
                                   |                                                     |
            CAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACGTCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCG
        801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
            GTCTTCTTGCCGTAGTTCCGGTTGAAGTTCTAGGCGGTGTTGCAGCTCCTGCCGTCGCACGTCGAGCGGCTGGTGATGGTCGTCTTGTGGGGGTAGCCGC
Case12      > Q  K  N  G  I  K  A  N  F  K  I  R  H  N  V  E  D  G  S  V  Q  L  A  D  H  Y  Q  Q  N  T  P  I  G  D
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                                   Bpu10             Bpu10
                                     |                 |
            ACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTTCCAGTCCGTCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTT
       901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
            TGCCGGGGCACGACGACGGGCTGTTGGTGATGGACTCGAAGGTCAGGCAGGACTCGTTTCTGGGGTTGCTCTTCGCGCTAGTGTACCAGGACGACCTCAA
Case12      >  G  P  V  L  L  P  D  N  H  Y  L  S  F  Q  S  V  L  S  K  D  P  N  E  K  R  D  H  M  V  L  L  E  F

                                                                                                      BseR1
                      Bpm1                    BsrG1                                                    Ale1
                        |                       |                                                        |
            CGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAACGTGGATGGCGGTAGCGGTGGCACCGGCAGCAAGGGCGAGGAGCTGTTCACCGGG
      1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
            GCACTGGCGGCGGCCCTAGTGAGAGCCGTACCTGCTCGACATGTTGCACCTACCGCCATCGCCACCGTGGCCGTCGTTCCCGCTCCTCGACAAGTGGCCC
Case12      > V  T  A  A  G  I  T  L  G  M  D  E  L  Y  N  V  D  G  G  S  G  G  T  G  S  K  G  E  E  L  F  T  G

                                                                                                        Bsg1
                                                                                                 Bcg1b   |
                                                                 Bcg1a                        BtgZ1  |   |
                                                                   |                            |  |   |
            GTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCC
      1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
            CACCACGGGTAGGACCAGCTCGACCTGCCGCTGCATTTGCCGGTGTTCAAGTCGCACAGGCCGCTCCCGCTCCCGCTACGGTGGATGCCGTTCGACTGGG
Case12      > V  V  P  I  L  V  E  L  D  G  D  V  N  G  H  K  F  S  V  S  G  E  G  E  G  D  A  T  Y  G  K  L  T  L

                                                BssS1
                          Eco57                  Ale1                          Xmn1          Eco57
                            |                      |                             |             |
            TGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTCGGCTACGGCCTGAAGTGCTTCGCCCGCTACCCCGACCA
      1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
            ACTTCGACTAGACGTGGTGGCCGTTCGACGGGCACGGGACCGGGTGGGAGCACTGGTGGGAGCCGATGCCGGACTTCACGAAGCGGGCGATGGGGCTGGT
Case12      >  K  L  I  C  T  T  G  K  L  P  V  P  W  P  T  L  V  T  T  L  G  Y  G  L  K  C  F  A  R  Y  P  D  H

                      Eci1
                        |
            CATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCC
      1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
            GTACTTCGTCGTGCTGAAGAAGTTCAGGCGGTACGGGCTTCCGATGCAGGTCCTCGCGTGGTAGAAGAAGTTCCTGCTGCCGTTGATGTTCTGGGCGCGG
Case12      > M  K  Q  H  D  F  F  K  S  A  M  P  E  G  Y  V  Q  E  R  T  I  F  F  K  D  D  G  N  Y  K  T  R  A
```

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                                SpDon
            SpDon              Ale1 |                                Eco57
                |                  | |                                  |
          GAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGGCTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACA
     1401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
          CTCCACTTCAAGCTCCCGCTGTGGGACCACTTGGCGTAGCTCGACTTCCCGTAGCCGAAGTTCCTCCTGCCGTTGTAGGACCCCGTGTTCGACCTCATGT
Case12      > E  V  K  F  E  G  D  T  L  V  N  R  I  E  L  K  G  I  G  F  K  E  D  G  N  I  L  G  H  K  L  E  Y  N

                     Pvu2
                   Bpm1 |                EcoR1
         Mlu1 Bcl1    | |             T7Ter   |                                          BtgZ1
            |    |    | |                 |   |                                            |
          ACACGCGTGATCAGCTGACCGAAGAACAGATTGCTGAATTCAAGGAAGCCTTCTCCCTATTTGATAAAGATGGCGATGGCACCATCACAACAAAGGAACT
     1501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
          TGTGCGCACTAGTCGACTGGCTTCTTGTCTAACGACTTAAGTTCCTTCGGAAGAGGGATAAACTATTTCTACCGCTACCGTGGTAGTGTTGTTTCCTTGA
Case12      >   T  R  D  Q  L  T  E  E  Q  I  A  E  F  K  E  A  F  S  L  F  D  K  D  G  D  G  T  I  T  T  K  E  L

                BspH1                Bmr1       AlwN1            Bcl1
                    |                  |           |               |
          TGGAACTGTCATGAGGTCACTGGGTCAGAACCCAACAGAAGCTGAATTGCAGGATATGATCAATGAAGTGGATGCTGATGGTAATGGCACCATTGACTTC
     1601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
          ACCTTGACAGTACTCCAGTGACCCAGTCTTGGGTTGTCTTCGACTTAACGTCCTATACTAGTTACTTCACCTACGACTACCATTACCGTGGTAACTGAAG
Case12      >  G  T  V  M  R  S  L  G  Q  N  P  T  E  A  E  L  Q  D  M  I  N  E  V  D  A  D  G  N  G  T  I  D  F

                                                T7Ter
                          SpAcc                 SpDon                 Bsm1                          BsrD1
                              |                     |                    |                              |
          CCCGAATTTTTGACTATGATGGCTAGAAAAATGAAAGATACAGATAGTGAAGAAGAAATCCGTGAGGCATTCCGAGTCTTTGACAAGGATGGCAATGGTT
     1701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
          GGGCTTAAAAACTGATACTACCGATCTTTTTACTTTCTATGTCTATCACTTCTTCTTTAGGCACTCCGTAAGGCTCAGAAACTGTTCCTACCGTTACCAA
Case12      > P  E  F  L  T  M  M  A  R  K  M  K  D  T  D  S  E  E  E  I  R  E  A  F  R  V  F  D  K  D  G  N  G  Y

                                 BspH1
                                  Bsg1
                               BmgB1 |                           T7Ter            Bcl1            BsmB1
                                   | |                              |               |                |
          ATATCAGTGCAGCAGAACTACGTCACGTCATGACAAACTTAGGAGAAAAACTAACAGATGAAGAAGTAGATGAAATGATCAGAGAAGCAGATATTGATGG
     1801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
          TATAGTCACGTCGTCTTGATGCAGTGCAGTACTGTTTGAATCCTCTTTTTGATTGTCTACTTCTTCATCTACTTTACTAGTCTCTTCGTCTATAACTACC
Case12      >   I  S  A  A  E  L  R  H  V  M  T  N  L  G  E  K  L  T  D  E  E  V  D  E  M  I  R  E  A  D  I  D  G
```

```
                                                   Not1
                Drd1  SpAcc   EcoR1         T7Ter     polyA    Eag1      Xba1   BsaB1
                  |      |       |             |         |       |         |       |
           AGACGGACAAGTCAACTATGAAGAATTCGTACAGATGATGACTGCAAAATAAAGCGGCCGCGACTCTAGATCATAATCAGCCATACCACATTTGTAGAGG
      1901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
           TCTGCCTGTTCAGTTGATACTTCTTAAGCATGTCTACTACTGACGTTTTATTTCGCCGGCGCTGAGATCTAGTATTAGTCGGTATGGTGTAAACATCTCC
Case12       >  D  G  Q  V  N  Y  E  E  F  V  Q  M  M  T  A  K  *

                                                                  Bsm1
                 SpDon   Dra1                                    Mfe1|        Hpa1       polyA    Psi1
                     |      |                                       ||           |           |       |
           TTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGG
      2001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
           AAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACC

           polyA                        polyA            Bts1 Bsm1                                    Afl2
               |                            |               |    |                                        |
           TTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAGGC
      2101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
           AATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTCCG

             SpDon        Ssp1                                                                          Psi1
                 |           |                                                                            |
           GTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTAT
      2201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
           CATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATA

                                                                 BsaXb                  Drd1    BsaXa
                                                                    |                      |        |
           AAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAA
      2301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
           TTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTT

                                BtgZ1
                                Dra3|                                                                SpAcc
                                   ||                                                                    |
           CCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAG
      2401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
           GGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTC
```

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                                Nae1
                            NgoM4 |                                     BsrB1
                                | |                                       |
      CCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCG
2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
      GGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGC

      GTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTT
2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
      CAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAA

                                      BciV1
                                   BspH1  |
        polyA                     BsrB1 |  |                            Ssp1  Ear1        Bsu36
            |                         | |  |                               |     |            |
      GTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGA
2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
      CAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCT

                                                                                      Nsi1
                                                                                    Sph1 |
            Eci1                                                                   BfrB1 |
          Pvu2 |                                      BseY1                   BstAP  | |
             | |                                        |                        |  | |
      AAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAA
2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
      TTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTT

                                                        Nsi1
                                                      Sph1 |
                                                     BfrB1 |
 SexA1                      BseY1                   BstAP  | |                        Eci1
     |                          |                       |  | |                          |
      CCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCAT
2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
      GGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTA
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                Eci1                                                                  Sfi1
     Eci1     Bmr1|       Eci1            Nco1                    polyA              Bgl1
       |         ||          |               |                       |                  |
      CCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTA
3001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
      GGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGAT

                                Avr2
                               Stu1|                                                          BspM1
           SpDon             BseR1  ||              Cla1              BsaB1                   BfuA1
             |                  |  ||                 |                  |                       |
      TTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGA
3101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
      AAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCT

                 Eag1                                      Bmr1
                    |                                        |
      TTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGT
3201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
      AACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACA

            Nar1
           Kas1|                        Drd1                                                  Msc1
              ||                          |                                                     |
      CAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGAC
3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
      GTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTG

                 Pvu2
           Fsp1    |        PflF1                        Eco57
              |    |            |                           |
      GGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCAC
3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
      CCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTG
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                                                                                   BtgZ1
                                                                              BspM1  |
 SpDon                          BciV1         BsrD1                         BfuA1  |
     |                              |             |                                |  |
      CTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATC
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      GAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAG

                                                        Sap1
                                                        Ear1                          BpuE1
                                                           |                             |
      GCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAG
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      CGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTC

                 Sph1                        Nco1                BtgZ1
                    |                           |                   |
      GCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTC
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      CGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAG

                BseY1
               Nae1 |                                                  Sap1
            NgoM4 | |        Rsr2         Eci1                        Ear1                    Eco57
                | | |           |             |                          |                       |
      ATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCT
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      TAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGA

                           BtgZ1
    BssS1                 BsrB1 |                                                  BsrB1          BstB1
       |                     | |                                                     |              |
      TCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATG
3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
      AGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTAC
```

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                                BssS1                                                       Nae1
                                BspM1                                                   NgoM4 |
                                BfuA1                       SpAcc                        Bpm1 |
                                    |                         |                            | |
     ACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCT
4001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
     TGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGA

                                                   Bpm1
                                               SpAcc  |
                                                Avr2  |
                                                   |  |
     GGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCG
4101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
     CCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGC

            polyA        polyA
                |            |
     CGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACC
4201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
     GCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGG

  Bsa1
     |
     CCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCG
4301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
     GGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGC

            BstAP
            AlwN1      Bsu36                            Dra1                Dra1
                |          |                               |                   |
     GGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTT
4401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
     CCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAA
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          BspH1
             |
      TGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTT
4501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
      ACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAA

      BpuE1                                                                          Eco57
          |                                                                            |
      CTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTG
4601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
      GACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGAC


                                        SpAcc
                                           |
      GCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCT
4701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
      CGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGA

                     AlwN1                      BpuE1
                        |                          |
      GCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGC
4801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
      CGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCG

                ApaL1     BseY1                                          SpAcc
                    |         |                                             |
      TGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCG
4901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
      ACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGC


                              BciV1
                            Eci1   |                    BssS1                                    SpAcc
                               |   |                       |                                        |
      AAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCC
5001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
      TTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGG
```

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                          Drd1            BpuE1                SpAcc     Eci1
                            |                |                    |        |
      TGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGG
5101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
      ACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCC

                           SpDon                                                      Nsi1
                          BspLU|                                                    BfrB1 |
                               ||                                                       | |
      TTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
5201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*||||||| 5287
      AAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aat2	**Afl2**	**Age1**	Ale1	AlwN1	**ApaL1**	**Ase1**	Avr2	**BamH1**	**Bcg1a**	**Bcg1b**	BciV1	Bcl1	BfrB1
BfuA1	Bgl1	**Blp1**	BmgB1	Bmr1	Bpm1	Bpu10	BpuE1	**Bsa1**	BsaB1	**BsaXa**	**BsaXb**	BseR1	BseY1
Bsg1	Bsm1	**BsmB1**	BspH1	**BspLU**	BspM1	BsrB1	BsrD1	**BsrG1**	**BssH2**	BssS1	BstAP	**BstB1**	Bsu36
BtgZ1	**Bts1**	**Cla1**	Dra1	**Dra3**	Drd1	Eag1	Ear1	Eci1	**Ecl2**	Eco57	EcoR1	**Fsp1**	**Hpa1**
Kas1	**Mfe1**	**Mlu1**	**Msc1**	Nae1	**Nar1**	Nco1	**Nde1**	NgoM4	**Nhe1**	**Not1**	Nsi1	**PflF1**	**PflM1**
polyA	Psi1	Pvu2	**Rsr2**	**Sac1**	Sap1	**SexA1**	**Sfi1**	**SnaB1**	SpAcc	SpDon	Sph1	Ssp1	**Stu1**
T7Ter	**Xba1**	**Xho1**	**Xmn1**										

Unique:

Afl2	**Age1**	**ApaL1**	**Ase1**	**BamH1**	**Bcg1a**	**Bcg1b**	**Blp1**	**Bsa1**	**BsaXa**	**BsaXb**	**BsmB1**	**BspLU**	**BsrG1**
BssH2	**BstB1**	**Bts1**	**Cla1**	**Dra3**	**Ecl2**	**Fsp1**	**Hpa1**	**Kas1**	**Mfe1**	**Mlu1**	**Msc1**	**Nar1**	**Nde1**
Nhe1	**Not1**	**PflF1**	**PflM1**	**Rsr2**	**Sac1**	**SexA1**	**Sfi1**	**SnaB1**	**Stu1**	**Xba1**	**Xho1**	**Xmn1**	

Not found:

Aar1	Acc65	Acl1	Afe1	Ahd1	Apa1	Asc1	AsiS1	Bae1a	Bae1b	Bbs1	BbvC1	Bgl2	BsiW1
BspE1	BstE2	BstX1	BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	EcoK	EcoN1	EcoRV	FCatB	FCatL
FCatR	FCatP	ScFRT	Fse1	FspA1	Hind3	I_Ceu	Kpn1	loxP	Nru1	Pac1	Pme1	Pml1	PshA1
PspOM	Pst1	Pvu1	R4atB	R4atL	R4atP	R4atR	Sac2	Sal1	SanD1	Sbf1	Sca1	Sgf1	SgrA1
Sma1	Spe1	Srf1	Swa1	T3RNA	T7RNA	PISce	Xcm1						

Excluded by site complexity:

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