Gateway® Case12-cyto entry clone 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). MCS sequence is shown in frame, the attL sites are underlined. Shaded regions correspond to DNA sequences transferred from the entry clone into the destination vector following recombination. Non-Case12 amino acids coded by those DNA sequences are shown in black, Case12 amino acids are shown in green.

```
                                   polyA                                          BsrD1  Psi1        BsrG1
                                     |                                              |      |            |
            TAGTTATTAGCCCCAAATAATGATTTTATTTTGACTGATAGTGACCTGTTCGTTGCAACAAATTGATAAGCAATGCTTTTTTATAATGCCAACTTTGTAC
        1   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 100
            ATCAATAATCGGGGTTTATTACTAAAATAAAACTGACTATCACTGGACAAGCAACGTTGTTTAACTATTCGTTACGAAAAAATATTACGGTTGAAACATG
attL1 site   >                                                                                                V  Q

                                                                                                  BamH1
                                                                                                 Sma1 |
                                                                                                Apa1| |
                                                                                            PspOM   || |
                                                                  Hind3                     Sac2|   || |
                                                        Xho1   Sac1 |  EcoR1      Sal1      Kpn1  ||   || |
                        Nhe1 Afe1   BpuE1 Bgl2    | Ecl2 | |BstB1 |     Pst1| Acc65   |  ||   || |  Age1
                                |    |        |    |    |    | | |    | |         ||      |   |  ||   || |      |
            AAAAAAGCAGGCTGCTAGCGCTACCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCTGCAGTCGACGGTACCGCGGGCCCGGGATCCACCGGTCGCCAC
      101   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 200
            TTTTTTCGTCCGACGATCGCGATGGCCTGAGTCTAGAGCTCGAGTTCGAAGCTTAAGACGTCAGCTGCCATGGCGCCCGGGCCCTAGGTGGCCAGCGGTG
MCS          >  K  S  R  L  L  A  L  P  D  S  D  L  E  L  K  L  R  I  L  Q  S  T  V  P  R  A  R  D  P  P  V  A  T
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                                                                  Xho1
                                                               Sac1  |
                                                            Ecl2 |   |
                 BmgB1                                   Blp1   | |   |
                    |                                       |   | |   |
     CATGTCATCACGTCGTAAGTGGAATAAGACAGGTCACGCAGTCAGAGCTATAGGTCGGCTGAGCTCACTCGAGAACGTCTATATCATGGCCGACAAGCAG
201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 300
     GTACAGTAGTGCAGCATTCACCTTATTCTGTCCAGTGCGTCAGTCTCGATATCCAGCCGACTCGAGTGAGCTCTTGCAGATATAGTACCGGCTGTTCGTC
Case12   >  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  Q

                       Eci1                                                   Bsg1
                          |                                                      |
     AAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACGTCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACG
301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 400
     TTCTTGCCGTAGTTCCGGTTGAAGTTCTAGGCGGTGTTGCAGCTCCTGCCGTCGCACGTCGAGCGGCTGGTGATGGTCGTCTTGTGGGGGTAGCCGCTGC
Case12   > 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  G

                                  Bpu10            Bpu10
                                     |                |
     GCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTTCCAGTCCGTCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGT
401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 500
     CGGGGCACGACGACGGGCTGTTGGTGATGGACTCGAAGGTCAGGCAGGACTCGTTTCTGGGGTTGCTCTTCGCGCTAGTGTACCAGGACGACCTCAAGCA
Case12   >   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  V

                                                                                                  BseR1
                 Bpm1                     BsrG1                                                   Ale1
                    |                        |                                                       |
     GACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAACGTGGATGGCGGTAGCGGTGGCACCGGCAGCAAGGGCGAGGAGCTGTTCACCGGGGTG
501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
     CTGGCGGCGGCCCTAGTGAGAGCCGTACCTGCTCGACATGTTGCACCTACCGCCATCGCCACCGTGGCCGTCGTTCCCGCTCCTCGACAAGTGGCCCCAC
Case12   >  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  V

                                                                                                 Bsg1
                                                                                            Bcg1b   |
                                                                   Bcg1a                 BtgZ1  |    |
                                                                     |                      |  |    |
     GTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGA
601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
     CACGGGTAGGACCAGCTCGACCTGCCGCTGCATTTGCCGGTGTTCAAGTCGCACAGGCCGCTCCCGCTCCCGCTACGGTGGATGCCGTTCGACTGGGACT
Case12   > 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  K
```

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                                                BssS1
                     Eco57                       Ale1                          Xmn1          Eco57
                        |                          |                              |             |
        AGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTCGGCTACGGCCTGAAGTGCTTCGCCCGCTACCCCGACCACAT
    701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
        TCGACTAGACGTGGTGGCCGTTCGACGGGCACGGGACCGGGTGGGAGCACTGGTGGGAGCCGATGCCGGACTTCACGAAGCGGGCGATGGGGCTGGTGTA
Case12    >  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  M

                 Eci1
                   |
        GAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAG
    801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
        CTTCGTCGTGCTGAAGAAGTTCAGGCGGTACGGGCTTCCGATGCAGGTCCTCGCGTGGTAGAAGAAGTTCCTGCTGCCGTTGATGTTCTGGGCGCGGCTC
Case12    >  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  E

                          SpDon
SpDon                    Ale1 |                                Eco57
   |                        | |                                   |
        GTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGGCTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACA
    901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
        CACTTCAAGCTCCCGCTGTGGGACCACTTGGCGTAGCTCGACTTCCCGTAGCCGAAGTTCCTCCTGCCGTTGTAGGACCCCGTGTTCGACCTCATGTTGT
Case12    > 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  T

                 Pvu2
              Bpm1 |                EcoR1
Mlu1 Bcl1     | |             T7Ter   |                                          BtgZ1
   |    |     | |                |    |                                             |
        CGCGTGATCAGCTGACCGAAGAACAGATTGCTGAATTCAAGGAAGCCTTCTCCCTATTTGATAAAGATGGCGATGGCACCATCACAACAAAGGAACTTGG
   1001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
        GCGCACTAGTCGACTGGCTTCTTGTCTAACGACTTAAGTTCCTTCGGAAGAGGGATAAACTATTTCTACCGCTACCGTGGTAGTGTTGTTTCCTTGAACC
Case12    >  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  G

         BspH1                Bmr1       AlwN1            Bcl1
            |                   |           |                |
        AACTGTCATGAGGTCACTGGGTCAGAACCCAACAGAAGCTGAATTGCAGGATATGATCAATGAAGTGGATGCTGATGGTAATGGCACCATTGACTTCCCC
   1101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
        TTGACAGTACTCCAGTGACCCAGTCTTGGGTTGTCTTCGACTTAACGTCCTATACTAGTTACTTCACCTACGACTACCATTACCGTGGTAACTGAAGGGG
Case12    >  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  P
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                                                T7Ter
                          SpAcc                 SpDon                 Bsm1                          BsrD1
                            |                     |                     |                             |
            GAATTTTTGACTATGATGGCTAGAAAAATGAAAGATACAGATAGTGAAGAAGAAATCCGTGAGGCATTCCGAGTCTTTGACAAGGATGGCAATGGTTATA
      1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
            CTTAAAAACTGATACTACCGATCTTTTTACTTTCTATGTCTATCACTTCTTCTTTAGGCACTCCGTAAGGCTCAGAAACTGTTCCTACCGTTACCAATAT
Case12      > 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  I

                                BspH1
                                 Bsg1
                              BmgB1 |                          T7Ter            Bcl1             BsmB1
                                  | |                            |                |                |
            TCAGTGCAGCAGAACTACGTCACGTCATGACAAACTTAGGAGAAAAACTAACAGATGAAGAAGTAGATGAAATGATCAGAGAAGCAGATATTGATGGAGA
      1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
            AGTCACGTCGTCTTGATGCAGTGCAGTACTGTTTGAATCCTCTTTTTGATTGTCTACTTCTTCATCTACTTTACTAGTCTCTTCGTCTATAACTACCTCT
Case12      >   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  D

                                                                Not1
             Drd1  SpAcc   EcoR1         T7Ter     polyA     Eag1            BseY1      BsrG1             Psi1
               |     |       |             |         |         |               |          |                |
            CGGACAAGTCAACTATGAAGAATTCGTACAGATGATGACTGCAAAATAAAGCGGCCGCGACTCTAGGACCCAGCTTTCTTGTACAAAGTTGGCATTATAA
      1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
            GCCTGTTCAGTTGATACTTCTTAAGCATGTCTACTACTGACGTTTTATTTCGCCGGCGCTGAGATCCTGGGTCGAAAGAACATGTTTCAACCGTAATATT
Case12/attL2 >  G  Q  V  N  Y  E  E  F  V  Q  M  M  T  A  K  *

            BsrD1                                     polyA                   BsaB1
                |                                       |                        |
            GAAAGCATTGCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGCTAGATCATAATCAGCCATACCACATTTGTAGA
      1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
            CTTTCGTAACGAATAGTTAAACAACGTTGCTTGTCCAGTGATAGTCAGTTTTATTTTAGTAATAAACGATCTAGTATTAGTCGGTATGGTGTAAACATCT
attL2 site

                                                                    Bsm1
                 SpDon   Dra1                                      Mfe1|        Hpa1       polyA    Psi1
                    |       |                                        ||           |           |        |
            GGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAAT
      1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
            CCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTA
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        polyA                        polyA            Bts1 Bsm1                                Afl2
          |                            |                |    |                                     |
      GGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAG
1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
      CCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTC

          SpDon        Ssp1
            |            |
      GCGTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTT
1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
      CGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAA

   Psi1                                                      BsaXb                  Drd1    BsaXa
      |                                                        |                       |        |
      ATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAA
1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
      TATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTT

                                BtgZ1
                                Dra3|                                                          SpAcc
                                   ||                                                             |
      AACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGG
2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
      TTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCC

                                   Nae1
                                NgoM4 |                                      BsrB1
                                    | |                                        |
      AGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAG
2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
      TCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATC

      CGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTAT
2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
      GCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATA
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                                        BciV1
                                      BspH1  |
          polyA                      BsrB1 |  |                            Ssp1  Ear1        Bsu36
            |                           | |  |                               |     |            |
      TTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCG
2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
      AACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGC

                                                                                                Nsi1
                                                                                              Sph1 |
              Eci1                                                                           BfrB1 |
            Pvu2 |                                      BseY1                            BstAP  | |
                 | |                                      |                                |   | |
      GAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGC
2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
      CTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCG

                                                          Nsi1
                                                        Sph1 |
                                                       BfrB1 |
   SexA1                      BseY1                   BstAP  | |                        Eci1
     |                          |                        |   | |                          |
      AACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCC
2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
      TTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGG

                Eci1                                                                          Sfi1
       Eci1     Bmr1|       Eci1            Nco1                    polyA                    Bgl1
         |        ||          |               |                       |                       |
      ATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGC
2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
      TAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCG

                                    Avr2
                                   Stu1|
            SpDon                BseR1  ||                Cla1                BsaB1
              |                    |  ||                  |                    |
      TATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATG
2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
      ATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTAC
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 BspM1
 BfuA1                Eag1                                        Bmr1
     |                  |                                           |
      GATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCT
 2801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
      CTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGA

              Nar1
             Kas1|                        Drd1                                                    Msc1
                 ||                          |                                                       |
      GTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACG
 2901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
      CAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGC

                     Pvu2
                Fsp1   |       PflF1                        Eco57
                    |   |           |                          |
      ACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTC
 3001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
      TGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAG

                                                                                   BtgZ1
                                                                              BspM1  |
   SpDon                          BciV1         BsrD1                        BfuA1  |
       |                              |             |                              |  |
      ACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACA
 3101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
      TGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGT

                                                          Sap1
                                                          Ear1                           BpuE1
                                                             |                              |
      TCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCC
 3201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
      AGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGG
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                 Sph1                        Nco1                BtgZ1
                    |                           |                   |
      AGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGAT
3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
      TCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTA

              BseY1
             Nae1 |                                                Sap1
          NgoM4 | |        Rsr2         Eci1                      Ear1                    Eco57
              | | |           |            |                         |                       |
      TCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCG
3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
      AGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGC

                         BtgZ1
      BssS1            BsrB1 |                                                BsrB1          BstB1
          |                | |                                                  |              |
      CTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAA
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      GAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTT

                              BssS1                                                                Nae1
                              BspM1                                                             NgoM4 |
                              BfuA1                        SpAcc                                 Bpm1 |
                                  |                          |                                     | |
      TGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGG
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      ACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCC

                                                   Bpm1
                                               SpAcc  |
                                                Avr2  |
                                                   |  |
      CTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACC
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      GACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGG
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                polyA        polyA
                   |            |
      CGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATA
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      GCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTAT

    Bsa1
      |
      CCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGT
3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
      GGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCA


                BstAP
                AlwN1      Bsu36                            Dra1               Dra1
                   |          |                               |                  |
      CGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTT
4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
      GCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAA


            BspH1
                |
      TTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTT
4101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
      AAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAA


        BpuE1                                                                          Eco57
           |                                                                              |
      TTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAC
4201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
      AAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTG


                                            SpAcc
                                              |
      TGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCT
4301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
      ACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGA
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                 AlwN1                    BpuE1
                    |                        |
     CTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGG
4401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
     GACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCC

                ApaL1     BseY1                                          SpAcc
                    |         |                                              |
     GCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCC
4501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
     CGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGG

                              BciV1
                            Eci1   |                    BssS1                                  SpAcc
                               |   |                       |                                      |
     CGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGT
4601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
     GCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCA

                            Drd1            BpuE1               SpAcc     Eci1
                               |               |                   |        |
     CCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTAC
4701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
     GGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATG

                              SpDon                                                   Nsi1
                             BspLU|                                                BfrB1 |
                                  ||                                                    | |
     GGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
4801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||  4889
     CCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Acc65	**Afe1**	**Afl2**	**Age1**	Ale1	AlwN1	**Apa1**	**ApaL1**	Avr2	**BamH1**	**Bcg1a**	**Bcg1b**	BciV1	Bcl1
BfrB1	BfuA1	**Bgl1**	**Bgl2**	**Blp1**	BmgB1	Bmr1	Bpm1	Bpu10	BpuE1	**Bsa1**	BsaB1	**BsaXa**	**BsaXb**
BseR1	BseY1	Bsg1	Bsm1	**BsmB1**	BspH1	**BspLU**	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1
Bsu36	BtgZ1	**Bts1**	**Cla1**	Dra1	**Dra3**	Drd1	Eag1	Ear1	Eci1	Ecl2	Eco57	EcoR1	**Fsp1**
Hind3	**Hpa1**	**Kas1**	**Kpn1**	**Mfe1**	**Mlu1**	**Msc1**	Nae1	**Nar1**	Nco1	NgoM4	**Nhe1**	**Not1**	Nsi1
PflF1	polyA	Psi1	**PspOM**	**Pst1**	Pvu2	**Rsr2**	Sac1	**Sac2**	**Sal1**	Sap1	**SexA1**	**Sfi1**	**Sma1**
SpAcc	SpDon	Sph1	Ssp1	**Stu1**	T7Ter	Xho1	**Xmn1**						

Unique:

Acc65	**Afe1**	**Afl2**	**Age1**	**Apa1**	**ApaL1**	**BamH1**	**Bcg1a**	**Bcg1b**	**Bgl1**	**Bgl2**	**Blp1**	**Bsa1**	**BsaXa**
BsaXb	**BsmB1**	**BspLU**	**Bts1**	**Cla1**	**Dra3**	**Fsp1**	**Hind3**	**Hpa1**	**Kas1**	**Kpn1**	**Mfe1**	**Mlu1**	**Msc1**
Nar1	**Nhe1**	**Not1**	**PflF1**	**PspOM**	**Pst1**	**Rsr2**	**Sac2**	**Sal1**	**SexA1**	**Sfi1**	**Sma1**	**Stu1**	**Xmn1**

Not found:

Aar1	Aat2	Acl1	Ahd1	Asc1	Ase1	AsiS1	Bae1a	Bae1b	Bbs1	BbvC1	BsiW1	BspE1	BssH2
BstE2	BstX1	BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	EcoK	EcoN1	EcoRV	FCatB	FCatL	FCatR
FCatP	ScFRT	Fse1	FspA1	I_Ceu	loxP	Nde1	Nru1	Pac1	PflM1	Pme1	Pml1	PshA1	Pvu1
R4atB	R4atL	R4atP	R4atR	SanD1	Sbf1	Sca1	Sgf1	SgrA1	SnaB1	Spe1	Srf1	Swa1	T3RNA
T7RNA	PISce	Xba1	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													