Gateway® HyPer-AS 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). The attL sites are underlined. Shaded region corresponds to DNA sequence transferred from the entry clone into the destination vector following recombination. Non-HyPer amino acids are shown in black, HyPer amino acids are shown in green.

```
                                        polyA                                          BsrD1  Psi1        BsrG1
                                            |                                              |     |            |
               TAGTTATTAGCCCCAAATAATGATTTTATTTTGACTGATAGTGACCTGTTCGTTGCAACAAATTGATAAGCAATGCTTTTTTATAATGCCAACTTTGTAC
            1  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 100
               ATCAATAATCGGGGTTTATTACTAAAATAAAACTGACTATCACTGGACAAGCAACGTTGTTTAACTATTCGTTACGAAAAAATATTACGGTTGAAACATG
attL1 site   >                                                                                                    Q
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```
                                                   BstX1
                                  Age1           Xcm1  |
                         Nhe1 Afe1   |       Nco1   |  |                   PflF1     BsrD1
                            |    |   |          |   |  |                       |         |
               AAAAAAGCAGGCTGCTAGCGCTACCGGTCGCCACCATGGAAATGGCTTCTCAACAGGGTGAGACTATGTCAGGACCATTGCATATCGGTCTAATCCCAAC
          101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 200
               TTTTTCGTCCGACGATCGCGATGGCCAGCGGTGGTACCTTTACCGAAGAGTTGTCCCACTCTGATACAGTCCTGGTAACGTATAGCCAGATTAGGGTTG
attL1/HyPer  >   K  S  R  L  L  A  L  P  V  A  T  M  E  M  A  S  Q  Q  G  E  T  M  S  G  P  L  H  I  G  L  I  P  T
```

```
                                                                                    EcoN1
            PflM1          SpDon   SpDon                                            BssS1                  Bmr1
                |              |       |                                                |                      |
               AGTTGGACCTTACTTACTTCCTCACATTATCCCAATGCTACACCAAACTTTCCCTAAACTTGAAATGTACCTTCACGAGGCACAGACTCATCAACTATTG
          201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 300
               TCAACCTGGAATGAATGAAGGAGTGTAATAGGGTTACGATGTGGTTTGAAAGGGATTTGAACTTTACATGGAAGTGCTCCGTGTCTGAGTAGTTGATAAC
HyPer        >  V  G  P  Y  L  L  P  H  I  I  P  M  L  H  Q  T  F  P  K  L  E  M  Y  L  H  E  A  Q  T  H  Q  L  L
```

```
                     Xcm1 SpDon                                         Bsm1
                        |     |                                            |
               GCCCAGTTAGATAGTGGTAAACTTGATTGTGTCATACTAGCTTTGGTAAAGGAATCCGAGGCATTCATAGAAGTGCCTCTTTTCGATGAACCTATGCTTT
          301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 400
               CGGGTCAATCTATCACCATTTGAACTAACACAGTATGATCGAAACCATTTCCTTAGGCTCCGTAAGTATCTTCACGGAGAAAAGCTACTTGGATACGAAA
HyPer        > A  Q  L  D  S  G  K  L  D  C  V  I  L  A  L  V  K  E  S  E  A  F  I  E  V  P  L  F  D  E  P  M  L  L

                                                     Bsm1
                 SpAcc          Nco1               Xmn1 |                                              Bts1
                     |             |                  | |                                                 |
               TAGCAATCTATGAAGATCACCCATGGGCCAATAGAGAATGCGTTCCAATGGCAGATTTGGCCGGTGAGAAACTTCTAATGCTTGAGGATGGACACTGCTT
          401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 500
               ATCGTTAGATACTTCTAGTGGGTACCCGGTTATCTCTTACGCAAGGTTACCGTCTAAACCGGCCACTCTTTGAAGATTACGAACTCCTACCTGTGACGAA
HyPer        >   A  I  Y  E  D  H  P  W  A  N  R  E  C  V  P  M  A  D  L  A  G  E  K  L  L  M  L  E  D  G  H  C  L

            BpuE1 Eci1       BpuE1
                |    |           |
               GAGGGATCAAGCTATGTCCGCCGGTTACAATTCAGATAACGTCTATATCATGGCCGACAAACAGAAGAATGGTATAAAGGCCAACTTCAAAATTAGACAT
          501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
               CTCCCTAGTTCGATACAGGCGGCCAATGTTAAGTCTATTGCAGATATAGTACCGGCTGTTTGTCTTCTTACCATATTTCCGGTTGAAGTTTTAATCTGTA
HyPer        >  R  D  Q  A  M  S  A  G  Y  N  S  D  N  V  Y  I  M  A  D  K  Q  K  N  G  I  K  A  N  F  K  I  R  H

                                                                                      SpDon
                                                                                          |
               AACGTGGAAGATGGTTCCGTACAACTAGCAGACCATTATCAACAGAACACCCCAATCGGTGACGGACCTGTTTTACTTCCAGATAACCACTACCTATCTT
          601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
               TTGCACCTTCTACCAAGGCATGTTGATCGTCTGGTAATAGTTGTCTTGTGGGGTTAGCCACTGCCTGGACAAAATGAAGGTCTATTGGTGATGGATAGAA
HyPer        > N  V  E  D  G  S  V  Q  L  A  D  H  Y  Q  Q  N  T  P  I  G  D  G  P  V  L  L  P  D  N  H  Y  L  S  F

               SpAcc                                      Dra3                       BpuE1
                   |                                         |                           |
               TTCAGTCTGTCCTATCCAAAGACCCAAATGAGAAAAGGGATCACATGGTGTTGCTTGAGTTCGTAACCGCTGCCGGTATTACTCTTGGTATGGATGAGCT
          701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
               AAGTCAGACAGGATAGGTTTCTGGGTTTACTCTTTTCCCTAGTGTACCACAACGAACTCAAGCATTGGCGACGGCCATAATGAGAACCATACCTACTCGA
HyPer        >   Q  S  V  L  S  K  D  P  N  E  K  R  D  H  M  V  L  L  E  F  V  T  A  A  G  I  T  L  G  M  D  E  L
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                                                     Ear1                             Ssp1                 BmgB1
                                                        |                                |                     |
                  ATACAATGTAGACGGAGGTAGTGGAGGTACAGGTTCCAAGGGAGAAGAGTTGTTCACAGGAGTTGTCCCAATATTAGTAGAACTTGATGGTGACGTGAAC
             801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
                  TATGTTACATCTGCCTCCATCACCTCCATGTCCAAGGTTCCCTCTTCTCAACAAGTGTCCTCAACAGGGTTATAATCATCTTGAACTACCACTGCACTTG
HyPer           >  Y  N  V  D  G  G  S  G  G  T  G  S  K  G  E  E  L  F  T  G  V  V  P  I  L  V  E  L  D  G  D  V  N

                                                                                 T7Ter
                                BspE1    SpDon           SpAcc                   Ase1|BsrG1                    Nco1
                                    |        |               |                      ||    |                       |
                  GGTCACAAATTTTCAGTCTCCGGAGAAGGTGAGGGTGACGCAACCTACGGAAAACTAACATTGAAATTAATCTGTACAACTGGAAAACTTCCTGTCCCAT
             901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
                  CCAGTGTTTAAAAGTCAGAGGCCTCTTCCACTCCCACTGCGTTGGATGCCTTTTGATTGTAACTTTAATTAGACATGTTGACCTTTTGAAGGACAGGGTA
HyPer           > G  H  K  F  S  V  S  G  E  G  E  G  D  A  T  Y  G  K  L  T  L  K  L  I  C  T  T  G  K  L  P  V  P  W

                Msc1             Bsu36          Dra1            EcoRV      Nde1                               Bsu36
                   |                 |             |                |         |                                   |
                  GGCCAACATTAGTAACAACCTTAGGTTACGGTTTAAAGTGCTTCGCAAGATATCCTGACCATATGAAGCAACATGACTTCTTCAAGAGTGCTATGCCTGA
            1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
                  CCGGTTGTAATCATTGTTGGAATCCAATGCCAAATTTCACGAAGCGTTCTATAGGACTGGTATACTTCGTTGTACTGAAGAAGTTCTCACGATACGGACT
HyPer           >   P  T  L  V  T  T  L  G  Y  G  L  K  C  F  A  R  Y  P  D  H  M  K  Q  H  D  F  F  K  S  A  M  P  E

                                                              Psi1           SpDon   Bae1b
                                                                 |               |       |
                  GGGATATGTGCAAGAGAGGACTATATTCTTCAAAGACGACGGTAATTATAAAACTAGGGCAGAAGTGAAGTTTGAGGGAGATACTTTGGTGAATAGAATA
            1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
                  CCCTATACACGTTCTCTCCTGATATAAGAAGTTTCTGCTGCCATTAATATTTTGATCCCGTCTTCACTTCAAACTCCCTCTATGAAACCACTTATCTTAT
HyPer           >  G  Y  V  Q  E  R  T  I  F  F  K  D  D  G  N  Y  K  T  R  A  E  V  K  F  E  G  D  T  L  V  N  R  I

                                                                                                          Eco57
                  Bae1a                           Ssp1                             Bcg1a     BstB1        BciV1
                      |                              |                                 |         |            |
                  GAGCTTAAAGGTATCGGATTCAAAGAGGACGGAAATATTCTTGGACACAAGCTAGAGTACAACGGAACCGGATTTTGCTTCGAAGCCGGTGCTGACGAGG
            1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
                  CTCGAATTTCCATAGCCTAAGTTTCTCCTGCCTTTATAAGAACCTGTGTTCGATCTCATGTTGCCTTGGCCTAAAACGAAGCTTCGGCCACGACTGCTCC
HyPer           > E  L  K  G  I  G  F  K  E  D  G  N  I  L  G  H  K  L  E  Y  N  G  T  G  F  C  F  E  A  G  A  D  E  D
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                  SpDon
              Bcg1b   |                                        BpuE1                                       Ear1
                  |   |                                            |                                          |
               ATACTCACTTCAGGGCTACATCACTAGAAACCTTGAGGAACATGGTAGCCGCAGGAAGTGGAATAACTTTGTTACCAGCACTTGCCGTGCCACCAGAGAG
         1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
               TATGAGTGAAGTCCCGATGTAGTGATCTTTGGAACTCCTTGTACCATCGGCGTCCTTCACCTTATTGAAACAATGGTCGTGAACGGCACGGTGGTCTCTC
HyPer        >   T  H  F  R  A  T  S  L  E  T  L  R  N  M  V  A  A  G  S  G  I  T  L  L  P  A  L  A  V  P  P  E  R

                                           Nsi1
                                        BfrB1 |                        BstX1                 SpDon
                                            | |                            |                     |
               GAAGAGGGATGGTGTAGTTTATCTTCCATGCATTAAACCAGAGCCAAGAAGGACCATTGGATTGGTCTACAGGCCAGGTTCACCATTGAGATCAAGGTAT
         1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
               CTTCTCCCTACCACATCAAATAGAAGGTACGTAATTTGGTCTCGGTTCTTCCTGGTAACCTAACCAGATGTCCGGTCCAAGTGGTAACTCTAGTTCCATA
HyPer        >  K  R  D  G  V  V  Y  L  P  C  I  K  P  E  P  R  R  T  I  G  L  V  Y  R  P  G  S  P  L  R  S  R  Y

                                                                                   BamH1
                          SpAcc                                                   Bts1 |                     BseY1
                              |                                                      | |                         |
               GAACAGTTAGCAGAGGCTATAAGAGCCAGGATGGATGGTCACTTTGATAAGGTTTTGAAGCAAGCAGTGTGAGGATCCACCGGATCTAGGTAACTGAACC
         1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
               CTTGTCAATCGTCTCCGATATTCTCGGTCCTACCTACCAGTGAAACTATTCCAAAACTTCGTTCGTCACACTCCTAGGTGGCCTAGATCCATTGACTTGG
HyPer        > E  Q  L  A  E  A  I  R  A  R  M  D  G  H  F  D  K  V  L  K  Q  A  V  *

                    BsrG1             Psi1   BsrD1                                        polyA
                        |                |       |                                            |
               CAGCTTTCTTGTACAAAGTTGGCATTATAAGAAAGCATTGCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGCTA
         1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
               GTCGAAAGAACATGTTTCAACCGTAATATTCTTTCGTAACGAATAGTTAAACAACGTTGCTTGTCCAGTGATAGTCAGTTTTATTTTAGTAATAAACGAT
attL2 site

                  Bcl1BsaB1                            SpDon   Dra1
                     |    |                                |      |
               GATAACTGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGC
         1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
               CTATTGACTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACG
```

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   Bsm1
  Mfe1|        Hpa1       polyA    Psi1      polyA                        polyA            Bts1 Bsm1
     ||           |           |       |          |                            |               |    |
      AATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCT
1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
      TTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGACGTAAGA

                                      Mlu1     SpDon        Ssp1
                                         |         |           |
      AGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAACGCGTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCA
1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
      TCAACACCAAACAGGTTTGAGTAGTTACATAGAATTGCGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGT

                                        Psi1
                                           |
      TTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCAC
2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
      AAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTG

                                                                    BtgZ1
 BsaXb                 Drd1    BsaXa                                Dra3|
     |                    |        |                                   ||
      TATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTGGGGTC
2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
      ATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAACCCCAG

                                                                       Nae1
                              SpAcc                                 NgoM4 |
                                  |                                     | |
      GAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAA
2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
      CTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTT

           BsrB1
               |
      GCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAG
2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
      CGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGTC
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                                                                                BciV1
                                                                             BspH1  |
                                               polyA                       BsrB1 |  |
                                                   |                           | |  |
      GTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAAT
2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
      CACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTA

                                                    Eci1
             Ssp1  Ear1        Bsu36              Pvu2 |                                      BseY1
                |     |            |                 | |                                          |
      GCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAG
2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
      CGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTCGTC

                        Nsi1                                                                    Nsi1
                      Sph1 |                                                                  Sph1 |
                     BfrB1 |                                                                 BfrB1 |
                  BstAP  | |            SexA1                 BseY1                       BstAP  | |
                      |  | |                |                         |                       |  | |
      GCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAA
2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
      CGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTT

                                                      Eci1
                       Eci1                 Eci1     Bmr1|       Eci1            Nco1
                          |                    |        ||          |               |
      TTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTT
2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
      AATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAAA

                                                                          Avr2
                           Sfi1                                          Stu1|
    polyA                  Bgl1                    SpDon             BseR1  ||              Cla1
        |                     |                        |                 |  ||                 |
      ATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAG
2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
      TAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTC
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                                      BspM1
          BsaB1                       BfuA1               Eag1                                       Bmr1
              |                           |                  |                                          |
      ACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAAC
2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
      TGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTG

                                                    Nar1
                                                   Kas1|                       Drd1
                                                      ||                          |
      AGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACT
3001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
      TCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGA

                                                          Pvu2
                                  Msc1                Fsp1   |       PflF1                       Eco57
                                     |                   |   |           |                           |
      GCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTA
3101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
      CGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGAT

                                        SpDon                         BciV1         BsrD1
                                            |                             |             |
      TTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTG
3201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
      AACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAAC

                      BtgZ1
                   BspM1  |                                                                     Sap1
                   BfuA1  |                                                                     Ear1
                       |  |                                                                        |
      ATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGA
3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
      TAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCT

                           BpuE1                         Sph1                       Nco1
                               |                            |                          |
      AGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTG
3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
      TCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAAC
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                                                       BseY1
                                                      Nae1 |
   BtgZ1                                           NgoM4 | |        Rsr2         Eci1
       |                                               | | |           |            |
      CCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTG
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      GGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCAC

      Sap1                                                        BtgZ1
      Ear1                   Eco57         BssS1                BsrB1 |
         |                       |             |                    | |
      ATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCT
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      TATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGA

                                                                     BssS1
                                                                     BspM1
                  BsrB1          BstB1                               BfuA1                      SpAcc
                      |              |                                   |                          |
      TGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATG
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      ACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATAC

                                     Nae1                                                   Bpm1
                                  NgoM4 |                                               SpAcc  |
                                   Bpm1 |                                                Avr2  |
                                      | |                                                   |  |
      AAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCT
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      TTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGA

                                                    polyA        polyA
                                                        |            |
      AACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAA
3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
      TTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAAACAAGTATTT
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                                         Bsa1
                                            |
      CGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCC
4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
      GCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGG

                                                    BstAP
                                                    AlwN1      Bsu36                            Dra1
                                                        |          |                               |
      CAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACT
4101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
      GTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGA

               Dra1                              BspH1
                  |                                  |
      TCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCC
4201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
      AGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGG

                                             BpuE1
                                                 |
      GTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGC
4301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
      CATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACG

                           Eco57                                               SpAcc
                               |                                                   |
      CGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCA
4401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
      GCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGT

                                                            AlwN1                     BpuE1
                                                                |                         |
      CTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGAC
4501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
      GAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTG
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                                                       ApaL1     BseY1
                                                           |         |
      TCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGAT
4601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
      AGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTA

                                                                       BciV1
               SpAcc                                               Eci1   |                    BssS1
                   |                                                   |   |                        |
      ACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAG
4701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
      TGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTC

                                     SpAcc                          Drd1            BpuE1
                                         |                             |                |
      GGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGG
4801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
      CCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCCGCC

                                                                      SpDon
    SpAcc     Eci1                                                   BspLU|
        |        |                                                       ||
      AGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTG
4901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
      TCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGAC

                           Nsi1
                        BfrB1 |
                            | |
      TGGATAACCGTATTACCGCCATGCAT
5001  |||||||||*|||||||||*|||||| 5026
      ACCTATTGGCATAATGGCGGTACGTA
```

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Found:

    Afe1    Age1   AlwN1   ApaL1    Ase1    Avr2   Bae1a   Bae1b   BamH1   Bcg1a   Bcg1b   BciV1    Bcl1   BfrB1
   BfuA1    Bgl1   BmgB1    Bmr1    Bpm1   BpuE1    Bsa1   BsaB1   BsaXa   BsaXb   BseR1   BseY1    Bsm1   BspE1
   BspH1   BspLU   BspM1   BsrB1   BsrD1   BsrG1   BssS1   BstAP   BstB1   BstX1   Bsu36   BtgZ1    Bts1    Cla1
    Dra1    Dra3    Drd1    Eag1    Ear1    Eci1   Eco57   EcoN1   EcoRV    Fsp1    Hpa1    Kas1    Mfe1    Mlu1
    Msc1    Nae1    Nar1    Nco1    Nde1   NgoM4    Nhe1    Nsi1   PflF1   PflM1   polyA    Psi1    Pvu2    Rsr2
    Sap1   SexA1    Sfi1   SpAcc   SpDon    Sph1    Ssp1    Stu1   T7Ter    Xcm1    Xmn1

Unique:

    Afe1    Age1   ApaL1    Ase1   Bae1a   Bae1b   BamH1   Bcg1a   Bcg1b    Bcl1    Bgl1   BmgB1    Bsa1   BsaXa
   BsaXb   BseR1   BspE1   BspLU    Cla1    Eag1   EcoN1   EcoRV    Fsp1    Hpa1    Kas1    Mfe1    Mlu1    Nar1
    Nde1    Nhe1   PflM1    Rsr2   SexA1    Sfi1    Stu1   T7Ter    Xmn1



Not found:

    Aar1    Aat2   Acc65    Acl1    Afl2    Ahd1    Ale1    Apa1    Asc1   AsiS1    Bbs1   BbvC1    Bgl2    Blp1
   Bpu10    Bsg1   BsiW1   BsmB1   BssH2   BstE2   BstZ1    _Chi    EcoK   EcoR1   FCatB   FCatL   FCatR   FCatP
   ScFRT    Fse1   FspA1   Hind3   I_Ceu    Kpn1    loxP    Not1    Nru1    Pac1    Pme1    Pml1   PshA1   PspOM
    Pst1    Pvu1   R4atB   R4atL   R4atP   R4atR    Sac1    Sac2    Sal1   SanD1    Sbf1    Sca1    Sgf1   SgrA1
    Sma1   SnaB1    Spe1    Srf1    Swa1   T3RNA   T7RNA   PISce    Xba1    Xho1

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
```