**Gateway® TagRFP-AS-C 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 region corresponds to DNA sequence transferred from the entry clone into the destination vector following recombination. Non-TagRFP amino acids are shown in black, TagRFP amino acids are shown in red.

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

                                          SpDon                                Nsi1
                                Age1     Ale1 |     SpDon                       Nde1
                        Nhe1 Afe1   |    Nco1 | |    Ear1 |                   BfrB1 |
                            |    |   |      | | |      | |                       | |
            AAAAAAGCAGGCTGCTAGCGCTACCGGTCGCCACCATGGTGAGTAAAGGTGAAGAGTTGATTAAAGAGAACATGCATATGAAGTTATACATGGAGGGAAC
      101   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 200
            TTTTTTCGTCCGACGATCGCGATGGCCAGCGGTGGTACCACTCATTTCCACTTCTCAACTAATTTCTCTTGTACGTATACTTCAATATGTACCTCCCTTG
attL1/TagRFP >  K  S  R  L  L  A  L  P  V  A  T  M  V  S  K  G  E  E  L  I  K  E  N  M  H  M  K  L  Y  M  E  G  T

                          BsrG1                                   SpAcc
                             |                                       |
            TGTCAATAATCACCACTTTAAGTGTACATCAGAGGGTGAGGGAAAGCCATACGAGGGAACCCAAACTATGAGAATCAAAGTAGTGGAGGGAGGTCCTCTT
      201   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 300
            ACAGTTATTAGTGGTGAAATTCACATGTAGTCTCCCACTCCCTTTCGGTATGCTCCCTTGGGTTTGATACTCTTAGTTTCATCACCTCCCTCCAGGAGAA
TagRFP      >  V  N  N  H  H  F  K  C  T  S  E  G  E  G  K  P  Y  E  G  T  Q  T  M  R  I  K  V  V  E  G  G  P  L
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            Ear1                                                                                                Dra1
              |                                                                                                   |
         CCATTTGCTTTTGATATACTAGCAACAAGTTTCATGTATGGTTCCAGGACCTTCATTAACCATACTCAGGGAATCCCTGACTTCTTTAAACAGTCTTTTC
     301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 400
         GGTAAACGAAAACTATATGATCGTTGTTCAAAGTACATACCAAGGTCCTGGAAGTAATTGGTATGAGTCCCTTAGGGACTGAAGAAATTTGTCAGAAAAG
TagRFP     > P  F  A  F  D  I  L  A  T  S  F  M  Y  G  S  R  T  F  I  N  H  T  Q  G  I  P  D  F  F  K  Q  S  F  P

                                BstE2
                   SpDon     Eco57|                  Drd1
                       |         ||                    |
         CTGAAGGTTTTACATGGGAGAGGGTTACCACTTACGAGGACGGTGGAGTCTTGACAGCAACCCAGGACACTTCATTACAAGATGGATGCCTAATATACAA
     401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 500
         GACTTCCAAAATGTACCCTCTCCCAATGGTGAATGCTCCTGCCACCTCAGAACTGTCGTTGGGTCCTGTGAAGTAATGTTCTACCTACGGATTATATGTT
TagRFP     >   E  G  F  T  W  E  R  V  T  T  Y  E  D  G  G  V  L  T  A  T  Q  D  T  S  L  Q  D  G  C  L  I  Y  N

           SpDon                          SpAcc
              |                              |
         TGTGAAAATTAGGGGTGTGAATTTCCCTAGTAACGGACCAGTTATGCAGAAGAAAACACTAGGTTGGGAAGCTAATACTGAAATGTTGTACCCTGCCGAC
     501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
         ACACTTTTAATCCCCACACTTAAAGGGATCATTGCCTGGTCAATACGTCTTCTTTTGTGATCCAACCCTTCGATTATGACTTTACAACATGGGACGGCTG
TagRFP     >  V  K  I  R  G  V  N  F  P  S  N  G  P  V  M  Q  K  K  T  L  G  W  E  A  N  T  E  M  L  Y  P  A  D

                                     Afl2                                   Dra1
                                       |                                      |
         GGAGGTTTAGAAGGTAGATCCGACATGGCCCTTAAGCTAGTCGGAGGTGGACACTTGATCTGTAACTTTAAAACCACATATAGGTCTAAGAAGCCAGCAA
     601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
         CCTCCAAATCTTCCATCTAGGCTGTACCGGGAATTCGATCAGCCTCCACCTGTGAACTAGACATTGAAATTTTGGTGTATATCCAGATTCTTCGGTCGTT
TagRFP     > G  G  L  E  G  R  S  D  M  A  L  K  L  V  G  G  G  H  L  I  C  N  F  K  T  T  Y  R  S  K  K  P  A  K

                                 SpDon          SpAcc
                                    |              |
         AGAATCTAAAAATGCCTGGTGTTTACTATGTGGACCATAGACTAGAAAGGATAAAAGAAGCAGACAAAGAAACTTACGTGGAGCAACATGAGGTCGCCGT
     701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
         TCTTAGATTTTTACGGACCACAAATGATACACCTGGTATCTGATCTTTCCTATTTTCTTCGTCTGTTTCTTTGAATGCACCTCGTTGTACTCCAGCGGCA
TagRFP     >   N  L  K  M  P  G  V  Y  Y  V  D  H  R  L  E  R  I  K  E  A  D  K  E  T  Y  V  E  Q  H  E  V  A  V
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                                                                                                                                Sac2
                                                                  BpuE1     Xho1    Hind3  EcoR1      Sal1      Kpn1  |
                                SpDon                          BspE1   | Bgl2   |   Sac1 |BstB1 |     Pst1| Acc65   |  |
                                   |                              |   |    |     |     |     |     |     |     |     |  |
            CGCTAGGTATTGCGACTTACCTTCCAAGCTAGGTCACAAATTGAACTCCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCTGCAGTCGACGGTACCGCG
        801 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*|||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 900
            GCGATCCATAACGCTGAATGGAAGGTTCGATCCAGTGTTTAACTTGAGGCCTGAGTCTAGAGCTCGAGTTCGAAGCTTAAGACGTCAGCTGCCATGGCGC
TagRFP/MCS  >  A  R  Y  C  D  L  P  S  K  L  G  H  K  L  N  S  G  L  R  S  R  A  Q  A  S  N  S  A  V  D  G  T  A

                 BamH1
                Sma1 |
               Apa1| |
        PspOM   || |                      BseY1      BsrG1             Psi1   BsrD1
            |   || |                         |          |                |       |
            GGCCCGGGATCCACCGGATCTAGGTAACTGAACCCAGCTTTCTTGTACAAAGTTGGCATTATAAGAAAGCATTGCTTATCAATTTGTTGCAACGAACAGG
        901 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 1000
            CCGGGCCCTAGGTGGCCTAGATCCATTGACTTGGGTCGAAAGAACATGTTTCAACCGTAATATTCTTTCGTAACGAATAGTTAAACAACGTTGCTTGTCC
MCS/attL2   > G  P  G  S  T  G  S  R  *

                     polyA                        Bcl1BsaB1                              SpDon   Dra1
                        |                            |    |                                 |       |
            TCACTATCAGTCAAAATAAAATCATTATTTGCTAGATAACTGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCAC
       1001 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 1100
            AGTGATAGTCAGTTTTATTTTAGTAATAAACGATCTATTGACTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTG
attL2 site  >

                                      Bsm1
                                     Mfe1|        Hpa1       polyA    Psi1      polyA
                                        ||           |           |       |          |
            ACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAA
       1101 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 1200
            TGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTT

              polyA            Bts1 Bsm1                                        Mlu1     SpDon        Ssp1
                  |                |    |                                          |          |           |
            TTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAACGCGTAAATTGTAAGCGTTAATATTTTGTT
       1201 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 1300
            AAAGTGTTTATTTCGTAAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTGCGCATTTAACATTCGCAATTATAAAACAA
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                                                                                Psi1
                                                                                  |
      AAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGG
1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
      TTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCC

                                  BsaXb                 Drd1    BsaXa
                                     |                    |        |
      TTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTAC
1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
      AACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATG

  BtgZ1
  Dra3|                                                        SpAcc
     ||                                                          |
      GTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAA
1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
      CACTTGGTAGTGGGATTAGTTCAAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTT

     Nae1
  NgoM4 |                                   BsrB1
      | |                                     |
      GCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCC
1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
      CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGG

                                                                                  polyA
                                                                                    |
      GCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATA
1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
      CGGCGCGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTAT

              BciV1
          BspH1  |                                                                  Eci1
        BsrB1 |  |                            Ssp1  Ear1        Bsu36              Pvu2 |
            | |  |                               |     |            |                 | |
      TGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAG
1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
      ACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTC
```

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                                                   Nsi1
                                                 Sph1 |
                                                BfrB1 |
                         BseY1                BstAP  | |            SexA1                    BseY1
                             |                    |  | |               |                       |
     TTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCC
1901 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 2000
     AATCCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGG

                           Nsi1
                         Sph1 |
                        BfrB1 |                                                        Eci1
                     BstAP  | |                        Eci1                 Eci1     Bmr1|       Eci1
                         |  | |                          |                    |        ||          |
     CAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGC
2001 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 2100
     GTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCG

                                                                  Sfi1
                 Nco1                    polyA                    Bgl1                     SpDon
                    |                        |                       |                        |
     CCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTT
2101 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 2200
     GGTAAGAGGCGGGGTACCGACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAA

       Avr2
      Stu1|                                                                BspM1
   BseR1  ||                Cla1                BsaB1                      BfuA1                Eag1
      |  ||                   |                   |                          |                   |
     GGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGG
2201 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 2300
     CCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACC

                                                                                          Nar1
                                  Bmr1                                                   Kas1|
                                     |                                                      ||
     GTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTG
2301 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 2400
     CACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAAC
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                                                                                                  Pvu2
                Drd1                                                  Msc1                  Fsp1   |
                  |                                                     |                     |   |
      TCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGA
2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
      AGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCT

   PflF1                        Eco57                                      SpDon
      |                            |                                          |
      CGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATC
2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
      GCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAG

                                                   BtgZ1
                                                BspM1  |
    BciV1         BsrD1                         BfuA1  |
      |             |                                |  |
      ATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGG
2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
      TACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACC

                            Sap1
                            Ear1                          BpuE1                        Sph1
                              |                             |                            |
      AAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGA
2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
      TTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCT

                                                                                      BseY1
                                                                                     Nae1 |
                Nco1                BtgZ1                                       NgoM4 | |
                  |                   |                                           | | |
      GGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCG
2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
      CCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGC
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                                        Sap1                                                        BtgZ1
  Rsr2          Eci1                    Ear1                    Eco57         BssS1               BsrB1 |
     |            |                       |                       |             |                   | |
      GACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTC
2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
      CTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAG

                                                  BsrB1          BstB1
                                                     |              |
      CCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCA
3001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
      GGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGT

   BssS1                                                        Nae1
   BspM1                                                      NgoM4 |
   BfuA1                      SpAcc                            Bpm1 |
      |                          |                              | |
      TCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCA
3101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
      AGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGT

                          Bpm1
                       SpAcc  |
                        Avr2  |                                                        polyA        polyA
                          |   |                                                           |            |
      TGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAA
3201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
      ACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTT

                                                                                  Bsa1
                                                                                    |
      TAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATAC
3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
      ATTTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATG
```

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                                                                                BstAP
                                                                                AlwN1      Bsu36
                                                                                    |          |
     GCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAG
3401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
     CGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTC

                          Dra1               Dra1                             BspH1
                             |                  |                                |
     GTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTA
3501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
     CAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAAT

                                                                        BpuE1
                                                                           |
     ACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACA
3601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
     TGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGT


                                                          Eco57
                                                             |
     AAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATA
3701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
     TTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTAT


            SpAcc                                                                          AlwN1
                |                                                                              |
     CTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGC
3801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
     GACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACG


                   BpuE1                                                                 ApaL1      BseY1
                      |                                                                      |          |
     CAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCC
3901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
     GTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGG
```

```
                                                SpAcc
                                                  |
      AGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGG
4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
      TCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCC


     BciV1
  Eci1   |                    BssS1                                    SpAcc
     |   |                       |                                        |
      TAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGA
4101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
      ATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACT


  Drd1            BpuE1               SpAcc     Eci1
     |                |                   |        |
      GCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCT
4201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
      CGCAGCTAAAAACACTACGAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGA


    SpDon                                                Nsi1
   BspLU|                                              BfrB1 |
       ||                                                 | |
      CACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
4301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4360
      GTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Acc65** | **Afe1** | **Afl2** | **Age1** | **Ale1** | AlwN1 | **Apa1** | **ApaL1** | Avr2 | **BamH1** | BciV1 | **Bcl1** | BfrB1 | BfuA1 |
| **Bgl1** | **Bgl2** | Bmr1 | Bpm1 | BpuE1 | **Bsa1** | BsaB1 | **BsaXa** | **BsaXb** | **BseR1** | BseY1 | Bsm1 | **BspE1** | BspH1 |
| **BspLU** | BspM1 | BsrB1 | BsrD1 | BsrG1 | BssS1 | BstAP | BstB1 | **BstE2** | Bsu36 | BtgZ1 | **Bts1** | **Cla1** | Dra1 |
| **Dra3** | Drd1 | **Eag1** | Ear1 | Eci1 | Eco57 | **EcoR1** | **Fsp1** | **Hind3** | **Hpa1** | **Kas1** | **Kpn1** | **Mfe1** | **Mlu1** |
| **Msc1** | Nae1 | **Nar1** | Nco1 | **Nde1** | NgoM4 | **Nhe1** | Nsi1 | **PflF1** | polyA | Psi1 | **PspOM** | **Pst1** | Pvu2 |
| **Rsr2** | **Sac1** | **Sac2** | **Sal1** | Sap1 | **SexA1** | **Sfi1** | **Sma1** | SpAcc | SpDon | Sph1 | Ssp1 | **Stu1** | **Xho1** |

Unique:

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Acc65** | **Afe1** | **Afl2** | **Age1** | **Ale1** | **Apa1** | **ApaL1** | **BamH1** | **Bcl1** | **Bgl1** | **Bgl2** | **Bsa1** | **BsaXa** | **BsaXb** |
| **BseR1** | **BspE1** | **BspLU** | **BstE2** | **Bts1** | **Cla1** | **Dra3** | **Eag1** | **EcoR1** | **Fsp1** | **Hind3** | **Hpa1** | **Kas1** | **Kpn1** |
| **Mfe1** | **Mlu1** | **Msc1** | **Nar1** | **Nde1** | **Nhe1** | **PflF1** | **PspOM** | **Pst1** | **Rsr2** | **Sac1** | **Sac2** | **Sal1** | **SexA1** |
| **Sfi1** | **Sma1** | **Stu1** | **Xho1** | | | | | | | | | | |

Not found:

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Aar1 | Aat2 | Acl1 | Ahd1 | Asc1 | Ase1 | AsiS1 | Bae1a | Bae1b | Bbs1 | BbvC1 | Bcg1a | Bcg1b | Blp1 |
| BmgB1 | Bpu10 | Bsg1 | BsiW1 | BsmB1 | BssH2 | BstX1 | BstZ1 | BxatB | BxatL | BxatR | BxatP | _Chi | EcoK |
| EcoN1 | EcoRV | FCatB | FCatL | FCatR | FCatP | ScFRT | Fse1 | FspA1 | I_Ceu | loxP | Not1 | Nru1 | Pac1 |
| PflM1 | Pme1 | Pml1 | PshA1 | Pvu1 | R4atB | R4atL | R4atP | R4atR | SanD1 | Sbf1 | Sca1 | Sgf1 | SgrA1 |
| SnaB1 | Spe1 | Srf1 | Swa1 | T3RNA | T7RNA | T7Ter | PISce | Xba1 | Xcm1 | Xmn1 | | | |

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 | | | | | | | | | | | | | |