pPhi-Yellow-dest1 vector restriction map

The data has not been verified by restriction digestion with each enzyme listed and does not take into account possible methylation sites. Enzymes that recognize unambiguous sequences less than 6 basepairs long are not included – for the more complete enzyme list please refer to the Table of restriction sites.

Unique sites 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 shown in frame, amino acids coded by MCS and MODC amino acids are shown in bold black.

```
        Ase1                                                                                Bgl1
          |                                                                                   |
     TAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCG
   1 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 100
     ATCAATAATTATCATTAGTTAATGCCCCAGTAATCAAGTATCGGGTATATACCTCAAGGCGCAATGTATTGAATGCCATTTACCGGGCGGACCGACTGGC

                          Aat2                                                  Aat2
                            |                                                     |
     CCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGT
 101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 200
     GGGTTGCTGGGGGCGGGTAACTGCAGTTATTACTGCATACAAGGGTATCATTGCGGTTATCCCTGAAAGGTAACTGCAGTTACCCACCTCATAAATGCCA

             Bgl1                  Nde1                        Aat2                  Bgl1  Bmr1
               |                     |                           |                     |     |
     AAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTA
 201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 300
     TTTGACGGGTGAACCGTCATGTAGTTCACATAGTATACGGTTCATGCGGGGGATAACTGCAGTTACTGCCATTTACCGGGCGGACCGTAATACGGGTCAT

                                          SnaB1                Nco1
                                            |                    |
     CATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGA
 301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 400
     GTACTGGAATACCCTGAAAGGATGAACCGTCATGTAGATGCATAATCAGTAGCGATAATGGTACCACTACGCCAAAACCGTCATGTAGTTACCCGCACCT
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                                                  Aat2                                                  Eci1
                                                    |                                                     |
        TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
    401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 500
        ATCGCCAAACTGAGTGCCCCTAAAGGTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT

                                                                                                Nhe1 Afe1
                                                                                                  |    |
        ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCGCTA
    501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
        TGTTGAGGCGGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT
PhiYFP-m    >                                                                                    L  A  L

                                                                  BamH1
                                                                 Sma1 |
                                                                Apa1| |
                                                           PspOM   || |
                                                           Sac2|   || |
                  Xho1    Hind3  EcoR1      Sal1      Kpn1  ||   || |                        Nar1
        BpuE1 Bgl2   |    Sac1 |BstB1 |     Pst1| Acc65   |  ||   || |  Age1                 Kas1|
                  |    |    |    |    |     |    |    |    ||   || |    |                      ||
        CCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCTGCAGTCGACGGTACCGCGGGCCCGGGATCCACCGGTCGCCACCATGAGCAGCGGCGCCCTGCTGT
    601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
        GGCCTGAGTCTAGAGCTCGAGTTCGAAGCTTAAGACGTCAGCTGCCATGGCGCCCGGGCCCTAGGTGGCCAGCGGTGGTACTCGTCGCCGCGGGACGACA
PhiYFP-m    >  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  M  S  S  G  A  L  L

                                                Eco57    Msc1                Sac2
                                                    |       |                   |
        TCCACGGCAAGATCCCCTACGTGGTGGAGATGGAGGGCGATGTGGATGGCCACACCTTCAGCATCCGCGGTAAGGGCTACGGCGATGCCAGCGTGGGCAA
    701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
        AGGTGCCGTTCTAGGGGATGCACCACCTCTACCTCCCGCTACACCTACCGGTGTGGAAGTCGTAGGCGCCATTCCCGATGCCGCTACGGTCGCACCCGTT
PhiYFP-m    > F  H  G  K  I  P  Y  V  V  E  M  E  G  D  V  D  G  H  T  F  S  I  R  G  K  G  Y  G  D  A  S  V  G  K
```

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                                                                                Nar1
                Bsg1                                                BstE2      Kas1|
                Bmr1                SgrA1                          Ale1 |     Bpm1     Bmr1||
                   |                    |                            | |        |        |||
                GGTGGATGCCCAGTTCATCTGCACCACCGGCGATGTGCCCGTGCCCTGGAGCACCCTGGTGACCACCCTGACCTACGGCGCCCAGTGCTTCGCCAAGTAC
            801 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 900
                CCACCTACGGGTCAAGTAGACGTGGTGGCCGCTACACGGGCACGGGACCTCGTGGGACCACTGGTGGGACTGGATGCCGCGGGTCACGAAGCGGTTCATG
PhiYFP-m     >  V  D  A  Q  F  I  C  T  T  G  D  V  P  V  P  W  S  T  L  V  T  T  L  T  Y  G  A  Q  C  F  A  K  Y

                           Xmn1          Eco57 Sph1                                Bsg1
                              |              |    |                                  |
                GGCCCCGAGCTGAAGGATTTCTACAAGAGCTGCATGCCCGATGGCTACGTGCAGGAGCGCACCATCACCTTCGAGGGCGATGGCAATTTCAAGACCCGCG
            901 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 1000
                CCGGGGCTCGACTTCCTAAAGATGTTCTCGACGTACGGGCTACCGATGCACGTCCTCGCGTGGTAGTGGAAGCTCCCGCTACCGTTAAAGTTCTGGGCGC
PhiYFP-m     >  G  P  E  L  K  D  F  Y  K  S  C  M  P  D  G  Y  V  Q  E  R  T  I  T  F  E  G  D  G  N  F  K  T  R

                                                                                  PflM1
                                                                                  BseY1
                                                                                Pml1  |
                BstE2                  BsrG1                    Msc1                Msc1   |  |
                    |                    |                        |                   |   |  |
                CCGAGGTGACCTTCGAGAATGGCAGCGTGTACAATCGCGTGAAGCTGAATGGCCAGGGCTTCAAGAAGGATGGCCACGTGCTGGGCAAGAATCTGGAGTT
           1001 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 1100
                GGCTCCACTGGAAGCTCTTACCGTCGCACATGTTAGCGCACTTCGACTTACCGGTCCCGAAGTTCTTCCTACCGGTGCACGACCCGTTCTTAGACCTCAA
PhiYFP-m     > A  E  V  T  F  E  N  G  S  V  Y  N  R  V  K  L  N  G  Q  G  F  K  K  D  G  H  V  L  G  K  N  L  E  F

                         Bpm1                                Sap1                     BssS1       Nae1
                        Bts1|  BsrG1                        Ear1               Bgl2Eco57  |    NgoM4 |
                           ||      |                           |                 |    |  |        | |
                CAATTTCACCCCCCACTGCCTGTACATCTGGGGCGATCAGGCCAATCACGGCCTGAAGAGCGCCTTCAAGATCTGCCACGAGATCGCCGGCAGCAAGGGC
           1101 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 1200
                GTTAAAGTGGGGGGTGACGGACATGTAGACCCCGCTAGTCCGGTTAGTGCCGGACTTCTCGCGGAAGTTCTAGACGGTGCTCTAGCGGCCGTCGTTCCCG
PhiYFP-m     >  N  F  T  P  H  C  L  Y  I  W  G  D  Q  A  N  H  G  L  K  S  A  F  K  I  C  H  E  I  A  G  S  K  G

                                                          ApaL1 Pml1                          Pml1   Blp1
                                                              |    |                             |      |
                GATTTCATCGTGGCCGATCACACCCAGATGAATACCCCCATCGGCGGCGGCCCCGTGCACGTGCCCGAGTACCACCACATGAGCTACCACGTGAAGCTGA
           1201 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 1300
                CTAAAGTAGCACCGGCTAGTGTGGGTCTACTTATGGGGGTAGCCGCCGCCGGGGCACGTGCACGGGCTCATGGTGGTGTACTCGATGGTGCACTTCGACT
PhiYFP-m     >  D  F  I  V  A  D  H  T  Q  M  N  T  P  I  G  G  G  P  V  H  V  P  E  Y  H  H  M  S  Y  H  V  K  L
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                                        Bsa1         BssH2                                Xho1  EcoRV  Nco1
                                          |             |                                    |      |     |
            GCAAGGATGTGACCGATCACCGCGATAATATGAGCCTGACGGAGACCGTGCGCGCCGTGGATTGCCGCAAGACCTACCTGGGATCTCGAGATATCAGCCA
      1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
            CGTTCCTACACTGGCTAGTGGCGCTATTATACTCGGACTGCCTCTGGCACGCGCGGCACCTAACGGCGTTCTGGATGGACCCTAGAGCTCTATAGTCGGT
PhiYFP-m    > S  K  D  V  T  D  H  R  D  N  M  S  L  T  E  T  V  R  A  V  D  C  R  K  T  Y  L  G  S  R  D  I  S  H

                   Nae1
                SgrA1 |                                                                          BstAP
                NgoM4 |                                                  BsrB1                  Pst1   |
                    | |                                                    |                     |   |
            TGGCTTCCCGCCGGCGGTGGCGGCGCAGGATGATGGCACGCTGCCCATGTCTTGTGCCCAGGAGAGCGGGATGGACCGTCACCCTGCAGCCTGTGCTTCT
      1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
            ACCGAAGGGCGGCCGCCACCGCCGCGTCCTACTACCGTGCGACGGGTACAGAACACGGGTCCTCTCGCCCTACCTGGCAGTGGGACGTCGGACACGAAGA
MODC        >  G  F  P  P  A  V  A  A  Q  D  D  G  T  L  P  M  S  C  A  Q  E  S  G  M  D  R  H  P  A  A  C  A  S

                                Eag1      Xba1   BsaB1                                  Dra1
                                  |         |      |                                      |
            GCTAGGATCAATGTGTAGGATCGGCCGCGACTCTAGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCC
      1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
            CGATCCTAGTTACACATCCTAGCCGGCGCTGAGATCTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGG
MODC        >  A  R  I  N  V  *

                                 Bsm1
                                Mfe1|        Hpa1                Psi1
                                   ||          |                  |
            CCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCAC
      1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
            GGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTG

                      Bts1 Bsm1                                Afl2                     Ssp1
                        |    |                                   |                        |
            AAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTGTAAGCGTTAATATTTTGTTAAAATT
      1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
            TTTATTTCGTAAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTCCGCATTTAACATTCGCAATTATAAAACAATTTTAA
```

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                                                                  Psi1
                                                                    |
      CGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGT
1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
      GCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCA

                              BsaXb                 Drd1    BsaXa                                Dra3
                                |                     |        |                                    |
      GTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAAC
1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
      CAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTG

                                                                                                  Nae1
                                                                                               NgoM4 |
                                                                                                   | |
      CATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGC
2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
      GTAGTGGGATTAGTTCAAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCG

                                        BsrB1
                                          |
      GAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCG
2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
      CTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGC

      CTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATC
2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
      GAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAG

        BciV1
     BspH1  |                                                                  Eci1
   BsrB1 |  |                            Ssp1  Ear1        Bsu36             Pvu2 |
       | |  |                              |     |           |                 | |
      CGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGG
2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
      GCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCC
```

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                                                Nsi1
                                              Sph1 |
                                             BfrB1 |
                     BseY1                  BstAP  | |            SexA1                    BseY1
                       |                       |  | |               |                       |
     TGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAG
2401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
     ACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTC

                       Nsi1
                     Sph1 |
                    BfrB1 |                                                        Eci1
                 BstAP  | |                       Eci1                 Eci1     Bmr1|       Eci1
                    |  | |                         |                    |        ||          |
     GCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTC
2501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
     CGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAG

                                                 Sfi1                                          Stu1
        Nco1                                     Bgl1                                       BseR1  |
          |                                        |                                          |  |
     TCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGC
2601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
     AGGCGGGGTACCGACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCG

                                                                 BspM1
  Avr2              Cla1              BsaB1                      BfuA1               Eag1
    |                 |                 |                          |                  |
     CTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAG
2701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
     GATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTC

                                                                                Nar1
                           Bmr1                                                Kas1|
                             |                                                    ||
     AGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGA
2801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
     TCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCT
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                                                                                  Pvu2
       Drd1                                                  Msc1                Fsp1   |       PflF1
          |                                                     |                   |   |           |
     CCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGT
2901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
     GGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACA

                        Eco57                                                                     BciV1
                            |                                                                        |
     CACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCT
3001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
     GTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGA

                                          BspM1
           BsrD1                          BfuA1
              |                               |
     GATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCG
3101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
     CTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGC

                        Sap1
                        Ear1                          BpuE1                         Sph1
                           |                              |                             |
     GTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCT
3201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
     CAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGA

                                                                                  BseY1
                                                                                 Nae1 |
           Nco1                                                             NgoM4 | |        Rsr2
              |                                                                 | | |           |
     CGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGC
3301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
     GCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCG
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                                Sap1
   Eci1                         Ear1                    Eco57         BssS1                BsrB1
      |                            |                       |             |                    |
     TATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATT
3401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
     ATAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAA

                                                                                                BssS1
                                                                                                BspM1
                                                BsrB1          BstB1                            BfuA1
                                                   |              |                                |
     CGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGA
3501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
     GCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCT

                                                                 Nae1
                                                              NgoM4 |
                                                               Bpm1 |
                                                                 | |
     GATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGG
3601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
     CTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACC

                   Bpm1
               Avr2  |
                   |  |
     AGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAAC
3701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
     TCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTG

                                                                     Bsa1
                                                                       |
     GCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGC
3801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
     CGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCG
```

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                                                                                BstAP
                                                                                AlwN1      Bsu36
                                                                                    |          |
     GTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACT
3901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
     CAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGA

                       Dra1               Dra1                                BspH1
                          |                  |                                   |
     CATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGA
4001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
     GTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACT

                                                                          BpuE1
                                                                              |
     GTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAA
4101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
     CAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTT

                                                   Eco57
                                                      |
     CCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCC
4201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
     GGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGG

                                                                                      AlwN1
                                                                                         |
     TTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGG
4301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
     AAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACC

             BpuE1                                                                ApaL1     BseY1
                |                                                                    |         |
     CGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTG
4401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
     GCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAAC
```

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                                                                                                   BciV1
                                                                                             Eci1   |
                                                                                                |   |
     GAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCG
4501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
     CTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGC

                       BssS1                                                                Drd1
                           |                                                                   |
     GCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCG
4601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
     CGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGC

           BpuE1                        Eci1                                                  BspLU
               |                            |                                                     |
     ATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATG
4701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
     TAAAAACACTACGAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTAC

                                                   Nsi1
                                                BfrB1 |
                                                    | |
     TTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
4801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||| 4854
     AAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aat2	**Acc65**	**Afe1**	**Afl2**	**Age1**	**Ale1**	AlwN1	**Apa1**	ApaL1	**Ase1**	Avr2	**BamH1**	BciV1	BfrB1
BfuA1	Bgl1	Bgl2	**Blp1**	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	**BsaXa**	**BsaXb**	**BseR1**	BseY1	Bsg1
Bsm1	BspH1	**BspLU**	BspM1	BsrB1	**BsrD1**	BsrG1	**BssH2**	BssS1	BstAP	BstB1	BstE2	Bsu36	Bts1
Cla1	Dra1	**Dra3**	Drd1	Eag1	Ear1	Eci1	Eco57	**EcoR1**	**EcoRV**	**Fsp1**	**Hind3**	**Hpa1**	Kas1
Kpn1	**Mfe1**	Msc1	Nae1	Nar1	Nco1	**Nde1**	NgoM4	**Nhe1**	Nsi1	**PflF1**	**PflM1**	Pml1	Psi1
PspOM	Pst1	Pvu2	**Rsr2**	**Sac1**	Sac2	**Sal1**	Sap1	**SexA1**	**Sfi1**	SgrA1	**Sma1**	**SnaB1**	Sph1
Ssp1	**Stu1**	**Xba1**	Xho1	**Xmn1**									

Unique:

Acc65	**Afe1**	**Afl2**	**Age1**	**Ale1**	**Apa1**	**Ase1**	**BamH1**	**Blp1**	**BsaXa**	**BsaXb**	**BseR1**	**BspLU**	**BsrD1**
BssH2	**Cla1**	**Dra3**	**EcoR1**	**EcoRV**	**Fsp1**	**Hind3**	**Hpa1**	**Kpn1**	**Mfe1**	**Nde1**	**Nhe1**	**PflF1**	**PflM1**
PspOM	**Rsr2**	**Sac1**	**Sal1**	**SexA1**	**Sfi1**	**Sma1**	**SnaB1**	**Stu1**	**Xba1**	**Xmn1**			

Not found:

Aar1	Acl1	Ahd1	Asc1	AsiS1	Bae1a	Bae1b	Bbs1	BbvC1	Bcg1a	Bcg1b	Bcl1	BmgB1	Bpu10
BsiW1	BsmB1	BspE1	BstX1	BstZ1	_Chi	EcoK	EcoN1	ScFRT	Fse1	FspA1	I_Ceu	loxP	Mlu1
Not1	Nru1	Pac1	Pme1	PshA1	Pvu1	SanD1	Sbf1	Sca1	Sgf1	Spe1	Srf1	Swa1	PISce
Xcm1													

Excluded by site complexity:

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