pTagCFP-N vector restriction map

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

Unique sites are shown in bold red. 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, amino acids coded by MCS are shown in black.

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

                          Aat2                  SpAcc                       Aat2
                            |                     |                           |
      CCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGT
  101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 200
      GGGTTGCTGGGGGCGGGTAACTGCAGTTATTACTGCATACAAGGGTATCATTGCGGTTATCCCTGAAAGGTAACTGCAGTTACCCACCTCATAAATGCCA

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

                                  BtgZ1 SnaB1                 Nco1
                                    |     |                     |
      CATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGA
  301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 400
      GTACTGGAATACCCTGAAAGGATGAACCGTCATGTAGATGCATAATCAGTAGCGATAATGGTACCACTACGCCAAAACCGTCATGTAGTTACCCGCACCT
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                                                   Aat2                                                  Eci1
                                                     |                                                     |
     TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 500
     ATCGCCAAACTGAGTGCCCCTAAAGGTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT

                                                                                                Nhe1 Afe1
                                                                                                  |    |
     ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCGCTA
501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
     TGTTGAGGCGGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT
MCS            >                                                                                P  L  A  L

                                                                                BamH1
                                                                               Sma1 |
                                                                              Apa1| |
                                                                     PspOM    || |
                                                                     Sac2|    || |
                                  Xho1    Hind3  EcoR1      Sal1      Kpn1  ||    || |
                        BpuE1 Bgl2   |    Sac1 |BstB1 |     Pst1| Acc65   |  ||    || |  Age1            BsrB1
                                |    |        |      |          ||       |  ||    || |     |                |
     CCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCTGCAGTCGACGGTACCGCGGGCCCGGGATCCACCGGTCGCCACCATGAGCGGGGGCGAGGAGCTGT
601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
     GGCCTGAGTCTAGAGCTCGAGTTCGAAGCTTAAGACGTCAGCTGCCATGGCGCCCGGGCCCTAGGTGGCCAGCGGTGGTACTCGCCCCCGCTCCTCGACA
MCS/TagCFP     > 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  G  G  E  E  L  F

                                                ApaL1
                 BseR1                         BmgB1|                                                BsaXa
                    |                             ||                                                    |
     TCGCTGGCATCGTGCCCGTGCTGATCGAGCTGGACGGCGACGTGCACGGCCACAAGTTCAGCGTGCGCGGTGAGGGAGAGGGCGACGCCGACTACGGCAA
701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
     AGCGACCGTAGCACGGGCACGACTAGCTCGACCTGCCGCTGCACGTGCCGGTGTTCAAGTCGCACGCGCCACTCCCTCTCCCGCTGCGGCTGATGCCGTT
TagCFP         >  A  G  I  V  P  V  L  I  E  L  D  G  D  V  H  G  H  K  F  S  V  R  G  E  G  E  G  D  A  D  Y  G  K
```

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                                BsaXb                                BstE2
            Bsg1               Bpm1  |                            Ale1 |                      BstAP
              |                  |  |                               | |                         |
            GCTGGAGATCAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTGGTGACCACCCTCGCCTGGGGCATCCAGTGCTTCGCCCGCTAC
      801   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
            CGACCTCTAGTTCAAGTAGACGTGGTGGCCGTTCGACGGGCACGGGACCGGGTGGGACCACTGGTGGGAGCGGACCCCGTAGGTCACGAAGCGGGCGATG
TagCFP    > L  E  I  K  F  I  C  T  T  G  K  L  P  V  P  W  P  T  L  V  T  T  L  A  W  G  I  Q  C  F  A  R  Y

                            Xmn1
                              |
            CCCGAGCACATGAAGATGAACGACTTCTTCAAGAGCGCCATGCCCGAGGGCTACATCCAGGAGCGCACCATCCACTTCCAGGACGACGGCAAGTACAAGA
      901   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
            GGGCTCGTGTACTTCTACTTGCTGAAGAAGTTCTCGCGGTACGGGCTCCCGATGTAGGTCCTCGCGTGGTAGGTGAAGGTCCTGCTGCCGTTCATGTTCT
TagCFP    > P  E  H  M  K  M  N  D  F  F  K  S  A  M  P  E  G  Y  I  Q  E  R  T  I  H  F  Q  D  D  G  K  Y  K  T

                                          SpDon
             Sac2 SpDon                  Ale1 |                                Eco57                    PflM1
               |     |                      | |                                  |                        |
            CCCGCGGCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCGTCGAGCTGAAGGGCGAGGGCTTCAAGGAGGACGGCAACATCCTGGGCCACAAGTT
     1001   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
            GGGCGCCGCTCCACTTCAAGCTCCCGCTGTGGGACCACTTGGCGCAGCTCGACTTCCCGCTCCCGAAGTTCCTCCTGCCGTTGTAGGACCCGGTGTTCAA
TagCFP    >  R  G  E  V  K  F  E  G  D  T  L  V  N  R  V  E  L  K  G  E  G  F  K  E  D  G  N  I  L  G  H  K  L

                              BsrG1                        Xcm1         Eci1        Bpm1
                                |                            |            |           |
            GGAGTACAGCGCCATCAGCGACAACGTGTACATCATGCCCGACAAGGCCAACAACGGCCTGGAGGCGAACTTCAAGATCCGCCACAACATCGAGGGCGGC
     1101   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
            CCTCATGTCGCGGTAGTCGCTGTTGCACATGTAGTACGGGCTGTTCCGGTTGTTGCCGGACCTCCGCTTGAAGTTCTAGGCGGTGTTGTAGCTCCCGCCG
TagCFP    > E  Y  S  A  I  S  D  N  V  Y  I  M  P  D  K  A  N  N  G  L  E  A  N  F  K  I  R  H  N  I  E  G  G

                                                                                      Eci1
                 Pvu2            Bsg1       Xcm1                  BtgZ1BsaB1         Bpu10 |
                   |               |          |                      |    |              | |
            GGCGTGCAGCTGGCCGACCACTACCAGACCAACGTGCCCCTGGGCGATGGCCCCGTGCTGATCCCCATCAACCACTACCTGAGCTGCCAGTCCGCCATCA
     1201   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
            CCGCACGTCGACCGGCTGGTGATGGTCTGGTTGCACGGGGACCCGCTACCGGGGCACGACTAGGGGTAGTTGGTGATGGACTCGACGGTCAGGCGGTAGT
TagCFP    > G  V  Q  L  A  D  H  Y  Q  T  N  V  P  L  G  D  G  P  V  L  I  P  I  N  H  Y  L  S  C  Q  S  A  I  S
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                                 Eco57                                                                  Not1
                                  Dra3                          Bpm1         PflM1                     Eag1
                                     |                             |             |                         |
      GCAAGGACCGCAACGAAGCCCGCGACCACATGGTGCTCCTGGAGTCCTTCAGCGCCTACTGCCACACCCACGGCATGGACGAGCTGTACCGCTAAAGCGG
1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
      CGTTCCTGGCGTTGCTTCGGGCGCTGGTGTACCACGAGGACCTCAGGAAGTCGCGGATGACGGTGTGGGTGCCGTACCTGCTCGACATGGCGATTTCGCC
TagCFP      >  K  D  R  N  E  A  R  D  H  M  V  L  L  E  S  F  S  A  Y  C  H  T  H  G  M  D  E  L  Y  R  *

                Xba1   BsaB1                            SpDon   Dra1
                   |       |                               |      |
      CCGCGACTCTAGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGA
1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
      GGCGCTGAGATCTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACT

       Bsm1
      Mfe1|        Hpa1       polyA    Psi1      polyA                        polyA            Bts1 Bsm1
         ||           |           |      |          |                           |                |    |
      ATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCA
1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
      TACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGACGT

                                     Afl2         SpDon        Ssp1
                                        |             |           |
      TTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAG
1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
      AAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTCCGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTC

                                          Psi1
                                            |
      CTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGT
1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
      GAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCA

                                                                                BtgZ1
     BsaXb                  Drd1     BsaXa                                      Dra3|
        |                      |         |                                        ||
      CCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGG
1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
      GGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACC
```

```
                                                                   Nae1
                                SpAcc                           NgoM4 |
                                   |                                | |
     GGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAA
1901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
     CCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTT

              BsrB1
                 |
     GAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCG
2001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
     CTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGC

                                                                                   BciV1
                                                                              BspH1  |
                                                polyA                      BsrB1 |   |
                                                   |                           | |   |
     TCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGAT
2101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
     AGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTA

                                                   Eci1
                Ssp1  Ear1        Bsu36            Pvu2 |                                        BseY1
                   |     |            |                | |                                           |
     AAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCA
2201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
     TTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGT

                          Nsi1                                                                    Nsi1
                        Sph1 |                                                                  Sph1 |
                       BfrB1 |                                                                 BfrB1 |
                     BstAP  | |            SexA1                      BseY1                   BstAP  | |
                            |  | |                |                        |                        |  | |
     GCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATC
2301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
     CGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAG
```

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                                                   Eci1
                        Eci1                 Eci1     Bmr1|       Eci1            Nco1
                          |                    |        ||          |               |
     TCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTT
2401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
     AGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAA

                                                                                   Avr2
                            Sfi1                                                  Stu1|
       polyA                Bgl1                      SpDon             BseR1   ||              Cla1
         |                    |                         |                 |    ||                |
     TTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCA
2501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
     AAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGT

                                        BspM1
                BsaB1                   BfuA1                 Eag1
                  |                       |                     |
     AGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCA
2601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
     TCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGT

                                                   Nar1
     Bmr1                                         Kas1|                        Drd1
       |                                            ||                           |
     CAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATG
2701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
     GTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTAC
```

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                                                   Pvu2
                                  Msc1                Fsp1   |       PflF1
                                     |                   |   |           |
     AACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCT
2801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
     TTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGA

 Eco57                                   SpDon                        BciV1         BsrD1
    |                                       |                            |             |
     GCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACG
2901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
     CGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGC

                        BtgZ1
                     BspM1  |                                                                   Sap1
                     BfuA1  |                                                                   Ear1
                        |   |                                                                     |
     CTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGG
3001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
     GAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACC

                            BpuE1                        Sph1                        Nco1
                               |                           |                           |
     ACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTG
3101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
     TGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGAC

                                                      BseY1
                                                     Nae1 |
      BtgZ1                                       NgoM4 | |        Rsr2         Eci1
         |                                          | | |           |            |
     CTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACC
3201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
     GAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGG
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          Sap1                                                  BtgZ1
          Ear1                   Eco57         BssS1                BsrB1 |
            |                      |             |                    | |
      CGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCC
3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
      GCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGG

                                                                  BssS1
                                                                  BspM1
                 BsrB1          BstB1                             BfuA1                      SpAcc
                    |              |                                |                          |
      TTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTC
3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
      AAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAG

                                  Nae1                                                      Bpm1
                                NgoM4 |                                                  SpAcc  |
                                 Bpm1 |                                                   Avr2  |
                                    | |                                                        |  |
      TATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGA
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      ATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCT

                                                        polyA        polyA
                                                           |            |
      GGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCA
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      CCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAAACAAGT

                                          Bsa1
                                            |
      TAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCAC
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      ATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTG
```

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                                                  BstAP
                                                  AlwN1      Bsu36                           Dra1
                                                      |          |                               |
     CCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAA
3801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
     GGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATT

                 Dra1                              BspH1
                    |                                 |
     AACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGA
3901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
     TTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCT

                                                BpuE1
                                                   |
     CCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGT
4001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
     GGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACA

                            Eco57                                                 SpAcc
                                |                                                     |
     TTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCC
4101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
     AACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGG

                                                                 AlwN1                     BpuE1
                                                                    |                          |
     ACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTT
4201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
     TGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAA

                                                            ApaL1     BseY1
                                                                |         |
     GGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTG
4301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
     CCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGAC
```

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                                                                   BciV1
                 SpAcc                                           Eci1   |                    BssS1
                     |                                              |   |                       |
      AGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCA
4401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
      TCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGT

                                        SpAcc                          Drd1            BpuE1
                                            |                             |                |
      CGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGG
4501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
      GCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCC

                                                                                SpDon
        SpAcc     Eci1                                                         BspLU|
            |        |                                                            ||
      GCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGAT
4601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
      CGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTA

                                 Nsi1
                             BfrB1 |
                                 | |
      TCTGTGGATAACCGTATTACCGCCATGCAT
4701  |||||||||*|||||||||*|||||||||* 4730
      AGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aat2	**Acc65**	**Afe1**	**Afl2**	**Age1**	Ale1	AlwN1	**Apa1**	ApaL1	**Ase1**	Avr2	**BamH1**	BciV1	BfrB1
BfuA1	Bgl1	**Bgl2**	**BmgB1**	Bmr1	Bpm1	**Bpu10**	BpuE1	**Bsa1**	BsaB1	BsaXa	BsaXb	BseR1	BseY1
Bsg1	Bsm1	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**	**Msc1**	Nae1	**Nar1**	Nco1	**Nde1**	NgoM4	**Nhe1**	**Not1**	Nsi1	**PflF1**	PflM1	polyA
Psi1	**PspOM**	**Pst1**	Pvu2	**Rsr2**	**Sac1**	Sac2	**Sal1**	Sap1	**SexA1**	**Sfi1**	**Sma1**	**SnaB1**	SpAcc
SpDon	Sph1	Ssp1	**Stu1**	**Xba1**	Xcm1	**Xho1**	**Xmn1**						

Unique:

Acc65	**Afe1**	**Afl2**	**Age1**	**Apa1**	**Ase1**	**BamH1**	**Bgl2**	**BmgB1**	**Bpu10**	**Bsa1**	**BspLU**	**BsrD1**	**BsrG1**
BstE2	**Bts1**	**Cla1**	**EcoR1**	**Fsp1**	**Hind3**	**Hpa1**	**Kas1**	**Kpn1**	**Mfe1**	**Msc1**	**Nar1**	**Nde1**	**Nhe1**
Not1	**PflF1**	**PspOM**	**Pst1**	**Rsr2**	**Sac1**	**Sal1**	**SexA1**	**Sfi1**	**Sma1**	**SnaB1**	**Stu1**	**Xba1**	**Xho1**
Xmn1													

Not found:

Aar1	Acl1	Ahd1	Asc1	AsiS1	Bae1a	Bae1b	Bbs1	BbvC1	Bcg1a	Bcg1b	Bcl1	Blp1	BsiW1
BsmB1	BspE1	BssH2	BstX1	BstZ1	_Chi	EcoK	EcoN1	EcoRV	ScFRT	Fse1	FspA1	I_Ceu	loxP
Mlu1	Nru1	Pac1	Pme1	Pml1	PshA1	Pvu1	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Spe1	Srf1
Swa1	T3RNA	T7RNA	T7Ter	PISce									

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													