pTagCFP-tubulin 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 bright blue. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site). TagCFP amino acids are shown in light blue. Tubulin amino acids are shown in orange.

```
          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

                                                                                ApaL1
         Age1            BsrB1                  BseR1                         BmgB1|
            |                |                      |                              ||
        CCGGTCGCCACCATGAGCGGGGGCGAGGAGCTGTTCGCTGGCATCGTGCCCGTGCTGATCGAGCTGGACGGCGACGTGCACGGCCACAAGTTCAGCGTGC
    601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
        GGCCAGCGGTGGTACTCGCCCCCGCTCCTCGACAAGCGACCGTAGCACGGGCACGACTAGCTCGACCTGCCGCTGCACGTGCCGGTGTTCAAGTCGCACG
TagCFP     >            M  S  G  G  E  E  L  F  A  G  I  V  P  V  L  I  E  L  D  G  D  V  H  G  H  K  F  S  V  R

                                                                  BsaXb                          BstE2
                                  BsaXa    Bsg1                  Bpm1  |                         Ale1 |
                                      |       |                     |  |                            | |
        GCGGTGAGGGAGAGGGCGACGCCGACTACGGCAAGCTGGAGATCAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTGGTGACCAC
    701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
        CGCCACTCCCTCTCCCGCTGCGGCTGATGCCGTTCGACCTCTAGTTCAAGTAGACGTGGTGGCCGTTCGACGGGCACGGGACCGGGTGGGACCACTGGTG
TagCFP     >  G  E  G  E  G  D  A  D  Y  G  K  L  E  I  K  F  I  C  T  T  G  K  L  P  V  P  W  P  T  L  V  T  T

                         BstAP                                  Xmn1
                            |                                      |
        CCTCGCCTGGGGCATCCAGTGCTTCGCCCGCTACCCCGAGCACATGAAGATGAACGACTTCTTCAAGAGCGCCATGCCCGAGGGCTACATCCAGGAGCGC
    801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
        GGAGCGGACCCCGTAGGTCACGAAGCGGGCGATGGGGCTCGTGTACTTCTACTTGCTGAAGAAGTTCTCGCGGTACGGGCTCCCGATGTAGGTCCTCGCG
TagCFP     >  L  A  W  G  I  Q  C  F  A  R  Y  P  E  H  M  K  M  N  D  F  F  K  S  A  M  P  E  G  Y  I  Q  E  R
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                                                                                  SpDon
                                                   Sac2 SpDon                    Ale1 |
                                                      |     |                       | |
            ACCATCCACTTCCAGGACGACGGCAAGTACAAGACCCGCGGCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCGTCGAGCTGAAGGGCGAGGGCT
       901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
            TGGTAGGTGAAGGTCCTGCTGCCGTTCATGTTCTGGGCGCCGCTCCACTTCAAGCTCCCGCTGTGGGACCACTTGGCGCAGCTCGACTTCCCGCTCCCGA
TagCFP      > T  I  H  F  Q  D  D  G  K  Y  K  T  R  G  E  V  K  F  E  G  D  T  L  V  N  R  V  E  L  K  G  E  G  F

             Eco57                     PflM1                        BsrG1                        Xcm1
                |                          |                            |                            |
            TCAAGGAGGACGGCAACATCCTGGGCCACAAGTTGGAGTACAGCGCCATCAGCGACAACGTGTACATCATGCCCGACAAGGCCAACAACGGCCTGGAGGC
      1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
            AGTTCCTCCTGCCGTTGTAGGACCCGGTGTTCAACCTCATGTCGCGGTAGTCGCTGTTGCACATGTAGTACGGGCTGTTCCGGTTGTTGCCGGACCTCCG
TagCFP      >   K  E  D  G  N  I  L  G  H  K  L  E  Y  S  A  I  S  D  N  V  Y  I  M  P  D  K  A  N  N  G  L  E  A

           Eci1        Bpm1                        Pvu2            Bsg1       Xcm1                  BtgZ1BsaB1
             |           |                           |               |          |                       |    |
            GAACTTCAAGATCCGCCACAACATCGAGGGCGGCGGCGTGCAGCTGGCCGACCACTACCAGACCAACGTGCCCCTGGGCGATGGCCCCGTGCTGATCCCC
      1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
            CTTGAAGTTCTAGGCGGTGTTGTAGCTCCCGCCGCCGCACGTCGACCGGCTGGTGATGGTCTGGTTGCACGGGGACCCGCTACCGGGGCACGACTAGGGG
TagCFP      > N  F  K  I  R  H  N  I  E  G  G  G  V  Q  L  A  D  H  Y  Q  T  N  V  P  L  G  D  G  P  V  L  I  P

                      Eci1                                                Eco57
                   Bpu10 |                                                Dra3                        Bpm1
                      | |                                                  |                           |
            ATCAACCACTACCTGAGCTGCCAGTCCGCCATCAGCAAGGACCGCAACGAAGCCCGCGACCACATGGTGCTCCTGGAGTCCTTCAGCGCCTACTGCCACA
      1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
            TAGTTGGTGATGGACTCGACGGTCAGGCGGTAGTCGTTCCTGGCGTTGCTTCGGGCGCTGGTGTACCACGAGGACCTCAGGAAGTCGCGGATGACGGTGT
TagCFP      > I  N  H  Y  L  S  C  Q  S  A  I  S  K  D  R  N  E  A  R  D  H  M  V  L  L  E  S  F  S  A  Y  C  H  T

                                  BspE1        Xho1
              PflM1             BsrB1 |     Bgl2   |                                Msc1
                |                 | |         |   |                                  |
            CCCACGGCATGGACGAGCTGTACCGCTCCGGACTCAGATCTCGAGTGCGTGAGTGCATCTCCATCCACGTTGGCCAGGCTGGTGTCCAGATTGGCAATGC
      1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
            GGGTGCCGTACCTGCTCGACATGGCGAGGCCTGAGTCTAGAGCTCACGCACTCACGTAGAGGTAGGTGCAACCGGTCCGACCACAGGTCTAACCGTTACG
TagCFP/Tubulin  H  G  M  D  E  L  Y  R  S  G  L  R  S  R  V  R  E  C  I  S  I  H  V  G  Q  A  G  V  Q  I  G  N  A
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            BseY1
          BsrD1 |                                   Msc1
         BstAP| |      Sac1                       BstX1   |                                  Eco57BseR1
             || |         |                           |   |                                      |    |
             CTGCTGGGAGCTCTACTGCCTGGAACACGGCATCCAGCCCGATGGCCAGATGCCAAGTGACAAGACCATTGGGGGAGGAGATGACTCCTTCAACACCTTC
        1401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
             GACGACCCTCGAGATGACGGACCTTGTGCCGTAGGTCGGGCTACCGGTCTACGGTTCACTGTTCTGGTAACCCCCTCCTCTACTGAGGAAGTTGTGGAAG
Tubulin     > C  W  E  L  Y  C  L  E  H  G  I  Q  P  D  G  Q  M  P  S  D  K  T  I  G  G  G  D  D  S  F  N  T  F

             SpAcc
          BsmB1   |                  Pml1   Sma1
             |    |                     |      |
             TTCAGTGAGACGGGCGCTGGCAAGCACGTGCCCCGGGCTGTGTTTGTAGACTTGGAACCCACAGTCATTGATGAAGTTCGCACTGGCACCTACCGCCAGC
        1501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
             AAGTCACTCTGCCCGCGACCGTTCGTGCACGGGGCCCGACACAAACATCTGAACCTTGGGTGTCAGTAACTACTTCAAGCGTGACCGTGGATGGCGGTCG
Tubulin     > F  S  E  T  G  A  G  K  H  V  P  R  A  V  F  V  D  L  E  P  T  V  I  D  E  V  R  T  G  T  Y  R  Q  L

                 Bpu10
               Sap1   |
               Ear1   |
                  |   |
             TCTTCCACCCTGAGCAGCTCATCACAGGCAAGGAAGATGCTGCCAATAACTATGCCCGAGGGCACTACACCATTGGCAAGGAGATCATTGACCTTGTGTT
        1601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
             AGAAGGTGGGACTCGTCGAGTAGTGTCCGTTCCTTCTACGACGGTTATTGATACGGGCTCCCGTGATGTGGTAACCGTTCCTCTAGTAACTGGAACACAA
Tubulin     >  F  H  P  E  Q  L  I  T  G  K  E  D  A  A  N  N  Y  A  R  G  H  Y  T  I  G  K  E  I  I  D  L  V  L

                                     Age1                          Xcm1
                                  Bbs1  |                         BstX1
              EcoR1            Eco57ApaL1|  |                     SpAcc |          Xmn1         SpDon
                  |                |    ||  |                         | |            |             |
             GGACCGAATTCGCAAGCTGGCTGACCAGTGCACCGGTCTTCAGGGCTTCTTGGTTTTCCACAGCTTTGGTGGGGGAACTGGTTCTGGGTTCACCTCCCTG
        1701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
             CCTGGCTTAAGCGTTCGACCGACTGGTCACGTGGCCAGAAGTCCCGAAGAACCAAAAGGTGTCGAAACCACCCCCTTGACCAAGACCCAAGTGGAGGGAC
Tubulin     > D  R  I  R  K  L  A  D  Q  C  T  G  L  Q  G  F  L  V  F  H  S  F  G  G  G  T  G  S  G  F  T  S  L
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                                                                  Bpm1            SpAcc
                     BsmB1                                   BseY1   |             Pvu2
                       |                                        |   |                |
      CTCATGGAACGTCTCTCAGTTGATTATGGCAAGAAGTCCAAGCTGGAGTTCTCCATTTACCCAGCACCCCAGGTTTCCACAGCTGTAGTTGAGCCCTACA
1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
      GAGTACCTTGCAGAGAGTCAACTAATACCGTTCTTCAGGTTCGACCTCAAGAGGTAAATGGGTCGTGGGGTCCAAAGGTGTCGACATCAACTCGGGATGT
Tubulin     > L  M  E  R  L  S  V  D  Y  G  K  K  S  K  L  E  F  S  I  Y  P  A  P  Q  V  S  T  A  V  V  E  P  Y  N

                 SpDon                                Bpm1                          PshA1              EcoRV
                    |                                   |                              |                  |
      ACTCCATCCTCACCACCCACACCACCCTGGAGCACTCTGATTGTGCCTTCATGGTAGACAATGAGGCCATCTATGACATCTGTCGTAGAAACCTCGATAT
1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
      TGAGGTAGGAGTGGTGGGTGTGGTGGGACCTCGTGAGACTAACACGGAAGTACCATCTGTTACTCCGGTAGATACTGTAGACAGCATCTTTGGAGCTATA
Tubulin     >   S  I  L  T  T  H  T  T  L  E  H  S  D  C  A  F  M  V  D  N  E  A  I  Y  D  I  C  R  R  N  L  D  I

                                                                Bts1
                                                                  |
      CGAGCGCCCAACCTACACTAACCTTAACCGCCTTATTAGCCAGATTGTGTCCTCCATCACTGCTTCCCTGAGATTTGATGGAGCCCTGAATGTTGACCTG
2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
      GCTCGCGGGTTGGATGTGATTGGAATTGGCGGAATAATCGGTCTAACACAGGAGGTAGTGACGAAGGGACTCTAAACTACCTCGGGACTTACAACTGGAC
Tubulin     >  E  R  P  T  Y  T  N  L  N  R  L  I  S  Q  I  V  S  S  I  T  A  S  L  R  F  D  G  A  L  N  V  D  L

                EcoR1        SexA1                             Msc1 Nde1              SpAcc
                   |            |                                |    |                  |
      ACAGAATTCCAGACCAACCTGGTGCCCTACCCCCGCATCCACTTCCCTCTGGCCACATATGCCCCTGTCATCTCTGCTGAGAAAGCCTACCATGAACAGC
2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
      TGTCTTAAGGTCTGGTTGGACCACGGGATGGGGGCGTAGGTGAAGGGAGACCGGTGTATACGGGGACAGTAGAGACGACTCTTTCGGATGGTACTTGTCG
Tubulin     > T  E  F  Q  T  N  L  V  P  Y  P  R  I  H  F  P  L  A  T  Y  A  P  V  I  S  A  E  K  A  Y  H  E  Q  L

                                                   SpDon                 SpDon
                   SpAcc                        BstX1  |               Nco1   |
                      |                            |  |                  |   |
      TTTCTGTAGCAGAGATCACCAATGCTTGCTTTGAGCCAGCCAACCAGATGGTGAAATGTGACCCTCGCCATGGTAAATACATGGCTTGCTGCCTGTTGTA
2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
      AAAGACATCGTCTCTAGTGGTTACGAACGAAACTCGGTCGGTTGGTCTACCACTTTACACTGGGAGCGGTACCATTTATGTACCGAACGACGGACAACAT
Tubulin     >   S  V  A  E  I  T  N  A  C  F  E  P  A  N  Q  M  V  K  C  D  P  R  H  G  K  Y  M  A  C  C  L  L  Y
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                 BmgB1                    BsrD1                                PflM1            Bgl1
                   |                        |                                    |                |
            CCGTGGTGACGTGGTTCCCAAAGATGTCAATGCTGCCATTGCCACCATCAAAACCAAGCGCAGCATCCAGTTTGTGGATTGGTGCCCCACTGGCTTCAAG
     2301   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
            GGCACCACTGCACCAAGGGTTTCTACAGTTACGACGGTAACGGTGGTAGTTTTGGTTCGCGTCGTAGGTCAAACACCTAACCACGGGGTGACCGAAGTTC
Tubulin       > R  G  D  V  V  P  K  D  V  N  A  A  I  A  T  I  K  T  K  R  S  I  Q  F  V  D  W  C  P  T  G  F  K

                                                  Msc1                     Blp1                  Bpu10
                                     Ale1   Bsa1  EcoN1                    Sph1|            BsrD1 BbvC1
                                        |      |     |                       ||                |     |
            GTTGGCATCAACTACCAGCCTCCCACTGTGGTGCCTGGTGGAGACCTGGCCAAGGTACAGAGAGCTGTGTGCATGCTGAGCAACACCACAGCCATTGCTG
     2401   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
            CAACCGTAGTTGATGGTCGGAGGGTGACACCACGGACCACCTCTGGACCGGTTCCATGTCTCTCGACACACGTACGACTCGTTGTGGTGTCGGTAACGAC
Tubulin       > V  G  I  N  Y  Q  P  P  T  V  V  P  G  G  D  L  A  K  V  Q  R  A  V  C  M  L  S  N  T  T  A  I  A  E

                Stu1                                                Bae1b                          Bae1a
                  |                                                   |                              |
            AGGCCTGGGCTCGCCTGGACCACAAGTTTGACCTGATGTATGCCAAGCGTGCCTTTGTTCACTGGTACGTGGGTGAGGGGATGGAGGAAGGCGAGTTTTC
     2501   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
            TCCGGACCCGAGCGGACCTGGTGTTCAAACTGGACTACATACGGTTCGCACGGAAACAAGTGACCATGCACCCACTCCCCTACCTCCTTCCGCTCAAAAG
Tubulin       >  A  W  A  R  L  D  H  K  F  D  L  M  Y  A  K  R  A  F  V  H  W  Y  V  G  E  G  M  E  E  G  E  F  S

                                     EcoN1             BpuE1    BseR1             SpDon
                                        |                 |        |                 |
            AGAGGCCCGTGAAGATATGGCTGCCCTTGAGAAGGATTATGAGGAGGTTGGTGTGGATTCTGTTGAAGGAGAGGGTGAGGAAGAAGGAGAGGAATACTAA
     2601   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
            TCTCCGGGCACTTCTATACCGACGGGAACTCTTCCTAATACTCCTCCAACCACACCTAAGACAACTTCCTCTCCCACTCCTTCTTCCTCTCCTTATGATT
Tubulin       > E  A  R  E  D  M  A  A  L  E  K  D  Y  E  E  V  G  V  D  S  V  E  G  E  G  E  E  E  G  E  E  Y  *

          BamH1        Xba1      Bcl1BsaB1                                SpDon   Dra1
            |            |         |    |                                  |       |
            GGATCCACCGGATCTAGATAACTGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGA
     2701   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
            CCTAGGTGGCCTAGATCTATTGACTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACT
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                 Bsm1
                Mfe1|        Hpa1       polyA    Psi1      polyA                        polyA
                   ||           |           |       |          |                           |
     AACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATT
2801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
     TTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAA

      Bts1 Bsm1                                       Mlu1     SpDon        Ssp1
          |    |                                        |         |           |
     TTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAACGCGTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTT
2901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
     AAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTGCGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAA

                                                   Psi1
                                                     |
     TTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTT
3001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
     AACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAA

                                                                                   BtgZ1
                 BsaXb                  Drd1    BsaXa                             Dra3|
                     |                     |        |                                ||
     TGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAAT
3101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
     ACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTA

                                                                                      Nae1
                                          SpAcc                                  NgoM4 |
                                             |                                        | |
     CAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAG
3201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
     GTTCAAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTC

                         BsrB1
                            |
     AAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCG
3301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
     TTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGC
```

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                                                                                                  BciV1
                                                                                               BspH1  |
                                                                                 polyA       BsrB1 |  |
                                                                                   |             | |  |
      CTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGAC
3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
      GATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTG

                                                                                 Eci1
                                 Ssp1  Ear1        Bsu36              Pvu2 |
                                    |     |           |                 | |
      AATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCC
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      TTATTGGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGG

                                          Nsi1
                                        Sph1 |
                                       BfrB1 |
          BseY1                     BstAP  | |            SexA1                     BseY1
              |                        |  | |                |                        |
      CCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGC
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      GGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACG

            Nsi1
          Sph1 |
         BfrB1 |                                                        Eci1
      BstAP  | |                       Eci1                 Eci1     Bmr1|       Eci1            Nco1
          |  | |                          |                   |        ||          |               |
      AAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGG
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      TTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACC
```

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                                                                                  Avr2
                                          Sfi1                                   Stu1|
                   polyA                  Bgl1                     SpDon       BseR1  ||
                     |                      |                         |              |  ||
     CTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGC
3801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
     GACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACG

                                                  BspM1
       Cla1                BsaB1                  BfuA1                Eag1
         |                   |                      |                   |
     AAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGC
3901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
     TTTCTAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCG

                                                                    Nar1
                Bmr1                                               Kas1|                        Drd1
                  |                                                  ||                          |
     TATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCG
4001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
     ATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGC

                                                                        Pvu2
                                            Msc1                   Fsp1   |        PflF1
                                              |                      |   |           |
     GTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGG
4101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
     CACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCC

            Eco57                                     SpDon                          BciV1         BsrD1
              |                                         |                              |             |
     AAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGG
4201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
     TTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCC
```

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                                 BtgZ1
                              BspM1  |
                              BfuA1  |
                                  |  |
     CGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATC
4301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
     GCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAG

           Sap1
           Ear1                          BpuE1                          Sph1                        Nco1
              |                             |                              |                           |
     AGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCA
4401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
     TCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGT

                                                                  BseY1
                                                                 Nae1 |
                 BtgZ1                                        NgoM4 | |        Rsr2         Eci1
                    |                                            | | |           |            |
     TGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATA
4501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
     ACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTAT

                   Sap1                                                          BtgZ1
                   Ear1                      Eco57         BssS1                BsrB1 |
                      |                        |             |                    | |
     GCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCG
4601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
     CGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGC

                                                                                  BssS1
                                                                                  BspM1
                                BsrB1          BstB1                              BfuA1
                                   |             |                                  |
     CCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCC
4701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
     GGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGG
```

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                                                 Nae1
                                              NgoM4 |
            SpAcc                              Bpm1 |
              |                                  | |
      ACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCC
4801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
      TGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGG

        Bpm1
    SpAcc  |
     Avr2  |                                                        polyA        polyA
       |   |                                                          |            |
      ACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGG
4901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
      TGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACC

                                                   Bsa1
                                                     |
      GTCGTTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTT
5001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
      CAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAA

                                                          BstAP
                          SpDon                           AlwN1      Bsu36
                            |                               |          |
      TCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTT
5101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
      AGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAA

            Dra1                Dra1                                BspH1
              |                   |                                   |
      AGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCA
5201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
      TCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGT

                                                        BpuE1
                                                          |
      CTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCA
5301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5400
      GACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGT
```

```
                                        Eco57                                                   SpAcc
                                           |                                                      |
     GCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGC
5401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5500
     CGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCG

                                                                                AlwN1
                                                                                  |
     CGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTG
5501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5600
     GCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCAC

  BpuE1                                                                   ApaL1     BseY1
     |                                                                       |         |
     TCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACC
5601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5700
     AGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGG

                                                                                          BciV1
                              SpAcc                                                  Eci1    |
                                 |                                                      |    |
     TACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAA
5701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5800
     ATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTT

           BssS1                                     SpAcc                            Drd1            BpuE1
              |                                        |                                |                |
     CAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATG
5801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5900
     GTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTAC

                                                                                        SpDon
                    SpAcc     Eci1                                                     BspLU|
                       |        |                                                          ||
     CTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCG
5901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6000
     GAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGC
```

```
                                          Nsi1
                                       BfrB1 |
                                           | |
            TTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
      6001  |||||||||*|||||||||*|||||||||*|||||||||*|| 6042
            AATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aat2	**Afe1**	Age1	Ale1	AlwN1	ApaL1	**Ase1**	Avr2	**Bae1a**	**Bae1b**	**BamH1**	**Bbs1**	**BbvC1**	BciV1
Bcl1	BfrB1	BfuA1	Bgl1	**Bgl2**	**Blp1**	BmgB1	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa
BsaXb	BseR1	BseY1	Bsg1	Bsm1	BsmB1	**BspE1**	BspH1	**BspLU**	BspM1	BsrB1	BsrD1	**BsrG1**	BssS1
BstAP	**BstB1**	**BstE2**	BstX1	Bsu36	BtgZ1	Bts1	**Cla1**	Dra1	Dra3	Drd1	**Eag1**	Ear1	Eci1
Eco57	EcoN1	EcoR1	**EcoRV**	**Fsp1**	**Hpa1**	**Kas1**	**Mfe1**	**Mlu1**	Msc1	Nae1	**Nar1**	Nco1	Nde1
NgoM4	**Nhe1**	Nsi1	**PflF1**	PflM1	**Pml1**	polyA	**PshA1**	Psi1	Pvu2	**Rsr2**	**Sac1**	**Sac2**	Sap1
SexA1	**Sfi1**	**Sma1**	**SnaB1**	SpAcc	SpDon	Sph1	Ssp1	Stu1	**Xba1**	Xcm1	**Xho1**	Xmn1	

Unique:

Afe1	**Ase1**	**Bae1a**	**Bae1b**	**BamH1**	**Bbs1**	**BbvC1**	**Bcl1**	**Bgl2**	**Blp1**	**BspE1**	**BspLU**	**BsrG1**	**BstB1**
BstE2	**Cla1**	**Eag1**	**EcoRV**	**Fsp1**	**Hpa1**	**Kas1**	**Mfe1**	**Mlu1**	**Nar1**	**Nhe1**	**PflF1**	**Pml1**	**PshA1**
Rsr2	**Sac1**	**Sac2**	**Sfi1**	**Sma1**	**SnaB1**	**Xba1**	**Xho1**						

Not found:

Aar1	Acc65	Acl1	Afl2	Ahd1	Apa1	Asc1	AsiS1	Bcg1a	Bcg1b	BsiW1	BssH2	BstZ1	_Chi
EcoK	ScFRT	Fse1	FspA1	Hind3	I_Ceu	Kpn1	loxP	Not1	Nru1	Pac1	Pme1	PspOM	Pst1
Pvu1	Sal1	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													