pCasper3-BG 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 red. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site). TagBFP amino acids are shown in blue, TagGFP2 amino acids are shown in green, Linker amino acids are shown in black.

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

                          Aat2                    SpAcc                         Aat2
                            |                       |                             |
     CCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGT
 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

                                                                  BamH1
                                                                 Sma1 |
                                                                Apa1| |
                                                            PspOM   || |
                          Hind3                             Sac2|   || |
                   Xho1   Sac1 |  EcoR1      Sal1      Kpn1  ||   || |
         BpuE1 Bgl2    | Ecl2 | |BstB1 |     Pst1| Acc65   |  ||   || |  Age1
             |    |   |    | | |    | |        ||     |   |  ||   || |     |
     CCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCTGCAGTCGACGGTACCGCGGGCCCGGGATCCACCGGTCGCCACCATGAGCGAGCTGATTAAGGAGA
601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
     GGCCTGAGTCTAGAGCTCGAGTTCGAAGCTTAAGACGTCAGCTGCCATGGCGCCCGGGCCCTAGGTGGCCAGCGGTGGTACTCGCTCGACTAATTCCTCT
TagBFP    >                                                                   M  S  E  L  I  K  E  N

                    BsrG1                                 ApaL1                       SpAcc
                      |                                     |                           |
     ACATGCACATGAAGCTGTACATGGAGGGCACCGTGGACAACCATCACTTCAAGTGCACATCCGAGGGCGAAGGCAAGCCCTACGAGGGCACCCAGACCAT
701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
     TGTACGTGTACTTCGACATGTACCTCCCGTGGCACCTGTTGGTAGTGAAGTTCACGTGTAGGCTCCCGCTTCCGTTCGGGATGCTCCCGTGGGTCTGGTA
TagBFP    >  M  H  M  K  L  Y  M  E  G  T  V  D  N  H  H  F  K  C  T  S  E  G  E  G  K  P  Y  E  G  T  Q  T  M

     GAGAATCAAGGTGGTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGCTACTAGCTTCCTCTACGGCAGCAAGACCTTCATCAACCACACCCAG
801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
     CTCTTAGTTCCACCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGATCGAAGGAGATGCCGTCGTTCTGGAAGTAGTTGGTGTGGGTC
TagBFP    >  R  I  K  V  V  E  G  G  P  L  P  F  A  F  D  I  L  A  T  S  F  L  Y  G  S  K  T  F  I  N  H  T  Q
```

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                                   Bsu36       SpDon                          Bbs1             Bpm1
                                     |           |                              |                |
            GGCATCCCCGACTTCTTCAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACATACGAAGACGGGGGCGTGCTGACCGCTACCCAGGACA
       901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
            CCGTAGGGGCTGAAGAAGTTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGGTGTATGCTTCTGCCCCCGCACGACTGGCGATGGGTCCTGT
TagBFP    > G  I  P  D  F  F  K  Q  S  F  P  E  G  F  T  W  E  R  V  T  T  Y  E  D  G  G  V  L  T  A  T  Q  D  T

                                                                 SpDon                            BseY1
                                                                   |                                |
            CCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACTTCACATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGA
      1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
            GGTCGGAGGTCCTGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCCACTTGAAGTGTAGGTTGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCT
TagBFP    >   S  L  Q  D  G  C  L  I  Y  N  V  K  I  R  G  V  N  F  T  S  N  G  P  V  M  Q  K  K  T  L  G  W  E

            BsmB1
         Stu1  |                                Bgl1                     BssS1          Eco57
            |  |                                  |                        |              |
            GGCCTTCACCGAGACGCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAAACGACATGGCCCTGAAGCTCGTGGGCGGGAGCCATCTGATCGCAAACATC
      1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
            CCGGAAGTGGCTCTGCGACATGGGGCGACTGCCGCCGGACCTTCCGTCTTTGCTGTACCGGGACTTCGAGCACCCGCCCTCGGTAGACTAGCGTTTGTAG
TagBFP    >  A  F  T  E  T  L  Y  P  A  D  G  G  L  E  G  R  N  D  M  A  L  K  L  V  G  G  S  H  L  I  A  N  I

                                BpuE1                                                SpAcc                Bsa1
                                   |                                                    |                   |
            AAGACCACATATAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCTGGCGTCTACTATGTGGACTACAGACTGGAAAGAATCAAGGAGGCCAACAACG
      1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
            TTCTGGTGTATATCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGACCGCAGATGATACACCTGATGTCTGACCTTTCTTAGTTCCTCCGGTTGTTGC
TagBFP    > K  T  T  Y  R  S  K  K  P  A  K  N  L  K  M  P  G  V  Y  Y  V  D  Y  R  L  E  R  I  K  E  A  N  N  E

                                         Bts1                                Hind3
            PshA1        BssS1 Dra3      Msc1| AlwN1          SpAcc          Bmr1 EcoR1
                |            |    |         ||     |              |              |     |
            AGACCTACGTCGAGCAGCACGAGGTGGCAGTGGCCAGATACTGCGACCTCCCTAGCAAACTGGGGCACAAGCTTGAATTCGGTGGTTCTGGTTCTGATGA
      1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
            TCTGGATGCAGCTCGTCGTGCTCCACCGTCACCGGTCTATGACGCTGGAGGGATCGTTTGACCCCGTGTTCGAACTTAAGCCACCAAGACCAAGACTACT
TagBFP    >   T  Y  V  E  Q  H  E  V  A  V  A  R  Y  C  D  L  P  S  K  L  G  H  K  L  E  F  G  G  S  G  S  D  E
```

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                                                                BseR1
                                   Kpn1                         Nae1|                                ApaL1
                Hind3            Acc65   | BsrB1              NgoM4 ||                              BmgB1|
                    |                |   |     |                  | ||                                   ||
           AGTTGATAAGCTTGGTGGTTCTGGTTCTGGTACCATGAGCGGGGGCGAGGAGCTGTTCGCCGGCATCGTGCCCGTGCTGATCGAGCTGGACGGCGACGTG
      1401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
           TCAACTATTCGAACCACCAAGACCAAGACCATGGTACTCGCCCCCGCTCCTCGACAAGCGGCCGTAGCACGGGCACGACTAGCTCGACCTGCCGCTGCAC
TagGFP2      >  V  D  K  L  G  G  S  G  S  G  T  M  S  G  G  E  E  L  F  A  G  I  V  P  V  L  I  E  L  D  G  D  V

                                                                                    BsaXb
                                                       BsaXa    Bsg1              Bpm1  |
                                                          |       |                 |  |
           CACGGCCACAAGTTCAGCGTGCGCGGCGAGGGCGAGGGCGACGCCGACTACGGCAAGCTGGAGATCAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGC
      1501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
           GTGCCGGTGTTCAAGTCGCACGCGCCGCTCCCGCTCCCGCTGCGGCTGATGCCGTTCGACCTCTAGTTCAAGTAGACGTGGTGGCCGTTCGACGGGCACG
TagGFP2      > H  G  H  K  F  S  V  R  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

                   BstE2
                  Ale1 |                      BstAP                                  Xmn1
                     | |                         |                                      |
           CCTGGCCCACCCTGGTGACCACCCTCTGCTACGGCATCCAGTGCTTCGCCCGCTACCCCGAGCACATGAAGATGAACGACTTCTTCAAGAGCGCCATGCC
      1601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
           GGACCGGGTGGGACCACTGGTGGGAGACGATGCCGTAGGTCACGAAGCGGGCGATGGGGCTCGTGTACTTCTACTTGCTGAAGAAGTTCTCGCGGTACGG
TagGFP2      >   W  P  T  L  V  T  T  L  C  Y  G  I  Q  C  F  A  R  Y  P  E  H  M  K  M  N  D  F  F  K  S  A  M  P

                                                                                                  SpDon
                        EcoK                                        Sac2 SpDon                   Ale1 |
                          |                                            |     |                     | |
           CGAGGGCTACATCCAGGAGCGCACCATCCAGTTCCAGGACGACGGCAAGTACAAGACCCGCGGCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGC
      1701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
           GCTCCCGATGTAGGTCCTCGCGTGGTAGGTCAAGGTCCTGCTGCCGTTCATGTTCTGGGCGCCGCTCCACTTCAAGCTCCCGCTGTGGGACCACTTGGCG
TagGFP2      > E  G  Y  I  Q  E  R  T  I  Q  F  Q  D  D  G  K  Y  K  T  R  G  E  V  K  F  E  G  D  T  L  V  N  R
```

```
                                                                                                BsrG1
                                                                                               Dra3 |
                                                                                             Eci1 | |
                                Eco57                       PflM1                    Bpm1  | | |
                                   |                           |                       |  | | |
            ATCGAGCTGAAGGGCAAGGACTTCAAGGAGGACGGCAACATCCTGGGCCACAAGCTGGAGTACAGCTTCAACAGCCACAACGTGTACATCCGCCCCGACA
      1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
            TAGCTCGACTTCCCGTTCCTGAAGTTCCTCCTGCCGTTGTAGGACCCGGTGTTCGACCTCATGTCGAAGTTGTCGGTGTTGCACATGTAGGCGGGGCTGT
TagGFP2       > I  E  L  K  G  K  D  F  K  E  D  G  N  I  L  G  H  K  L  E  Y  S  F  N  S  H  N  V  Y  I  R  P  D  K

                   Xcm1                     Bpm1                          Pvu2            Bsg1       Xcm1
                     |                         |                             |               |          |
            AGGCCAACAACGGCCTGGAGGCTAACTTCAAGACCCGCCACAACATCGAGGGCGGCGGCGTGCAGCTGGCCGACCACTACCAGACCAACGTGCCCCTGGG
      1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
            TCCGGTTGTTGCCGGACCTCCGATTGAAGTTCTGGGCGGTGTTGTAGCTCCCGCCGCCGCACGTCGACCGGCTGGTGATGGTCTGGTTGCACGGGGACCC
TagGFP2       >   A  N  N  G  L  E  A  N  F  K  T  R  H  N  I  E  G  G  G  V  Q  L  A  D  H  Y  Q  T  N  V  P  L  G

                                                                                                  Eco57
                           BsaB1          Bpu10                                                   Dra3
                             |              |                                                       |
            CGACGGCCCCGTGCTGATCCCCATCAACCACTACCTGAGCACTCAGACCAAGATCAGCAAGGACCGCAACGAGGCCCGCGACCACATGGTGCTCCTGGAG
      2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
            GCTGCCGGGGCACGACTAGGGGTAGTTGGTGATGGACTCGTGAGTCTGGTTCTAGTCGTTCCTGGCGTTGCTCCGGGCGCTGGTGTACCACGAGGACCTC
TagGFP2       >  D  G  P  V  L  I  P  I  N  H  Y  L  S  T  Q  T  K  I  S  K  D  R  N  E  A  R  D  H  M  V  L  L  E

                                                      Not1
                 AlwN1 Bpm1          PflM1      BsrG1 SpDon  Eag1      Xba1   BsaB1
                     |    |             |          |     |     |         |       |
            TCCTTCAGCGCCTGCTGCCACACCCACGGCATGGACGAGCTGTACAGGTAAGCGGCCGCGACTCTAGATCATAATCAGCCATACCACATTTGTAGAGGTT
      2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
            AGGAAGTCGCGGACGACGGTGTGGGTGCCGTACCTGCTCGACATGTCCATTCGCCGGCGCTGAGATCTAGTATTAGTCGGTATGGTGTAAACATCTCCAA
TagGFP2       > S  F  S  A  C  C  H  T  H  G  M  D  E  L  Y  R  *

                                                                Bsm1
                 SpDon   Dra1                                  Mfe1|        Hpa1       polyA    Psi1
                    |      |                                     ||           |           |       |
            TTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTT
      2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
            AATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAA
```

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    polyA                        polyA            Bts1 Bsm1                                Afl2
      |                            |                |    |                                     |
      ACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAGGCGT
2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
      TGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTCCGCA

      SpDon        Ssp1                                                                          Psi1
        |            |                                                                              |
      AAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAA
2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
      TTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATT

                                                                BsaXb                 Drd1    BsaXa
                                                                  |                     |        |
      ATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACC
2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
      TAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGG

                                BtgZ1
                                Dra3|                                                   SpAcc
                                   ||                                                      |
      GTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCC
2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
      CAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGG

                                   Nae1
                                NgoM4 |                                   BsrB1
                                    | |                                     |
      CCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGT
2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
      GGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCA

      CACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGT
2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
      GTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACA
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                                   BciV1
                                 BspH1  |
      polyA                     BsrB1 |  |                            Ssp1  Ear1        Bsu36
          |                         | |  |                               |     |            |
      TTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAA
2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
      AATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTT

                                                                                      Nsi1
                                                                                    Sph1 |
          Eci1                                                                     BfrB1 |
         Pvu2 |                                       BseY1                    BstAP  | |            SexA1
            | |                                          |                          |  | |                |
      GAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACC
3001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
      CTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGG

                                                   Nsi1
                                                 Sph1 |
                                                BfrB1 |
                         BseY1                BstAP  | |                        Eci1
                             |                    |  | |                          |
      AGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCC
3101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
      TCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGG

             Eci1                                                                      Sfi1
   Eci1     Bmr1|       Eci1            Nco1                   polyA                   Bgl1
      |        ||          |               |                      |                      |
      CGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATT
3201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
      GCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAA

                                Avr2
                               Stu1|                                                                BspM1
         SpDon             BseR1  ||              Cla1                BsaB1                        BfuA1
             |                 |  ||                |                    |                            |
      CCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATT
3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
      GGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAA
```

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                Eag1                                        Bmr1
                  |                                           |
      GCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA
3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
      CGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGT

          Nar1
         Kas1|                        Drd1                                                    Msc1
            ||                          |                                                       |
      GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGG
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      CGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCC

                Pvu2
           Fsp1   |       PflF1                        Eco57                                    SpDon
             |    |          |                           |                                          |
      GCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCT
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      CGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGA

                                                                                   BtgZ1
                                                                              BspM1  |
                            BciV1         BsrD1                               BfuA1  |
                                |             |                                   |  |
      TGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      ACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCG

                                                  Sap1
                                                  Ear1                            BpuE1
                                                    |                               |
      ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGC
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      TAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCG
```

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                Sph1                        Nco1                BtgZ1
                   |                           |                   |
     TCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCAT
3901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
     AGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTA

            BseY1
           Nae1 |                                                Sap1
       NgoM4 | |        Rsr2         Eci1                       Ear1                    Eco57
           | | |           |            |                          |                        |
     CGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTC
4001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
     GCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAG

                       BtgZ1
  BssS1               BsrB1 |                                                BsrB1          BstB1
     |                   | |                                                   |              |
     CTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGAC
4101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
     GAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTG

                           BssS1                                                          Nae1
                           BspM1                                                       NgoM4 |
                           BfuA1                       SpAcc                            Bpm1 |
                               |                          |                                | |
     CGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGG
4201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
     GCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACC

                                                  Bpm1
                                              SpAcc  |
                                               Avr2  |
                                                  |  |
     ATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCG
4301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
     TACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGC
```

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          polyA        polyA                                                                  Bsa1
              |            |                                                                     |
     CTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCC
4401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
     GATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGG

     ACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGG
4501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
     TGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCC

          BstAP
          AlwN1      Bsu36                            Dra1               Dra1
              |          |                               |                  |
     GCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTG
4601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
     CGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAAC

       BspH1
           |
     ATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCT
4701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
     TATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGA

    BpuE1                                                                    Eco57
       |                                                                        |
     GCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGC
4801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
     CGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCG

                                     SpAcc
                                        |
     TTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGC
4901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
     AAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACG
```

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                 AlwN1                      BpuE1
                    |                          |
     TAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTG
5001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
     ATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGAC

             ApaL1     BseY1                                          SpAcc
                 |         |                                              |
     AACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAA
5101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
     TTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTT

                            BciV1
                         Eci1   |                    BssS1                                  SpAcc
                            |   |                       |                                      |
     GGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTG
5201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
     CCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGAC

                         Drd1            BpuE1                SpAcc     Eci1
                            |                |                   |        |
     TCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTT
5301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5400
     AGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAA

                           SpDon                                                   Nsi1
                          BspLU|                                                BfrB1 |
                               ||                                                    | |
     CCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
5401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*||||| 5485
     GGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aat2	Acc65	**Afe1**	**Afl2**	**Age1**	Ale1	AlwN1	**Apa1**	ApaL1	**Ase1**	Avr2	**BamH1**	**Bbs1**	BciV1
BfrB1	BfuA1	Bgl1	**Bgl2**	**BmgB1**	Bmr1	Bpm1	**Bpu10**	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1
BseY1	Bsg1	Bsm1	**BsmB1**	BspH1	**BspLU**	BspM1	BsrB1	**BsrD1**	BsrG1	BssS1	BstAP	BstB1	**BstE2**
Bsu36	BtgZ1	Bts1	**Cla1**	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	**Ecl2**	Eco57	**EcoK**	EcoR1
Fsp1	Hind3	**Hpa1**	**Kas1**	Kpn1	**Mfe1**	Msc1	Nae1	**Nar1**	Nco1	**Nde1**	NgoM4	**Nhe1**	**Not1**
Nsi1	**PflF1**	PflM1	polyA	**PshA1**	Psi1	**PspOM**	**Pst1**	Pvu2	**Rsr2**	**Sac1**	Sac2	**Sal1**	Sap1
SexA1	**Sfi1**	**Sma1**	**SnaB1**	SpAcc	SpDon	Sph1	Ssp1	Stu1	**Xba1**	Xcm1	**Xho1**	**Xmn1**	

Unique:

Afe1	**Afl2**	**Age1**	**Apa1**	**Ase1**	**BamH1**	**Bbs1**	**Bgl2**	**BmgB1**	**Bpu10**	**BsmB1**	**BspLU**	**BsrD1**	**BstE2**
Cla1	**Ecl2**	**EcoK**	**Fsp1**	**Hpa1**	**Kas1**	**Mfe1**	**Nar1**	**Nde1**	**Nhe1**	**Not1**	**PflF1**	**PshA1**	**PspOM**
Pst1	**Rsr2**	**Sac1**	**Sal1**	**SexA1**	**Sfi1**	**Sma1**	**SnaB1**	**Xba1**	**Xho1**	**Xmn1**			

Not found:

Aar1	Acl1	Ahd1	Asc1	AsiS1	Bae1a	Bae1b	BbvC1	Bcg1a	Bcg1b	Bcl1	Blp1	BsiW1	BspE1
BssH2	BstX1	BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	EcoN1	EcoRV	FCatB	FCatL	FCatR	FCatP
ScFRT	Fse1	FspA1	I_Ceu	loxP	Mlu1	Nru1	Pac1	Pme1	Pml1	Pvu1	R4atB	R4atL	R4atP
R4atR	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													