pTagBFP-actin 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 bold blue, beta-Actin 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
                                                                                                    |
        ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCGGTC
    501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
        TGTTGAGGCGGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCCAG

                                                BsrG1                                 ApaL1
                                                  |                                     |
        GCCACCATGAGCGAGCTGATTAAGGAGAACATGCACATGAAGCTGTACATGGAGGGCACCGTGGACAACCATCACTTCAAGTGCACATCCGAGGGCGAAG
    601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
        CGGTGGTACTCGCTCGACTAATTCCTCTTGTACGTGTACTTCGACATGTACCTCCCGTGGCACCTGTTGGTAGTGAAGTTCACGTGTAGGCTCCCGCTTC
TagBFP      >      M  S  E  L  I  K  E  N  M  H  M  K  L  Y  M  E  G  T  V  D  N  H  H  F  K  C  T  S  E  G  E  G

          SpAcc
              |
        GCAAGCCCTACGAGGGCACCCAGACCATGAGAATCAAGGTGGTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGCTACTAGCTTCCTCTACGG
    701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
        CGTTCGGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCCACCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGATCGAAGGAGATGCC
TagBFP      >  K  P  Y  E  G  T  Q  T  M  R  I  K  V  V  E  G  G  P  L  P  F  A  F  D  I  L  A  T  S  F  L  Y  G

                                                                  Bsu36       SpDon
                                                                    |           |
        CAGCAAGACCTTCATCAACCACACCCAGGGCATCCCCGACTTCTTCAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACATACGAAGAC
    801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
        GTCGTTCTGGAAGTAGTTGGTGTGGGTCCCGTAGGGGCTGAAGAAGTTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGGTGTATGCTTCTG
TagBFP      >  S  K  T  F  I  N  H  T  Q  G  I  P  D  F  F  K  Q  S  F  P  E  G  F  T  W  E  R  V  T  T  Y  E  D

       Bbs1            Bpm1                                                                SpDon
         |                |                                                                    |
        GGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACTTCACATCCAACGGCCCTG
    901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
        CCCCCGCACGACTGGCGATGGGTCCTGTGGTCGGAGGTCCTGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCCACTTGAAGTGTAGGTTGCCGGGAC
TagBFP      > G  G  V  L  T  A  T  Q  D  T  S  L  Q  D  G  C  L  I  Y  N  V  K  I  R  G  V  N  F  T  S  N  G  P  V
```

```
                                   BsmB1
                         BseY1    Stu1  |                                  Bgl1                      BssS1
                             |       |  |                                     |                         |
            TGATGCAGAAGAAAACACTCGGCTGGGAGGCCTTCACCGAGACGCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAAACGACATGGCCCTGAAGCTCGT
      1001  |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 1100
            ACTACGTCTTCTTTTGTGAGCCGACCCTCCGGAAGTGGCTCTGCGACATGGGGCGACTGCCGCCGGACCTTCCGTCTTTGCTGTACCGGGACTTCGAGCA
TagBFP      >  M  Q  K  K  T  L  G  W  E  A  F  T  E  T  L  Y  P  A  D  G  G  L  E  G  R  N  D  M  A  L  K  L  V

                  Eco57                                BpuE1
                      |                                   |
            GGGCGGGAGCCATCTGATCGCAAACATCAAGACCACATATAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCTGGCGTCTACTATGTGGACTACAGA
      1101  |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 1200
            CCCGCCCTCGGTAGACTAGCGTTTGTAGTTCTGGTGTATATCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGACCGCAGATGATACACCTGATGTCT
TagBFP      > G  G  S  H  L  I  A  N  I  K  T  T  Y  R  S  K  K  P  A  K  N  L  K  M  P  G  V  Y  Y  V  D  Y  R

                                                                  Bts1                                Hind3
         SpAcc                  Bsa1       PshA1       BssS1 Dra3      Msc1| AlwN1          SpAcc          Bmr1
             |                     |           |           |    |         ||     |              |             |
            CTGGAAAGAATCAAGGAGGCCAACAACGAGACCTACGTCGAGCAGCACGAGGTGGCAGTGGCCAGATACTGCGACCTCCCTAGCAAACTGGGGCACAAGC
      1201  |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 1300
            GACCTTTCTTAGTTCCTCCGGTTGTTGCTCTGGATGCAGCTCGTCGTGCTCCACCGTCACCGGTCTATGACGCTGGAGGGATCGTTTGACCCCGTGTTCG
TagBFP      > L  E  R  I  K  E  A  N  N  E  T  Y  V  E  Q  H  E  V  A  V  A  R  Y  C  D  L  P  S  K  L  G  H  K  L

                                                                                                  Nae1
                          Xho1                                                                 NgoM4 |
             BspE1     Bgl2   |              EcoRV     BsaXb  Sal1                        BsaXa  | |
                 |        |   |                 |         |     |                            |  | |
            TTAATTCCGGACTCAGATCTCGAGCTATGGATGATGATATCGCCGCGCTCGTCGTCGACAACGGCTCCGGCATGTGCAAGGCCGGCTTCGCGGGCGACGA
      1301  |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 1400
            AATTAAGGCCTGAGTCTAGAGCTCGATACCTACTACTATAGCGGCGCGAGCAGCAGCTGTTGCCGAGGCCGTACACGTTCCGGCCGAAGCGCCCGCTGCT
TagBFP/actin >  N  S  G  L  R  S  R  A  M  D  D  D  I  A  A  L  V  V  D  N  G  S  G  M  C  K  A  G  F  A  G  D  D

                Sma1
                Bgl1                      Nar1
               Bbs1|                     Kas1|
                   ||                        ||
            TGCCCCCCGGGCCGTCTTCCCCTCCATCGTGGGGCGCCCCAGGCACCAGGGCGTGATGGTGGGCATGGGTCAGAAGGATTCCTATGTGGGCGACGAGGCC
      1401  |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 1500
            ACGGGGGGCCCGGCAGAAGGGGAGGTAGCACCCCGCGGGGTCCGTGGTCCCGCACTACCACCCGTACCCAGTCTTCCTAAGGATACACCCGCTGCTCCGG
beta-Actin  > A  P  R  A  V  F  P  S  I  V  G  R  P  R  H  Q  G  V  M  V  G  M  G  Q  K  D  S  Y  V  G  D  E  A
```

```
                                                  Eco57                  Bmr1
                                                    |                      |
            CAGAGCAAGAGAGGCATCCTCACCCTGAAGTACCCCATCGAGCACGGCATCGTCACCAACTGGGACGACATGGAGAAAATCTGGCACCACACCTTCTACA
      1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
            GTCTCGTTCTCTCCGTAGGAGTGGGACTTCATGGGGTAGCTCGTGCCGTAGCAGTGGTTGACCCTGCTGTACCTCTTTTAGACCGTGGTGTGGAAGATGT
beta-Actin   > Q  S  K  R  G  I  L  T  L  K  Y  P  I  E  H  G  I  V  T  N  W  D  D  M  E  K  I  W  H  H  T  F  Y  N

                                       BseR1
                                    Dra3   |
                                   BstAP   |                                                  Bsa1
                                       |   |                                                    |
            ATGAGCTGCGTGTGGCTCCCGAGGAGCACCCCGTGCTGCTGACCGAGGCCCCCCTGAACCCCAAGGCCAACCGCGAGAAGATGACCCAGATCATGTTTGA
      1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
            TACTCGACGCACACCGAGGGCTCCTCGTGGGGCACGACGACTGGCTCCGGGGGGACTTGGGGTTCCGGTTGGCGCTCTTCTACTGGGTCTAGTACAAACT
beta-Actin   >   E  L  R  V  A  P  E  E  H  P  V  L  L  T  E  A  P  L  N  P  K  A  N  R  E  K  M  T  Q  I  M  F  E

                     BseY1                                                                          PflF1
                         |                                                                              |
            GACCTTCAACACCCCAGCCATGTACGTTGCTATCCAGGCTGTGCTATCCCTGTACGCCTCTGGCCGTACCACTGGCATCGTGATGGACTCCGGTGACGGG
      1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
            CTGGAAGTTGTGGGGTCGGTACATGCAACGATAGGTCCGACACGATAGGGACATGCGGAGACCGGCATGGTGACCGTAGCACTACCTGAGGCCACTGCCC
beta-Actin   >  T  F  N  T  P  A  M  Y  V  A  I  Q  A  V  L  S  L  Y  A  S  G  R  T  T  G  I  V  M  D  S  G  D  G

                     Bcg1a
       BstE2         Dra3|  SpAcc                      Bcg1b   Xcm1                                BspH1
           |            ||      |                          |      |                                    |
            GTCACCCACACTGTGCCCATCTACGAGGGGTATGCCCTCCCCCATGCCATCCTGCGTCTGGACCTGGCTGGCCGGGACCTGACTGACTACCTCATGAAGA
      1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
            CAGTGGGTGTGACACGGGTAGATGCTCCCCATACGGGAGGGGGTACGGTAGGACGCAGACCTGGACCGACCGGCCCTGGACTGACTGATGGAGTACTTCT
beta-Actin   > V  T  H  T  V  P  I  Y  E  G  Y  A  L  P  H  A  I  L  R  L  D  L  A  G  R  D  L  T  D  Y  L  M  K  I

                                  SpDon  Eag1  BsrB1           BsaXa                        BsaXb
                                      |     |      |               |                            |
            TCCTCACCGAGCGCGGCTACAGCTTCACCACCACGGCCGAGCGGGAAATCGTGCGTGACATTAAGGAGAAGCTGTGCTACGTCGCCCTGGACTTCGAGCA
      1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
            AGGAGTGGCTCGCGCCGATGTCGAAGTGGTGGTGCCGGCTCGCCCTTTAGCACGCACTGTAATTCCTCTTCGACACGATGCAGCGGGACCTGAAGCTCGT
beta-Actin   >   L  T  E  R  G  Y  S  F  T  T  T  A  E  R  E  I  V  R  D  I  K  E  K  L  C  Y  V  A  L  D  F  E  Q
```

```
                                  Sap1
                                  Ear1
                                SpAcc|                                                  BsrD1
                 Msc1   BseR1        Xcm1  ||                 Bpm1     Drd1                  BsrB1         Bsu36
                    |       |           |  ||                    |        |                      |             |
            AGAGATGGCCACGGCTGCTTCCAGCTCCTCCCTGGAGAAGAGCTACGAGCTGCCTGACGGCCAGGTCATCACCATTGGCAATGAGCGGTTCCGCTGCCCT
       2001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
            TCTCTACCGGTGCCGACGAAGGTCGAGGAGGGACCTCTTCTCGATGCTCGACGGACTGCCGGTCCAGTAGTGGTAACCGTTACTCGCCAAGGCGACGGGA
beta-Actin   >  E  M  A  T  A  A  S  S  S  S  L  E  K  S  Y  E  L  P  D  G  Q  V  I  T  I  G  N  E  R  F  R  C  P

                      SpAcc
                     Ear1 |                                                  BspH1        BmgB1
                        | |                                                     |            |
            GAGGCACTCTTCCAGCCTTCCTTCCTGGGCATGGAGTCCTGTGGCATCCACGAAACTACCTTCAACTCCATCATGAAGTGTGACGTGGACATCCGCAAAG
       2101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
            CTCCGTGAGAAGGTCGGAAGGAAGGACCCGTACCTCAGGACACCGTAGGTGCTTTGATGGAAGTTGAGGTAGTACTTCACACTGCACCTGTAGGCGTTTC
beta-Actin   > E  A  L  F  Q  P  S  F  L  G  M  E  S  C  G  I  H  E  T  T  F  N  S  I  M  K  C  D  V  D  I  R  K  D

                                                      BsrD1                      Bts1         BseY1
                                                          |                          |             |
            ACCTGTACGCCAACACAGTGCTGTCTGGCGGCACCACCATGTACCCTGGCATTGCCGACAGGATGCAGAAGGAGATCACTGCCCTGGCACCCAGCACAAT
       2201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
            TGGACATGCGGTTGTGTCACGACAGACCGCCGTGGTGGTACATGGGACCGTAACGGCTGTCCTACGTCTTCCTCTAGTGACGGGACCGTGGGTCGTGTTA
beta-Actin   >   L  Y  A  N  T  V  L  S  G  G  T  T  M  Y  P  G  I  A  D  R  M  Q  K  E  I  T  A  L  A  P  S  T  M

                   BsrD1
                BseR1  |
               BsaB1|  |       Bpu10       Sca1                                                  BsaB1
                   ||  |           |          |                                                      |
            GAAGATCAAGATCATTGCTCCTCCTGAGCGCAAGTACTCCGTGTGGATCGGCGGCTCCATCCTGGCCTCGCTGTCCACCTTCCAGCAGATGTGGATCAGC
       2301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
            CTTCTAGTTCTAGTAACGAGGAGGACTCGCGTTCATGAGGCACACCTAGCCGCCGAGGTAGGACCGGAGCGACAGGTGGAAGGTCGTCTACACCTAGTCG
beta-Actin   >  K  I  K  I  I  A  P  P  E  R  K  Y  S  V  W  I  G  G  S  I  L  A  S  L  S  T  F  Q  Q  M  W  I  S

                                                          BamH1        Xba1      Bcl1BsaB1
                                                              |           |         |    |
            AAGCAGGAGTATGACGAGTCCGGCCCCTCCATCGTCCACCGCAAATGCTTCTAGGGATCCACCGGATCTAGATAACTGATCATAATCAGCCATACCACAT
       2401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
            TTCGTCCTCATACTGCTCAGGCCGGGGAGGTAGCAGGTGGCGTTTACGAAGATCCCTAGGTGGCCTAGATCTATTGACTAGTATTAGTCGGTATGGTGTA
beta-Actin   > K  Q  E  Y  D  E  S  G  P  S  I  V  H  R  K  C  F  *
```

```
                                                                                  Bsm1
                 SpDon   Dra1                                                  Mfe1|        Hpa1       polyA
                     |      |                                                     ||           |           |
      TTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGC
2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
      AACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCG

     Psi1      polyA                        polyA            Bts1 Bsm1
       |          |                            |                |    |
      TTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTA
2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
      AATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACAT

        Mlu1     SpDon        Ssp1
           |         |           |
      TCTTAACGCGTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAA
2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
      AGAATTGCGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTT

          Psi1                                                          BsaXb                 Drd1
             |                                                             |                     |
      ATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAG
2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
      TAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTC

                                      BtgZ1
 BsaXa                                Dra3|                                                        SpAcc
     |                                   ||                                                             |
      GGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCC
2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
      CCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGG

                                         Nae1
                                      NgoM4 |                                     BsrB1
                                          | |                                         |
      TAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCA
3001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
      ATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGT
```

```
      AGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAA
3101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
      TCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTT

                                                  BciV1
                                               BspH1  |
                  polyA                       BsrB1 |  |                            Ssp1  Ear1
                      |                           | |  |                              |     |
      CCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCC
3201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
      GGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCAGG

                                                                                                  Nsi1
                                                                                                Sph1 |
                      Eci1                                                                     BfrB1 |
 Bsu36              Pvu2 |                                        BseY1                    BstAP  | |
     |                 | |                                           |                        |  | |
      TGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATT
3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
      ACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAA

                                                                    Nsi1
                                                                  Sph1 |
                                                                 BfrB1 |
          SexA1                      BseY1                    BstAP  | |                        Eci1
              |                          |                        |  | |                           |
      AGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAAC
3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
      TCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTG

                        Eci1                                                                      Sfi1
                Eci1     Bmr1|       Eci1            Nco1                   polyA                  Bgl1
                   |        ||          |               |                       |                     |
      TCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCC
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      AGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGG
```

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                                                Avr2
                                               Stu1|
                      SpDon             BseR1  ||              Cla1              BsaB1
                          |                 |  ||                |                 |
      TCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAA
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      AGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTT

        BspM1
        BfuA1               Eag1                                        Bmr1
            |                  |                                           |
      CAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGT
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      GTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACA

                       Nar1
                      Kas1|                       Drd1
                         ||                          |
      TCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCT
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      AGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGA

                            Pvu2
    Msc1                Fsp1   |       PflF1                        Eco57
       |                   |   |           |                           |
      GGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTG
3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
      CCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGAC

                                                                                                  BtgZ1
                                                                                              BspM1  |
          SpDon                          BciV1         BsrD1                                  BfuA1  |
              |                              |             |                                      |  |
      TCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAG
4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
      AGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTC
```

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                                                                  Sap1
                                                                  Ear1                          BpuE1
                                                                    |                             |
      CGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACT
4101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
      GCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGA

                          Sph1                        Nco1                BtgZ1
                             |                           |                   |
      GTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTT
4201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
      CAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAA

                        BseY1
                       Nae1 |                                                Sap1
                    NgoM4 | |        Rsr2         Eci1                      Ear1                   Eco57
                        | | |           |            |                         |                       |
      TCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGG
4301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
      AGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCC

                                   BtgZ1
             BssS1                BsrB1 |                                                BsrB1
                |                    | |                                                    |
      CTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGG
4401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
      GACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCC

                                      BssS1
                                      BspM1
   BstB1                              BfuA1                      SpAcc
       |                                 |                          |
      TTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGG
4501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
      AAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCC
```

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       Nae1                                                  Bpm1
    NgoM4 |                                             SpAcc  |
     Bpm1 |                                              Avr2  |
        | |                                                 |  |
      ACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGA
4601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
      TGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCT

                      polyA        polyA
                          |            |
      AGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCT
4701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
      TCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGA

           Bsa1
              |
      GTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAG
4801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
      CAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTC

                      BstAP
                      AlwN1      Bsu36                            Dra1               Dra1
                          |          |                               |                  |
      CCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAA
4901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
      GGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTT

                   BspH1
                      |
      GATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGAT
5001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
      CTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTA

               BpuE1                                                                          Eco57
                   |                                                                              |
      CCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGA
5101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
      GGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCT
```

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                                                SpAcc
                                                   |
      AGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATA
5201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
      TCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTAT

                            AlwN1                     BpuE1
                                |                         |
      CCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAG
5301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5400
      GGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTC

                        ApaL1     BseY1                                                 SpAcc
                            |         |                                                     |
      CGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCA
5401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5500
      GCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGT

                                       BciV1
                                    Eci1   |                    BssS1
                                       |   |                         |
      CGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCT
5501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5600
      GCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGA

       SpAcc                          Drd1            BpuE1               SpAcc     Eci1
           |                             |                |                   |        |
      TTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCC
5601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5700
      AATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGG

                                      SpDon                                                      Nsi1
                                     BspLU|                                                   BfrB1 |
                                          ||                                                       | |
      TTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
5701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||| 5796
      AAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aat2	AlwN1	ApaL1	**Ase1**	Avr2	**BamH1**	Bbs1	**Bcg1a**	**Bcg1b**	BciV1	**Bcl1**	BfrB1	BfuA1	Bgl1
Bgl2	**BmgB1**	Bmr1	Bpm1	**Bpu10**	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsm1	**BsmB1**
BspE1	BspH1	**BspLU**	BspM1	BsrB1	BsrD1	**BsrG1**	BssS1	BstAP	**BstB1**	**BstE2**	Bsu36	BtgZ1	Bts1
Cla1	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	**EcoRV**	**Fsp1**	**Hind3**	**Hpa1**	Kas1	**Mfe1**
Mlu1	Msc1	Nae1	Nar1	Nco1	**Nde1**	NgoM4	**Nhe1**	Nsi1	PflF1	polyA	**PshA1**	Psi1	Pvu2
Rsr2	**Sal1**	Sap1	**Sca1**	**SexA1**	**Sfi1**	**Sma1**	**SnaB1**	SpAcc	SpDon	Sph1	Ssp1	Stu1	**Xba1**
Xcm1	**Xho1**												

Unique:

Ase1	**BamH1**	**Bcg1a**	**Bcg1b**	**Bcl1**	**Bgl2**	**BmgB1**	**Bpu10**	**BsmB1**	**BspE1**	**BspLU**	**BsrG1**	**BstB1**	**BstE2**
Cla1	**EcoRV**	**Fsp1**	**Hind3**	**Hpa1**	**Mfe1**	**Mlu1**	**Nde1**	**Nhe1**	**PshA1**	**Rsr2**	**Sal1**	**Sca1**	**SexA1**
Sfi1	**Sma1**	**SnaB1**	**Xba1**	**Xho1**									

Not found:

Aar1	Acc65	Acl1	Afe1	Afl2	Age1	Ahd1	Ale1	Apa1	Asc1	AsiS1	Bae1a	Bae1b	BbvC1
Blp1	Bsg1	BsiW1	BssH2	BstX1	BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	Ecl2	EcoK	EcoN1
EcoR1	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	I_Ceu	Kpn1	loxP	Not1	Nru1	Pac1
PflM1	Pme1	Pml1	PspOM	Pst1	Pvu1	R4atB	R4atL	R4atP	R4atR	Sac1	Sac2	SanD1	Sbf1
Sgf1	SgrA1	Spe1	Srf1	Swa1	T3RNA	T7RNA	T7Ter	PISce	Xmn1				

Excluded by site complexity:

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