pTagYFP-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 bold blue. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site). TagYFP amino acids are shown in orange, 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

                                                Aat2                                                Eci1
                                                  |                                                   |
      TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
  401 |********|********|********|********|********|********|********|********|********|********|********| 500
      ATCGCCAAACTGAGTGCCCCTAAAGGTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT
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                                                                                                                Nhe1 Afe1
                                                                                                                   |    |
            ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCGCTA
        501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
            TGTTGAGGCGGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT

                                                BseR1
                                                Nae1|                                ApaL1
             Age1       Nco1                   NgoM4 ||                             BmgB1|
                |          |                       | ||                                 ||
            CCGGTCGCCACCATGGTTAGCAAAGGCGAGGAGCTGTTCGCCGGCATCGTGCCCGTGCTGATCGAGCTGGACGGCGACGTGCACGGCCACAAGTTCAGCG
        601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
            GGCCAGCGGTGGTACCAATCGTTTCCGCTCCTCGACAAGCGGCCGTAGCACGGGCACGACTAGCTCGACCTGCCGCTGCACGTGCCGGTGTTCAAGTCGC
TagYFP        >            M  V  S  K  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

                                                                   BsaXb                                BstE2
                                       BsaXa    Bsg1              Bpm1  |                             Ale1 |
                                           |       |                 |  |                                | |
            TGCGCGGCGAGGGCGAGGGCGACGCCGACTACGGCAAGCTGGAGATCAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTGGTGAC
        701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
            ACGCGCCGCTCCCGCTCCCGCTGCGGCTGATGCCGTTCGACCTCTAGTTCAAGTAGACGTGGTGGCCGTTCGACGGGCACGGGACCGGGTGGGACCACTG
TagYFP        >   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  W  P  T  L  V  T

                                                                          Xmn1
                                                                            |
            CACCCTCACCTACGGCGTACAGTGCTTCGCCCGCTACCCCAAGCACATGAAGATGAACGACTTCTTCAAGAGCGCCATGCCCGAGGGCTACATCCAGGAG
        801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
            GTGGGAGTGGATGCCGCATGTCACGAAGCGGGCGATGGGGTTCGTGTACTTCTACTTGCTGAAGAAGTTCTCGCGGTACGGGCTCCCGATGTAGGTCCTC
TagYFP        >  T  L  T  Y  G  V  Q  C  F  A  R  Y  P  K  H  M  K  M  N  D  F  F  K  S  A  M  P  E  G  Y  I  Q  E

                                                                                   SpDon
                          Ear1                      Sac2 SpDon                    Ale1 |
                             |                         |     |                        | |
            CGCACCATCCTCTTCCAAGACGACGGCAAGTACAAGACCCGCGGCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCAAGG
        901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
            GCGTGGTAGGAGAAGGTTCTGCTGCCGTTCATGTTCTGGGCGCCGCTCCACTTCAAGCTCCCGCTGTGGGACCACTTGGCGTAGCTCGACTTCCCGTTCC
TagYFP        > R  T  I  L  F  Q  D  D  G  K  Y  K  T  R  G  E  V  K  F  E  G  D  T  L  V  N  R  I  E  L  K  G  K  D
```

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                 Eco57                    PflM1                  Bpm1                              Xcm1
                    |                        |                     |                                 |
            ACTTCAAGGAGGACGGCAACATCCTGGGCCACAAGCTGGAGTACAGCTTCAACAGCCACAACGTCTACATCACCCCCGACAAGGCCAACAACGGCCTGGA
      1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
            TGAAGTTCCTCCTGCCGTTGTAGGACCCGGTGTTCGACCTCATGTCGAAGTTGTCGGTGTTGCAGATGTAGTGGGGGCTGTTCCGGTTGTTGCCGGACCT
TagYFP        >  F  K  E  D  G  N  I  L  G  H  K  L  E  Y  S  F  N  S  H  N  V  Y  I  T  P  D  K  A  N  N  G  L  E

          SpDon           Bpm1                        Pvu2           Bsg1       Xcm1
            |               |                           |              |          |
            GGTGAACTTCAAGACCCGCCACAACATCGAGGGCGGCGGCGTGCAGCTGGCCGACCACTACCAGACCAACGTGCCCCTGGGCGACGGCCCCGTGCTGATC
      1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
            CCACTTGAAGTTCTGGGCGGTGTTGTAGCTCCCGCCGCCGCACGTCGACCGGCTGGTGATGGTCTGGTTGCACGGGGACCCGCTGCCGGGGCACGACTAG
TagYFP        >  V  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  D  G  P  V  L  I

                                                                                                          Pst1
          BsaB1          Bpu10                                                Dra3                  AlwN1 Bpm1
            |              |                                                     |                       |    |
            CCCATCAACCACTACCTGAGCTACCAGACCGACATCAGCAAGGACCGCAACGAGGCCCGCGACCACATGGTGCTCCTGGAGTCCGTCAGCGCCTGCAGCC
      1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
            GGGTAGTTGGTGATGGACTCGATGGTCTGGCTGTAGTCGTTCCTGGCGTTGCTCCGGGCGCTGGTGTACCACGAGGACCTCAGGCAGTCGCGGACGTCGG
TagYFP        > P  I  N  H  Y  L  S  Y  Q  T  D  I  S  K  D  R  N  E  A  R  D  H  M  V  L  L  E  S  V  S  A  C  S  H

                                  BspE1        Xho1
                PflM1            BsrB1 |     Bgl2   |              EcoRV     BsaXb  Sal1
                   |                 | |        |   |                 |         |     |
            ACACCCACGGCATGGACGAGCTGTACCGCTCCGGACTCAGATCTCGAGCTATGGATGATGATATCGCCGCGCTCGTCGTCGACAACGGCTCCGGCATGTG
      1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
            TGTGGGTGCCGTACCTGCTCGACATGGCGAGGCCTGAGTCTAGAGCTCGATACCTACTACTATAGCGGCGCGAGCAGCAGCTGTTGCCGAGGCCGTACAC
TagYFP/actin >  T  H  G  M  D  E  L  Y  R  S  G  L  R  S  R  A  M  D  D  D  I  A  A  L  V  V  D  N  G  S  G  M  C

                Nae1                    Sma1
            NgoM4 |                     Bgl1                    Nar1
         BsaXa  | |                    Bbs1|                   Kas1|
            |   | |                      ||                      ||
            CAAGGCCGGCTTCGCGGGCGACGATGCCCCCCGGGCCGTCTTCCCCTCCATCGTGGGGCGCCCCAGGCACCAGGGCGTGATGGTGGGCATGGGTCAGAAG
      1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
            GTTCCGGCCGAAGCGCCCGCTGCTACGGGGGGCCCGGCAGAAGGGGAGGTAGCACCCCGCGGGGTCCGTGGTCCCGCACTACCACCCGTACCCAGTCTTC
beta-actin    >  K  A  G  F  A  G  D  D  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
```

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                                                                                Eco57                   Bmr1
                                                                                  |                       |
            GATTCCTATGTGGGCGACGAGGCCCAGAGCAAGAGAGGCATCCTCACCCTGAAGTACCCCATCGAGCACGGCATCGTCACCAACTGGGACGACATGGAGA
      1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
            CTAAGGATACACCCGCTGCTCCGGGTCTCGTTCTCTCCGTAGGAGTGGGACTTCATGGGGTAGCTCGTGCCGTAGCAGTGGTTGACCCTGCTGTACCTCT
beta-actin  > D  S  Y  V  G  D  E  A  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

                                                                  BseR1
                                                              Dra3   |
                                                             BstAP   |
                                                                 |   |
            AAATCTGGCACCACACCTTCTACAATGAGCTGCGTGTGGCTCCCGAGGAGCACCCCGTGCTGCTGACCGAGGCCCCCCTGAACCCCAAGGCCAACCGCGA
      1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
            TTTAGACCGTGGTGTGGAAGATGTTACTCGACGCACACCGAGGGCTCCTCGTGGGGCACGACGACTGGCTCCGGGGGGACTTGGGGTTCCGGTTGGCGCT
beta-actin  >  I  W  H  H  T  F  Y  N  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

                        Bsa1                BseY1
                          |                   |
            GAAGATGACCCAGATCATGTTTGAGACCTTCAACACCCCAGCCATGTACGTTGCTATCCAGGCTGTGCTATCCCTGTACGCCTCTGGCCGTACCACTGGC
      1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
            CTTCTACTGGGTCTAGTACAAACTCTGGAAGTTGTGGGGTCGGTACATGCAACGATAGGTCCGACACGATAGGGACATGCGGAGACCGGCATGGTGACCG
beta-actin  >  K  M  T  Q  I  M  F  E  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

                          BstE2        Bcg1a
                        PflF1 |        Dra3|  SpAcc                      Bcg1b   Xcm1
                            | |           ||      |                          |      |
            ATCGTGATGGACTCCGGTGACGGGGTCACCCACACTGTGCCCATCTACGAGGGGTATGCCCTCCCCCATGCCATCCTGCGTCTGGACCTGGCTGGCCGGG
      1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
            TAGCACTACCTGAGGCCACTGCCCCAGTGGGTGTGACACGGGTAGATGCTCCCCATACGGGAGGGGGTACGGTAGGACGCAGACCTGGACCGACCGGCCC
beta-actin  > I  V  M  D  S  G  D  G  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

                    BspH1                                 SpDon  Eag1  BsrB1          BsaXa
                      |                                     |     |      |              |
            ACCTGACTGACTACCTCATGAAGATCCTCACCGAGCGCGGCTACAGCTTCACCACCACGGCCGAGCGGGAAATCGTGCGTGACATTAAGGAGAAGCTGTG
      1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
            TGGACTGACTGATGGAGTACTTCTAGGAGTGGCTCGCGCCGATGTCGAAGTGGTGGTGCCGGCTCGCCCTTTAGCACGCACTGTAATTCCTCTTCGACAC
beta-actin  >  L  T  D  Y  L  M  K  I  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
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                                                   Sap1
                                                   Ear1
                                                 SpAcc|
                    BsaXb                 Msc1   BseR1        Xcm1  ||                 Bpm1     Drd1
                      |                     |       |           |  ||                   |        |
            CTACGTCGCCCTGGACTTCGAGCAAGAGATGGCCACGGCTGCTTCCAGCTCCTCCCTGGAGAAGAGCTACGAGCTGCCTGACGGCCAGGTCATCACCATT
      2001  |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 2100
            GATGCAGCGGGACCTGAAGCTCGTTCTCTACCGGTGCCGACGAAGGTCGAGGAGGGACCTCTTCTCGATGCTCGACGGACTGCCGGTCCAGTAGTGGTAA
beta-actin   >  Y  V  A  L  D  F  E  Q  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

                BsrD1                        SpAcc
                BsrB1         Bsu36          Ear1 |                                                   BspH1
                   |            |             | |                                                       |
            GGCAATGAGCGGTTCCGCTGCCCTGAGGCACTCTTCCAGCCTTCCTTCCTGGGCATGGAGTCCTGTGGCATCCACGAAACTACCTTCAACTCCATCATGA
      2101  |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 2200
            CCGTTACTCGCCAAGGCGACGGGACTCCGTGAGAAGGTCGGAAGGAAGGACCCGTACCTCAGGACACCGTAGGTGCTTTGATGGAAGTTGAGGTAGTACT
beta-actin   > G  N  E  R  F  R  C  P  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

               BmgB1                                                          BsrD1
                  |                                                              |
            AGTGTGACGTGGACATCCGCAAAGACCTGTACGCCAACACAGTGCTGTCTGGCGGCACCACCATGTACCCTGGCATTGCCGACAGGATGCAGAAGGAGAT
      2201  |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 2300
            TCACACTGCACCTGTAGGCGTTTCTGGACATGCGGTTGTGTCACGACAGACCGCCGTGGTGGTACATGGGACCGTAACGGCTGTCCTACGTCTTCCTCTA
beta-actin   >   C  D  V  D  I  R  K  D  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

                                          BsrD1
                                       BseR1  |
          Bts1         BseY1             BsaB1|  |       Bpu10       Sca1
             |            |                 ||  |           |          |
            CACTGCCCTGGCACCCAGCACAATGAAGATCAAGATCATTGCTCCTCCTGAGCGCAAGTACTCCGTGTGGATCGGCGGCTCCATCCTGGCCTCGCTGTCC
      2301  |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 2400
            GTGACGGGACCGTGGGTCGTGTTACTTCTAGTTCTAGTAACGAGGAGGACTCGCGTTCATGAGGCACACCTAGCCGCCGAGGTAGGACCGGAGCGACAGG
beta-actin   >  T  A  L  A  P  S  T  M  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

                           BsaB1                                                          BamH1        Xba1
                              |                                                              |           |
            ACCTTCCAGCAGATGTGGATCAGCAAGCAGGAGTATGACGAGTCCGGCCCCTCCATCGTCCACCGCAAATGCTTCTAGGGATCCACCGGATCTAGATAAC
      2401  |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 2500
            TGGAAGGTCGTCTACACCTAGTCGTTCGTCCTCATACTGCTCAGGCCGGGGAGGTAGCAGGTGGCGTTTACGAAGATCCCTAGGTGGCCTAGATCTATTG
beta-actin   > T  F  Q  Q  M  W  I  S  K  Q  E  Y  D  E  S  G  P  S  I  V  H  R  K  C  F  *
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                                                                                                                Bsm1
   Bcl1BsaB1                                SpDon   Dra1                                                    Mfe1|
      |    |                                    |      |                                                        ||
      TGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGT
2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
      ACTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACA

         Hpa1       polyA    Psi1      polyA                        polyA            Bts1 Bsm1
            |           |       |          |                            |                |    |
      TGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGT
2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
      ACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGACGTAAGATCAACA

                                Mlu1     SpDon        Ssp1
                                   |         |           |
      GGTTTGTCCAAACTCATCAATGTATCTTAACGCGTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTT
2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
      CCAAACAGGTTTGAGTAGTTACATAGAATTGCGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAA

                                 Psi1                                                                BsaXb
                                    |                                                                    |
      AACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAA
2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
      TTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATT

                                                                 BtgZ1
                 Drd1    BsaXa                                   Dra3|
                    |        |                                      ||
      AGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTG
2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
      TCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCCAGCTCCAC

                                                                    Nae1
                        SpAcc                                   NgoM4 |
                           |                                        | |
      CCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAA
3001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
      GGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTT
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     BsrB1
        |
      GGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCA
3101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
      CCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGTCCACCGT

                                                                                   BciV1
                                                                              BspH1  |
                                                polyA                       BsrB1 |  |
                                                    |                           | |  |
      CTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCA
3201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
      GAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGT

                                                Eci1
       Ssp1  Ear1        Bsu36              Pvu2 |                                        BseY1
          |     |            |                 | |                                           |
      ATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAA
3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
      TATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTT

                  Nsi1                                                                      Nsi1
                Sph1 |                                                                    Sph1 |
               BfrB1 |                                                                   BfrB1 |
            BstAP  | |            SexA1                      BseY1                     BstAP  | |
                |  | |                |                         |                         |  | |
      GTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTC
3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
      CATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAG

                                                Eci1
                 Eci1                  Eci1     Bmr1|       Eci1            Nco1                   polyA
                    |                    |        ||          |              |                      |
      AGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTAT
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      TCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAAATAAATA
```

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                                                                Avr2
                    Sfi1                                       Stu1|
                    Bgl1                    SpDon            BseR1  ||              Cla1
                       |                       |                |  ||                |
     GCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGA
3601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
     CGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCT

                             BspM1
   BsaB1                     BfuA1              Eag1                                    Bmr1
      |                         |                 |                                       |
     TGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAA
3701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
     ACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTT
                                                Nar1
                                               Kas1|                      Drd1
                                                  ||                        |
     TCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGA
3801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
     AGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCT

                                                   Pvu2
                            Msc1                Fsp1   |       PflF1                       Eco57
                               |                   |   |           |                           |
     CGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGC
3901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
     GCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCG

                                  SpDon                          BciV1         BsrD1
                                     |                              |             |
     GAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGG
4001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
     CTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCC
```

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                 BtgZ1
             BspM1  |                                                          Sap1
             BfuA1  |                                                          Ear1
                 |  |                                                             |
     CTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCA
4101 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 4200
     GATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGT

                     BpuE1                          Sph1                        Nco1                BtgZ1
                         |                             |                           |                   |
     TCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAAT
4201 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 4300
     AGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTA

                                                BseY1
                                               Nae1 |                                                Sap1
                                            NgoM4 | |        Rsr2         Eci1                      Ear1
                                                | | |           |            |                          |
     ATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTG
4301 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 4400
     TAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAAC

                                                          BtgZ1
                         Eco57         BssS1                BsrB1 |
                             |             |                   | |
     CTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGA
4401 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 4500
     GACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCT

                                                            BssS1
                                                            BspM1
              BsrB1          BstB1                          BfuA1                      SpAcc
                 |              |                              |                          |
     GTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGT
4501 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 4600
     CAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCA
```

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                              Nae1                                                  Bpm1
                            NgoM4 |                                             SpAcc  |
                             Bpm1 |                                              Avr2  |
                                | |                                                 |  |
     TGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGA
4601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
     ACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACT

                                          polyA        polyA
                                              |            |
     AACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGG
4701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
     TTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCC

                                 Bsa1
                                    |
     GTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTT
4801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
     CAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAA

                                          BstAP
                                          AlwN1      Bsu36                            Dra1
                                              |          |                                |
     CGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTT
4901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
     GCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAA

        Dra1                                BspH1
           |                                    |
     TTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAA
5001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
     AATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTT

                                       BpuE1
                                          |
     AAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATC
5101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
     TTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAG
```

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                 Eco57                                                 SpAcc
                    |                                                    |
     AAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAA
5201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
     TTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTT

                                                      AlwN1                    BpuE1
                                                         |                        |
     GAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGA
5301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5400
     CTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCT

                                                 ApaL1     BseY1
                                                    |         |
     CGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTAC
5401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5500
     GCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATG

                                                                BciV1
        SpAcc                                                Eci1   |                    BssS1
            |                                                   |   |                       |
     AGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCT
5501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5600
     TCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGA

                                SpAcc                           Drd1            BpuE1               SpAcc
                                   |                               |                |                   |
     TCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTA
5601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5700
     AGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCCGCCTCGGAT

                                                                 SpDon
       Eci1                                                     BspLU|
           |                                                       ||
     TGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATA
5701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5800
     ACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTAT
```

```
                          Nsi1
                       BfrB1 |
                           | |
            ACCGTATTACCGCCATGCAT
      5801  |||||||||*|||||||||* 5820
            TGGCATAATGGCGGTACGTA
```

Found:

Aat2	**Afe1**	**Age1**	Ale1	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	Bsg1	Bsm1	**BspE1**	BspH1	**BspLU**	BspM1	BsrB1	BsrD1	BssS1	BstAP	**BstB1**	BstE2	Bsu36
BtgZ1	Bts1	**Cla1**	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	**EcoRV**	**Fsp1**	**Hpa1**	Kas1
Mfe1	**Mlu1**	Msc1	Nae1	Nar1	Nco1	**Nde1**	NgoM4	**Nhe1**	Nsi1	PflF1	PflM1	polyA	Psi1
Pst1	Pvu2	**Rsr2**	**Sac2**	**Sal1**	Sap1	**Sca1**	**SexA1**	**Sfi1**	**Sma1**	**SnaB1**	SpAcc	SpDon	Sph1
Ssp1	**Stu1**	**Xba1**	Xcm1	**Xho1**	**Xmn1**								

Unique:

Afe1	**Age1**	**Ase1**	**BamH1**	**Bbs1**	**Bcg1a**	**Bcg1b**	**Bcl1**	**Bgl2**	**BspE1**	**BspLU**	**BstB1**	**Cla1**	**EcoRV**
Fsp1	**Hpa1**	**Mfe1**	**Mlu1**	**Nde1**	**Nhe1**	**Pst1**	**Rsr2**	**Sac2**	**Sal1**	**Sca1**	**SexA1**	**Sfi1**	**Sma1**
SnaB1	**Stu1**	**Xba1**	**Xho1**	**Xmn1**									

Not found:

Aar1	Acc65	Acl1	Afl2	Ahd1	Apa1	Asc1	AsiS1	Bae1a	Bae1b	BbvC1	Blp1	BsiW1	BsmB1
BsrG1	BssH2	BstX1	BstZ1	_Chi	EcoK	EcoN1	EcoR1	ScFRT	Fse1	FspA1	Hind3	I_Ceu	Kpn1
loxP	Not1	Nru1	Pac1	Pme1	Pml1	PshA1	PspOM	Pvu1	Sac1	SanD1	Sbf1	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													