pTagRFP-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). TagRFP amino acids are shown in red, beta-actin amino acids are shown in dark-green, linker amino acids are shown in black.

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

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

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

                                  BtgZ1 SnaB1                 Nco1
                                    |     |                     |
      CATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGA
  301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 400
      GTACTGGAATACCCTGAAAGGATGAACCGTCATGTAGATGCATAATCAGTAGCGATAATGGTACCACTACGCCAAAACCGTCATGTAGTTACCCGCACCT

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

                      Ale1      Sap1
             Age1       Nco1 |      Ear1                                  BsrG1                                ApaL1
                |          | |         |                                    |                                    |
            CCGGTCGCCACCATGGTGTCTAAGGGCGAAGAGCTGATTAAGGAGAACATGCACATGAAGCTGTACATGGAGGGCACCGTGAACAACCACCACTTCAAGT
        601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
            GGCCAGCGGTGGTACCACAGATTCCCGCTTCTCGACTAATTCCTCTTGTACGTGTACTTCGACATGTACCTCCCGTGGCACTTGTTGGTGGTGAAGTTCA
pTagRFP      >            M  V  S  K  G  E  E  L  I  K  E  N  M  H  M  K  L  Y  M  E  G  T  V  N  N  H  H  F  K  C

                                SpAcc
                                  |
            GCACATCCGAGGGCGAAGGCAAGCCCTACGAGGGCACCCAGACCATGAGAATCAAGGTGGTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGC
        701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
            CGTGTAGGCTCCCGCTTCCGTTCGGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCCACCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCG
pTagRFP      >  T  S  E  G  E  G  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

                                                                                   Bsu36       SpDon
                                                                                     |           |
            TACCAGCTTCATGTACGGCAGCAGAACCTTCATCAACCACACCCAGGGCATCCCCGACTTCTTTAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGA
        801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
            ATGGTCGAAGTACATGCCGTCGTCTTGGAAGTAGTTGGTGTGGGTCCCGTAGGGGCTGAAGAAATTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCT
pTagRFP      >  T  S  F  M  Y  G  S  R  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

                          Bbs1            Bpm1                                                      SpDon
                            |                |                                                         |
            GTCACCACATACGAAGACGGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACT
        901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
            CAGTGGTGTATGCTTCTGCCCCCGCACGACTGGCGATGGGTCCTGTGGTCGGAGGTCCTGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCCACTTGA
pTagRFP      > V  T  T  Y  E  D  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
```

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                                                BseY1                                                Bgl1
                                                  |                                                   |
            TCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCAACACCGAGATGCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAAGCGA
      1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
            AGGGTAGGTTGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCTCCGGTTGTGGCTCTACGACATGGGGCGACTGCCGCCGGACCTTCCGTCTTCGCT
pTagRFP      >  P  S  N  G  P  V  M  Q  K  K  T  L  G  W  E  A  N  T  E  M  L  Y  P  A  D  G  G  L  E  G  R  S  D

                      BssS1          Eco57                                  BpuE1
                        |              |                                       |
            CATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACTTCAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGCGTC
      1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
            GTACCGGGACTTCGAGCACCCGCCCCCGGTGGACTAGACGTTGAAGTTCTGGTGTATGTCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCGCAG
pTagRFP      >  M  A  L  K  L  V  G  G  G  H  L  I  C  N  F  K  T  T  Y  R  S  K  K  P  A  K  N  L  K  M  P  G  V

                         SpAcc
                         PflM1                   Bsa1       PshA1       BssS1 Dra3      Msc1  AlwN1
                           |                       |           |           |    |         |      |
            TACTATGTGGACCACAGACTGGAAAGAATCAAGGAGGCCGACAAAGAGACCTACGTCGAGCAGCACGAGGTGGCTGTGGCCAGATACTGCGACCTCCCTA
      1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
            ATGATACACCTGGTGTCTGACCTTTCTTAGTTCCTCCGGCTGTTTCTCTGGATGCAGCTCGTCGTGCTCCACCGACACCGGTCTATGACGCTGGAGGGAT
pTagRFP      > Y  Y  V  D  H  R  L  E  R  I  K  E  A  D  K  E  T  Y  V  E  Q  H  E  V  A  V  A  R  Y  C  D  L  P  S

                                              Xho1                                                      NgoM4
          SpAcc          Bmr1    BspE1     Bgl2   |              EcoRV     BsaXb  Sal1                  BsaXa  |
            |              |        |        |    |                |         |     |                       |   |
            GCAAACTGGGGCACAAACTTAATTCCGGACTCAGATCTCGAGCTATGGATGATGATATCGCCGCGCTCGTCGTCGACAACGGCTCCGGCATGTGCAAGGC
      1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
            CGTTTGACCCCGTGTTTGAATTAAGGCCTGAGTCTAGAGCTCGATACCTACTACTATAGCGGCGCGAGCAGCAGCTGTTGCCGAGGCCGTACACGTTCCG
pTagRFP/actin>  K  L  G  H  K  L  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

                                 Sma1
                                 Bgl1                     Nar1
           Nae1                 Bbs1|                    Kas1|
            |                     ||                       ||
            CGGCTTCGCGGGCGACGATGCCCCCCGGGCCGTCTTCCCCTCCATCGTGGGGCGCCCCAGGCACCAGGGCGTGATGGTGGGCATGGGTCAGAAGGATTCC
      1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
            GCCGAAGCGCCCGCTGCTACGGGGGGCCCGGCAGAAGGGGAGGTAGCACCCCGCGGGGTCCGTGGTCCCGCACTACCACCCGTACCCAGTCTTCCTAAGG
beta-actin   >  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  D  S
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                                                SpDon                   Eco57                   Bmr1
                                                   |                       |                       |
            TATGTGGGCGACGAGGCCCAGAGCAAGAGAGGCATCCTCACCCTGAAGTACCCCATCGAGCACGGCATCGTCACCAACTGGGACGACATGGAGAAAATCT
      1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
            ATACACCCGCTGCTCCGGGTCTCGTTCTCTCCGTAGGAGTGGGACTTCATGGGGTAGCTCGTGCCGTAGCAGTGGTTGACCCTGCTGTACCTCTTTTAGA
beta-actin  > 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  I  W

                                                                   BseR1
                                                             Dra3    |
                                                            BstAP    |
                                                                |    |
            GGCACCACACCTTCTACAATGAGCTGCGTGTGGCTCCCGAGGAGCACCCCGTGCTGCTGACCGAGGCCCCCCTGAACCCCAAGGCCAACCGCGAGAAGAT
      1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
            CCGTGGTGTGGAAGATGTTACTCGACGCACACCGAGGGCTCCTCGTGGGGCACGACGACTGGCTCCGGGGGGACTTGGGGTTCCGGTTGGCGCTCTTCTA
beta-actin  >  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  K  M

                     Bsa1                 BseY1
                       |                     |
            GACCCAGATCATGTTTGAGACCTTCAACACCCCAGCCATGTACGTTGCTATCCAGGCTGTGCTATCCCTGTACGCCTCTGGCCGTACCACTGGCATCGTG
      1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
            CTGGGTCTAGTACAAACTCTGGAAGTTGTGGGGTCGGTACATGCAACGATAGGTCCGACACGATAGGGACATGCGGAGACCGGCATGGTGACCGTAGCAC
beta-actin  >  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  I  V

                          BstE2        Bcg1a
                        PflF1 |        Dra3|  SpAcc                      Bcg1b   Xcm1
                            | |           ||      |                          |      |
            ATGGACTCCGGTGACGGGGTCACCCACACTGTGCCCATCTACGAGGGGTATGCCCTCCCCCATGCCATCCTGCGTCTGGACCTGGCTGGCCGGGACCTGA
      1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
            TACCTGAGGCCACTGCCCCAGTGGGTGTGACACGGGTAGATGCTCCCCATACGGGAGGGGGTACGGTAGGACGCAGACCTGGACCGACCGGCCCTGGACT
beta-actin  > 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  L  T

                     BspH1                                SpDon  Eag1  BsrB1           BsaXa
                        |                                    |     |      |               |
            CTGACTACCTCATGAAGATCCTCACCGAGCGCGGCTACAGCTTCACCACCACGGCCGAGCGGGAAATCGTGCGTGACATTAAGGAGAAGCTGTGCTACGT
      1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
            GACTGATGGAGTACTTCTAGGAGTGGCTCGCGCCGATGTCGAAGTGGTGGTGCCGGCTCGCCCTTTAGCACGCACTGTAATTCCTCTTCGACACGATGCA
beta-actin  >  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  Y  V
```

```
                                                   Sap1
                                                   Ear1
                                                 SpAcc|
              BsaXb                 Msc1   BseR1        Xcm1  ||                 Bpm1     Drd1
                  |                    |       |           |  ||                    |        |
              CGCCCTGGACTTCGAGCAAGAGATGGCCACGGCTGCTTCCAGCTCCTCCCTGGAGAAGAGCTACGAGCTGCCTGACGGCCAGGTCATCACCATTGGCAAT
        2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
              GCGGGACCTGAAGCTCGTTCTCTACCGGTGCCGACGAAGGTCGAGGAGGGACCTCTTCTCGATGCTCGACGGACTGCCGGTCCAGTAGTGGTAACCGTTA
beta-actin    >  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  G  N

            BsrD1                        SpAcc
            BsrB1         Bsu36          Ear1 |                                                   BspH1
                |             |             | |                                                      |
              GAGCGGTTCCGCTGCCCTGAGGCACTCTTCCAGCCTTCCTTCCTGGGCATGGAGTCCTGTGGCATCCACGAAACTACCTTCAACTCCATCATGAAGTGTG
        2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
              CTCGCCAAGGCGACGGGACTCCGTGAGAAGGTCGGAAGGAAGGACCCGTACCTCAGGACACCGTAGGTGCTTTGATGGAAGTTGAGGTAGTACTTCACAC
beta-actin    > 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  C  D

           BmgB1                                                          BsrD1                       Bts1
               |                                                             |                           |
              ACGTGGACATCCGCAAAGACCTGTACGCCAACACAGTGCTGTCTGGCGGCACCACCATGTACCCTGGCATTGCCGACAGGATGCAGAAGGAGATCACTGC
        2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
              TGCACCTGTAGGCGTTTCTGGACATGCGGTTGTGTCACGACAGACCGCCGTGGTGGTACATGGGACCGTAACGGCTGTCCTACGTCTTCCTCTAGTGACG
beta-actin    >   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  T  A

                                     BsrD1
                                  BseR1  |
                BseY1             BsaB1|  |       Bpu10       Sca1
                    |                 ||  |           |          |
              CCTGGCACCCAGCACAATGAAGATCAAGATCATTGCTCCTCCTGAGCGCAAGTACTCCGTGTGGATCGGCGGCTCCATCCTGGCCTCGCTGTCCACCTTC
        2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
              GGACCGTGGGTCGTGTTACTTCTAGTTCTAGTAACGAGGAGGACTCGCGTTCATGAGGCACACCTAGCCGCCGAGGTAGGACCGGAGCGACAGGTGGAAG
beta-actin    >  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  T  F

                  BsaB1                                                                BamH1        Xba1      Bcl1
                      |                                                                   |           |         |
              CAGCAGATGTGGATCAGCAAGCAGGAGTATGACGAGTCCGGCCCCTCCATCGTCCACCGCAAATGCTTCTAGGGATCCACCGGATCTAGATAACTGATCA
        2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
              GTCGTCTACACCTAGTCGTTCGTCCTCATACTGCTCAGGCCGGGGAGGTAGCAGGTGGCGTTTACGAAGATCCCTAGGTGGCCTAGATCTATTGACTAGT
beta-actin    > 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
 BsaB1                                SpDon   Dra1                                            Mfe1|
     |                                    |      |                                                ||
      TAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGT
2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
      ATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACA

   Hpa1       polyA    Psi1      polyA                        polyA            Bts1 Bsm1
      |           |       |          |                            |                |    |
      TAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTG
2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
      ATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGACGTAAGATCAACACCAAAC

                          Mlu1     SpDon        Ssp1
                             |         |           |
      TCCAAACTCATCAATGTATCTTAACGCGTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAA
2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
      AGGTTTGAGTAGTTACATAGAATTGCGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTT

                           Psi1                                                          BsaXb
                              |                                                             |
      TAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACG
2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
      ATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGC

                                                     BtgZ1
           Drd1    BsaXa                             Dra3|
              |        |                                ||
      TGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAA
2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
      ACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCCAGCTCCACGGCATT
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                                                   Nae1
                 SpAcc                           NgoM4 |                                  BsrB1
                    |                                | |                                     |
     AGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCG
3001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
     TCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGC

     GGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTC
3101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
     CCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAG

                                                          BciV1
                                                        BspH1  |
                                polyA                  BsrB1 |  |                          Ssp1
                                   |                       | |  |                            |
     GGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATA
3201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
     CCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTAT

                                     Eci1
      Ear1        Bsu36             Pvu2 |                                   BseY1
        |            |                 | |                                     |
     TTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGC
3301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
     AACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACG

           Nsi1                                                                      Nsi1
         Sph1 |                                                                    Sph1 |
        BfrB1 |                                                                   BfrB1 |
     BstAP  | |            SexA1                      BseY1                    BstAP  | |
         |  | |                |                        |                          |  | |
     AAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAAC
3401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
     TTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTG
```

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                                   Eci1
     Eci1                 Eci1     Bmr1|       Eci1            Nco1                   polyA
        |                    |        ||          |               |                      |
CATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAG
3501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
GTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAAATAAATACGTCTC

                                                   Avr2
         Sfi1                                      Stu1|
         Bgl1                    SpDon            BseR1  ||              Cla1              BsaB1
           |                        |                |  ||                |                  |
GCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGA
3601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
CGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCTACTCCT

                   BspM1
                   BfuA1               Eag1                                        Bmr1
                      |                  |                                           |
TCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCT
3701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
AGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGA

                                  Nar1
                                 Kas1|                       Drd1
                                    ||                         |
GCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGC
3801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
CGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCG

                                      Pvu2
                Msc1                Fsp1   |       PflF1                      Eco57
                  |                   |    |          |                         |
AGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTG
3901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
TCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCAC
```

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                        SpDon                        BciV1         BsrD1
                            |                            |             |
     CCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCT
4001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
     GGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGA

         BtgZ1
      BspM1  |                                                                  Sap1
      BfuA1  |                                                                  Ear1
          |  |                                                                     |
     GCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGG
4101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
     CGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCC

              BpuE1                        Sph1                        Nco1                BtgZ1
                  |                            |                           |                   |
     GCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATG
4201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
     CGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTAC

                                       BseY1
                                      Nae1 |                                                  Sap1
                                   NgoM4 | |        Rsr2         Eci1                       Ear1
                                       | | |          |            |                            |
     GTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAG
4301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
     CACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTC

                                                  BtgZ1
                Eco57         BssS1               BsrB1 |
                    |             |                   | |
     AGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTT
4401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
     TCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAA
```

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                                                  BssS1
                                                  BspM1
      BsrB1          BstB1                        BfuA1                      SpAcc
          |              |                           |                          |
      CTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCT
4501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
      GACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGA

                        Nae1                                                  Bpm1
                     NgoM4 |                                              SpAcc  |
                      Bpm1 |                                               Avr2  |
                           | |                                                  |  |
      TCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACG
4601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
      AGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGC

                                        polyA        polyA
                                            |            |
      GAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTTCGG
4701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
      CTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCC

                            Bsa1                                                                  SpDon
                               |                                                                     |
      TCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGGGTG
4801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
      AGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCAC

                                        BstAP
                                        AlwN1      Bsu36                          Dra1
                                            |          |                              |
      AAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATT
4901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
      TTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAA

   Dra1                                 BspH1
      |                                    |
      TAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATC
5001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
      ATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAG
```

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                                BpuE1
                                   |
      AAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGC
5101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
      TTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCG

               Eco57                                                SpAcc
                  |                                                    |
      TACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTC
5201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
      ATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAG

                                                AlwN1                     BpuE1
                                                   |                         |
      TGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAG
5301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5400
      ACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATC

                                            ApaL1     BseY1
                                               |         |
      TTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTG
5401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5500
      AATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCAC

                                                         BciV1
   SpAcc                                              Eci1   |                    BssS1
      |                                                  |   |                       |
      AGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGG
5501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5600
      TCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCC

                         SpAcc                          Drd1            BpuE1               SpAcc
                            |                             |               |                     |
      GGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAA
5601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5700
      CCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCCGCCTCGGATACCTTT
```

```
                                                                SpDon
          Eci1                                                 BspLU|
             |                                                     ||
              AACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTA
        5701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5800
              TTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCAT

              TTACCGCCA
        5801  ||||||||| 5809
              AATGGCGGT
```

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	Bsm1	**BspE1**	BspH1	**BspLU**	BspM1	BsrB1	BsrD1	**BsrG1**	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	**PshA1**
Psi1	Pvu2	**Rsr2**	**Sal1**	Sap1	**Sca1**	**SexA1**	**Sfi1**	**Sma1**	**SnaB1**	SpAcc	SpDon	Sph1	Ssp1
Stu1	**Xba1**	Xcm1	**Xho1**										

Unique:

Afe1	**Age1**	**Ale1**	**Ase1**	**BamH1**	**Bcg1a**	**Bcg1b**	**Bcl1**	**Bgl2**	**BmgB1**	**Bpu10**	**BspE1**	**BspLU**	**BsrG1**
BstB1	**BstE2**	**Cla1**	**EcoRV**	**Fsp1**	**Hpa1**	**Mfe1**	**Mlu1**	**Nde1**	**Nhe1**	**PflM1**	**PshA1**	**Rsr2**	**Sal1**
Sca1	**SexA1**	**Sfi1**	**Sma1**	**SnaB1**	**Stu1**	**Xba1**	**Xho1**						

Not found:

Aar1	Acc65	Acl1	Afl2	Ahd1	Apa1	Asc1	AsiS1	Bae1a	Bae1b	BbvC1	Blp1	Bsg1	BsiW1
BsmB1	BssH2	BstX1	BstZ1	_Chi	EcoK	EcoN1	EcoR1	ScFRT	Fse1	FspA1	Hind3	I_Ceu	Kpn1
loxP	Not1	Nru1	Pac1	Pme1	Pml1	PspOM	Pst1	Pvu1	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													