pCase12-cyto 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).

```
          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

                                                                                BamH1
                                                                               Sma1 |
                                                                              Apa1| |
                                                                         PspOM   || |
                                                                         Sac2|   || |
                                Xho1    Hind3  EcoR1      Sal1      Kpn1  ||   || |
                        BpuE1 Bgl2   |   Sac1 |BstB1 |     Pst1| Acc65   |  ||   || |  Age1                BmgB1
                            |    |   |      | |    | |        ||     |   |  ||   || |     |                   |
            CCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCTGCAGTCGACGGTACCGCGGGCCCGGGATCCACCGGTCGCCACCATGTCATCACGTCGTAAGTGGA
        601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
            GGCCTGAGTCTAGAGCTCGAGTTCGAAGCTTAAGACGTCAGCTGCCATGGCGCCCGGGCCCTAGGTGGCCAGCGGTGGTACAGTAGTGCAGCATTCACCT
Case12      >                                                                                   M  S  S  R  R  K  W  N

                                                   Xho1
                                                  SpDon
                                         Blp1  Sac1  |                                                  Eci1
                                                |     |  |                                                  |
            ATAAGACAGGTCACGCAGTCAGAGCTATAGGTCGGCTGAGCTCACTCGAGAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTT
        701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
            TATTCTGTCCAGTGCGTCAGTCTCGATATCCAGCCGACTCGAGTGAGCTCTTGCAGATATAGTACCGGCTGTTCGTCTTCTTGCCGTAGTTCCGGTTGAA
Case12      >  K  T  G  H  A  V  R  A  I  G  R  L  S  S  L  E  N  V  Y  I  M  A  D  K  Q  K  N  G  I  K  A  N  F

                                                                  Bsg1
                                                                    |
            CAAGATCCGCCACAACGTCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAAC
        801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
            GTTCTAGGCGGTGTTGCAGCTCCTGCCGTCGCACGTCGAGCGGCTGGTGATGGTCGTCTTGTGGGGGTAGCCGCTGCCGGGGCACGACGACGGGCTGTTG
Case12      >  K  I  R  H  N  V  E  D  G  S  V  Q  L  A  D  H  Y  Q  Q  N  T  P  I  G  D  G  P  V  L  L  P  D  N
```

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                Bpu10            Bpu10                                                          Bpm1
                  |                |                                                              |
            CACTACCTGAGCTTCCAGTCCGTCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCG
       901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
            GTGATGGACTCGAAGGTCAGGCAGGACTCGTTTCTGGGGTTGCTCTTCGCGCTAGTGTACCAGGACGACCTCAAGCACTGGCGGCGGCCCTAGTGAGAGC
Case12      > H  Y  L  S  F  Q  S  V  L  S  K  D  P  N  E  K  R  D  H  M  V  L  L  E  F  V  T  A  A  G  I  T  L  G

                                                                                  BseR1
                     BsrG1                                                         Ale1
                       |                                                              |
            GCATGGACGAGCTGTACAACGTGGATGGCGGTAGCGGTGGCACCGGCAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGA
      1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
            CGTACCTGCTCGACATGTTGCACCTACCGCCATCGCCACCGTGGCCGTCGTTCCCGCTCCTCGACAAGTGGCCCCACCACGGGTAGGACCAGCTCGACCT
Case12      >   M  D  E  L  Y  N  V  D  G  G  S  G  G  T  G  S  K  G  E  E  L  F  T  G  V  V  P  I  L  V  E  L  D

                                                                                     Bsg1
                                                                                Bcg1b   |
                                   Bcg1a                                      BtgZ1  |   |                    Eco57
                                     |                                          |  |   |                      |
            CGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAG
      1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
            GCCGCTGCATTTGCCGGTGTTCAAGTCGCACAGGCCGCTCCCGCTCCCGCTACGGTGGATGCCGTTCGACTGGGACTTCGACTAGACGTGGTGGCCGTTC
Case12      >  G  D  V  N  G  H  K  F  S  V  S  G  E  G  E  G  D  A  T  Y  G  K  L  T  L  K  L  I  C  T  T  G  K

                          BssS1
                           Ale1                          Xmn1          Eco57                   Eci1
                             |                             |              |                       |
            CTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTCGGCTACGGCCTGAAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGT
      1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
            GACGGGCACGGGACCGGGTGGGAGCACTGGTGGGAGCCGATGCCGGACTTCACGAAGCGGGCGATGGGGCTGGTGTACTTCGTCGTGCTGAAGAAGTTCA
Case12      > L  P  V  P  W  P  T  L  V  T  T  L  G  Y  G  L  K  C  F  A  R  Y  P  D  H  M  K  Q  H  D  F  F  K  S

                                                                                 SpDon                  Ale1
                                                                                   |                      |
            CCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCT
      1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
            GGCGGTACGGGCTTCCGATGCAGGTCCTCGCGTGGTAGAAGAAGTTCCTGCTGCCGTTGATGTTCTGGGCGCGGCTCCACTTCAAGCTCCCGCTGTGGGA
Case12      >   A  M  P  E  G  Y  V  Q  E  R  T  I  F  F  K  D  D  G  N  Y  K  T  R  A  E  V  K  F  E  G  D  T  L

                                                                                                  Pvu2
```

```
                                                                                                  Bpm1 |
          SpDon                                Eco57                                   Mlu1 Bcl1   | |
              |                                    |                                       |    |   | |
              GGTGAACCGCATCGAGCTGAAGGGCATCGGCTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACGCGTGATCAGCTGACCGAAGAA
        1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
              CCACTTGGCGTAGCTCGACTTCCCGTAGCCGAAGTTCCTCCTGCCGTTGTAGGACCCCGTGTTCGACCTCATGTTGTGCGCACTAGTCGACTGGCTTCTT
Case12      >  V  N  R  I  E  L  K  G  I  G  F  K  E  D  G  N  I  L  G  H  K  L  E  Y  N  T  R  D  Q  L  T  E  E

                  EcoR1
               T7Ter   |                                                BtgZ1                BspH1
                   |   |                                                  |                    |
              CAGATTGCTGAATTCAAGGAAGCCTTCTCCCTATTTGATAAAGATGGCGATGGCACCATCACAACAAAGGAACTTGGAACTGTCATGAGGTCACTGGGTC
        1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
              GTCTAACGACTTAAGTTCCTTCGGAAGAGGGATAAACTATTTCTACCGCTACCGTGGTAGTGTTGTTTCCTTGAACCTTGACAGTACTCCAGTGACCCAG
Case12      > Q  I  A  E  F  K  E  A  F  S  L  F  D  K  D  G  D  G  T  I  T  T  K  E  L  G  T  V  M  R  S  L  G  Q

             Bmr1       AlwN1            Bcl1                                                                SpAcc
                |           |               |                                                                   |
              AGAACCCAACAGAAGCTGAATTGCAGGATATGATCAATGAAGTGGATGCTGATGGTAATGGCACCATTGACTTCCCCGAATTTTTGACTATGATGGCTAG
        1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
              TCTTGGGTTGTCTTCGACTTAACGTCCTATACTAGTTACTTCACCTACGACTACCATTACCGTGGTAACTGAAGGGGCTTAAAAACTGATACTACCGATC
Case12      >   N  P  T  E  A  E  L  Q  D  M  I  N  E  V  D  A  D  G  N  G  T  I  D  F  P  E  F  L  T  M  M  A  R

                           T7Ter
                           SpDon                 Bsm1                          BsrD1
                               |                   |                              |
              AAAAATGAAAGATACAGATAGTGAAGAAGAAATCCGTGAGGCATTCCGAGTCTTTGACAAGGATGGCAATGGTTATATCAGTGCAGCAGAACTACGTCAC
        1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
              TTTTTACTTTCTATGTCTATCACTTCTTCTTTAGGCACTCCGTAAGGCTCAGAAACTGTTCCTACCGTTACCAATATAGTCACGTCGTCTTGATGCAGTG
Case12      >  K  M  K  D  T  D  S  E  E  E  I  R  E  A  F  R  V  F  D  K  D  G  N  G  Y  I  S  A  A  E  L  R  H

            BspH1
             Bsg1
         BmgB1 |                           T7Ter            Bcl1            BsmB1          Drd1  SpAcc   EcoR1
             | |                               |               |                |             |      |       |
              GTCATGACAAACTTAGGAGAAAAACTAACAGATGAAGAAGTAGATGAAATGATCAGAGAAGCAGATATTGATGGAGACGGACAAGTCAACTATGAAGAAT
        1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
              CAGTACTGTTTGAATCCTCTTTTTGATTGTCTACTTCTTCATCTACTTTACTAGTCTCTTCGTCTATAACTACCTCTGCCTGTTCAGTTGATACTTCTTA
Case12      > V  M  T  N  L  G  E  K  L  T  D  E  E  V  D  E  M  I  R  E  A  D  I  D  G  D  G  Q  V  N  Y  E  E  F
```

```
                                 Not1
                T7Ter     polyA    Eag1      Xba1   BsaB1                            SpDon   Dra1
                   |         |       |         |       |                                |      |
        TCGTACAGATGATGACTGCAAAATAAAGCGGCCGCGACTCTAGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCA
1901    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
        AGCATGTCTACTACTGACGTTTTATTTCGCCGGCGCTGAGATCTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGT
Case12      >   V  Q  M  M  T  A  K  *

                                     Bsm1
                                    Mfe1|        Hpa1       polyA    Psi1      polyA
                                       ||           |           |       |          |
        CACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAA
2001    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
        GTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTT

           polyA            Bts1 Bsm1                                    Afl2         SpDon        Ssp1
               |               |    |                                       |            |           |
        ATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTGTAAGCGTTAATATTTTGT
2101    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
        TAAAGTGTTTATTTCGTAAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTCCGCATTTAACATTCGCAATTATAAAACA

                                                                                Psi1
                                                                                  |
        TAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGG
2201    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
        ATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCC

                                     BsaXb                 Drd1    BsaXa
                                        |                    |        |
        GTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTA
2301    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
        CAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGAT

      BtgZ1
      Dra3|                                                      SpAcc
          ||                                                        |
        CGTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAA
2401    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
        GCACTTGGTAGTGGGATTAGTTCAAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTT
```

```
        Nae1
     NgoM4 |                                   BsrB1
         | |                                     |
        AGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACC
2501    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
        TCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGG

                                                                                        polyA
                                                                                          |
        CGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAAT
2601    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
        GCGGCGCGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTA

                 BciV1
              BspH1  |                                                                    Eci1
            BsrB1 |  |                              Ssp1  Ear1        Bsu36              Pvu2 |
                | |  |                                 |     |            |                 | |
        ATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCA
2701    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
        TACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGT

                                                                  Nsi1
                                                                Sph1 |
                                                               BfrB1 |
                                BseY1                     BstAP  | |            SexA1
                                   |                         |  | |                |
        GTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCC
2801    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
        CAATCCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGG

                                  Nsi1
                                Sph1 |
                               BfrB1 |                                                          Eci1
 BseY1                       BstAP  | |                          Eci1                  Eci1     Bmr1|       Eci1
     |                          |  | |                             |                     |        ||          |
        CCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCG
2901    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
        GGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGC
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                                                          Sfi1
                Nco1                    polyA             Bgl1                    SpDon
                  |                       |                 |                       |
     CCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTT
3001 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 3100
     GGGTAAGAGGCGGGGTACCGACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAA

        Avr2
       Stu1|                                                        BspM1
   BseR1  ||              Cla1              BsaB1                   BfuA1                Eag1
       |  ||                |                 |                       |                   |
     TGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTG
3101 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 3200
     ACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAAC

                                                                                          Nar1
                                Bmr1                                                     Kas1|
                                  |                                                        ||
     GGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTT
3201 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 3300
     CCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAA

                                                                                              Pvu2
            Drd1                                                  Msc1                Fsp1   |
              |                                                     |                   |    |
     GTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCG
3301 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 3400
     CAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGC

    PflF1                       Eco57                                   SpDon
       |                          |                                       |
     ACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCAT
3401 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 3500
     TGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTA
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                                                   BtgZ1
                                                BspM1  |
     BciV1         BsrD1                        BfuA1  |
        |             |                            |  |
      CATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATG
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      GTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTAC

                              Sap1
                              Ear1                          BpuE1                        Sph1
                                 |                             |                            |
      GAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCG
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      CTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGC

                                                                                          BseY1
                                                                                         Nae1 |
                  Nco1               BtgZ1                                            NgoM4 | |
                     |                  |                                                 | | |
      AGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGC
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      TCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCG

                                        Sap1
   Rsr2         Eci1                    Ear1                  Eco57         BssS1                BsrB1
      |            |                       |                     |             |                    |
      GGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCT
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      CCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGA

 BtgZ1                                                BsrB1          BstB1
    |                                                    |              |
      CCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCC
3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
      GGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGG
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    BssS1                                                   Nae1
    BspM1                                                NgoM4 |
    BfuA1                      SpAcc                      Bpm1 |
        |                          |                        | |
      ATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTC
 4001 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 4100
      TAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAG

                         Bpm1
                     SpAcc  |
                      Avr2  |                                                   polyA        polyA
                         |  |                                                      |           |
      ATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGA
 4101 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 4200
      TACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCT

                                                                          Bsa1
                                                                            |
      ATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATA
 4201 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 4300
      TATTTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTAT

                                                                          BstAP
                                          SpDon                           AlwN1      Bsu36
                                             |                               |          |
      CGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCA
 4301 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 4400
      GCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGT

                            Dra1              Dra1                            BspH1
                              |                 |                               |
      GGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTT
 4401 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 4500
      CCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAA

                                                                        BpuE1
                                                                          |
      AACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAAC
 4501 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 4600
      TTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTG
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                                                          Eco57
                                                            |
      AAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAAT
4601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
      TTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTA

              SpAcc                                                                          AlwN1
                  |                                                                            |
      ACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTG
4701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
      TGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGAC

                     BpuE1                                                                ApaL1     BseY1
                        |                                                                   |         |
      CCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCC
4801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
      GGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGG

                                                 SpAcc
                                                    |
      CAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCG
4901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
      GTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGC

      BciV1
   Eci1   |                    BssS1                                   SpAcc
      |   |                       |                                       |
      GTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTG
5001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
      CATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAAC

   Drd1            BpuE1               SpAcc     Eci1
      |               |                   |        |
      AGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGC
5101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
      TCGCAGCTAAAAACACTACGAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACG
```

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            SpDon                                                Nsi1
           BspLU|                                             BfrB1 |
               ||                                                 | |
          TCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
5201      |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*| 5261
          AGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aat2	**Acc65**	**Afe1**	**Afl2**	**Age1**	Ale1	AlwN1	**Apa1**	**ApaL1**	**Ase1**	Avr2	**BamH1**	**Bcg1a**	**Bcg1b**
BciV1	Bcl1	BfrB1	BfuA1	Bgl1	**Bgl2**	**Blp1**	BmgB1	Bmr1	Bpm1	Bpu10	BpuE1	**Bsa1**	BsaB1
BsaXa	**BsaXb**	BseR1	BseY1	Bsg1	Bsm1	**BsmB1**	BspH1	**BspLU**	BspM1	BsrB1	BsrD1	**BsrG1**	BssS1
BstAP	BstB1	Bsu36	BtgZ1	**Bts1**	**Cla1**	Dra1	**Dra3**	Drd1	Eag1	Ear1	Eci1	Eco57	EcoR1
Fsp1	**Hind3**	**Hpa1**	**Kas1**	**Kpn1**	**Mfe1**	**Mlu1**	**Msc1**	Nae1	**Nar1**	Nco1	**Nde1**	NgoM4	**Nhe1**
Not1	Nsi1	**PflF1**	polyA	Psi1	**PspOM**	**Pst1**	Pvu2	**Rsr2**	Sac1	**Sac2**	**Sal1**	Sap1	**SexA1**
Sfi1	**Sma1**	**SnaB1**	SpAcc	SpDon	Sph1	Ssp1	**Stu1**	T7Ter	**Xba1**	Xho1	**Xmn1**		

Unique:

Acc65	**Afe1**	**Afl2**	**Age1**	**Apa1**	**ApaL1**	**Ase1**	**BamH1**	**Bcg1a**	**Bcg1b**	**Bgl2**	**Blp1**	**Bsa1**	**BsaXa**
BsaXb	**BsmB1**	**BspLU**	**BsrG1**	**Bts1**	**Cla1**	**Dra3**	**Fsp1**	**Hind3**	**Hpa1**	**Kas1**	**Kpn1**	**Mfe1**	**Mlu1**
Msc1	**Nar1**	**Nde1**	**Nhe1**	**Not1**	**PflF1**	**PspOM**	**Pst1**	**Rsr2**	**Sac2**	**Sal1**	**SexA1**	**Sfi1**	**Sma1**
SnaB1	**Stu1**	**Xba1**	**Xmn1**										

Not found:

Aar1	Acl1	Ahd1	Asc1	AsiS1	Bae1a	Bae1b	Bbs1	BbvC1	BsiW1	BspE1	BssH2	BstE2	BstX1
BstZ1	_Chi	EcoK	EcoN1	EcoRV	ScFRT	Fse1	FspA1	I_Ceu	loxP	Nru1	Pac1	PflM1	Pme1
Pml1	PshA1	Pvu1	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Spe1	Srf1	Swa1	T3RNA	T7RNA	PISce
Xcm1													

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													