peNirFP-N 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). MCS sequence is shown in frame, amino acids encoded by MCS are shown in black.

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

                         Aat2                    SpAcc                        Aat2
                            |                       |                            |
     CCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGT
 101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 200
     GGGTTGCTGGGGGCGGGTAACTGCAGTTATTACTGCATACAAGGGTATCATTGCGGTTATCCCTGAAAGGTAACTGCAGTTACCCACCTCATAAATGCCA

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

                                 BtgZ1 SnaB1                 Nco1
                                    |     |                    |
     CATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGA
 301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 400
     GTACTGGAATACCCTGAAAGGATGAACCGTCATGTAGATGCATAATCAGTAGCGATAATGGTACCACTACGCCAAAACCGTCATGTAGTTACCCGCACCT
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                                                   Aat2                                                  Eci1
                                                     |                                                     |
     TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 500
     ATCGCCAAACTGAGTGCCCCTAAAGGTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT

                                                                                                Nhe1 Afe1
                                                                                                  |    |
     ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCGCTA
501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
     TGTTGAGGCGGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT
MCS     >                                                                                     L  A  L

                                                                  BamH1
                                                                 Sma1 |
                                                                Apa1| |
                                                            PspOM   || |
                                   Hind3                    Sac2|   || |
                          Xho1    Sac1 |  EcoR1      Sal1      Kpn1  ||   || |
                      BpuE1 Bgl2   | Ecl2 | |BstB1 |     Pst1| Acc65   |  ||   || |  Age1       Nco1
                          |    |    |    | | |    | |         ||      |  ||   || |     |          |
     CCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCTGCAGTCGACGGTACCGCGGGCCCGGGATCCACCGGTCGCCACCATGGGAGAGGATAGCGAGCTGA
601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
     GGCCTGAGTCTAGAGCTCGAGTTCGAAGCTTAAGACGTCAGCTGCCATGGCGCCCGGGCCCTAGGTGGCCAGCGGTGGTACCCTCTCCTATCGCTCGACT
MCS/NirFP  > P  D  S  D  L  E  L  K  L  R  I  L  Q  S  T  V  P  R  A  R  D  P  P  V  A  T  M  G  E  D  S  E  L  I

                                BsrG1                                ApaL1                    SpAcc
                                  |                                    |                        |
     TCTCCGAGAACATGCACACGAAACTGTACATGGAGGGCACCGTGAACGGCCACCACTTCAAGTGCACATCCGAGGGCGAAGGCAAGCCCTACGAGGGCAC
701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
     AGAGGCTCTTGTACGTGTGCTTTGACATGTACCTCCCGTGGCACTTGCCGGTGGTGAAGTTCACGTGTAGGCTCCCGCTTCCGTTCGGGATGCTCCCGTG
NirFP      >  S  E  N  M  H  T  K  L  Y  M  E  G  T  V  N  G  H  H  F  K  C  T  S  E  G  E  G  K  P  Y  E  G  T

     CCAGACCTGTAAGATCAAGGTGGTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGCTACCAGCTTCATGTACGGCAGCAAAACCTTTATCAAC
801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
     GGTCTGGACATTCTAGTTCCACCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTCGAAGTACATGCCGTCGTTTTGGAAATAGTTG
NirFP      >  Q  T  C  K  I  K  V  V  E  G  G  P  L  P  F  A  F  D  I  L  A  T  S  F  M  Y  G  S  K  T  F  I  N
```

```
                                                Bsu36       SpDon                          Bbs1
                                                   |           |                             |
            CACACCCAGGGCATCCCCGACTTCTTTAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGGATCACCACATACGAAGACGGGGGCGTGCTGACCGCTA
     901    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
            GTGTGGGTCCCGTAGGGGCTGAAGAAATTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCCTAGTGGTGTATGCTTCTGCCCCCGCACGACTGGCGAT
NirFP     > H  T  Q  G  I  P  D  F  F  K  Q  S  F  P  E  G  F  T  W  E  R  I  T  T  Y  E  D  G  G  V  L  T  A  T
```

```
          Bpm1
            |
            CCCAGGACACCAGCCTCCAGAACGGCTGCCTCATCTACAACGTCAAGATCAACGGGGTGAACTTCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACT
    1001    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
            GGGTCCTGTGGTCGGAGGTCTTGCCGACGGAGTAGATGTTGCAGTTCTAGTTGCCCCACTTGAAGGGTAGGTTGCCGGGACACTACGTCTTCTTTTGTGA
NirFP     >   Q  D  T  S  L  Q  N  G  C  L  I  Y  N  V  K  I  N  G  V  N  F  P  S  N  G  P  V  M  Q  K  K  T  L
```

```
                                                                                   Bsg1       Eco57
          BseY1                                 PshA1                            BssS1  |       BpuE1 Bts1
            |                                      |                                |  |           |    |
            CGGCTGGGAGGCCAACACCGAGATGCTGTACCCCGCTGACAGCGGTCTGAGAGGCCATAATCAGATGGCCCTGAAGCTCGTGGGCGGGGGCTACCTGCAC
    1101    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
            GCCGACCCTCCGGTTGTGGCTCTACGACATGGGGCGACTGTCGCCAGACTCTCCGGTATTAGTCTACCGGGACTTCGAGCACCCGCCCCCGATGGACGTG
NirFP     > G  W  E  A  N  T  E  M  L  Y  P  A  D  S  G  L  R  G  H  N  Q  M  A  L  K  L  V  G  G  G  Y  L  H
```

```
         BspM1                        BpuE1                                          SpAcc
            |                            |                                              |
            TGCTCCCTCAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGCTTCTACTTCGTGGACCGTAAACTGGAAAGAATCAAGGAGG
    1201    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
            ACGAGGGAGTTCTGGTGTATGTCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCGAAGATGAAGCACCTGGCATTTGACCTTTCTTAGTTCCTCC
NirFP     > C  S  L  K  T  T  Y  R  S  K  K  P  A  K  N  L  K  M  P  G  F  Y  F  V  D  R  K  L  E  R  I  K  E  A
```

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                                                                                                                  Not1
                                                                                                                  Eag1
                                                                                                                  Bsg1
                                                                                                               BsrB1|
                                                                                                          Blp1    ||
                                                                                                        Pvu2|     ||
                 Bsa1       PshA1       BssS1           Msc1  AlwN1          BspM1           Bmr1||     ||
                    |           |           |              |      |              |              |||     ||
                 CCGACAAAGAGACCTACGTCGAGCAGCACGAGATGGCTGTGGCCAGGTACTGCGACCTGCCTAGCAAACTGGGGCACAGCTGAGCGGCCGCGTGACAAGC
          1301   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
                 GGCTGTTTCTCTGGATGCAGCTCGTCGTGCTCTACCGACACCGGTCCATGACGCTGGACGGATCGTTTGACCCCGTGTCGACTCGCCGGCGCACTGTTCG
NirFP        >   D  K  E  T  Y  V  E  Q  H  E  M  A  V  A  R  Y  C  D  L  P  S  K  L  G  H  S  *

                    BamH1
                  Pml1  |
                 Eco57  |                          SanD1
                     |  |                             |
                 TGCACGTGGATCCTGAGAACTTCAGGGTGAGTCTATGGGACCCTTGATGTTTTCTTTCCCCTTCTTTTCTATGGTTAAGTTCATGTCATAGGAAGGGGAT
          1401   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
                 ACGTGCACCTAGGACTCTTGAAGTCCCACTCAGATACCCTGGGAACTACAAAAGAAAGGGGAAGAAAAGATACCAATTCAAGTACAGTATCCTTCCCCTA

                                                                                                   polyA         Mfe1
                                                                                                      |             |
                 AAGTAACAGGGTACAGTTTAGAATGGGAAACAGACGAATGATTGCATCAGTGTGGAAGTCTCAGGATCGTTTTAGTTTCTTTTATTTGCTGTTCATAACA
          1501   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
                 TTCATTGTCCCATGTCAAATCTTACCCTTTGTCTGCTTACTAACGTAGTCACACCTTCAGAGTCCTAGCAAAATCAAAGAAAATAAACGACAAGTATTGT

                                                                  SpDon
                                                                     |
                 ATTGTTTTCTTTTGTTTAATTCTTGCTTTCTTTTTTTTTCTTCTCCGCAATTTTTACTATTATACTTAATGCCTTAACATTGTGTATAACAAAAGGAAAT
          1601   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
                 TAACAAAAGAAAACAAATTAAGAACGAAAGAAAAAAAAAGAAGAGGCGTTAAAAATGATAATATGAATTACGGAATTGTAACACATATTGTTTTCCTTTA

                 ATCTCTGAGATACATTAAGTAACTTAAAAAAAAACTTTACACAGTCTGCCTAGTACATTACTATTTGGAATATATGTGTGCTTATTTGCATATTCATAAT
          1701   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
                 TAGAGACTCTATGTAATTCATTGAATTTTTTTTGAAATGTGTCAGACGGATCATGTAATGATAAACCTTATATACACACGAATAAACGTATAAGTATTA
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                polyA     polyA                                                    BsrG1
                    |         |                                                        |
     CTCCCTACTTTATTTTCTTTTATTTTTAATTGATACATAATCATTATACATATTTATGGGTTAAAGTGTAATGTTTTAATATGTGTACACATATTGACCA
1801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
     GAGGGATGAAATAAAAGAAAATAAAAATTAACTATGTATTAGTAATATGTATAAATACCCAATTTCACATTACAAAATTATACACATGTGTATAACTGGT

                                Dra1
                                   |
     AATCAGGGTAATTTTGCATTTGTAATTTTAAAAAATGCTTTCTTCTTTTAATATACTTTTTTGTTTATCTTATTTCTAATACTTTCCCTAATCTCTTTCT
1901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
     TTAGTCCCATTAAAACGTAAACATTAAAATTTTTTACGAAAGAAGAAAATTATATGAAAAAACAAATAGAATAAAGATTATGAAAGGGATTAGAGAAAGA

     SpAcc                                                                              Ssp1
         |                                                                                 |
     TTCAGGGCAATAATGATACAATGTATCATGCCTCTTTGCACCATTCTAAAGAATAACAGTGATAATTTCTGGGTTAAGGCAATAGCAATATTTCTGCATA
2001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
     AAGTCCCGTTATTACTATGTTACATAGTACGGAGAAACGTGGTAAGATTTCTTATTGTCACTATTAAAGACCCAATTCCGTTATCGTTATAAAGACGTAT

      Ssp1                      SpDon                                                   polyA
         |                         |                                                       |
     TAAATATTTCTGCATATAAATTGTAACTGATGTAAGAGGTTTCATATTGCTAATAGCAGCTACAATCCAGCTACCATTCTGCTTTTATTTTATGGTTGGG
2101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
     ATTTATAAAGACGTATATTTAACATTGACTACATTCTCCAAAGTATAACGATTATCGTCGATGTTAGGTCGATGGTAAGACGAAAATAAAATACCAACCC

                                                                                 AlwN1
                                                                            SpAcc  |
                                                                                |  |
     ATAAGGCTGGATTATTCTGAGTCCAAGCTAGGCCCTTTTGCTAATCATGTTCATACTTCTTATCTTCCTCCCACAGCTCCTGGGCAACGTGCTGGTCTGT
2201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
     TATTCCGACCTAATAAGACTCAGGTTCGATCCGGGAAAACGATTAGTACAAGTATGAAGAATAGAAGGAGGGTGTCGAGGACCCGTTGCACGACCAGACA

                BstX1    EcoR1                                  Bsg1
                   |        |                                      |
     GTGCTGGCCCATCACTTTGGCAAAGAATTCACCCCACCAGTGCAGGCTGCCTATCAGAAAGTGGTGGCTGGTGTGGCTAATGCCCTGGCCCACAAGTATC
2301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
     CACGACCGGGTAGTGAAACCGTTTCTTAAGTGGGGTGGTCACGTCCGACGGATAGTCTTTCACCACCGACCACACCGATTACGGGACCGGGTGTTCATAG
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                                                                                                Bmr1
                                                                                                  |
      ACTAAGCTCGCTTTCTTGCTGTCCAATTTCTATTAAAGGTTCCTTTGTTCCCTAAGTCCAACTACTAAACTGGGGGATATTATGAAGGGCCTTGAGCATT
2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
      TGATTCGAGCGAAAGAACGACAGGTTAAAGATAATTTCCAAGGAAACAAGGGATTCAGGTTGATGATTTGACCCCCTATAATACTTCCCGGAACTCGTAA

             BpuE1
             Xba1|  BsaB1                                SpDon   Dra1
                ||      |                                   |      |
      GGATTCTGCCTCTAGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAA
2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
      CCTAAGACGGAGATCTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTT

          Bsm1
         Mfe1|        Hpa1       polyA    Psi1      polyA                        polyA            Bts1
             ||           |           |       |          |                           |               |
      TGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACT
2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
      ACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGA


   Bsm1                                  Afl2         SpDon        Ssp1
      |                                     |             |            |
      GCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAAT
2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
      CGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTCCGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTA


                                                Psi1
                                                  |
      CAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAG
2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
      GTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTC

                                                                                  BtgZ1
        BsaXb                    Drd1     BsaXa                                  Dra3|
            |                       |         |                                     ||
      AGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTT
2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
      TCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAA
```

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                                                                   Nae1
                                  SpAcc                          NgoM4 |
                                      |                              | |
     TGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGG
3001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
     ACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCC

                BsrB1
                    |
     GAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGC
3101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
     CTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCG

                                                                                      BciV1
                                                                                  BspH1  |
                                                polyA                            BsrB1 |  |
                                                  |                                 | |  |
     GCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCT
3201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
     CGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGA

                                                      Eci1
                  Ssp1  Ear1        Bsu36             Pvu2 |
                    |     |            |                 | |
     GATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCC
3301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
     CTATTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGG

                              Nsi1
                            Sph1 |                                                                  Sph1
                           BfrB1 |                                                                 BfrB1
 BseY1                   BstAP  | |            SexA1                      BseY1                   BstAP  |
     |                       |  | |                |                         |                       |  |
     CCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGC
3401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
     GGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACG
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                                                        Eci1
   Nsi1                      Eci1                 Eci1     Bmr1|       Eci1            Nco1
      |                         |                    |        ||          |               |
      ATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAAT
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      TAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTA

                                                                                  Avr2
                                 Sfi1                                             Stu1|
          polyA                  Bgl1                      SpDon             BseR1  ||              Cla1
              |                     |                         |                 |  ||                 |
      TTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGA
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      AAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTCTAGCT

                 BsaB1                        BspM1                Eag1
                    |                            |                   |
      TCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGG
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      AGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACC

                                                          Nar1
        Bmr1                                             Kas1|                        Drd1
           |                                                ||                          |
      GCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGA
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      CGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACT

                                                      Pvu2
                                       Msc1                Fsp1   |        PflF1
                                          |                   |   |            |
      ATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTG
3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
      TACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGAC
```

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    Eco57                                       SpDon                          BciV1         BsrD1
      |                                           |                              |             |
      GCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCAT
4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
      CGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTA

                            BtgZ1
                         BspM1  |
                            |   |
      ACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC
4101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
      TGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAG

   Sap1
   Ear1                           BpuE1                          Sph1                        Nco1
     |                              |                              |                           |
      TGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGC
4201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
      ACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACG

                                                                BseY1
                                                               Nae1 |
         BtgZ1                                               NgoM4 | |        Rsr2         Eci1
            |                                                    | | |           |            |
      CTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCT
4301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
      GACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGA

            Sap1                                                          BtgZ1
            Ear1                      Eco57         BssS1                 BsrB1 |
               |                        |             |                     | |
      ACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATC
4401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
      TGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAG
```

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                                                                  BssS1
                        BsrB1          BstB1                      BspM1
                            |              |                          |
     GCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCC
4501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
     CGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGG

                                        Nae1                                                   Bpm1
                                      NgoM4 |                                              SpAcc  |
   SpAcc                               Bpm1 |                                               Avr2  |
       |                                   | |                                                  |  |
     TTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGG
4601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
     AAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCC

                                                        polyA        polyA
                                                            |            |
     GGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGT
4701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
     CCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAAACA

                                            Bsa1
                                              |
     TCATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCC
4801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
     AGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGG

                                                        BstAP
                                                        AlwN1      Bsu36
                                                            |          |
     CACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATT
4901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
     GTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAA
```

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   Dra1               Dra1                              BspH1
      |                  |                                 |
      TAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTC
5001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
      ATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAG

                                                  BpuE1
                                                     |
      AGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTT
5101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
      TCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAA

                                Eco57                                                 SpAcc
                                   |                                                     |
      TGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAG
5201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
      ACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATC

                                                                  AlwN1                     BpuE1
                                                                     |                         |
      GCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGG
5301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5400
      CGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCC

                                                                ApaL1     BseY1
                                                                   |         |
      GTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAA
5401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5500
      CAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTT
```

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                                                                   BciV1
                    SpAcc                                        Eci1   |
                        |                                           |   |
     CTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGC
5501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5600
     GACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCG

  BssS1                                 SpAcc                        Drd1            BpuE1
     |                                      |                           |                |
     GCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGG
5601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5700
     CGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCC

                                                                   SpDon
          SpAcc     Eci1                                         BspLU|
              |        |                                            ||
     GGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCT
5701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5800
     CCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGA

                                Nsi1
                            BfrB1 |
                                | |
     GATTCTGTGGATAACCGTATTACCGCCATGCAT
5801 |||||||||*|||||||||*|||||||||*||| 5833
     CTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aat2	**Acc65**	**Afe1**	**Afl2**	**Age1**	AlwN1	**Apa1**	ApaL1	**Ase1**	Avr2	BamH1	**Bbs1**	BciV1	BfrB1
Bgl1	**Bgl2**	**Blp1**	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	**BsaXa**	**BsaXb**	**BseR1**	BseY1	Bsg1	Bsm1
BspH1	**BspLU**	BspM1	BsrB1	**BsrD1**	BsrG1	BssS1	BstAP	BstB1	**BstX1**	Bsu36	BtgZ1	Bts1	**Cla1**
Dra1	**Dra3**	Drd1	Eag1	Ear1	Eci1	**Ecl2**	Eco57	EcoR1	**Fsp1**	**Hind3**	**Hpa1**	**Kas1**	**Kpn1**
Mfe1	Msc1	Nae1	**Nar1**	Nco1	**Nde1**	NgoM4	**Nhe1**	**Not1**	Nsi1	**PflF1**	**Pml1**	polyA	PshA1
Psi1	**PspOM**	**Pst1**	Pvu2	**Rsr2**	**Sac1**	**Sac2**	**Sal1**	**SanD1**	Sap1	**SexA1**	**Sfi1**	**Sma1**	**SnaB1**
SpAcc	SpDon	Sph1	Ssp1	**Stu1**	**Xba1**	**Xho1**							

Unique:

Acc65	**Afe1**	**Afl2**	**Age1**	**Apa1**	**Ase1**	**Bbs1**	**Bgl2**	**Blp1**	**BsaXa**	**BsaXb**	**BseR1**	**BspLU**	**BsrD1**
BstX1	**Cla1**	**Dra3**	**Ecl2**	**Fsp1**	**Hind3**	**Hpa1**	**Kas1**	**Kpn1**	**Nar1**	**Nde1**	**Nhe1**	**Not1**	**PflF1**
Pml1	**PspOM**	**Pst1**	**Rsr2**	**Sac1**	**Sac2**	**Sal1**	**SanD1**	**SexA1**	**Sfi1**	**Sma1**	**SnaB1**	**Stu1**	**Xba1**
Xho1													

Not found:

Aar1	Acl1	Ahd1	Ale1	Asc1	AsiS1	Bae1a	Bae1b	BbvC1	Bcg1a	Bcg1b	Bcl1	BmgB1	Bpu10
BsiW1	BsmB1	BspE1	BssH2	BstE2	BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	EcoK	EcoN1	EcoRV
FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	I_Ceu	loxP	Mlu1	Nru1	Pac1	PflM1	Pme1
Pvu1	R4atB	R4atL	R4atP	R4atR	Sbf1	Sca1	Sgf1	SgrA1	Spe1	Srf1	Swa1	T3RNA	T7RNA
T7Ter	PISce	Xcm1	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													