pHyper-dMito 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).

Mitochondrial targeting signals (MTS-1 and MTS-2) are shown in bold black and bold green.

```
        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
                                                                                                         |
               ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCATGT
          501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
               TGTTGAGGCGGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGTACA
MTS-1        >                                                                                                 M  S

                                                           Bmr1         BssH2             PflM1
                                                              |             |                 |
               CCGTCCTGACGCCGCTGCTGCTGCGGGGCTTGACAGGCTCGGCCCGGCGGCTCCCAGTGCCGCGCGCCAAGATCCATTCGTTGGGGGATCTGTCCGTCCT
          601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
               GGCAGGACTGCGGCGACGACGACGCCCCGAACTGTCCGAGCCGGGCCGCCGAGGGTCACGGCGCGCGGTTCTAGGTAAGCAACCCCCTAGACAGGCAGGA
MTS-1/MTS-2  >   V  L  T  P  L  L  L  R  G  L  T  G  S  A  R  R  L  P  V  P  R  A  K  I  H  S  L  G  D  L  S  V  L

                                                    Bmr1         BssH2             PflM1 BamH1  Age1
                                                       |             |                 |     |     |
               GACGCCGCTGCTGCTGCGGGGCTTGACAGGCTCGGCCCGGCGGCTCCCAGTGCCGCGCGCCAAGATCCATTCGTTGGGGGATCCACCGGTCGCCACCGAG
          701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
               CTGCGGCGACGACGACGCCCCGAACTGTCCGAGCCGGGCCGCCGAGGGTCACGGCGCGCGGTTCTAGGTAAGCAACCCCCTAGGTGGCCAGCGGTGGCTC
MTS-2/Hyper  >  T  P  L  L  L  R  G  L  T  G  S  A  R  R  L  P  V  P  R  A  K  I  H  S  L  G  D  P  P  V  A  T  E

                                          Rsr2
                                      BspE1  |                                               Bsg1
                         Bgl1     PflF1   |  |                                            BspM1 |
          BstX1        BsmB1|    Bsg1 |   |  |                         SpAcc              BfuA1 |
              |            ||       | |   |  |                             |                  | |
               ATGGCAAGCCAGCAGGGCGAGACGATGTCCGGACCGCTGCACATTGGTTTGATTCCCACAGTTGGACCGTACCTGCTACCGCATATTATCCCTATGCTGC
          801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
               TACCGTTCGGTCGTCCCGCTCTGCTACAGGCCTGGCGACGTGTAACCAAACTAAGGGTGTCAACCTGGCATGGACGATGGCGTATAATAGGGATACGACG
Hyper        > M  A  S  Q  Q  G  E  T  M  S  G  P  L  H  I  G  L  I  P  T  V  G  P  Y  L  L  P  H  I  I  P  M  L  H
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                                                                  PflM1
                                                                  AlwN1
                                                                      |
               ACCAGACCTTTCCAAAGCTGGAAATGTATCTGCATGAAGCACAGACCCACCAGTTACTGGCGCAACTGGACAGCGGCAAACTCGATTGCGTGATCCTCGC
          901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
               TGGTCTGGAAAGGTTTCGACCTTTACATAGACGTACTTCGTGTCTGGGTGGTCAATGACCGCGTTGACCTGTCGCCGTTTGAGCTAACGCACTAGGAGCG
Hyper        >   Q  T  F  P  K  L  E  M  Y  L  H  E  A  Q  T  H  Q  L  L  A  Q  L  D  S  G  K  L  D  C  V  I  L  A

              SpDon            Bsm1                                         SpAcc
                  |               |                                             |
               GCTGGTGAAAGAGAGCGAAGCATTCATTGAAGTGCCGTTGTTTGATGAGCCAATGTTGCTGGCTATCTATGAAGATCACCCGTGGGCGAACCGCGAATGC
         1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
               CGACCACTTTCTCTCGCTTCGTAAGTAACTTCACGGCAACAAACTACTCGGTTACAACGACCGATAGATACTTCTAGTGGGCACCCGCTTGGCGCTTACG
Hyper        >  L  V  K  E  S  E  A  F  I  E  V  P  L  F  D  E  P  M  L  L  A  I  Y  E  D  H  P  W  A  N  R  E  C

                                                                                            Nae1
                                                                                         NgoM4 |
            Bsm1           Bgl1                                              Eci1      BsrD1 | |           PflF1
               |              |                                                 |          | | |               |
               GTACCGATGGCCGATCTGGCAGGGGAAAAACTGCTGATGCTGGAAGATGGTCACTGTTTGCGCGATCAGGCAATGTCCGCCGGCTACAACAGCGACAACG
         1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
               CATGGCTACCGGCTAGACCGTCCCCTTTTTGACGACTACGACCTTCTACCAGTGACAAACGCGCTAGTCCGTTACAGGCGGCCGATGTTGTCGCTGTTGC
Hyper        > V  P  M  A  D  L  A  G  E  K  L  L  M  L  E  D  G  H  C  L  R  D  Q  A  M  S  A  G  Y  N  S  D  N  V

                                                     Eci1                                                     Bsg1
                                                        |                                                        |
               TCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACGTCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCA
         1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
               AGATATAGTACCGGCTGTTCGTCTTCTTGCCGTAGTTCCGGTTGAAGTTCTAGGCGGTGTTGCAGCTCCTGCCGTCGCACGTCGAGCGGCTGGTGATGGT
Hyper        >   Y  I  M  A  D  K  Q  K  N  G  I  K  A  N  F  K  I  R  H  N  V  E  D  G  S  V  Q  L  A  D  H  Y  Q

                                                               Bpu10             Bpu10
                                                                   |                 |
               GCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTTCCAGTCCGTCCTGAGCAAAGACCCCAACGAGAAGCGCGAT
         1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
               CGTCTTGTGGGGGTAGCCGCTGCCGGGGCACGACGACGGGCTGTTGGTGATGGACTCGAAGGTCAGGCAGGACTCGTTTCTGGGGTTGCTCTTCGCGCTA
Hyper        >  Q  N  T  P  I  G  D  G  P  V  L  L  P  D  N  H  Y  L  S  F  Q  S  V  L  S  K  D  P  N  E  K  R  D
```

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                                             Bpm1                    BsrG1
                                                |                        |
               CACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAACGTGGATGGCGGTAGCGGTGGCACCGGCAGCAAGG
         1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
               GTGTACCAGGACGACCTCAAGCACTGGCGGCGGCCCTAGTGAGAGCCGTACCTGCTCGACATGTTGCACCTACCGCCATCGCCACCGTGGCCGTCGTTCC
Hyper        > H  M  V  L  L  E  F  V  T  A  A  G  I  T  L  G  M  D  E  L  Y  N  V  D  G  G  S  G  G  T  G  S  K  G

                            BseR1
                             Ale1                                                       Bcg1a
                                |                                                           |
               GCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGC
         1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
               CGCTCCTCGACAAGTGGCCCCACCACGGGTAGGACCAGCTCGACCTGCCGCTGCATTTGCCGGTGTTCAAGTCGCACAGGCCGCTCCCGCTCCCGCTACG
Hyper        >   E  E  L  F  T  G  V  V  P  I  L  V  E  L  D  G  D  V  N  G  H  K  F  S  V  S  G  E  G  E  G  D  A

                           Bsg1
                      Bcg1b   |                                               BssS1
                   BtgZ1  |   |                    Eco57                       Ale1                          Xmn1
                       |  |   |                        |                          |                             |
               CACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTCGGCTACGGCCTGAAGTGC
         1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
               GTGGATGCCGTTCGACTGGGACTTCGACTAGACGTGGTGGCCGTTCGACGGGCACGGGACCGGGTGGGAGCACTGGTGGGAGCCGATGCCGGACTTCACG
Hyper        >  T  Y  G  K  L  T  L  K  L  I  C  T  T  G  K  L  P  V  P  W  P  T  L  V  T  T  L  G  Y  G  L  K  C

                       Eco57                   Eci1
                           |                      |
               TTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACG
         1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
               AAGCGGGCGATGGGGCTGGTGTACTTCGTCGTGCTGAAGAAGTTCAGGCGGTACGGGCTTCCGATGCAGGTCCTCGCGTGGTAGAAGAAGTTCCTGCTGC
Hyper        > F  A  R  Y  P  D  H  M  K  Q  H  D  F  F  K  S  A  M  P  E  G  Y  V  Q  E  R  T  I  F  F  K  D  D  G

                                                         SpDon
                                 SpDon                  Ale1 |                                Eco57
                                     |                     | |                                    |
               GCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGGCTTCAAGGAGGACGGCAACATCCT
         1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
               CGTTGATGTTCTGGGCGCGGCTCCACTTCAAGCTCCCGCTGTGGGACCACTTGGCGTAGCTCGACTTCCCGTAGCCGAAGTTCCTCCTGCCGTTGTAGGA
Hyper        >   N  Y  K  T  R  A  E  V  K  F  E  G  D  T  L  V  N  R  I  E  L  K  G  I  G  F  K  E  D  G  N  I  L
```

```
                                     Age1  Bpm1                             Eci1                          Fsp1
                                        |     |                                |                             |
               GGGGCACAAGCTGGAGTACAACGGCACCGGTTTCTGTTTTGAAGCCGGGGCGGATGAAGATACACACTTCCGCGCGACCAGCCTGGAAACTCTGCGCAAC
         1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
               CCCCGTGTTCGACCTCATGTTGCCGTGGCCAAAGACAAAACTTCGGCCCCGCCTACTTCTATGTGTGAAGGCGCGCTGGTCGGACCTTTGAGACGCGTTG
Hyper        >  G  H  K  L  E  Y  N  G  T  G  F  C  F  E  A  G  A  D  E  D  T  H  F  R  A  T  S  L  E  T  L  R  N

           BspM1
           BfuA1                                 Afe1                                     BtgZ1
               |                                    |                                         |
               ATGGTGGCGGCAGGTAGCGGGATCACTTTACTGCCAGCGCTGGCTGTGCCGCCGGAGCGCAAACGCGATGGGGTTGTTTATCTGCCGTGCATTAAGCCGG
         2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
               TACCACCGCCGTCCATCGCCCTAGTGAAATGACGGTCGCGACCGACACGGCGGCCTCGCGTTTGCGCTACCCCAACAAATAGACGGCACGTAATTCGGCC
Hyper        > M  V  A  A  G  S  G  I  T  L  L  P  A  L  A  V  P  P  E  R  K  R  D  G  V  V  Y  L  P  C  I  K  P  E

                                                           Fsp1             Pvu2                            Msc1
                                                              |                |                               |
               AACCACGCCGCACTATTGGCCTGGTTTATCGTCCTGGCTCACCGCTGCGCAGCCGCTATGAGCAGCTGGCAGAGGCCATCCGCGCAAGAATGGATGGCCA
         2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
               TTGGTGCGGCGTGATAACCGGACCAAATAGCAGGACCGAGTGGCGACGCGTCGGCGATACTCGTCGACCGTCTCCGGTAGGCGCGTTCTTACCTACCGGT
Hyper        >   P  R  R  T  I  G  L  V  Y  R  P  G  S  P  L  R  S  R  Y  E  Q  L  A  E  A  I  R  A  R  M  D  G  H

                                             Not1
                          Dra1          Dra1 Eag1      Xba1   BsaB1                            SpDon   Dra1
                             |             |    |         |       |                                |      |
               TTTCGATAAAGTTTTAAAACAGGCGGTTTAAAGCGGCCGCGACTCTAGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACC
         2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
               AAAGCTATTTCAAAATTTTGTCCGCCAAATTTCGCCGGCGCTGAGATCTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGG
Hyper        >  F  D  K  V  L  K  Q  A  V  *
                                                    Bsm1
                                                   Mfe1|        Hpa1       polyA    Psi1      polyA
                                                      ||           |           |       |          |
               TCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCAT
         2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
               AGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTA
```

```
              polyA            Bts1 Bsm1                                  Afl2         SpDon        Ssp1
                  |               |    |                                     |             |           |
      CACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTGTAAGCGTTAATAT
2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
      GTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTCCGCATTTAACATTCGCAATTATA

                                                                                Psi1
                                                                                   |
      TTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAG
2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
      AAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTC

                                         BsaXb                 Drd1    BsaXa
                                             |                    |        |
      ATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCC
2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
      TATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGG

        BtgZ1
        Dra3|                                                         SpAcc
           ||                                                             |
      CACTACGTGAACCATCACCCTAATCAAGTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACG
2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
      GTGATGCACTTGGTAGTGGGATTAGTTCAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGC

           Nae1
        NgoM4 |                                    BsrB1
            | |                                        |
      GGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACC
2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
      CCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGG

                                                                                       polyA
                                                                                           |
      ACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATT
2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
      TGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAA
```

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                    BciV1
                 BspH1  |                                                                   Eci1
               BsrB1 |  |                            Ssp1  Ear1        Bsu36              Pvu2 |
                   | |  |                               |     |            |                 | |
      CAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTG
3001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
      GTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACAC

                                                                Nsi1
                                                              Sph1 |
                                                             BfrB1 |
                                  BseY1                   BstAP  | |            SexA1
                                      |                       |  | |                |
      TGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAG
3101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
      ACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTC

                                    Nsi1
                                  Sph1 |
                                 BfrB1 |                                                      Eci1
      BseY1                   BstAP  | |                       Eci1                 Eci1     Bmr1|
          |                       |  | |                          |                    |        ||
      GCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAG
3201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
      CGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTC

                                                                   Sfi1
     Eci1            Nco1                   polyA                  Bgl1                    SpDon
        |               |                       |                     |                        |
      TTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGC
3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
      AAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCG
```

```
              Avr2
             Stu1|                                                            BspM1
         BseR1  ||              Cla1              BsaB1                       BfuA1               Eag1
             |  ||                 |                  |                           |                  |
      TTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCC
3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
      AAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGG

                                                                                            Nar1
                                         Bmr1                                              Kas1|
                                            |                                                 ||
      GCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTC
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      CGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAG

                                                                                                  Pvu2
                   Drd1                                                   Msc1                Fsp1   |
                      |                                                      |                   |   |
      TTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGT
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      AAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACA

         PflF1                       Eco57                                      SpDon
             |                           |                                          |
      GCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTA
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      CGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCAT

                                                              BtgZ1
                                                           BspM1  |
          BciV1         BsrD1                              BfuA1  |
              |             |                                  |  |
      TCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTC
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      AGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAG
```

```
                                    Sap1
                                    Ear1                           BpuE1                         Sph1
                                       |                               |                            |
      GGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGA
3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
      CCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCT

                                                                                               BseY1
                                                                                              Nae1 |
                        Nco1               BtgZ1                                           NgoM4 | |
                           |                   |                                               | | |
      CGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGT
4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
      GCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCA

                                              Sap1
        Rsr2         Eci1                     Ear1                   Eco57         BssS1
           |            |                        |                       |             |
      GTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCG
4101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
      CACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGC

      BtgZ1
    BsrB1 |                                               BsrB1          BstB1
        | |                                                   |             |
      CCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAAC
4201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
      GGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTG

         BssS1                                                               Nae1
         BspM1                                                            NgoM4 |
         BfuA1                      SpAcc                                  Bpm1 |
             |                         |                                      | |
      CTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGG
4301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
      GACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCC
```

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                                Bpm1
                            SpAcc  |
                             Avr2  |                                                        polyA
                                |  |                                                            |
      ATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAG
4401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
      TAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTC

     polyA                                                                       Bsa1
         |                                                                          |
      ACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGC
4501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
      TGTCTTATTTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCG

                                                                                            BstAP
                                                                                            AlwN1
                                                                                                |
      CAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAG
4601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
      GTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATC

   Bsu36                            Dra1               Dra1                              BspH1
       |                               |                  |                                  |
      CCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAAT
4701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
      GGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTA

                                                                                     BpuE1
                                                                                         |
      CCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTG
4801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
      GGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAAC

                                                                   Eco57
                                                                       |
      CAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATAC
4901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
      GTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATG
```

```
                   SpAcc                                                                            AlwN1
                       |                                                                                |
      CAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGC
5001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
      GTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCG

                          BpuE1                                                                ApaL1
                              |                                                                    |
      TGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACA
5101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
      ACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGT

     BseY1                                             SpAcc
         |                                                 |
      CAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGT
5201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
      GTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCA

           BciV1
        Eci1   |                    BssS1                                    SpAcc
           |   |                        |                                        |
      ATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTG
5301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5400
      TAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGAC

        Drd1            BpuE1               SpAcc     Eci1
           |                |                   |        |
      ACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCT
5401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5500
      TGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGA

          SpDon                                                    Nsi1
         BspLU|                                                 BfrB1 |
             ||                                                     | |
      TTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
5501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||| 5566
      AAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aat2 **Afe1** **Afl2** Age1 Ale1 AlwN1 **ApaL1** **Ase1** Avr2 **BamH1** **Bcg1a** **Bcg1b** BciV1 BfrB1
BfuA1 Bgl1 Bmr1 Bpm1 Bpu10 BpuE1 **Bsa1** BsaB1 **BsaXa** **BsaXb** BseR1 BseY1 Bsg1 Bsm1
BsmB1 **BspE1** BspH1 **BspLU** BspM1 BsrB1 BsrD1 **BsrG1** BssH2 BssS1 BstAP **BstB1** **BstX1** Bsu36
BtgZ1 **Bts1** **Cla1** Dra1 **Dra3** Drd1 Eag1 Ear1 Eci1 Eco57 Fsp1 **Hpa1** **Kas1** **Mfe1**
Msc1 Nae1 **Nar1** Nco1 **Nde1** NgoM4 **Nhe1** **Not1** Nsi1 PflF1 PflM1 polyA Psi1 Pvu2
Rsr2 Sap1 **SexA1** **Sfi1** **SnaB1** SpAcc SpDon Sph1 Ssp1 **Stu1** **Xba1** **Xmn1**

Unique:

Afe1 **Afl2** **ApaL1** **Ase1** **BamH1** **Bcg1a** **Bcg1b** **Bsa1** **BsaXa** **BsaXb** **BsmB1** **BspE1** **BspLU** **BsrG1**
BstB1 **BstX1** **Bts1** **Cla1** **Dra3** **Hpa1** **Kas1** **Mfe1** **Nar1** **Nde1** **Nhe1** **Not1** **SexA1** **Sfi1**
SnaB1 **Stu1** **Xba1** **Xmn1**

```
Not found:

    Aar1    Acc65    Acl1    Ahd1    Apa1    Asc1   AsiS1   Bae1a   Bae1b    Bbs1   BbvC1    Bcl1    Bgl2    Blp1

   BmgB1   BsiW1   BstE2   BstZ1    _Chi    EcoK   EcoN1   EcoR1   EcoRV   ScFRT    Fse1   FspA1   Hind3   I_Ceu

    Kpn1    loxP    Mlu1    Nru1    Pac1    Pme1    Pml1   PshA1   PspOM    Pst1    Pvu1    Sac1    Sac2    Sal1

   SanD1    Sbf1    Sca1    Sgf1   SgrA1    Sma1    Spe1    Srf1    Swa1   T3RNA   T7RNA   T7Ter   PISce    Xcm1

   Xho1

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
```