pFusionRed-PDHA1 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 base pairs 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).

FusionRed amino acids are shown in red, human pyruvate dehydrogenase (lipoamide) alpha 1 (PDHA1) amino acids are shown in green, linker amino acids are shown in black.

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

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

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

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

                                                                                                   Nhe1
                                                                                                     |
        ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCACCG
    501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
        TGTTGAGGCGGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGTGGC

                                                        Nae1
                                BsmB1                 NgoM4 |
                                  |                     | |
        CCACCATGAGGAAGATGCTCGCCGCCGTCTCCCGCGTGCTGTCTGGCGCTTCTCAGAAGCCGGCAAGCAGAGTGCTGGTAGCATCCCGTAATTTTGCAAA
    601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
        GGTGGTACTCCTTCTACGAGCGGCGGCAGAGGGCGCACGACAGACCGCGAAGAGTCTTCGGCCGTTCGTCTCACGACCATCGTAGGGCATTAAAACGTTT
PDHA1     >     M  R  K  M  L  A  A  V  S  R  V  L  S  G  A  S  Q  K  P  A  S  R  V  L  V  A  S  R  N  F  A  N

          BstAP                                 SpAcc                     Ale1     SpDon
              |                                   |                         |         |
        TGATGCTACATTTGAAATTAAGAAATGTGACCTTCACCGGCTGGAAGAAGGCCCTCCTGTCACAACAGTGCTCACCAGGGAGGATGGGCTCAAATACTAC
    701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
        ACTACGATGTAAACTTTAATTCTTTACACTGGAAGTGGCCGACCTTCTTCCGGGAGGACAGTGTTGTCACGAGTGGTCCCTCCTACCCGAGTTTATGATG
PDHA1     >  D  A  T  F  E  I  K  K  C  D  L  H  R  L  E  E  G  P  P  V  T  T  V  L  T  R  E  D  G  L  K  Y  Y

                                                Pvu2                                  Ale1          Hind3
                                                  |                                     |               |
        AGGATGATGCAGACTGTACGCCGAATGGAGTTGAAAGCAGATCAGCTGTATAAACAGAAAATTATTCGTGGTTTCTGTCACTTGTGTGATGGTCAGGAAG
    801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
        TCCTACTACGTCTGACATGCGGCTTACCTCAACTTTCGTCTAGTCGACATATTTGTCTTTTAATAAGCACCAAAGACAGTGAACACACTACCAGTCCTTC
PDHA1     > R  M  M  Q  T  V  R  R  M  E  L  K  A  D  Q  L  Y  K  Q  K  I  I  R  G  F  C  H  L  C  D  G  Q  E  A
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                                Nae1
                             NgoM4 |         Bpm1                    Bgl1           SpDon    Sma1
                                 | |            |                      |               |       |
            CTTGCTGTGTGGGCCTGGAGGCCGGCATCAACCCCACAGACCATCTCATCACAGCCTACCGGGCTCACGGCTTTACTTTCACCCGGGGCCTTTCCGTCCG
       901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
            GAACGACACACCCGGACCTCCGGCCGTAGTTGGGGTGTCTGGTAGAGTAGTGTCGGATGGCCCGAGTGCCGAAATGAAAGTGGGCCCCGGAAAGGCAGGC
PDHA1          >   C  C  V  G  L  E  A  G  I  N  P  T  D  H  L  I  T  A  Y  R  A  H  G  F  T  F  T  R  G  L  S  V  R

                                                                                                   SpAcc
                         SpAcc                       SpAcc              Cla1  BspLU            Bcg1b |          BsaXa
                             |                           |                 |      |                | |              |
            AGAAATTCTCGCAGAGCTTACAGGACGAAAAGGAGGTTGTGCTAAAGGGAAAGGAGGATCGATGCACATGTATGCCAAGAACTTCTACGGGGGCAATGGC
      1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
            TCTTTAAGAGCGTCTCGAATGTCCTGCTTTTCCTCCAACACGATTTCCCTTTCCTCCTAGCTACGTGTACATACGGTTCTTGAAGATGCCCCCGTTACCG
PDHA1          >  E  I  L  A  E  L  T  G  R  K  G  G  C  A  K  G  K  G  G  S  M  H  M  Y  A  K  N  F  Y  G  G  N  G

            BspM1
             Aar1                      BsaXb
      BsrD1  |        Bcg1a          BseY1|                                          Bcg1a
          |  |            |           ||                                              |
            ATCGTGGGAGCGCAGGTGCCCCTGGGCGCTGGGATTGCTCTAGCCTGTAAGTATAATGGAAAAGATGAGGTCTGCCTGACTTTATATGGCGATGGTGCTG
      1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
            TAGCACCCTCGCGTCCACGGGGACCCGCGACCCTAACGAGATCGGACATTCATATTACCTTTTCTACTCCAGACGGACTGAAATATACCGCTACCACGAC
PDHA1          > I  V  G  A  Q  V  P  L  G  A  G  I  A  L  A  C  K  Y  N  G  K  D  E  V  C  L  T  L  Y  G  D  G  A  A

                                Hind3
             BtgZ1    Bcg1b BstB1  |  SpDon                                  SpAcc
                 |        |     |  |      |                                     |
            CTAACCAGGGCCAGATATTCGAAGCTTACAACATGGCAGCTTTGTGGAAATTACCTTGTATTTTCATCTGTGAGAATAATCGCTATGGAATGGGAACGTC
      1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
            GATTGGTCCCGGTCTATAAGCTTCGAATGTTGTACCGTCGAAACACCTTTAATGGAACATAAAAGTAGACACTCTTATTAGCGATACCTTACCCTTGCAG
PDHA1          >   N  Q  G  Q  I  F  E  A  Y  N  M  A  A  L  W  K  L  P  C  I  F  I  C  E  N  N  R  Y  G  M  G  T  S

                   BsrB1              SpAcc                                          EcoRV
                       |                  |                                              |
            TGTTGAGAGAGCGGCAGCCAGCACTGATTACTACAAGAGAGGCGATTTCATTCCTGGGCTGAGAGTGGATGGAATGGATATCCTGTGCGTCCGAGAGGCA
      1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
            ACAACTCTCTCGCCGTCGGTCGTGACTAATGATGTTCTCTCCGCTAAAGTAAGGACCCGACTCTCACCTACCTTACCTATAGGACACGCAGGCTCTCCGT
PDHA1          >  V  E  R  A  A  A  S  T  D  Y  Y  K  R  G  D  F  I  P  G  L  R  V  D  G  M  D  I  L  C  V  R  E  A
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                                 SpAcc         Apa1
                              Bgl2  |    PspOM   |  BstX1       Pst1                                  Drd1
                                 |  |         |   |      |           |                                     |
            ACAAGGTTTGCTGCTGCCTATTGTAGATCTGGGAAGGGGCCCATCCTGATGGAGCTGCAGACTTACCGTTACCACGGACACAGTATGAGTGACCCTGGAG
      1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
            TGTTCCAAACGACGACGGATAACATCTAGACCCTTCCCCGGGTAGGACTACCTCGACGTCTGAATGGCAATGGTGCCTGTGTCATACTCACTGGGACCTC
PDHA1     > T  R  F  A  A  A  Y  C  R  S  G  K  G  P  I  L  M  E  L  Q  T  Y  R  Y  H  G  H  S  M  S  D  P  G  V

                        Bpm1
                 BssS1  |  Xmn1     SpDon  SpDon    BpuE1                        SpDon
                     |  |     |          |      |        |                           |
            TCAGTTACCGTACACGAGAAGAAATTCAGGAAGTAAGAAGTAAGAGTGACCCTATTATGCTTCTCAAGGACAGGATGGTGAACAGCAATCTTGCCAGTGT
      1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
            AGTCAATGGCATGTGCTCTTCTTTAAGTCCTTCATTCTTCATTCTCACTGGGATAATACGAAGAGTTCCTGTCCTACCACTTGTCGTTAGAACGGTCACA
PDHA1     >   S  Y  R  T  R  E  E  I  Q  E  V  R  S  K  S  D  P  I  M  L  L  K  D  R  M  V  N  S  N  L  A  S  V

                                                                                                      Bpm1
                                                                                          Sap1      BsaXb |
              SpAcc                 SpDon                 Bmr1             Eag1    Bpu10     Ear1     BseY1| |
                 |                     |                    |                |        |        |         || |
            GGAAGAACTAAAGGAAATTGATGTGGAAGTGAGGAAGGAGATTGAGGATGCTGCCCAGTTTGCCACGGCCGATCCTGAGCCACCTTTGGAAGAGCTGGGC
      1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
            CCTTCTTGATTTCCTTTAACTACACCTTCACTCCTTCCTCTAACTCCTACGACGGGTCAAACGGTGCCGGCTAGGACTCGGTGGAAACCTTCTCGACCCG
PDHA1     >  E  E  L  K  E  I  D  V  E  V  R  K  E  I  E  D  A  A  Q  F  A  T  A  D  P  E  P  P  L  E  E  L  G

                           BsaXa                   PflM1                        BspE1   BamH1  Age1
                              |                       |                            |       |     |
            TACCACATCTACTCCAGCGACCCACCTTTTGAAGTTCGTGGTGCCAATCAGTGGATCAAGTTTAAGTCAGTCAGTAGCTCCGGAGGGGATCCACCGGTCG
      1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
            ATGGTGTAGATGAGGTCGCTGGGTGGAAAACTTCAAGCACCACGGTTAGTCACCTAGTTCAAATTCAGTCAGTCATCGAGGCCTCCCCTAGGTGGCCAGC
PDHA1     > Y  H  I  Y  S  S  D  P  P  F  E  V  R  G  A  N  Q  W  I  K  F  K  S  V  S  S  S  G  G  D  P  P  V  A

                SpDon
               Ale1 |
            Nco1 | |                                 BsrG1                                ApaL1
                | | |                                   |                                    |
            CCACCATGGTGAGCGAGCTGATTAAGGAGAACATGCCCATGAAGCTGTACATGGAGGGCACCGTGAACAACCACCACTTCAAGTGCACATCCGAGGGCGA
      1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
            GGTGGTACCACTCGCTCGACTAATTCCTCTTGTACGGGTACTTCGACATGTACCTCCCGTGGCACTTGTTGGTGGTGAAGTTCACGTGTAGGCTCCCGCT
FusionRed >   T  M  V  S  E  L  I  K  E  N  M  P  M  K  L  Y  M  E  G  T  V  N  N  H  H  F  K  C  T  S  E  G  E
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                 SpAcc
                    |
            AGGCAAGCCCTACGAGGGCACCCAGACCATGAGAATCAAGGTCGTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGCTACCAGCTTCATGTAC
      1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
            TCCGTTCGGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCCAGCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTCGAAGTACATG
FusionRed    >  G  K  P  Y  E  G  T  Q  T  M  R  I  K  V  V  E  G  G  P  L  P  F  A  F  D  I  L  A  T  S  F  M  Y

                                                                                Bsu36       SpDon
                                                                                   |           |
            GGCAGCAGAACCTTCATCAAGCACCCTCCGGGCATCCCCGACTTCTTTAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACATACGAAG
      2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
            CCGTCGTCTTGGAAGTAGTTCGTGGGAGGCCCGTAGGGGCTGAAGAAATTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGGTGTATGCTTC
FusionRed    > G  S  R  T  F  I  K  H  P  P  G  I  P  D  F  F  K  Q  S  F  P  E  G  F  T  W  E  R  V  T  T  Y  E  D

            Bbs1             Bpm1                                                                  BseY1
               |                |                                                                      |
            ACGGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGGTTAGAGGGGTGAACTTCCCAGCCAACGGCCC
      2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
            TGCCCCCGCACGACTGGCGATGGGTCCTGTGGTCGGAGGTCCTGCCGACGGAGTAGATGTTGCAGTTCCAATCTCCCCACTTGAAGGGTCGGTTGCCGGG
FusionRed    >   G  G  V  L  T  A  T  Q  D  T  S  L  Q  D  G  C  L  I  Y  N  V  K  V  R  G  V  N  F  P  A  N  G  P

                                          BsmB1
                              BseY1    Stu1  |                                   Bgl1                     BssS1
                                 |       |  |                                      |                        |
            TGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCTCCACCGAGACGATGTACCCCGCTGACGGCGGCCTGGAAGGCGCATGTGACATGGCCCTGAAGCTC
      2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
            ACACTACGTCTTCTTTTGTGAGCCGACCCTCCGGAGGTGGCTCTGCTACATGGGGCGACTGCCGCCGGACCTTCCGCGTACACTGTACCGGGACTTCGAG
FusionRed    >  V  M  Q  K  K  T  L  G  W  E  A  S  T  E  T  M  Y  P  A  D  G  G  L  E  G  A  C  D  M  A  L  K  L

                                                                  BpuE1
                      Eco57        Bsa1                       BpuE1  |
                         |            |                          |  |
            GTGGGCGGGGGCCACCTGATCTGCAACCTTGAGACCACATACAGATCCAAGAAACCCGCTACGAACCTCAAGATGCCCGGCGTCTACAACGTGGACCACA
      2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
            CACCCGCCCCCGGTGGACTAGACGTTGGAACTCTGGTGTATGTCTAGGTTCTTTGGGCGATGCTTGGAGTTCTACGGGCCGCAGATGTTGCACCTGGTGT
FusionRed    > V  G  G  G  H  L  I  C  N  L  E  T  T  Y  R  S  K  K  P  A  T  N  L  K  M  P  G  V  Y  N  V  D  H  R
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           SpAcc
           PflM1                  Bsa1       PshA1       BssS1 Dra3      Msc1                            SpDon
              |                     |           |           |    |         |                                |
           GACTGGAAAGAATCAAGGAGGCCGACGATGAGACCTACGTCGAGCAGCACGAGGTGGCTGTGGCCAGATACTCTACTGGTGGCGCTGGTGATGGAGGTAA
      2401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
           CTGACCTTTCTTAGTTCCTCCGGCTGCTACTCTGGATGCAGCTCGTCGTGCTCCACCGACACCGGTCTATGAGATGACCACCGCGACCACTACCTCCATT
FusionRed    >   L  E  R  I  K  E  A  D  D  E  T  Y  V  E  Q  H  E  V  A  V  A  R  Y  S  T  G  G  A  G  D  G  G  K

             Not1
             Eag1
           BsrB1|      Xba1   BsaB1                            SpDon   Dra1
               ||         |       |                               |      |
           ATGAGCGGCCGCGACTCTAGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACA
      2501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
           TACTCGCCGGCGCTGAGATCTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGT
FusionRed    >  *

                    Bsm1
                   Mfe1|        Hpa1       polyA    Psi1      polyA                        polyA
                      ||           |           |       |          |                            |
           TAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTT
      2601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
           ATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAA


           Bts1 Bsm1                                  Afl2         SpDon        Ssp1
              |    |                                     |            |           |
           TCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGT
      2701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
           AGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTCCGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACA


                                                     Psi1
                                                       |
           TAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGA
      2801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
           ATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCT
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                                                                   BtgZ1
            BsaXb                 Drd1    BsaXa                    Dra3|
                |                    |        |                       ||
     ACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAG
2901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
     TGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTC

                                                                      Nae1
                                       SpAcc                       NgoM4 |
                                           |                          | |
     TTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAG
3001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
     AAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTC

                     BsrB1
                         |
     GAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTAC
3101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
     CTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATG

                                                                                          BciV1
                                                                                       BspH1  |
                                                                polyA                 BsrB1 |  |
                                                                    |                    | |  |
     AGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATA
3201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
     TCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTAT

                                                                Eci1
                        Ssp1  Ear1        Bsu36              Pvu2 |
                           |     |            |                 | |
     ACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAG
3301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
     TGGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTC
```

```
                                Nsi1
                              Sph1 |
                             BfrB1 |
      BseY1                  BstAP  | |            SexA1                    BseY1
          |                      |  | |               |                       |
      GCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAG
3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
      CGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTC

        Nsi1
      Sph1 |
     BfrB1 |                                                   Eci1
  BstAP  | |                      Eci1                 Eci1     Bmr1|       Eci1            Nco1
      |  | |                         |                   |        ||          |               |
      CATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGA
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      GTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACT

                                                                                      Avr2
                                  Sfi1                                               Stu1|
                polyA             Bgl1                     SpDon             BseR1  ||
                    |                |                        |                  |  ||
      CTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAG
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      GATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTC

    Cla1              BsaB1                       BspM1               Eag1
      |                  |                           |                  |
      ATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATG
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      TAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATAC

                                                                Nar1
             Bmr1                                               Kas1|                        Drd1
                |                                                  ||                          |
      ACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGC
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      TGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACG
```

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                                                                  Pvu2
                                          Msc1                Fsp1   |       PflF1
                                             |                   |   |           |
     CCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGG
3901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
     GGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCC

        Eco57                                     SpDon                        BciV1         BsrD1
           |                                        |                            |             |
     GACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGC
4001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
     CTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCG

                                 BtgZ1
                              BspM1  |
                                  |  |
     TGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGA
4101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
     ACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCT

       Sap1
       Ear1                           BpuE1                        Sph1                        Nco1
          |                              |                            |                           |
     TGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGC
4201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
     ACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCG

                                                                 BseY1
                                                                Nae1 |
                 BtgZ1                                       NgoM4 | |        Rsr2         Eci1
                     |                                           | | |           |            |
     GATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGT
4301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
     CTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCA
```

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                Sap1                                                    BtgZ1
                Ear1                    Eco57         BssS1                BsrB1 |
                   |                        |             |                    | |
     TGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTT
4401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
     ACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAA

                                                                                BssS1
                           BsrB1          BstB1                                BspM1
                               |              |                                    |
     CTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCG
4501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
     GATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGC

                                            Nae1
                                         NgoM4 |                                                SpAcc
       SpAcc                              Bpm1 |                                                 Avr2
           |                                 | |                                                    |
     CCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCC
4601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
     GGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGG

    Bpm1                                                        polyA        polyA
      |                                                             |            |
     TAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCG
4701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
     ATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGC

                                                   Bsa1
                                                     |
     TTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCC
4801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
     AAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGG
```

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                                                                BstAP
                                                                AlwN1      Bsu36
                                                                   |          |
     CACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGAT
4901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
     GTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTA

       Dra1                Dra1                                BspH1
          |                   |                                   |
     TGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGA
5001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
     ACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACT


                                                         BpuE1
                                                            |
     GCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGG
5101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
     CGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCC


                                    Eco57                                                   SpAcc
                                       |                                                       |
     TGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTA
5201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
     ACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCAT


                                                                     AlwN1                     BpuE1
                                                                        |                         |
     GTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTT
5301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5400
     CAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAA


                                                                   ApaL1     BseY1
                                                                      |         |
     ACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACA
5401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5500
     TGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGT
```

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                                                                   BciV1
                        SpAcc                                   Eci1   |
                            |                                      |   |
     CCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGG
5501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5600
     GGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCC

       BssS1                                    SpAcc                          Drd1            BpuE1
           |                                        |                              |                |
     AGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCG
5601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5700
     TCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGC

                                                                                  SpDon
                 SpAcc     Eci1                                                 BspLU|
                     |        |                                                     ||
     TCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTAT
5701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5800
     AGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATA

                                   Nsi1
                                BfrB1 |
                                    | |
     CCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
5801 |||||||||*|||||||||*|||||||||*|||||||| 5838
     GGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aar1	Aat2	**Afl2**	**Age1**	Ale1	AlwN1	**Apa1**	ApaL1	**Ase1**	Avr2	**BamH1**	**Bbs1**	Bcg1a	Bcg1b
BciV1	BfrB1	Bgl1	**Bgl2**	Bmr1	Bpm1	**Bpu10**	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	**BseR1**	BseY1
Bsm1	BsmB1	**BspE1**	BspH1	BspLU	BspM1	BsrB1	BsrD1	**BsrG1**	BssS1	BstAP	BstB1	**BstX1**	Bsu36
BtgZ1	**Bts1**	Cla1	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	**EcoRV**	**Fsp1**	Hind3	**Hpa1**
Kas1	**Mfe1**	Msc1	Nae1	**Nar1**	Nco1	**Nde1**	NgoM4	**Nhe1**	**Not1**	Nsi1	**PflF1**	PflM1	polyA
PshA1	Psi1	**PspOM**	**Pst1**	Pvu2	**Rsr2**	Sap1	**SexA1**	**Sfi1**	**Sma1**	**SnaB1**	SpAcc	SpDon	Sph1
Ssp1	Stu1	**Xba1**	**Xmn1**										

Unique:

Aar1	**Afl2**	**Age1**	**Apa1**	**Ase1**	**BamH1**	**Bbs1**	**Bgl2**	**Bpu10**	**BseR1**	**BspE1**	**BsrG1**	**BstX1**	**Bts1**
EcoRV	**Fsp1**	**Hpa1**	**Kas1**	**Mfe1**	**Nar1**	**Nde1**	**Nhe1**	**Not1**	**PflF1**	**PshA1**	**PspOM**	**Pst1**	**Rsr2**
SexA1	**Sfi1**	**Sma1**	**SnaB1**	**Xba1**	**Xmn1**								

Not found:

Acc65	Acl1	Afe1	Ahd1	Asc1	AsiS1	Bae1a	Bae1b	BbvC1	Bcl1	Blp1	BmgB1	Bsg1	BsiW1
BssH2	BstE2	BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	Ecl2	EcoK	EcoN1	EcoR1	FCatB	FCatL
FCatR	FCatP	ScFRT	Fse1	FspA1	I_Ceu	Kpn1	loxP	Mlu1	Nru1	Pac1	Pme1	Pml1	Pvu1
R4atB	R4atL	R4atP	R4atR	Sac1	Sac2	Sal1	SanD1	Sbf1	Sca1	Sgf1	SgrA1	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													