pmKate2-keratin 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). mKate2 amino acids are shown in red, keratin 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
                                                                                                         |
               ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCACCA
          501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
               TGTTGAGGCGGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGTGGT
keratin      >                                                                                                    M

                                                                         BseY1
                                                                       Nar1  |      Nar1
                    SpDon                       Age1                  Kas1|  |     Kas1| Eag1
                        |                          |                     ||  |        ||    |
               TGAGCTTCACCACTCGCTCCACCTTCTCCACCAACTACCGGTCCCTGGGCTCTGTCCAGGCGCCCAGCTACGGCGCCCGGCCGGTCAGCAGCGCGGCCAG
          601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
               ACTCGAAGTGGTGAGCGAGGTGGAAGAGGTGGTTGATGGCCAGGGACCCGAGACAGGTCCGCGGGTCGATGCCGCGGGCCGGCCAGTCGTCGCGCCGGTC
keratin      >   S  F  T  T  R  S  T  F  S  T  N  Y  R  S  L  G  S  V  Q  A  P  S  Y  G  A  R  P  V  S  S  A  A  S

                        BseY1                                _Chi
                        AlwN1                        Eco57BsrB1 |                                   Msc1
                            |                            |    | |                                      |
               CGTCTATGCAGGCGCTGGGGGCTCTGGTTCCCGGATCTCCGTGTCCCGCTCCACCAGCTTCAGGGGCGGCATGGGGTCCGGGGGCCTGGCCACCGGGATA
          701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
               GCAGATACGTCCGCGACCCCCGAGACCAAGGGCCTAGAGGCACAGGGCGAGGTGGTCGAAGTCCCCGCCGTACCCCAGGCCCCCGGACCGGTGGCCCTAT
keratin      >  V  Y  A  G  A  G  G  S  G  S  R  I  S  V  S  R  S  T  S  F  R  G  G  M  G  S  G  G  L  A  T  G  I

                                                Bsa1                                       SpDon            Bsa1
                                                   |                                           |               |
               GCCGGGGGTCTGGCAGGAATGGGAGGCATCCAGAACGAGAAGGAGACCATGCAAAGCCTGAACGACCGCCTGGCCTCTTACCTGGACAGAGTGAGGAGCC
          801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
               CGGCCCCCAGACCGTCCTTACCCTCCGTAGGTCTTGCTCTTCCTCTGGTACGTTTCGGACTTGCTGGCGGACCGGAGAATGGACCTGTCTCACTCCTCGG
keratin      > A  G  G  L  A  G  M  G  G  I  Q  N  E  K  E  T  M  Q  S  L  N  D  R  L  A  S  Y  L  D  R  V  R  S  L
```

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                  BseR1         Bpm1                 Bpm1          SanD1  Ahd1     AlwN1                  Bpm1
                      |            |                    |              |     |         |                     |
               TGGAGACCGAGAACCGGAGGCTGGAGAGCAAAATCCGGGAGCACTTGGAGAAGAAGGGACCCCAGGTCAGAGACTGGAGCCATTACTTCAAGATCATCGA
          901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
               ACCTCTGGCTCTTGGCCTCCGACCTCTCGTTTTAGGCCCTCGTGAACCTCTTCTTCCCTGGGGTCCAGTCTCTGACCTCGGTAATGAAGTTCTAGTAGCT
keratin      >   E  T  E  N  R  R  L  E  S  K  I  R  E  H  L  E  K  K  G  P  Q  V  R  D  W  S  H  Y  F  K  I  I  E

               Bsu36      Bgl2                                          Pst1                                Drd1
                   |         |                                             |                                  |
               GGACCTGAGGGCTCAGATCTTCGCAAATACTGTGGACAATGCCCGCATCGTTCTGCAGATTGACAATGCCCGTCTTGCTGCTGATGACTTTAGAGTCAAG
         1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
               CCTGGACTCCCGAGTCTAGAAGCGTTTATGACACCTGTTACGGGCGTAGCAAGACGTCTAACTGTTACGGGCAGAACGACGACTACTGAAATCTCAGTTC
keratin      >  D  L  R  A  Q  I  F  A  N  T  V  D  N  A  R  I  V  L  Q  I  D  N  A  R  L  A  A  D  D  F  R  V  K

                                        PflM1                                                           Pvu2
                           Msc1       SpAcc |           Nco1                                           Pst1|
                              |           | |              |                                              ||
               TATGAGACAGAGCTGGCCATGCGCCAGTCTGTGGAGAACGACATCCATGGGCTCCGCAAGGTCATTGATGACACCAATATCACACGACTGCAGCTGGAGA
         1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
               ATACTCTGTCTCGACCGGTACGCGGTCAGACACCTCTTGCTGTAGGTACCCGAGGCGTTCCAGTAACTACTGTGGTTATAGTGTGCTGACGTCGACCTCT
keratin      > Y  E  T  E  L  A  M  R  Q  S  V  E  N  D  I  H  G  L  R  K  V  I  D  D  T  N  I  T  R  L  Q  L  E  T

                                               Sap1
                                               Ear1
                                              BseR1
          BpuE1           Bpm1              BspH1 |      Ear1        SpDon    Stu1
              |              |                  | |         |            |       |
               CAGAGATCGAGGCTCTCAAGGAGGAGCTGCTCTTCATGAAGAAGAACCACGAAGAGGAAGTAAAAGGCCTACAAGCCCAGATTGCCAGCTCTGGGTTGAC
         1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
               GTCTCTAGCTCCGAGAGTTCCTCCTCGACGAGAAGTACTTCTTCTTGGTGCTTCTCCTTCATTTTCCGGATGTTCGGGTCTAACGGTCGAGACCCAACTG
keratin      >   E  I  E  A  L  K  E  E  L  L  F  M  K  K  N  H  E  E  E  V  K  G  L  Q  A  Q  I  A  S  S  G  L  T

                                                                        Apa1
                                                     BstX1         PspOM   |
                                                         |             |   |
               CGTGGAGGTAGATGCCCCCAAATCTCAGGACCTCGCCAAGATCATGGCAGACATCCGGGCCCAATATGACGAGCTGGCTCGGAAGAACCGAGAGGAGCTA
         1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
               GCACCTCCATCTACGGGGGTTTAGAGTCCTGGAGCGGTTCTAGTACCGTCTGTAGGCCCGGGTTATACTGCTCGACCGAGCCTTCTTGGCTCTCCTCGAT
keratin      >  V  E  V  D  A  P  K  S  Q  D  L  A  K  I  M  A  D  I  R  A  Q  Y  D  E  L  A  R  K  N  R  E  E  L
```

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                  Sca1                            BseR1              Bpu10
                 BseR1      Bsa1                Ale1  |  SpDon       BbvC1      BsmB1               BsmB1
                     |         |                   |  |      |           |          |                   |
               GACAAGTACTGGTCTCAGCAGATTGAGGAGAGCACCACAGTGCTCACCACACAGTCTGCTGAGGTTGGAGCTGCTGAGACGACGCTCACAGAGCTGAGAC
         1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
               CTGTTCATGACCAGAGTCGTCTAACTCCTCTCGTGGTGTCACGAGTGGTGTGTCAGACGACTCCAACCTCGACGACTCTGCTGCGAGTGTCTCGACTCTG
keratin       >D  K  Y  W  S  Q  Q  I  E  E  S  T  T  V  L  T  T  Q  S  A  E  V  G  A  A  E  T  T  L  T  E  L  R  R

                                                                                  EcoN1
                                                                               Bsu36  |
                         BsaXb                                                  SpAcc|  |
              Ahd1      PflM1|                         BsaXa                Eco57 ||  |
                 |          ||                             |                    | ||  |
               GTACAGTCCAGTCCTTGGAGATCGACCTGGACTCCATGAGAAATCTGAAGGCCAGCTTGGAGAACAGCCTGAGGGAGGTGGAGGCCCGCTACGCCCTACA
         1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
               CATGTCAGGTCAGGAACCTCTAGCTGGACCTGAGGTACTCTTTAGACTTCCGGTCGAACCTCTTGTCGGACTCCCTCCACCTCCGGGCGATGCGGGATGT
keratin       >  T  V  Q  S  L  E  I  D  L  D  S  M  R  N  L  K  A  S  L  E  N  S  L  R  E  V  E  A  R  Y  A  L  Q

                                                                   Sma1
              T7Ter   Bsg1  BamH1                              BpuE1  |
                  |      |      |                                  |  |
               GATGGAGCAGCTCAACGGGATCCTGCTGCACCTTGAGTCAGAGCTGGCACAGACCCGGGCAGAGGGACAGCGCCAGGCCCAGGAGTATGAGGCCCTGCTG
         1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
               CTACCTCGTCGAGTTGCCCTAGGACGACGTGGAACTCAGTCTCGACCGTGTCTGGGCCCGTCTCCCTGTCGCGGTCCGGGTCCTCATACTCCGGGACGAC
keratin       > M  E  Q  L  N  G  I  L  L  H  L  E  S  E  L  A  Q  T  R  A  E  G  Q  R  Q  A  Q  E  Y  E  A  L  L

                                                Bpm1
                                                   |
               AACATCAAGGTCAAGCTGGAGGCTGAGATCGCCACCTACCGCCGCCTGCTGGAAGATGGCGAGGACTTTAATCTTGGTGATGCCTTGGACAGCAGCAACT
         1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
               TTGTAGTTCCAGTTCGACCTCCGACTCTAGCGGTGGATGGCGGCGGACGACCTTCTACCGCTCCTGAAATTAGAACCACTACGGAACCTGTCGTCGTTGA
keratin       >N  I  K  V  K  L  E  A  E  I  A  T  Y  R  R  L  L  E  D  G  E  D  F  N  L  G  D  A  L  D  S  S  N  S

                                                                 Bsa1                                EcoR1
                                                                    |                                    |
               CCATGCAAACCATCCAAAAGACCACCACCCGCCGGATAGTGGATGGCAAAGTGGTGTCTGAGACCAATGACACCAAAGTTCTGAGGCATCGAATTCTGCA
         1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
               GGTACGTTTGGTAGGTTTTCTGGTGGTGGGCGGCCTATCACCTACCGTTTCACCACAGACTCTGGTTACTGTGGTTTCAAGACTCCGTAGCTTAAGACGT
keratin       >  M  Q  T  I  Q  K  T  T  T  R  R  I  V  D  G  K  V  V  S  E  T  N  D  T  K  V  L  R  H  R  I  L  Q
```

```
                                BamH1
                               Sma1 |
                              Apa1| |
                         PspOM   || |
                         Sac2|   || |                SpDon
            Sal1      Kpn1  ||   || |               Ale1 |
           Pst1| Acc65   |  ||   || |  Age1       Nco1 | |                                 BsrG1
              ||     |   |  ||   || |     |          | | |                                     |
               GTCGACGGTACCGCGGGCCCGGGATCCACCGGTCGCCACCATGGTGAGCGAGCTGATTAAGGAGAACATGCACATGAAGCTGTACATGGAGGGCACCGTG
         1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
               CAGCTGCCATGGCGCCCGGGCCCTAGGTGGCCAGCGGTGGTACCACTCGCTCGACTAATTCCTCTTGTACGTGTACTTCGACATGTACCTCCCGTGGCAC
mKate2       >  S  T  V  P  R  A  R  D  P  P  V  A  T  M  V  S  E  L  I  K  E  N  M  H  M  K  L  Y  M  E  G  T  V

                            ApaL1                SpAcc
                                |                         |
               AACAACCACCACTTCAAGTGCACATCCGAGGGCGAAGGCAAGCCCTACGAGGGCACCCAGACCATGAGAATCAAGGCGGTCGAGGGCGGCCCTCTCCCCT
         2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
               TTGTTGGTGGTGAAGTTCACGTGTAGGCTCCCGCTTCCGTTCGGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCCGCCAGCTCCCGCCGGGAGAGGGGA
mKate2       > N  N  H  H  F  K  C  T  S  E  G  E  G  K  P  Y  E  G  T  Q  T  M  R  I  K  A  V  E  G  G  P  L  P  F

               TCGCCTTCGACATCCTGGCTACCAGCTTCATGTACGGCAGCAAAACCTTCATCAACCACACCCAGGGCATCCCCGACTTCTTTAAGCAGTCCTTCCCCGA
         2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
               AGCGGAAGCTGTAGGACCGATGGTCGAAGTACATGCCGTCGTTTTGGAAGTAGTTGGTGTGGGTCCCGTAGGGGCTGAAGAAATTCGTCAGGAAGGGGCT
mKate2       >   A  F  D  I  L  A  T  S  F  M  Y  G  S  K  T  F  I  N  H  T  Q  G  I  P  D  F  F  K  Q  S  F  P  E

                   SpDon                          Bbs1             Bpm1
                       |                             |                |
               GGGCTTCACATGGGAGAGAGTCACCACATACGAAGACGGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTC
         2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
               CCCGAAGTGTACCCTCTCTCAGTGGTGTATGCTTCTGCCCCCGCACGACTGGCGATGGGTCCTGTGGTCGGAGGTCCTGCCGACGGAGTAGATGTTGCAG
mKate2       >  G  F  T  W  E  R  V  T  T  Y  E  D  G  G  V  L  T  A  T  Q  D  T  S  L  Q  D  G  C  L  I  Y  N  V

                                                                                 Bsa1
                                                                     BseY1    Stu1  |
                                                                         |       |  |
               AAGATCAGAGGGGTGAACTTCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCTCCACCGAGACCCTGTACCCCGCTGACGGCG
         2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
               TTCTAGTCTCCCCACTTGAAGGGTAGGTTGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCTCCGGAGGTGGCTCTGGGACATGGGGCGACTGCCGC
mKate2       > K  I  R  G  V  N  F  P  S  N  G  P  V  M  Q  K  K  T  L  G  W  E  A  S  T  E  T  L  Y  P  A  D  G  G
```

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                            Bgl1          Bgl1       BssS1          Eco57                    Bbs1          BpuE1
                               |             |           |              |                       |              |
                         GCCTGGAAGGCAGAGCCGACATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACTTGAAGACCACATACAGATCCAAGAAACCCGCTAAGAA
                   2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
                         CGGACCTTCCGTCTCGGCTGTACCGGGACTTCGAGCACCCGCCCCCGGTGGACTAGACGTTGAACTTCTGGTGTATGTCTAGGTTCTTTGGGCGATTCTT
          mKate2       >   L  E  G  R  A  D  M  A  L  K  L  V  G  G  G  H  L  I  C  N  L  K  T  T  Y  R  S  K  K  P  A  K  N

                                                             Bbs1
                                                         SpAcc  |               Bsa1       PshA1       BssS1 Dra3      Msc1
                                                             |  |                  |           |           |    |         |
                         CCTCAAGATGCCCGGCGTCTACTATGTGGACAGAAGACTGGAAAGAATCAAGGAGGCCGACAAAGAGACCTACGTCGAGCAGCACGAGGTGGCTGTGGCC
                   2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
                         GGAGTTCTACGGGCCGCAGATGATACACCTGTCTTCTGACCTTTCTTAGTTCCTCCGGCTGTTTCTCTGGATGCAGCTCGTCGTGCTCCACCGACACCGG
          mKate2       >  L  K  M  P  G  V  Y  Y  V  D  R  R  L  E  R  I  K  E  A  D  K  E  T  Y  V  E  Q  H  E  V  A  V  A

                                                              Not1
                                                              Eag1
                         AlwN1          SpAcc          Bmr1 BsrB1|      Xba1   BsaB1                            SpDon   Dra1
                             |              |             |     ||         |       |                                |      |
                         AGATACTGCGACCTCCCTAGCAAACTGGGGCACAGATGAGCGGCCGCGACTCTAGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTA
                   2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
                         TCTATGACGCTGGAGGGATCGTTTGACCCCGTGTCTACTCGCCGGCGCTGAGATCTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAAT
          mKate2       > R  Y  C  D  L  P  S  K  L  G  H  R  *

                                                                     Bsm1
                                                                    Mfe1|        Hpa1       polyA    Psi1      polyA
                                                                       ||           |           |       |          |
                         AAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAATAAAGCA
                   2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
                         TTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGT

                                        polyA            Bts1 Bsm1                                  Afl2         SpDon
                                            |               |    |                                     |             |
                         ATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTGTAAGCG
                   2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
                         TATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTCCGCATTTAACATTCGC
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       Ssp1                                                                            Psi1
          |                                                                               |
      TTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATA
2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
      AATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTAT

                                                BsaXb                Drd1    BsaXa
                                                    |                    |        |
      GACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGC
3001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
      CTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCG

               BtgZ1
               Dra3|                                                         SpAcc
                  ||                                                             |
      GATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAG
3101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
      CTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTC

                  Nae1
               NgoM4 |                                    BsrB1
                   | |                                        |
      CTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGT
3201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
      GAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCA

                                                                                              polyA
                                                                                                  |
      AACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAA
3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
      TTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATT


                           BciV1
                        BspH1  |                                                                   Eci1
                      BsrB1 |  |                            Ssp1  Ear1        Bsu36              Pvu2 |
                          | |  |                               |     |            |                 | |
      ATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTG
3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
      TATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACAC
```

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                                                                       Nsi1
                                                                     Sph1 |
                                                                    BfrB1 |
                                         BseY1                   BstAP  | |            SexA1
                                             |                       |  | |                |
      GAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAG
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      CTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTC

                                           Nsi1
                                         Sph1 |
                                        BfrB1 |                                                      Eci1
             BseY1                   BstAP  | |                       Eci1                 Eci1     Bmr1|
                 |                       |  | |                          |                    |        ||
      TCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTC
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      AGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAG

                                                                          Sfi1
            Eci1            Nco1                   polyA                  Bgl1                    SpDon
               |               |                       |                     |                        |
      CGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTG
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      GCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCAC

                     Avr2
                    Stu1|                                                            BspM1
                BseR1  ||              Cla1              BsaB1                       BfuA1
                    |  ||                 |                  |                           |
      AGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTC
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      TCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAG

                                                                                                   Nar1
     Eag1                                       Bmr1                                              Kas1|
        |                                          |                                                 ||
      TCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGC
3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
      AGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCG
```

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                          Drd1                                                   Msc1                Fsp1
                             |                                                      |                   |
      CCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCG
4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
      GGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGC

     Pvu2       PflF1                       Eco57                                  SpDon
        |           |                           |                                          |
      CAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGA
4101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
      GTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCT

                                                                     BtgZ1
                                                                  BspM1  |
                 BciV1         BsrD1                              BfuA1  |
                     |             |                                  |  |
      GAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCA
4201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
      CTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGT

                                           Sap1
                                           Ear1                           BpuE1
                                              |                               |
      CGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCA
4301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
      GCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGT

                                                                                                     Nae1
    Sph1                       Nco1               BtgZ1                                          NgoM4 |
       |                          |                   |                                               | |
      TGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCG
4401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
      ACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGC
```

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                                                     Sap1
  BseY1        Rsr2         Eci1                     Ear1                   Eco57         BssS1
      |           |            |                        |                       |             |
      GCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTAC
4501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
      CGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATG


             BtgZ1
           BsrB1 |                                               BsrB1          BstB1
               | |                                                   |              |
      GGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGAC
4601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
      CCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTG


                BssS1                                                               Nae1
                BspM1                                                            NgoM4 |
                BfuA1                 SpAcc                                       Bpm1 |
                    |                          |                                     | |
      GCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAG
4701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
      CGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTC


                                       Bpm1
                                   SpAcc  |
                                    Avr2  |                                                        polyA
                                       |  |                                                            |
      CGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAA
4801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
      GCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTT


            polyA                                                                   Bsa1
                |                                                                      |
      TAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCA
4901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
      ATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGT
```

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                                                                                                     BstAP
                                                                                                     AlwN1
                                                                                                         |
      TTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCT
5001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
      AACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGA

          Bsu36                            Dra1               Dra1                              BspH1
              |                               |                  |                                  |
      GCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGA
5101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
      CGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACT

                                                                                            BpuE1
                                                                                                |
      CCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTG
5201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
      GGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGAC

                                                                          Eco57
                                                                              |
      CTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCG
5301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5400
      GACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGC

                          SpAcc
                              |
      CAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTAC
5401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5500
      GTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATG

       AlwN1                     BpuE1
           |                         |
      CAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTC
5501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5600
      GTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAG
```

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  ApaL1     BseY1                                             SpAcc
      |         |                                                 |
      GTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCG
5601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5700
      CACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGC


                  BciV1
               Eci1   |                    BssS1                                    SpAcc
                  |   |                        |                                        |
      GACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCC
5701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5800
      CTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGG


               Drd1            BpuE1               SpAcc     Eci1
                  |                |                   |        |
      ACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTG
5801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5900
      TGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAAC


                 SpDon                                                    Nsi1
                BspLU|                                                 BfrB1 |
                    ||                                                     | |
      CTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
5901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*||| 5973
      GACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

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Found:

     Aat2    Acc65     Afl2     Age1     Ahd1     Ale1    AlwN1     Apa1    ApaL1     Ase1     Avr2    BamH1     Bbs1    BbvC1
    BciV1    BfrB1    BfuA1     Bgl1     Bgl2     Bmr1     Bpm1    Bpu10    BpuE1     Bsa1    BsaB1    BsaXa    BsaXb    BseR1
    BseY1     Bsg1     Bsm1    BsmB1    BspH1    BspLU    BspM1    BsrB1    BsrD1    BsrG1    BssS1    BstAP    BstB1    BstX1
    Bsu36    BtgZ1     Bts1     _Chi     Cla1     Dra1     Dra3     Drd1     Eag1     Ear1     Eci1    Eco57    EcoN1    EcoR1
     Fsp1     Hpa1     Kas1     Kpn1     Mfe1     Msc1     Nae1     Nar1     Nco1     Nde1    NgoM4     Nhe1     Not1     Nsi1
    PflF1    PflM1    polyA    PshA1     Psi1    PspOM     Pst1     Pvu2     Rsr2     Sac2     Sal1    SanD1     Sap1     Sca1
    SexA1     Sfi1     Sma1    SnaB1    SpAcc    SpDon     Sph1     Ssp1     Stu1    T7Ter     Xba1

Unique:

    Acc65     Afl2     Ase1    BbvC1     Bgl2    Bpu10     Bsg1    BspLU    BsrD1    BsrG1    BstB1    BstX1     Bts1     _Chi
     Cla1    EcoN1    EcoR1     Fsp1     Hpa1     Kpn1     Mfe1     Nde1     Nhe1     Not1    PflF1    PshA1     Rsr2     Sac2
     Sal1    SanD1     Sca1    SexA1     Sfi1    SnaB1    T7Ter     Xba1



Not found:

     Aar1     Acl1     Afe1     Asc1    AsiS1    Bae1a    Bae1b    Bcg1a    Bcg1b     Bcl1     Blp1    BmgB1    BsiW1    BspE1
    BssH2    BstE2    BstZ1    BxatB    BxatL    BxatR    BxatP     Ecl2     EcoK    EcoRV    FCatB    FCatL    FCatR    FCatP
    ScFRT     Fse1    FspA1    Hind3    I_Ceu     loxP     Mlu1     Nru1     Pac1     Pme1     Pml1     Pvu1    R4atB    R4atL
    R4atP    R4atR     Sac1     Sbf1     Sgf1    SgrA1     Spe1     Srf1     Swa1    T3RNA    T7RNA    PISce     Xcm1     Xho1
     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
```