pmKate2-paxillin 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, paxillin 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

                                                                                                             Nco1
                                                                                                        Bcg1a   |
                                                                                                      Nhe1  |   |
                                                                                                         |  |   |
               ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCACCA
          501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
               TGTTGAGGCGGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGTGGT
paxillin      >                                                                                                   M

                                Bgl1  Bcg1b                              Age1
                                   |      |                                 |
               TGGACGACCTCGATGCCTTACTGGCAGACCTGGAATCCACCACCTCGCATATCTCTAAGCGACCGGTGTTTCTAACAGAGGAAACGCCTTACTCCTACCC
          601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
               ACCTGCTGGAGCTACGGAATGACCGTCTGGACCTTAGGTGGTGGAGCGTATAGAGATTCGCTGGCCACAAAGATTGTCTCCTTTGCGGAATGAGGATGGG
paxillin      >  D  D  L  D  A  L  L  A  D  L  E  S  T  T  S  H  I  S  K  R  P  V  F  L  T  E  E  T  P  Y  S  Y  P

                         SnaB1                    SgrA1
                             |                        |
               AACTGGAAACCATACGTACCAGGAGATTGCTGTGCCACCGCCGGTGCCCCCGCCGCCTTCCAGTGAGGCCCTAAATGGCACTGTGATTGACCCCTTAGAC
          701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
               TTGACCTTTGGTATGCATGGTCCTCTAACGACACGGTGGCGGCCACGGGGGCGGCGGAAGGTCACTCCGGGATTTACCGTGACACTAACTGGGGAATCTG
paxillin      > T  G  N  H  T  Y  Q  E  I  A  V  P  P  P  V  P  P  P  P  S  S  E  A  L  N  G  T  V  I  D  P  L  D

                    BseY1               _Chi         Bmr1                    Bpm1                        BsmB1
                        |                  |            |                       |                            |
               CAGTGGCAACCCAGCGTGTCCAGATACGGCCACCAGCAACCTCAGTCCCAGTCTCCGATATACAGCTCTAGTGCCAAAAGCTCCAGTGCCTCTGTTCCTA
          801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
               GTCACCGTTGGGTCGCACAGGTCTATGCCGGTGGTCGTTGGAGTCAGGGTCAGAGGCTATATGTCGAGATCACGGTTTTCGAGGTCACGGAGACAAGGAT
paxillin      >Q  W  Q  P  S  V  S  R  Y  G  H  Q  Q  P  Q  S  Q  S  P  I  Y  S  S  S  A  K  S  S  S  A  S  V  P  R
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                                                             BseR1
                                                           BsrG1 |
                    Blp1                                  Pml1 | |                          Pst1
                       |                                     | | |                             |
               GAGACGGGCTCAGCTCCCCTTCTCCCCGTGCCAGTGAGGAGGAACACGTGTACAGCTTCCCAAACAAGCAGAAGTCTGCAGAACCATCTCCCACAATGAC
          901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
               CTCTGCCCGAGTCGAGGGGAAGAGGGGCACGGTCACTCCTCCTTGTGCACATGTCGAAGGGTTTGTTCGTCTTCAGACGTCTTGGTAGAGGGTGTTACTG
paxillin     >   D  G  L  S  S  P  S  P  R  A  S  E  E  E  H  V  Y  S  F  P  N  K  Q  K  S  A  E  P  S  P  T  M  T

                  Xcm1                                                  Bsm1       Bmr1    SpAcc
                     |                                                     |          |        |
               CAGCACCTCCCTGGGCAGCAACCTCTCGGAACTGGACAGGCTTCTCCTGGAACTGAATGCTGTTCAACATAATCCCCCCAGTGGCTTCTCAGCAGATGAA
         1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
               GTCGTGGAGGGACCCGTCGTTGGAGAGCCTTGACCTGTCCGAAGAGGACCTTGACTTACGACAAGTTGTATTAGGGGGGTCACCGAAGAGTCGTCTACTT
paxillin     >  S  T  S  L  G  S  N  L  S  E  L  D  R  L  L  L  E  L  N  A  V  Q  H  N  P  P  S  G  F  S  A  D  E

                                                                                   Pst1
                                                                               Bsg1   |
                           Bts1                     SpDon                    SpAcc|   |              SpAcc
                              |                         |                        ||   |                  |
               GTCAGCAGAAGCCCATCACTGCCCAATGTGACCGGACCTCACTATGTCATCCCAGAGAGCAGCAGCTCTGCAGGAGGGAAGGCTGCACCCCCTACAAAAG
         1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
               CAGTCGTCTTCGGGTAGTGACGGGTTACACTGGCCTGGAGTGATACAGTAGGGTCTCTCGTCGTCGAGACGTCCTCCCTTCCGACGTGGGGGATGTTTTC
paxillin     > V  S  R  S  P  S  L  P  N  V  T  G  P  H  Y  V  I  P  E  S  S  S  S  A  G  G  K  A  A  P  P  T  K  E

                                                                                            Sac1
                                                   Bmr1                                   Ecl2 |  Bmr1  Bpm1 AlwN1
                                                      |                                      | |     |     |     |
               AAAAACCAAAGCGGAATGGTGGGCGTGGGATTGAAGATGTGCGTCCCAGTGTGGAGAGCCTGCTGGATGAGCTGGAGAGCTCTGTGCCAAGCCCAGTCCC
         1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
               TTTTTGGTTTCGCCTTACCACCCGCACCCTAACTTCTACACGCAGGGTCACACCTCTCGGACGACCTACTCGACCTCTCGAGACACGGTTCGGGTCAGGG
paxillin     >   K  P  K  R  N  G  G  R  G  I  E  D  V  R  P  S  V  E  S  L  L  D  E  L  E  S  S  V  P  S  P  V  P

                                                                                                    BssS1
                                   SpDon      BseY1                         Eco57               SpAcc   |
                                       |          |                             |                   |   |
               TGCAATCACTGTGAGCCAAGGGGAGGTGAGCAGCCCCCAGCGTGTCAACGCCAGTCAGCAGCAGACCCGTATCTCTGCTTCTTCAGCTACACGAGAACTG
         1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
               ACGTTAGTGACACTCGGTTCCCCTCCACTCGTCGGGGGTCGCACAGTTGCGGTCAGTCGTCGTCTGGGCATAGAGACGAAGAAGTCGATGTGCTCTTGAC
paxillin     >  A  I  T  V  S  Q  G  E  V  S  S  P  Q  R  V  N  A  S  Q  Q  Q  T  R  I  S  A  S  S  A  T  R  E  L
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                                                                 Nae1
                                                              NgoM4 |                                PflM1
                                                                  | |                                    |
               GATGAGCTGATGGCGTCCCTCTCTGACTTTAAGTTCATGGCACAGGGGAAAGCCGGCGGCAGCAGCTCCCCACCATCCACCACCCCAAAGCCTGGCAGTC
         1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
               CTACTCGACTACCGCAGGGAGAGACTGAAATTCAAGTACCGTGTCCCCTTTCGGCCGCCGTCGTCGAGGGGTGGTAGGTGGTGGGGTTTCGGACCGTCAG
paxillin     > D  E  L  M  A  S  L  S  D  F  K  F  M  A  Q  G  K  A  G  G  S  S  S  P  P  S  T  T  P  K  P  G  S  Q

                                                                                                             BseY1
                                                                                                         BspM1   |
             Pvu2       BseY1          Pst1                      Bmr1                       SpAcc        BfuA1   |
                |           |             |                         |                           |            |   |
               AGCTGGACACCATGCTGGGAAGTCTGCAGTCTGACCTGAACAAACTGGGGGTAGCGACGGTCGCCAAGGGTGTGTGCGGAGCCTGCAAGAAGCCGATTGC
         1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
               TCGACCTGTGGTACGACCCTTCAGACGTCAGACTGGACTTGTTTGACCCCCATCGCTGCCAGCGGTTCCCACACACGCCTCGGACGTTCTTCGGCTAACG
paxillin     >   L  D  T  M  L  G  S  L  Q  S  D  L  N  K  L  G  V  A  T  V  A  K  G  V  C  G  A  C  K  K  P  I  A

                                                 Bpu10                BstAP
                             Nco1          Bbs1 Bsg1 |               Bts1 |       Xcm1       BseR1         BsrB1
                                |             |    | |                  | |          |           |             |
               TGGGCAGGTAGTTACAGCCATGGGGAAGACCTGGCACCCTGAGCACTTCGTCTGCACCCACTGCCAGGAGGAGATTGGATCACGGAACTTCTTTGAGCGG
         1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
               ACCCGTCCATCAATGTCGGTACCCCTTCTGGACCGTGGGACTCGTGAAGCAGACGTGGGTGACGGTCCTCCTCTAACCTAGTGCCTTGAAGAAACTCGCC
paxillin     >  G  Q  V  V  T  A  M  G  K  T  W  H  P  E  H  F  V  C  T  H  C  Q  E  E  I  G  S  R  N  F  F  E  R

                        SpAcc                BseR1    Ear1                     BsrD1
                            |                    |       |                         |
               GATGGGCAGCCCTACTGTGAGAAGGACTATCACAACCTCTTCTCTCCTCGCTGCTACTACTGCAATGGGCCAATCCTTGATAAAGTGGTGACGGCTTTGG
         1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
               CTACCCGTCGGGATGACACTCTTCCTGATAGTGTTGGAGAAGAGAGGAGCGACGATGATGACGTTACCCGGTTAGGAACTATTTCACCACTGCCGAAACC
paxillin     > D  G  Q  P  Y  C  E  K  D  Y  H  N  L  F  S  P  R  C  Y  Y  C  N  G  P  I  L  D  K  V  V  T  A  L  D

                                                                              BspH1
                 BmgB1                  Bmr1                               Xmn1   |      Eco57
                     |                     |                                  |   |          |
               ACAGGACGTGGCACCCTGAACACTTTTTCTGTGCCCAGTGTGGAGTTTTCTTTGGACCTGAAGGATTTCATGAGAAGGATGGCAAAGCCTATTGCCGCAA
         1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
               TGTCCTGCACCGTGGGACTTGTGAAAAAGACACGGGTCACACCTCAAAAGAAACCTGGACTTCCTAAAGTACTCTTCCTACCGTTTCGGATAACGGCGTT
paxillin     >   R  T  W  H  P  E  H  F  F  C  A  Q  C  G  V  F  F  G  P  E  G  F  H  E  K  D  G  K  A  Y  C  R  K
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                                                       Srf1
                      BspLU                            Sma1                                    Dra3
                          |                               |                                       |
               GGACTACTTTGACATGTTTGCTCCCAAGTGTGGAGGCTGTGCCCGGGCTATCCTGGAAAATTACATTTCTGCCTTAAACACCCTGTGGCACCCTGAGTGC
         1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
               CCTGATGAAACTGTACAAACGAGGGTTCACACCTCCGACACGGGCCCGATAGGACCTTTTAATGTAAAGACGGAATTTGTGGGACACCGTGGGACTCACG
paxillin     >  D  Y  F  D  M  F  A  P  K  C  G  G  C  A  R  A  I  L  E  N  Y  I  S  A  L  N  T  L  W  H  P  E  C

                                     Bcg1b                             Bcg1a                   BssS1       Sac2
                                         |                                 |                       |          |
               TTTGTCTGTCGGGAATGTTTCACACCGTTCATCAACGGCAGCTTCTTCGAGCACGACGGGCAGCCCTACTGCGAGGTGCATTACCACGAGCGCCGCGGCT
         2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
               AAACAGACAGCCCTTACAAAGTGTGGCAAGTAGTTGCCGTCGAAGAAGCTCGTGCTGCCGGTCGGGATGACGCTCCACGTAATGGTGCTCGCGGCGCCGA
paxillin     > F  V  C  R  E  C  F  T  P  F  I  N  G  S  F  F  E  H  D  G  Q  P  Y  C  E  V  H  Y  H  E  R  R  G  S

                                                      Bts1  Nco1                           BpuE1
                                                         |     |                               |
               CGCTGTGCTCTGGCTGCCAGAAGCCCATCACGGGACGCTGCATCACTGCCATGGGCAAGAAATTTCACCCCGAACACTTTGTCTGTGCCTTCTGCCTCAA
         2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
               GCGACACGAGACCGACGGTCTTCGGGTAGTGCCCTGCGACGTAGTGACGGTACCCGTTCTTTAAAGTGGGGCTTGTGAAACAGACACGGAAGACGGAGTT
paxillin     >   L  C  S  G  C  Q  K  P  I  T  G  R  C  I  T  A  M  G  K  K  F  H  P  E  H  F  V  C  A  F  C  L  K

                                                                                                Hind3
                                                                                        Xho1   Sac1 |  EcoR1
                                                                              BpuE1  Ear1  | Ecl2 | |BstB1 |
                                                                                  |     |  |    | | |    | |
               GCAGCTCAACAAAGGAACCTTCAAAGAACAGAACGACAAGCCCTACTGTCAGAACTGCTTTCTCAAACTCTTCTGTCTCGAGCTCAAGCTTCGAATTCTG
         2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
               CGTCGAGTTGTTTCCTTGGAAGTTTCTTGTCTTGCTGTTCGGGATGACAGTCTTGACGAAAGAGTTTGAGAAGACAGAGCTCGAGTTCGAAGCTTAAGAC
paxillin     >  Q  L  N  K  G  T  F  K  E  Q  N  D  K  P  Y  C  Q  N  C  F  L  K  L  F  C  L  E  L  K  L  R  I  L
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                                  BamH1
                                 Sma1 |
                                Apa1| |
                           PspOM   || |
                           Sac2|   || |                SpDon
              Sal1      Kpn1  ||   || |               Ale1 |
             Pst1| Acc65   |  ||   || |  Age1       Nco1 | |                                 BsrG1
                ||     |   |  ||   || |     |          | | |                                     |
               CAGTCGACGGTACCGCGGGCCCGGGATCCACCGGTCGCCACCATGGTGAGCGAGCTGATTAAGGAGAACATGCACATGAAGCTGTACATGGAGGGCACCG
         2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
               GTCAGCTGCCATGGCGCCCGGGCCCTAGGTGGCCAGCGGTGGTACCACTCGCTCGACTAATTCCTCTTGTACGTGTACTTCGACATGTACCTCCCGTGGC
mKate2       > Q  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
                                  |                         |
               TGAACAACCACCACTTCAAGTGCACATCCGAGGGCGAAGGCAAGCCCTACGAGGGCACCCAGACCATGAGAATCAAGGCGGTCGAGGGCGGCCCTCTCCC
         2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
               ACTTGTTGGTGGTGAAGTTCACGTGTAGGCTCCCGCTTCCGTTCGGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCCGCCAGCTCCCGCCGGGAGAGGG
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

               CTTCGCCTTCGACATCCTGGCTACCAGCTTCATGTACGGCAGCAAAACCTTCATCAACCACACCCAGGGCATCCCCGACTTCTTTAAGCAGTCCTTCCCC
         2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
               GAAGCGGAAGCTGTAGGACCGATGGTCGAAGTACATGCCGTCGTTTTGGAAGTAGTTGGTGTGGGTCCCGTAGGGGCTGAAGAAATTCGTCAGGAAGGGG
mKate2       >  F  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

                     SpDon                          Bbs1             Bpm1
                         |                             |                |
               GAGGGCTTCACATGGGAGAGAGTCACCACATACGAAGACGGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACG
         2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
               CTCCCGAAGTGTACCCTCTCTCAGTGGTGTATGCTTCTGCCCCCGCACGACTGGCGATGGGTCCTGTGGTCGGAGGTCCTGCCGACGGAGTAGATGTTGC
mKate2       > E  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  |
                                                                           |       |  |
               TCAAGATCAGAGGGGTGAACTTCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCTCCACCGAGACCCTGTACCCCGCTGACGG
         2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
               AGTTCTAGTCTCCCCACTTGAAGGGTAGGTTGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCTCCGGAGGTGGCTCTGGGACATGGGGCGACTGCC
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
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                    Bgl1          Bgl1       BssS1          Eco57                    Bbs1          BpuE1
                       |             |           |              |                       |              |
               CGGCCTGGAAGGCAGAGCCGACATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACTTGAAGACCACATACAGATCCAAGAAACCCGCTAAG
         2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
               GCCGGACCTTCCGTCTCGGCTGTACCGGGACTTCGAGCACCCGCCCCCGGTGGACTAGACGTTGAACTTCTGGTGTATGTCTAGGTTCTTTGGGCGATTC
mKate2       >  G  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

                                                     Bbs1
                                                 SpAcc  |               Bsa1       PshA1       BssS1 Dra3
                                                     |  |                  |           |           |    |
               AACCTCAAGATGCCCGGCGTCTACTATGTGGACAGAAGACTGGAAAGAATCAAGGAGGCCGACAAAGAGACCTACGTCGAGCAGCACGAGGTGGCTGTGG
         2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
               TTGGAGTTCTACGGGCCGCAGATGATACACCTGTCTTCTGACCTTTCTTAGTTCCTCCGGCTGTTTCTCTGGATGCAGCTCGTCGTGCTCCACCGACACC
mKate2       > N  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
           Msc1  AlwN1          SpAcc          Bmr1 BsrB1|      Xba1   BsaB1                            SpDon
              |      |              |             |     ||         |       |                                |
               CCAGATACTGCGACCTCCCTAGCAAACTGGGGCACAGATGAGCGGCCGCGACTCTAGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTT
         3001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
               GGTCTATGACGCTGGAGGGATCGTTTGACCCCGTGTCTACTCGCCGGCGCTGAGATCTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAA
mKate2       >   R  Y  C  D  L  P  S  K  L  G  H  R  *

                                                             Bsm1
            Dra1                                            Mfe1|        Hpa1       polyA    Psi1      polyA
               |                                               ||           |           |       |          |
               TAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAG
         3101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
               ATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTC

                                polyA            Bts1 Bsm1                                  Afl2         SpDon
                                    |               |    |                                     |             |
               CAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTGTAAG
         3201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
               GTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTCCGCATTTAACATTC
```

```
         Ssp1                                                                            Psi1
            |                                                                               |
      CGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAA
3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
      GCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTT

                                                  BsaXb                 Drd1    BsaXa
                                                      |                    |        |
      TAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGG
3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
      ATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCC

                 BtgZ1
                 Dra3|                                                         SpAcc
                    ||                                                             |
      GCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAG
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      CGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATC

                    Nae1
                 NgoM4 |                                    BsrB1
                     | |                                        |
      AGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGC
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      TCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCG

                                                                                                polyA
                                                                                                    |
      GTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCT
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      CATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGA

                             BciV1
                          BspH1  |                                                                   Eci1
                        BsrB1 |  |                            Ssp1  Ear1        Bsu36              Pvu2 |
                            | |  |                               |     |            |                 | |
      AAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTG
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      TTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGAC
```

```
                                                                         Nsi1
                                                                       Sph1 |
                                                                      BfrB1 |
                                           BseY1                   BstAP  | |            SexA1
                                               |                       |  | |                |
      TGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAA
3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
      ACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTT

                                             Nsi1
                                           Sph1 |
                                          BfrB1 |
               BseY1                   BstAP  | |                       Eci1                 Eci1
                   |                       |  | |                          |                    |
      AGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAAC
4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
      TCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTG

   Eci1                                                                     Sfi1
  Bmr1|       Eci1            Nco1                   polyA                  Bgl1                    SpDon
     ||          |               |                       |                     |                        |
      TCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAG
4101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
      AGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATC

                       Avr2
                      Stu1|                                                            BspM1
                  BseR1  ||              Cla1              BsaB1                       BfuA1
                      |  ||                 |                  |                           |
      TGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGT
4201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
      ACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCA

                                                                                                     Nar1
       Eag1                                       Bmr1                                              Kas1|
          |                                          |                                                 ||
      TCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGC
4301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
      AGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCG
```

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                            Drd1                                                   Msc1
                               |                                                      |
      GCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTG
4401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
      CGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAAC


       Pvu2
   Fsp1   |       PflF1                       Eco57                                    SpDon
      |   |           |                           |                                          |
      CGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCC
4501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
      GCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGG


                                                                       BtgZ1
                                                                    BspM1  |
                   BciV1         BsrD1                              BfuA1  |
                       |             |                                  |  |
      GAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAG
4601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
      CTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTC


                                             Sap1
                                             Ear1                          BpuE1
                                                |                              |
      CACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAG
4701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
      GTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTC


      Sph1                      Nco1               BtgZ1                                          NgoM4
         |                         |                   |                                               |
      CATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGC
4801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
      GTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCG
```

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    BseY1                                              Sap1
   Nae1 |        Rsr2         Eci1                     Ear1                   Eco57         BssS1
      | |           |            |                        |                       |             |
      CGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTT
4901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
      GCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAA


               BtgZ1
             BsrB1 |                                               BsrB1          BstB1
                 | |                                                   |              |
      ACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCG
5001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
      TGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGC


                  BssS1                                                               Nae1
                  BspM1                                                            NgoM4 |
                  BfuA1                      SpAcc                                  Bpm1 |
                      |                          |                                     | |
      ACGCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCC
5101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
      TGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGG


                                         Bpm1
                                     SpAcc  |
                                      Avr2  |
                                         |  |
      AGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGC
5201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
      TCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCG


 polyA        polyA                                                                       Bsa1
     |            |                                                                          |
      AATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCC
5301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5400
      TTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGG
```

```
      CATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCC
5401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5500
      GTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGG

 BstAP
 AlwN1      Bsu36                            Dra1               Dra1                              BspH1
     |          |                               |                  |                                  |
      CTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCAT
5501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5600
      GACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTA

                                                                                              BpuE1
                                                                                                  |
      GACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATC
5601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5700
      CTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAG

                                                                            Eco57
                                                                                |
      TGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAG
5701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5800
      ACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTC

                            SpAcc
                                |
      CGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTT
5801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5900
      GCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAA

         AlwN1                     BpuE1
             |                         |
      ACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGT
5901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6000
      TGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCA
```

```
    ApaL1     BseY1                                             SpAcc
        |         |                                                 |
      TCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGG
6001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6100
      AGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCC


                    BciV1
                 Eci1   |                    BssS1                                    SpAcc
                    |   |                        |                                        |
      CGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCG
6101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6200
      GCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGC


                 Drd1            BpuE1               SpAcc     Eci1
                    |                |                   |        |
      CCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTT
6201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6300
      GGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAA


                   SpDon                                                    Nsi1
                  BspLU|                                                 BfrB1 |
                      ||                                                     | |
      TGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
6301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*||||| 6375
      ACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aat2 **Acc65** **Afl2** Age1 **Ale1** AlwN1 **Apa1** ApaL1 **Ase1** Avr2 **BamH1** Bbs1 Bcg1a Bcg1b
BciV1 BfrB1 BfuA1 Bgl1 **Blp1** **BmgB1** Bmr1 Bpm1 **Bpu10** BpuE1 Bsa1 BsaB1 **BsaXa** **BsaXb**
BseR1 BseY1 Bsg1 Bsm1 **BsmB1** BspH1 BspLU BspM1 BsrB1 BsrD1 BsrG1 BssS1 BstAP BstB1
Bsu36 BtgZ1 Bts1 **_Chi** **Cla1** Dra1 Dra3 Drd1 Eag1 Ear1 Eci1 Ecl2 Eco57 **EcoR1**
Fsp1 **Hind3** **Hpa1** **Kas1** **Kpn1** **Mfe1** Msc1 Nae1 **Nar1** Nco1 **Nde1** NgoM4 **Nhe1** **Not1**
Nsi1 **PflF1** **PflM1** **Pml1** polyA **PshA1** Psi1 **PspOM** Pst1 Pvu2 **Rsr2** Sac1 Sac2 **Sal1**
Sap1 **SexA1** **Sfi1** **SgrA1** Sma1 SnaB1 SpAcc SpDon Sph1 **Srf1** Ssp1 Stu1 **Xba1** Xcm1
Xho1 **Xmn1**

Unique:

Acc65 **Afl2** **Ale1** **Apa1** **Ase1** **BamH1** **Blp1** **BmgB1** **Bpu10** **BsaXa** **BsaXb** **BsmB1** **_Chi** **Cla1**
EcoR1 **Fsp1** **Hind3** **Hpa1** **Kas1** **Kpn1** **Mfe1** **Nar1** **Nde1** **Nhe1** **Not1** **PflF1** **PflM1** **Pml1**
PshA1 **PspOM** **Rsr2** **Sal1** **SexA1** **Sfi1** **SgrA1** **Srf1** **Xba1** **Xho1** **Xmn1**

Not found:

Aar1 Acl1 Afe1 Ahd1 Asc1 AsiS1 Bae1a Bae1b BbvC1 Bcl1 Bgl2 BsiW1 BspE1 BssH2
BstE2 BstX1 BstZ1 BxatB BxatL BxatR BxatP EcoK EcoN1 EcoRV FCatB FCatL FCatR FCatP
ScFRT Fse1 FspA1 I_Ceu loxP Mlu1 Nru1 Pac1 Pme1 Pvu1 R4atB R4atL R4atP R4atR
SanD1 Sbf1 Sca1 Sgf1 Spe1 Swa1 T3RNA T7RNA T7Ter PISce

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