pmKate2-clathrin vector restriction map

The data has not been verified by restriction digestion with each enzyme listed and does not take into account possible methylation sites. Enzymes that recognize unambiguous sequences less than 6 basepairs long are not included – for the more complete enzyme list please refer to the Table of restriction sites.

Unique sites are shown in bold blue. The location given specifies the 3’ end of the cut DNA (the base to the left of the cut site). mKate2 amino acids are shown in red, clathrin 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 Afe1
                                                                                                         |    |
               ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCGCTA
          501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
               TGTTGAGGCGGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT


                         SpDon
                        Ale1 |
           Age1       Nco1 | |                                 BsrG1                                ApaL1
              |          | | |                                     |                                    |
               CCGGTAGCCACCATGGTGAGCGAGCTGATTAAGGAGAACATGCACATGAAGCTGTACATGGAGGGCACCGTGAACAACCACCACTTCAAGTGCACATCCG
          601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
               GGCCATCGGTGGTACCACTCGCTCGACTAATTCCTCTTGTACGTGTACTTCGACATGTACCTCCCGTGGCACTTGTTGGTGGTGAAGTTCACGTGTAGGC
mKate2       >             M  V  S  E  L  I  K  E  N  M  H  M  K  L  Y  M  E  G  T  V  N  N  H  H  F  K  C  T  S  E

                          SpAcc
                              |
               AGGGCGAAGGCAAGCCCTACGAGGGCACCCAGACCATGAGAATCAAGGCGGTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGCTACCAGCTT
          701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
               TCCCGCTTCCGTTCGGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCCGCCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTCGAA
mKate2       >   G  E  G  K  P  Y  E  G  T  Q  T  M  R  I  K  A  V  E  G  G  P  L  P  F  A  F  D  I  L  A  T  S  F

                                                                               Bsu36       SpDon
                                                                                   |           |
               CATGTACGGCAGCAAAACCTTCATCAACCACACCCAGGGCATCCCCGACTTCTTTAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACA
          801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
               GTACATGCCGTCGTTTTGGAAGTAGTTGGTGTGGGTCCCGTAGGGGCTGAAGAAATTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGGTGT
mKate2       >  M  Y  G  S  K  T  F  I  N  H  T  Q  G  I  P  D  F  F  K  Q  S  F  P  E  G  F  T  W  E  R  V  T  T
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                      Bbs1             Bpm1
                         |                |
               TACGAAGACGGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACTTCCCATCCA
          901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
               ATGCTTCTGCCCCCGCACGACTGGCGATGGGTCCTGTGGTCGGAGGTCCTGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCCACTTGAAGGGTAGGT
mKate2       > Y  E  D  G  G  V  L  T  A  T  Q  D  T  S  L  Q  D  G  C  L  I  Y  N  V  K  I  R  G  V  N  F  P  S  N

                                                     Bsa1
                                         BseY1    Stu1  |                                 Bgl1          Bgl1
                                             |       |  |                                    |             |
               ACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCTCCACCGAGACCCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAGCCGACATGGCCCT
         1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
               TGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCTCCGGAGGTGGCTCTGGGACATGGGGCGACTGCCGCCGGACCTTCCGTCTCGGCTGTACCGGGA
mKate2       >   G  P  V  M  Q  K  K  T  L  G  W  E  A  S  T  E  T  L  Y  P  A  D  G  G  L  E  G  R  A  D  M  A  L

               BssS1          Eco57                    Bbs1          BpuE1
                   |              |                       |              |
               GAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACTTGAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGCGTCTACTATGTG
         1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
               CTTCGAGCACCCGCCCCCGGTGGACTAGACGTTGAACTTCTGGTGTATGTCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCGCAGATGATACAC
mKate2       >  K  L  V  G  G  G  H  L  I  C  N  L  K  T  T  Y  R  S  K  K  P  A  K  N  L  K  M  P  G  V  Y  Y  V

                       Bbs1
                   SpAcc  |               Bsa1       PshA1       BssS1 Dra3      Msc1  AlwN1          SpAcc
                       |  |                  |           |           |    |         |      |              |
               GACAGAAGACTGGAAAGAATCAAGGAGGCCGACAAAGAGACCTACGTCGAGCAGCACGAGGTGGCTGTGGCCAGATACTGCGACCTCCCTAGCAAACTGG
         1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
               CTGTCTTCTGACCTTTCTTAGTTCCTCCGGCTGTTTCTCTGGATGCAGCTCGTCGTGCTCCACCGACACCGGTCTATGACGCTGGAGGGATCGTTTGACC
mKate2       > D  R  R  L  E  R  I  K  E  A  D  K  E  T  Y  V  E  Q  H  E  V  A  V  A  R  Y  C  D  L  P  S  K  L  G

                                               Hind3
                             BpuE1     Xho1   Sac1 |  EcoR1      Sal1
                 Bmr1    BspE1   | Bgl2   | Ecl2 | |BstB1 |     Pst1|
                    |        |   |    |   |    | | |    | |        ||
               GGCACAAACTTAATTCCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCTGCAGTCGACATGGCTGATGACTTTGGCTTCTTCTCGTCGTCGGAGAGTGG
         1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
               CCGTGTTTGAATTAAGGCCTGAGTCTAGAGCTCGAGTTCGAAGCTTAAGACGTCAGCTGTACCGACTACTGAAACCGAAGAAGAGCAGCAGCCTCTCACC
mKate2/Clath >   H  K  L  N  S  G  L  R  S  R  A  Q  A  S  N  S  A  V  D  M  A  D  D  F  G  F  F  S  S  S  E  S  G
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                                          BseR1
                                         Not1 |
                                         Eag1 |        BseY1
                   Bgl1                 Eci1| |     Bgl1   |
                      |                    || |        |   |
               TGCCCCGGAGGCGGCGGAGGAGGACCCGGCGGCCGCCTTCCTGGCCCAGCAGGAGAGCGAGATTGCAGGCATAGAGAACGACGAGGGCTTCGGGGCACCT
         1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
               ACGGGGCCTCCGCCGCCTCCTCCTGGGCCGCCGGCGGAAGGACCGGGTCGTCCTCTCGCTCTAACGTCCGTATCTCTTGCTGCTCCCGAAGCCCCGTGGA
Clathrin     >  A  P  E  A  A  E  E  D  P  A  A  A  F  L  A  Q  Q  E  S  E  I  A  G  I  E  N  D  E  G  F  G  A  P

                BspM1
                BfuA1
                 Aar1                         BssS1
              Nae1  |                        Apa1 |
           NgoM4 |  |                   PspOM   | |                             PshA1
               | |  |                       |   | |                                 |
               GCCGGCAGCCATGCGGCCCCCGCACAGCCGGGCCCCACGAGTGGGGCTGGTTCTGAGGACATGGGGACCACAGTCAATGGAGATGTGTTTCAGGAGGCCA
         1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
               CGGCCGTCGGTACGCCGGGGGCGTGTCGGCCCGGGGTGCTCACCCCGACCAAGACTCCTGTACCCCTGGTGTCAGTTACCTCTACACAAAGTCCTCCGGT
Clathrin     > A  G  S  H  A  A  P  A  Q  P  G  P  T  S  G  A  G  S  E  D  M  G  T  T  V  N  G  D  V  F  Q  E  A  N

                                     BstAP                                                                  SpAcc
                                   BsrD1 |                                                                BseR1 |
                                       | |                                                                    | |
               ACGGTCCTGCTGATGGCTACGCAGCCATTGCCCAGGCTGACAGGCTGACCCAGGAGCCTGAGAGCATCCGCAAGTGGCGAGAGGAGCAGAGGAAACGGCT
         1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
               TGCCAGGACGACTACCGATGCGTCGGTAACGGGTCCGACTGTCCGACTGGGTCCTCGGACTCTCGTAGGCGTTCACCGCTCTCCTCGTCTCCTTTGCCGA
Clathrin     >   G  P  A  D  G  Y  A  A  I  A  Q  A  D  R  L  T  Q  E  P  E  S  I  R  K  W  R  E  E  Q  R  K  R  L

                                                                          SpAcc                  Bpm1
                                                                        Xcm1  |              BseR1  |
                                                                           |  |                  |  |
               GCAAGAGCTGGATGCTGCATCTAAGGTCACGGAACAGGAATGGCGGGAGAAGGCCAAGAAGGACCTGGAGGAGTGGAACCAGCGCCAGAGTGAACAAGTA
         1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
               CGTTCTCGACCTACGACGTAGATTCCAGTGCCTTGTCCTTACCGCCCTCTTCCGGTTCTTCCTGGACCTCCTCACCTTGGTCGCGGTCTCACTTGTTCAT
Clathrin     >  Q  E  L  D  A  A  S  K  V  T  E  Q  E  W  R  E  K  A  K  K  D  L  E  E  W  N  Q  R  Q  S  E  Q  V
```

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                                                                                        Dra3
                                                                                     Xcm1  |
                                                        BseR1     Bsa1             BseR1|  |          BseY1
                                                            |        |                 ||  |              |
               GAGAAGAACAAGATCAACAACCGGGCATCCGAGGAGGCTTTCGTGAAGGAATCCAAGGAGGAGACCCCAGGCACAGAGTGGGAGAAGGTGGCCCAGCTAT
         1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
               CTCTTCTTGTTCTAGTTGTTGGCCCGTAGGCTCCTCCGAAAGCACTTCCTTAGGTTCCTCCTCTGGGGTCCGTGTCTCACCCTCTTCCACCGGGTCGATA
Clathrin     > E  K  N  K  I  N  N  R  A  S  E  E  A  F  V  K  E  S  K  E  E  T  P  G  T  E  W  E  K  V  A  Q  L  C

                                      BstAP Bts1                                              Drd1  Eco57 BamH1
                                          |    |                                                 |      |     |
               GTGACTTCAACCCCAAGAGCAGCAAGCAGTGCAAAGATGTGTCCCGCCTGCGCTCGGTGCTCATGTCCCTGAAGCAGACGCCACTGTCCCGCTAGGGATC
         1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
               CACTGAAGTTGGGGTTCTCGTCGTTCGTCACGTTTCTACACAGGGCGGACGCGAGCCACGAGTACAGGGACTTCGTCTGCGGTGACAGGGCGATCCCTAG
Clathrin     >   D  F  N  P  K  S  S  K  Q  C  K  D  V  S  R  L  R  S  V  L  M  S  L  K  Q  T  P  L  S  R  *

                   Xba1      Bcl1BsaB1                            SpDon   Dra1
                      |         |    |                                |      |
               CACCGGATCTAGATAACTGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACAT
         2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
               GTGGCCTAGATCTATTGACTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTA

                       Bsm1
                      Mfe1|        Hpa1       polyA    Psi1      polyA                        polyA
                         ||           |           |       |          |                            |
               AAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTT
         2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
               TTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAA

           Bts1 Bsm1                                      Mlu1     SpDon        Ssp1
              |    |                                         |         |           |
               CACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAACGCGTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTT
         2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
               GTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTGCGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAA
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                                                   Psi1
                                                      |
      AAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAA
2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
      TTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTT

                                                                               BtgZ1
            BsaXb                 Drd1    BsaXa                                Dra3|
                |                    |        |                                   ||
      CAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGT
2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
      GTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCA

                                                                                  Nae1
                                         SpAcc                                 NgoM4 |
                                             |                                     | |
      TTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGG
2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
      AAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCC

                      BsrB1
                          |
      AAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACA
2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
      TTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGT

                                                                                           BciV1
                                                                                        BspH1  |
                                                          polyA                       BsrB1 |  |
                                                              |                           | |  |
      GGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAA
2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
      CCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATT

                                                               Eci1
                        Ssp1  Ear1        Bsu36              Pvu2 |
                           |     |            |                 | |
      CCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGG
2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
      GGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCC
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                                   Nsi1
                                 Sph1 |
                                BfrB1 |
     BseY1                   BstAP  | |            SexA1                     BseY1
         |                       |  | |                |                         |
      CTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGC
2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
      GAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCG

       Nsi1
     Sph1 |
    BfrB1 |                                                      Eci1
 BstAP  | |                       Eci1                 Eci1     Bmr1|       Eci1            Nco1
     |  | |                          |                    |        ||          |               |
      ATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGAC
3001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
      TACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTG

                                                                                     Avr2
                                      Sfi1                                          Stu1|
               polyA                  Bgl1                    SpDon             BseR1  ||
                   |                     |                        |                 |  ||
      TAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGA
3101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
      ATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTCT

                                                 BspM1
   Cla1              BsaB1                       BfuA1               Eag1
      |                  |                           |                  |
      TCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGA
3201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
      AGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACT

                                                               Nar1
            Bmr1                                              Kas1|                      Drd1
               |                                                 ||                          |
      CTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCC
3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
      GACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGG
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                                                                     Pvu2
                                             Msc1                Fsp1   |       PflF1
                                                |                   |   |           |
      CTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGG
3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
      GACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCC

        Eco57                                      SpDon                         BciV1         BsrD1
            |                                          |                             |             |
      ACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCT
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      TGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGA

                                 BtgZ1
                              BspM1  |
                              BfuA1  |
                                  |  |
      GCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGAT
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      CGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTA

       Sap1
       Ear1                           BpuE1                         Sph1                       Nco1
          |                               |                            |                          |
      GATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCG
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      CTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGC

                                                                  BseY1
                                                                 Nae1 |
              BtgZ1                                           NgoM4 | |        Rsr2         Eci1
                  |                                               | | |           |            |
      ATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTT
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      TACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAA
```

```
                 Sap1                                                        BtgZ1
                 Ear1                   Eco57         BssS1                BsrB1 |
                    |                       |             |                    | |
      GGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTC
3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
      CCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAG

                                                                                BssS1
                                                                                BspM1
                             BsrB1          BstB1                               BfuA1
                                 |              |                                   |
      TATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCGC
4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
      ATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCG

                                                Nae1
                                             NgoM4 |                                               SpAcc
       SpAcc                                  Bpm1 |                                                Avr2
           |                                     | |                                                   |
      CGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCT
4101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
      GCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGA

   Bpm1                                                        polyA        polyA
      |                                                            |            |
      AGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGT
4201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
      TCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGCA

                                                    Bsa1
                                                       |
      TTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCC
4301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
      AACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGG
```

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                                                               BstAP
                                                               AlwN1      Bsu36
                                                                   |          |
      ACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATT
4401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
      TGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAA

       Dra1               Dra1                              BspH1
          |                  |                                  |
      GATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAG
4501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
      CTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTC

                                                        BpuE1
                                                            |
      CGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGT
4601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
      GCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCA

                                      Eco57                                               SpAcc
                                          |                                                   |
      GGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAG
4701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
      CCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATC

                                                                       AlwN1                     BpuE1
                                                                           |                         |
      TTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTA
4801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
      AATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAAT

                                                                  ApaL1     BseY1
                                                                      |         |
      CCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACAC
4901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
      GGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTG
```

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                                                                                  BciV1
                          SpAcc                                                Eci1   |
                              |                                                   |   |
      CGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGA
5001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
      GCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCT

       BssS1                                    SpAcc                          Drd1            BpuE1
           |                                        |                             |                |
      GAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGT
5101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
      CTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCA

                                                                                 SpDon
               SpAcc     Eci1                                                   BspLU|
                   |        |                                                       ||
      CAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATC
5201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
      GTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAG

                                      Nsi1
                                   BfrB1 |
                                       | |
      CCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
5301  |||||||||*|||||||||*|||||||||*||||||| 5337
      GGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aar1 Aat2 **Afe1** **Age1** **Ale1** AlwN1 **Apa1** ApaL1 **Ase1** Avr2 **BamH1** Bbs1 BciV1 **Bcl1**
BfrB1 BfuA1 Bgl1 **Bgl2** Bmr1 Bpm1 BpuE1 Bsa1 BsaB1 **BsaXa** **BsaXb** BseR1 BseY1 Bsm1
BspE1 BspH1 **BspLU** BspM1 BsrB1 BsrD1 **BsrG1** BssS1 BstAP BstB1 Bsu36 BtgZ1 Bts1 **Cla1**
Dra1 Dra3 Drd1 Eag1 Ear1 Eci1 **Ecl2** Eco57 **EcoR1** **Fsp1** **Hind3** **Hpa1** **Kas1** **Mfe1**
Mlu1 Msc1 Nae1 **Nar1** Nco1 **Nde1** NgoM4 **Nhe1** **Not1** Nsi1 **PflF1** polyA PshA1 Psi1
PspOM **Pst1** Pvu2 **Rsr2** **Sac1** **Sal1** Sap1 **SexA1** **Sfi1** **SnaB1** SpAcc SpDon Sph1 Ssp1
Stu1 **Xba1** Xcm1 **Xho1**

Unique:

Aar1 **Afe1** **Age1** **Ale1** **Apa1** **Ase1** **BamH1** **Bcl1** **Bgl2** **BsaXa** **BsaXb** **BspE1** **BspLU** **BsrG1**
Cla1 **Ecl2** **EcoR1** **Fsp1** **Hind3** **Hpa1** **Kas1** **Mfe1** **Mlu1** **Nar1** **Nde1** **Nhe1** **Not1** **PflF1**
PspOM **Pst1** **Rsr2** **Sac1** **Sal1** **SexA1** **Sfi1** **SnaB1** **Xba1** **Xho1**

Not found:

Acc65 Acl1 Afl2 Ahd1 Asc1 AsiS1 Bae1a Bae1b BbvC1 Bcg1a Bcg1b Blp1 BmgB1 Bpu10
Bsg1 BsiW1 BsmB1 BssH2 BstE2 BstX1 BstZ1 BxatB BxatL BxatR BxatP _Chi EcoK EcoN1
EcoRV FCatB FCatL FCatR FCatP ScFRT Fse1 FspA1 I_Ceu Kpn1 loxP Nru1 Pac1 PflM1
Pme1 Pml1 Pvu1 R4atB R4atL R4atP R4atR Sac2 SanD1 Sbf1 Sca1 Sgf1 SgrA1 Sma1
Spe1 Srf1 Swa1 T3RNA T7RNA T7Ter PISce 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