pmKate2-actinin 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, alpha-actinin 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

                                Hind3
                        Xho1   Sac1 |
              BpuE1 Bgl2   | Ecl2 | |                                                   Ear1     Xcm1         Bmr1
                  |    |   |    | | |                                                      |        |            |
               CCGGACTCAGATCTCGAGCTCAAGCTTCGCACCATCATGGACCATTATGATTCTCAGCAAACCAACGATTACATGCAGCCAGAAGAGGACTGGGACCGGG
          601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
               GGCCTGAGTCTAGAGCTCGAGTTCGAAGCGTGGTAGTACCTGGTAATACTAAGAGTCGTTTGGTTGCTAATGTACGTCGGTCTTCTCCTGACCCTGGCCC
Actinin      >                                     M  D  H  Y  D  S  Q  Q  T  N  D  Y  M  Q  P  E  E  D  W  D  R  D

                    BspM1                                                         EcoN1
                    BfuA1    SpAcc                                              BspE1 |                     Ear1
                        |        |                                                  | |                        |
               ACCTGCTCCTGGACCCGGCCTGGGAGAAGCAGCAGAGAAAGACATTCACGGCATGGTGTAACTCCCACCTCCGGAAGGCGGGGACACAGATCGAGAACAT
          701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
               TGGACGAGGACCTGGGCCGGACCCTCTTCGTCGTCTCTTTCTGTAAGTGCCGTACCACATTGAGGGTGGAGGCCTTCCGCCCCTGTGTCTAGCTCTTGTA
Actinin      >   L  L  L  D  P  A  W  E  K  Q  Q  R  K  T  F  T  A  W  C  N  S  H  L  R  K  A  G  T  Q  I  E  N  I

                                                      Eco57       SpDon  Bpm1  Msc1                BsaXb ApaL1
                                                          |           |     |     |                    |     |
               CGAAGAGGACTTCCGGGATGGCCTGAAGCTCATGCTGCTGCTGGAGGTCATCTCAGGTGAACGCTTGGCCAAGCCAGAGCGAGGCAAGATGAGAGTGCAC
          801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
               GCTTCTCCTGAAGGCCCTACCGGACTTCGAGTACGACGACGACCTCCAGTAGAGTCCACTTGCGAACCGGTTCGGTCTCGCTCCGTTCTACTCTCACGTG
Actinin      >  E  E  D  F  R  D  G  L  K  L  M  L  L  L  E  V  I  S  G  E  R  L  A  K  P  E  R  G  K  M  R  V  H
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             Bgl2            BsaXa                                                                     SpDon
                |                |                                                                         |
               AAGATCTCCAACGTCAACAAGGCCCTGGATTTCATAGCCAGCAAAGGCGTCAAACTGGTGTCCATCGGAGCCGAAGAAATCGTGGATGGGAATGTGAAGA
          901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
               TTCTAGAGGTTGCAGTTGTTCCGGGACCTAAAGTATCGGTCGTTTCCGCAGTTTGACCACAGGTAGCCTCGGCTTCTTTAGCACCTACCCTTACACTTCT
Actinin      > K  I  S  N  V  N  K  A  L  D  F  I  A  S  K  G  V  K  L  V  S  I  G  A  E  E  I  V  D  G  N  V  K  M

                                                                  Ear1
                                                              Eco57  |
                                                                  |  |
               TGACCCTGGGCATGATCTGGACCATCATCCTGCGCTTTGCCATCCAGGACATCTCCGTGGAAGAGACTTCAGCCAAGGAAGGGCTGCTCCTGTGGTGTCA
         1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
               ACTGGGACCCGTACTAGACCTGGTAGTAGGACGCGAAACGGTAGGTCCTGTAGAGGCACCTTCTCTGAAGTCGGTTCCTTCCCGACGAGGACACCACAGT
Actinin      >   T  L  G  M  I  W  T  I  I  L  R  F  A  I  Q  D  I  S  V  E  E  T  S  A  K  E  G  L  L  L  W  C  Q

                                                             SpAcc
                                                                 |
               GAGAAAGACAGCCCCTTACAAAAATGTCAACATCCAGAACTTCCACATAAGCTGGAAGGATGGCCTCGGCTTCTGTGCTTTGATCCACCGACACCGGCCC
         1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
               CTCTTTCTGTCGGGGAATGTTTTTACAGTTGTAGGTCTTGAAGGTGTATTCGACCTTCCTACCGGAGCCGAAGACACGAAACTAGGTGGCTGTGGCCGGG
Actinin      >  R  K  T  A  P  Y  K  N  V  N  I  Q  N  F  H  I  S  W  K  D  G  L  G  F  C  A  L  I  H  R  H  R  P

                     SpAcc     SpAcc                                        BmgB1                           BstX1
                         |         |                                            |                               |
               GAGCTGATTGACTACGGGAAGCTGCGGAAGGATGATCCACTCACAAATCTGAATACGGCTTTTGACGTGGCAGAGAAGTACCTGGACATCCCCAAGATGC
         1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
               CTCGACTAACTGATGCCCTTCGACGCCTTCCTACTAGGTGAGTGTTTAGACTTATGCCGAAAACTGCACCGTCTCTTCATGGACCTGTAGGGGTTCTACG
Actinin      > E  L  I  D  Y  G  K  L  R  K  D  D  P  L  T  N  L  N  T  A  F  D  V  A  E  K  Y  L  D  I  P  K  M  L

                           Bbs1                            BspH1      Drd1                  Xcm1           Bgl1
                              |                                |         |                     |              |
               TGGATGCCGAAGACATCGTTGGAACTGCCCGACCGGATGAGAAAGCCATCATGACTTACGTGTCTAGCTTCTACCACGCCTTCTCTGGAGCCCAGAAGGC
         1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
               ACCTACGGCTTCTGTAGCAACCTTGACGGGCTGGCCTACTCTTTCGGTAGTACTGAATGCACAGATCGAAGATGGTGCGGAAGAGACCTCGGGTCTTCCG
Actinin      >   D  A  E  D  I  V  G  T  A  R  P  D  E  K  A  I  M  T  Y  V  S  S  F  Y  H  A  F  S  G  A  Q  K  A
```

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                                                                                   Bbs1                   Eci1
                 Bpm1    Eci1                                                  SpAcc  |       Msc1    Xcm1   |
                    |       |                                                      |  |          |       |   |
               GGAGACAGCAGCCAATCGCATCTGCAAGGTGTTGGCCGTCAACCAGGAGAACGAGCAGCTTATGGAAGACTACGAGAAGCTGGCCAGTGATCTGTTGGAG
         1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
               CCTCTGTCGTCGGTTAGCGTAGACGTTCCACAACCGGCAGTTGGTCCTCTTGCTCGTCGAATACCTTCTGATGCTCTTCGACCGGTCACTAGACAACCTC
Actinin       > E  T  A  A  N  R  I  C  K  V  L  A  V  N  Q  E  N  E  Q  L  M  E  D  Y  E  K  L  A  S  D  L  L  E

                                                                      BstAP
                                                                     Sph1 |                                Nar1
                                                                   Nsi1 | |                               Kas1|
            BamH1                                        Bpm1   BfrB1 | | |       AlwN1         Bsg1     Bpm1||
                |                                           |       | | | |           |            |        |||
               TGGATCCGCCGCACAATCCCGTGGCTGGAGAACCGGGTGCCCGAGAACACCATGCATGCCATGCAACAGAAGCTGGAGGACTTCCGGGACTACCGGCGCC
         1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
               ACCTAGGCGGCGTGTTAGGGCACCGACCTCTTGGCCCACGGGCTCTTGTGGTACGTACGGTACGTTGTCTTCGACCTCCTGAAGGCCCTGATGGCCGCGG
Actinin       >W  I  R  R  T  I  P  W  L  E  N  R  V  P  E  N  T  M  H  A  M  Q  Q  K  L  E  D  F  R  D  Y  R  R  L

                                                  Bsg1                  Pst1
                                              Pvu2   |              Bpm1   |          Blp1
                                                 |   |                 |   |             |
               TGCACAAGCCGCCCAAGGTGCAGGAGAAGTGCCAGCTGGAGATCAACTTCAACACGCTGCAGACCAAGCTGCGGCTCAGCAACCGGCCTGCCTTCATGCC
         1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
               ACGTGTTCGGCGGGTTCCACGTCCTCTTCACGGTCGACCTCTAGTTGAAGTTGTGCGACGTCTGGTTCGACGCCGAGTCGTTGGCCGGACGGAAGTACGG
Actinin       >  H  K  P  P  K  V  Q  E  K  C  Q  L  E  I  N  F  N  T  L  Q  T  K  L  R  L  S  N  R  P  A  F  M  P

                                                     BspM1
                                                     BfuA1                     Bpm1
                                 Bsa1                 Aar1  EcoN1           SpAcc |             BseR1  BspE1
                                    |                    |      |               | |                |      |
               CTCTGAGGGCAGGATGGTCTCGGACATCAACAATGCCTGGGGCTGCCTGGAGCAGGTGGAGAAGGGCTATGAGGAGTGGTTGCTGAATGAGATCCGGAGG
         1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
               GAGACTCCCGTCCTACCAGAGCCTGTAGTTGTTACGGACCCCGACGGACCTCGTCCACCTCTTCCCGATACTCCTCACCAACGACTTACTCTAGGCCTCC
Actinin       > S  E  G  R  M  V  S  D  I  N  N  A  W  G  C  L  E  Q  V  E  K  G  Y  E  E  W  L  L  N  E  I  R  R
```

```
                                 Bpm1                 Stu1    BssS1  Stu1                                   Bsa1
                                    |                    |        |     |                                      |
               CTGGAGCGACTGGACCACCTGGCAGAGAAGTTCCGGCAGAAGGCCTCCATCCACGAGGCCTGGACTGACGGCAAAGAGGCCATGCTGCGACAGAAGGACT
         1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
               GACCTCGCTGACCTGGTGGACCGTCTCTTCAAGGCCGTCTTCCGGAGGTAGGTGCTCCGGACCTGACTGCCGTTTCTCCGGTACGACGCTGTCTTCCTGA
Actinin      > L  E  R  L  D  H  L  A  E  K  F  R  Q  K  A  S  I  H  E  A  W  T  D  G  K  E  A  M  L  R  Q  K  D  Y

                               BpuE1     Stu1                 Stu1                                 BtgZ1
                                   |        |                    |                                     |
               ATGAGACCGCCACCCTCTCGGAGATCAAGGCCTTGCTCAAGAAGCATGAGGCCTTCGAGAGTGACCTGGCTGCCCACCAGGACCGTGTGGAGCAGATTGC
         1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
               TACTCTGGCGGTGGGAGAGCCTCTAGTTCCGGAACGAGTTCTTCGTACTCCGGAAGCTCTCACTGGACCGACGGGTGGTCCTGGCACACCTCGTCTAACG
Actinin      >   E  T  A  T  L  S  E  I  K  A  L  L  K  K  H  E  A  F  E  S  D  L  A  A  H  Q  D  R  V  E  Q  I  A

                             Sac1
                           Ecl2 |                 Bmr1    Dra3                  Bgl2                      PspOM
                              | |                    |       |                     |                          |
               CGCCATCGCACAGGAGCTCAATGAGCTGGACTATTATGACTCACCCAGTGTCAACGCCCGTTGCCAAAAGATCTGTGACCAGTGGGACAATCTGGGGGCC
         2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
               GCGGTAGCGTGTCCTCGAGTTACTCGACCTGATAATACTGAGTGGGTCACAGTTGCGGGCAACGGTTTTCTAGACACTGGTCACCCTGTTAGACCCCCGG
Actinin      >  A  I  A  Q  E  L  N  E  L  D  Y  Y  D  S  P  S  V  N  A  R  C  Q  K  I  C  D  Q  W  D  N  L  G  A

                                           Rsr2          Bpm1                 Bpm1
           Apa1                         BsrB1 |       Bsa1  |             Pvu2   |   Bsg1       Bgl1
              |                             | |          |  |                |   |      |          |
               CTAACTCAGAAGCGAAGGGAAGCTCTGGAGCGGACCGAGAAACTGCTGGAGACCATTGACCAGCTGTACTTGGAGTATGCCAAGCGGGCTGCACCCTTCA
         2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
               GATTGAGTCTTCGCTTCCCTTCGAGACCTCGCCTGGCTCTTTGACGACCTCTGGTAACTGGTCGACATGAACCTCATACGGTTCGCCCGACGTGGGAAGT
Actinin      > L  T  Q  K  R  R  E  A  L  E  R  T  E  K  L  L  E  T  I  D  Q  L  Y  L  E  Y  A  K  R  A  A  P  F  N

                                               BspM1
                                               BfuA1
                                             Sbf1  |                                 BseR1
                              Nco1           Pst1  |      ApaL1                     AlwN1|
                                 |              |  |          |                         ||
               ACAACTGGATGGAGGGGGCCATGGAGGACCTGCAGGACACCTTCATTGTGCACACCATTGAGGAGATCCAGGGACTGACCACAGCCCATGAGCAGTTCAA
         2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
               TGTTGACCTACCTCCCCCGGTACCTCCTGGACGTCCTGTGGAAGTAACACGTGTGGTAACTCCTCTAGGTCCCTGACTGGTGTCGGGTACTCGTCAAGTT
Actinin      >   N  W  M  E  G  A  M  E  D  L  Q  D  T  F  I  V  H  T  I  E  E  I  Q  G  L  T  T  A  H  E  Q  F  K
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                                              Msc1                                             BmgB1
                                                 |                                                 |
               GGCCACCCTCCCTGATGCCGACAAGGAGCGCCTGGCCATCCTGGGCATCCACAATGAGGTGTCCAAGATTGTCCAGACCTACCACGTCAATATGGCGGGC
         2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
               CCGGTGGGAGGGACTACGGCTGTTCCTCGCGGACCGGTAGGACCCGTAGGTGTTACTCCACAGGTTCTAACAGGTCTGGATGGTGCAGTTATACCGCCCG
Actinin      >  A  T  L  P  D  A  D  K  E  R  L  A  I  L  G  I  H  N  E  V  S  K  I  V  Q  T  Y  H  V  N  M  A  G

                                                                            BstAP
                                    Bsu36                        Pml1     Pvu2  |
                                        |                           |        |  |
               ACCAACCCCTACACAACCATCACGCCTCAGGAGATCAATGGCAAATGGGACCACGTGCGGCAGCTGGTGCCTCGGAGGGACCAAGCTCTGACGGAGGAGC
         2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
               TGGTTGGGGATGTGTTGGTAGTGCGGAGTCCTCTAGTTACCGTTTACCCTGGTGCACGCCGTCGACCACGGAGCCTCCCTGGTTCGAGACTGCCTCCTCG
Actinin      > T  N  P  Y  T  T  I  T  P  Q  E  I  N  G  K  W  D  H  V  R  Q  L  V  P  R  R  D  Q  A  L  T  E  E  H

                                                                                BamH1
                                                                              Apa1  |
              Sph1 BseR1                                                 PspOM   |  |
                 |     |                                                     |   |  |
               ATGCCCGACAGCAGCACAATGAGAGGCTACGCAAGCAGTTTGGAGCCCAGGCCAATGTCATCGGGCCCTGGATCCAGACCAAGATGGAGGAGATCGGGAG
         2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
               TACGGGCTGTCGTCGTGTTACTCTCCGATGCGTTCGTCAAACCTCGGGTCCGGTTACAGTAGCCCGGGACCTAGGTCTGGTTCTACCTCCTCTAGCCCTC
Actinin      >   A  R  Q  Q  H  N  E  R  L  R  K  Q  F  G  A  Q  A  N  V  I  G  P  W  I  Q  T  K  M  E  E  I  G  R

                                                                   Sap1
                                                                   Ear1
                               SanD1                            BspM1 |
                             Nsi1  |                            BfuA1 |
            BseR1         BfrB1 |  |             Blp1     Bpm1   Aar1 |                               Bcl1  Pvu2
                |             | |  |                |        |      | |                                  |     |
               GATCTCCATTGAGATGCATGGGACCCTGGAGGACCAGCTCAGCCACCTGCGGCAGTATGAGAAGAGCATCGTCAACTACAAGCCAAAGATTGATCAGCTG
         2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
               CTAGAGGTAACTCTACGTACCCTGGGACCTCCTGGTCGAGTCGGTGGACGCCGTCATACTCTTCTCGTAGCAGTTGATGTTCGGTTTCTAACTAGTCGAC
Actinin      >  I  S  I  E  M  H  G  T  L  E  D  Q  L  S  H  L  R  Q  Y  E  K  S  I  V  N  Y  K  P  K  I  D  Q  L
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                                                                         Nco1                           Pvu2
                   _Chi       Bpm1                                     Xcm1 |        Ale1    BseY1  BtgZ1  |
                      |          |                                        | |           |        |      |  |
               GAGGGCGACCACCAGCTCATCCAGGAGGCGCTCATCTTCGACAACAAGCACACCAACTACACCATGGAGCACATCCGTGTGGGCTGGGAGCAGCTGCTCA
         2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
               CTCCCGCTGGTGGTCGAGTAGGTCCTCCGCGAGTAGAAGCTGTTGTTCGTGTGGTTGATGTGGTACCTCGTGTAGGCACACCCGACCCTCGTCGACGAGT
Actinin      > E  G  D  H  Q  L  I  Q  E  A  L  I  F  D  N  K  H  T  N  Y  T  M  E  H  I  R  V  G  W  E  Q  L  L  T

           SpDon                                   AlwN1   Sma1                                Xmn1
               |                                       |      |                                   |
               CCACCATCGCCAGGACCATCAATGAGGTAGAGAACCAGATCCTGACCCGGGATGCCAAGGGCATCAGCCAGGAGCAGATGAATGAGTTCCGGGCCTCCTT
         2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
               GGTGGTAGCGGTCCTGGTAGTTACTCCATCTCTTGGTCTAGGACTGGGCCCTACGGTTCCCGTAGTCGGTCCTCGTCTACTTACTCAAGGCCCGGAGGAA
Actinin      >   T  I  A  R  T  I  N  E  V  E  N  Q  I  L  T  R  D  A  K  G  I  S  Q  E  Q  M  N  E  F  R  A  S  F

                                             SanD1  Bmr1          BseR1
                                                 |     |              |
               CAACCACTTTGACCGGGATCACTCCGGCACACTGGGTCCCGAGGAGTTCAAAGCCTGCCTCATCAGCTTGGGTTATGATATTGGCAACGACCCCCAGGGA
         2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
               GTTGGTGAAACTGGCCCTAGTGAGGCCGTGTGACCCAGGGCTCCTCAAGTTTCGGACGGAGTAGTCGAACCCAATACTATAACCGTTGCTGGGGGTCCCT
Actinin      >  N  H  F  D  R  D  H  S  G  T  L  G  P  E  E  F  K  A  C  L  I  S  L  G  Y  D  I  G  N  D  P  Q  G

                    BstAP     BspH1                    BstX1                  Stu1          Ahd1
                        |         |                        |                     |             |
               GAAGCAGAATTTGCCCGCATCATGAGCATTGTGGACCCCAACCGCCTGGGGGTAGTGACATTCCAGGCCTTCATTGACTTCATGTCCCGCGAGACAGCCG
         3001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
               CTTCGTCTTAAACGGGCGTAGTACTCGTAACACCTGGGGTTGGCGGACCCCCATCACTGTAAGGTCCGGAAGTAACTGAAGTACAGGGCGCTCTGTCGGC
Actinin      > E  A  E  F  A  R  I  M  S  I  V  D  P  N  R  L  G  V  V  T  F  Q  A  F  I  D  F  M  S  R  E  T  A  D

                            PflF1PflM1                 BseY1                  Nco1
                                |    |                     |                     |
               ACACAGATACAGCAGACCAAGTCATGGCTTCCTTCAAGATCCTGGCTGGGGACAAGAACTACATTACCATGGACGAGCTGCGCCGCGAGCTGCCACCCGA
         3101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
               TGTGTCTATGTCGTCTGGTTCAGTACCGAAGGAAGTTCTAGGACCGACCCCTGTTCTTGATGTAATGGTACCTGCTCGACGCGGCGCTCGACGGTGGGCT
Actinin      >   T  D  T  A  D  Q  V  M  A  S  F  K  I  L  A  G  D  K  N  Y  I  T  M  D  E  L  R  R  E  L  P  P  D
```

```
                                                                                    Ahd1
           BtgZ1      Sca1                                                        BspLU|                 BpuE1
               |         |                                                            ||                      |
               CCAGGCTGAGTACTGCATCGCGCGGATGGCCCCCTACACCGGCCCCGACTCCGTGCCAGGTGCTCTGGACTACATGTCCTTCTCCACGGCGCTGTACGGC
         3201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
               GGTCCGACTCATGACGTAGCGCGCCTACCGGGGGATGTGGCCGGGGCTGAGGCACGGTCCACGAGACCTGATGTACAGGAAGAGGTGCCGCGACATGCCG
Actinin      >  Q  A  E  Y  C  I  A  R  M  A  P  Y  T  G  P  D  S  V  P  G  A  L  D  Y  M  S  F  S  T  A  L  Y  G

                                                             BamH1
                                                            Sma1 |
                                                           Apa1| |
                                                      PspOM   || |
                                                      Sac2|   || |                SpDon
                              EcoR1      Sal1      Kpn1  ||   || |               Ale1 |
                       Hind3BstB1 |     Pst1| Acc65   |  ||   || |  Age1       Nco1 | |
                           |    | |        ||     |   |  ||   || |     |          | | |
               GAGAGTGACCTCAAGCTTCGAATTCTGCAGTCGACGGTACCGCGGGCCCGGGATCCACCGGTCGCCACCATGGTGAGCGAGCTGATTAAGGAGAACATGC
         3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
               CTCTCACTGGAGTTCGAAGCTTAAGACGTCAGCTGCCATGGCGCCCGGGCCCTAGGTGGCCAGCGGTGGTACCACTCGCTCGACTAATTCCTCTTGTACG
Actinin/mKate2 E  S  D  L  K  L  R  I  L  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

                    BsrG1                                ApaL1                     SpAcc
                        |                                    |                         |
               ACATGAAGCTGTACATGGAGGGCACCGTGAACAACCACCACTTCAAGTGCACATCCGAGGGCGAAGGCAAGCCCTACGAGGGCACCCAGACCATGAGAAT
         3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
               TGTACTTCGACATGTACCTCCCGTGGCACTTGTTGGTGGTGAAGTTCACGTGTAGGCTCCCGCTTCCGTTCGGGATGCTCCCGTGGGTCTGGTACTCTTA
mKate2       >   M  K  L  Y  M  E  G  T  V  N  N  H  H  F  K  C  T  S  E  G  E  G  K  P  Y  E  G  T  Q  T  M  R  I

               CAAGGCGGTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGCTACCAGCTTCATGTACGGCAGCAAAACCTTCATCAACCACACCCAGGGCATC
         3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
               GTTCCGCCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTCGAAGTACATGCCGTCGTTTTGGAAGTAGTTGGTGTGGGTCCCGTAG
mKate2       >  K  A  V  E  G  G  P  L  P  F  A  F  D  I  L  A  T  S  F  M  Y  G  S  K  T  F  I  N  H  T  Q  G  I

                                                SpDon                          Bbs1             Bpm1
                                                    |                             |                |
               CCCGACTTCTTTAAGCAGTCCTTCCCCGAGGGCTTCACATGGGAGAGAGTCACCACATACGAAGACGGGGGCGTGCTGACCGCTACCCAGGACACCAGCC
         3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
               GGGCTGAAGAAATTCGTCAGGAAGGGGCTCCCGAAGTGTACCCTCTCTCAGTGGTGTATGCTTCTGCCCCCGCACGACTGGCGATGGGTCCTGTGGTCGG
mKate2       > P  D  F  F  K  Q  S  F  P  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
```

```
                                                                                                              Bsa1
                                                                                                  BseY1    Stu1  |
                                                                                                      |       |  |
               TCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACTTCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCTC
         3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
               AGGTCCTGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCCACTTGAAGGGTAGGTTGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCTCCGGAG
mKate2       >   Q  D  G  C  L  I  Y  N  V  K  I  R  G  V  N  F  P  S  N  G  P  V  M  Q  K  K  T  L  G  W  E  A  S

                                               Bgl1          Bgl1       BssS1          Eco57
                                                  |             |           |              |
               CACCGAGACCCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAGCCGACATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACTTGAAGACC
         3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
               GTGGCTCTGGGACATGGGGCGACTGCCGCCGGACCTTCCGTCTCGGCTGTACCGGGACTTCGAGCACCCGCCCCCGGTGGACTAGACGTTGAACTTCTGG
mKate2       >  T  E  T  L  Y  P  A  D  G  G  L  E  G  R  A  D  M  A  L  K  L  V  G  G  G  H  L  I  C  N  L  K  T

                                                                                Bbs1
            Bbs1          BpuE1                                             SpAcc  |               Bsa1
               |              |                                                 |  |                  |
               ACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGCGTCTACTATGTGGACAGAAGACTGGAAAGAATCAAGGAGGCCGACAAAGAGACCT
         3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
               TGTATGTCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCGCAGATGATACACCTGTCTTCTGACCTTTCTTAGTTCCTCCGGCTGTTTCTCTGGA
mKate2       > T  Y  R  S  K  K  P  A  K  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

                                                                                 Not1
                                                                                 Eag1
          PshA1       BssS1 Dra3      Msc1  AlwN1          SpAcc          Bmr1 BsrB1|      Xba1   BsaB1
              |           |    |         |      |              |             |     ||         |       |
               ACGTCGAGCAGCACGAGGTGGCTGTGGCCAGATACTGCGACCTCCCTAGCAAACTGGGGCACAGATGAGCGGCCGCGACTCTAGATCATAATCAGCCATA
         4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
               TGCAGCTCGTCGTGCTCCACCGACACCGGTCTATGACGCTGGAGGGATCGTTTGACCCCGTGTCTACTCGCCGGCGCTGAGATCTAGTATTAGTCGGTAT
mKate2       >   V  E  Q  H  E  V  A  V  A  R  Y  C  D  L  P  S  K  L  G  H  R  *

                                                                                        Bsm1
                               SpDon   Dra1                                            Mfe1|        Hpa1
                                   |      |                                               ||           |
               CCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTAT
         4101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
               GGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATA
```

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  polyA    Psi1      polyA                            polyA            Bts1 Bsm1
      |       |          |                            |               |    |
      TGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATC
4201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
      ACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAG

          Afl2         SpDon        Ssp1
             |             |           |
      AATGTATCTTAAGGCGTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATC
4301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
      TTACATAGAATTCCGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAG

                Psi1                                                         BsaXb                 Drd1
                   |                                                             |                    |
      GGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACG
4401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
      CCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGC

                                            BtgZ1
       BsaXa                                Dra3|
           |                                   ||
      TCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCG
4501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
      AGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGC

                                               Nae1
      SpAcc                                 NgoM4 |                                    BsrB1
          |                                     | |                                        |
      GAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCG
4601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
      CTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGC

      CTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGC
4701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
      GACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACG
```

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                                                        BciV1
                                                     BspH1  |
                       polyA                       BsrB1 |  |                            Ssp1  Ear1
                           |                           | |  |                               |     |
      GCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAA
4801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
      CGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCCTT


                                                                                                    Nsi1
                                                                                                  Sph1 |
                            Eci1                                                                 BfrB1 |
       Bsu36              Pvu2 |                                      BseY1                   BstAP  | |
           |                 | |                                          |                       |  | |
      GAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATC
4901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
      CTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAG


                                                                        Nsi1
                                                                      Sph1 |
                                                                     BfrB1 |
                SexA1                     BseY1                   BstAP  | |                       Eci1
                    |                         |                       |  | |                          |
      TCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCC
5001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
      AGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGG


                              Eci1
                    Eci1     Bmr1|       Eci1            Nco1                  polyA
                       |        ||          |               |                       |
      CCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCC
5101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
      GGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGG
```

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                                                  Avr2
   Sfi1                                          Stu1|
   Bgl1                    SpDon             BseR1  ||              Cla1              BsaB1
      |                        |                 |  ||                 |                  |
      TCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATG
5201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
      AGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTAC

              BspM1
              BfuA1               Eag1                                       Bmr1
                  |                  |                                          |
      ATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCG
5301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5400
      TAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGC

                            Nar1
                           Kas1|                       Drd1
                              ||                          |
      CCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATC
5401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5500
      GGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAG

                                  Pvu2
          Msc1                Fsp1   |       PflF1                       Eco57
             |                   |   |           |                           |
      GTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGAT
5501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5600
      CACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCTA

                                                                                                  BtgZ1
                                                                                               BspM1  |
                SpDon                     BciV1         BsrD1                              BfuA1  |
                    |                             |             |                                  |  |
      CTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACC
5601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5700
      GAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGG
```

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                                                                        Sap1
                                                                        Ear1
                                                                           |
      ACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGC
5701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5800
      TGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCG

   BpuE1                         Sph1                       Nco1               BtgZ1
       |                            |                          |                   |
      CGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGC
5801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5900
      GCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCG

                               BseY1
                              Nae1 |                                              Sap1
                           NgoM4 | |        Rsr2         Eci1                     Ear1
                               | | |           |            |                        |
      CGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCG
5901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6000
      GCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGC

                                          BtgZ1
     Eco57         BssS1                BsrB1 |                                               BsrB1
         |             |                    | |                                                   |
      AATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACT
6001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6100
      TTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGA

                                             BssS1
                                             BspM1
         BstB1                               BfuA1                      SpAcc
             |                                   |                          |
      CTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTT
6101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6200
      GACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAA
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             Nae1                                                   Bpm1
          NgoM4 |                                               SpAcc  |
           Bpm1 |                                                Avr2  |
              | |                                                   |  |
      TCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAAT
6201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6300
      AGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTA

                            polyA        polyA
                                |            |
      ACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGG
6301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6400
      TGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACC

                 Bsa1
                    |
      CACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGC
6401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6500
      GTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCG

                            BstAP
                            AlwN1      Bsu36                            Dra1               Dra1
                                |          |                               |                  |
      TCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTA
6501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6600
      AGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGAT

                         BspH1
                             |
      GGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCT
6601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6700
      CCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGA
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                     BpuE1
                         |
      TGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTT
6701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6800
      ACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAA


   Eco57                                             SpAcc
       |                                                 |
      TTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCC
6801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6900
      AAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGG


                                    AlwN1                 BpuE1
                                        |                     |
      TACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAG
6901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7000
      ATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTC


                               ApaL1     BseY1                                             SpAcc
                                   |         |                                                 |
      GCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAA
7001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7100
      CGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTT


                                               BciV1
                                            Eci1   |                    BssS1
                                               |   |                        |
      GCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTG
7101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7200
      CGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGAC
```

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             SpAcc                          Drd1            BpuE1               SpAcc     Eci1
                 |                             |                |                   |        |
      GTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAAC
7201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7300
      CATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTG


                                              SpDon
                                             BspLU|                                                 BfrB1
                                                 ||                                                     |
      GCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGC
7301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7400
      CGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACG


   Nsi1
      |
      AT
7401  || 7402
      TA
```

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Found:

    Aar1    Aat2   Acc65    Afe1    Afl2    Age1    Ahd1    Ale1   AlwN1    Apa1   ApaL1    Ase1    Avr2   BamH1
    Bbs1   BciV1    Bcl1   BfrB1   BfuA1    Bgl1    Bgl2    Blp1   BmgB1    Bmr1    Bpm1   BpuE1    Bsa1   BsaB1
   BsaXa   BsaXb   BseR1   BseY1    Bsg1    Bsm1   BspE1   BspH1   BspLU   BspM1   BsrB1   BsrD1   BsrG1   BssS1
   BstAP   BstB1   BstX1   Bsu36   BtgZ1    Bts1    _Chi    Cla1    Dra1    Dra3    Drd1    Eag1    Ear1    Eci1
    Ecl2   Eco57   EcoN1   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   SanD1    Sap1    Sbf1    Sca1   SexA1    Sfi1    Sma1   SnaB1   SpAcc   SpDon
    Sph1    Ssp1    Stu1    Xba1    Xcm1    Xho1    Xmn1

Unique:

   Acc65    Afe1    Afl2    Age1    Ase1    Bcl1   BsrD1   BsrG1    Bts1    _Chi    Cla1   EcoR1    Fsp1    Hpa1
    Kpn1    Mfe1    Nde1    Nhe1    Not1   PflM1    Pml1   PshA1    Sac2    Sal1    Sbf1    Sca1   SexA1    Sfi1
   SnaB1    Xba1    Xho1    Xmn1

Not found:

    Acl1    Asc1   AsiS1   Bae1a   Bae1b   BbvC1   Bcg1a   Bcg1b   Bpu10   BsiW1   BsmB1   BssH2   BstE2   BstZ1
   BxatB   BxatL   BxatR   BxatP    EcoK   EcoRV   FCatB   FCatL   FCatR   FCatP   ScFRT    Fse1   FspA1   I_Ceu
    loxP    Mlu1    Nru1    Pac1    Pme1    Pvu1   R4atB   R4atL   R4atP   R4atR    Sgf1   SgrA1    Spe1    Srf1
    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
```