pTagRFP-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). TagRFP 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

                        Xho1    Hind3
              BpuE1 Bgl2   |   Sac1 |                                                   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
```

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                                 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                 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|   || |
                              EcoR1      Sal1      Kpn1  ||   || |               Ale1      Sap1
                       Hind3BstB1 |     Pst1| Acc65   |  ||   || |  Age1       Nco1 |      Ear1
                           |    | |        ||     |   |  ||   || |     |          | |         |
               GAGAGTGACCTCAAGCTTCGAATTCTGCAGTCGACGGTACCGCGGGCCCGGGATCCACCGGTCGCCACCATGGTGTCTAAGGGCGAAGAGCTGATTAAGG
         3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
               CTCTCACTGGAGTTCGAAGCTTAAGACGTCAGCTGCCATGGCGCCCGGGCCCTAGGTGGCCAGCGGTGGTACCACAGATTCCCGCTTCTCGACTAATTCC
Actinin/TagRFP>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  K  G  E  E  L  I  K  E

                             BsrG1                                ApaL1                     SpAcc
                                 |                                    |                         |
               AGAACATGCACATGAAGCTGTACATGGAGGGCACCGTGAACAACCACCACTTCAAGTGCACATCCGAGGGCGAAGGCAAGCCCTACGAGGGCACCCAGAC
         3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
               TCTTGTACGTGTACTTCGACATGTACCTCCCGTGGCACTTGTTGGTGGTGAAGTTCACGTGTAGGCTCCCGCTTCCGTTCGGGATGCTCCCGTGGGTCTG
TagRFP       >   N  M  H  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

               CATGAGAATCAAGGTGGTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGCTACCAGCTTCATGTACGGCAGCAGAACCTTCATCAACCACACC
         3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
               GTACTCTTAGTTCCACCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTCGAAGTACATGCCGTCGTCTTGGAAGTAGTTGGTGTGG
TagRFP       >  M  R  I  K  V  V  E  G  G  P  L  P  F  A  F  D  I  L  A  T  S  F  M  Y  G  S  R  T  F  I  N  H  T

                                             Bsu36       SpDon                          Bbs1             Bpm1
                                                 |           |                             |                |
               CAGGGCATCCCCGACTTCTTTAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACATACGAAGACGGGGGCGTGCTGACCGCTACCCAGG
         3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
               GTCCCGTAGGGGCTGAAGAAATTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGGTGTATGCTTCTGCCCCCGCACGACTGGCGATGGGTCC
TagRFP       > Q  G  I  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
```

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                                                            SpDon                                          BseY1
                                                                |                                              |
               ACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACTTCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTG
         3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
               TGTGGTCGGAGGTCCTGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCCACTTGAAGGGTAGGTTGCCGGGACACTACGTCTTCTTTTGTGAGCCGAC
TagRFP       >   T  S  L  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

                                                        Bgl1                     BssS1          Eco57
                                                           |                         |              |
               GGAGGCCAACACCGAGATGCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAAGCGACATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAAC
         3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
               CCTCCGGTTGTGGCTCTACGACATGGGGCGACTGCCGCCGGACCTTCCGTCTTCGCTGTACCGGGACTTCGAGCACCCGCCCCCGGTGGACTAGACGTTG
TagRFP       >  E  A  N  T  E  M  L  Y  P  A  D  G  G  L  E  G  R  S  D  M  A  L  K  L  V  G  G  G  H  L  I  C  N

                                                                                     SpAcc
                                   BpuE1                                             PflM1                  Bsa1
                                       |                                                 |                     |
               TTCAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGCGTCTACTATGTGGACCACAGACTGGAAAGAATCAAGGAGGCCGACA
         3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
               AAGTTCTGGTGTATGTCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCGCAGATGATACACCTGGTGTCTGACCTTTCTTAGTTCCTCCGGCTGT
TagRFP       > F  K  T  T  Y  R  S  K  K  P  A  K  N  L  K  M  P  G  V  Y  Y  V  D  H  R  L  E  R  I  K  E  A  D  K

                                                                                                Not1
                                                                                                Eag1
                   PshA1       BssS1 Dra3      Msc1  AlwN1          SpAcc          Bmr1       BsrB1|      Xba1
                       |           |    |         |      |              |             |           ||         |
               AAGAGACCTACGTCGAGCAGCACGAGGTGGCTGTGGCCAGATACTGCGACCTCCCTAGCAAACTGGGGCACAAACTTAATTGAGCGGCCGCGACTCTAGA
         4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
               TTCTCTGGATGCAGCTCGTCGTGCTCCACCGACACCGGTCTATGACGCTGGAGGGATCGTTTGACCCCGTGTTTGAATTAACTCGCCGGCGCTGAGATCT
TagRFP       >   E  T  Y  V  E  Q  H  E  V  A  V  A  R  Y  C  D  L  P  S  K  L  G  H  K  L  N  *

                                                                                                       Bsm1
             BsaB1                            SpDon   Dra1                                            Mfe1|
                 |                                |      |                                               ||
               TCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGT
         4101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
               AGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACA
```

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      Hpa1       polyA    Psi1      polyA                        polyA            Bts1 Bsm1
         |           |       |          |                            |               |    |
      TGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGT
4201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
      ACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGACGTAAGATCAACACCA

                         Afl2         SpDon        Ssp1
                            |             |           |
      TTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAAC
4301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
      AACAGGTTTGAGTAGTTACATAGAATTCCGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTG

                               Psi1                                                         BsaXb
                                  |                                                             |
      CAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGA
4401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
      GTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCT

                                                           BtgZ1
              Drd1    BsaXa                                Dra3|
                 |        |                                   ||
      ACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCG
4501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
      TGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCCAGCTCCACGGC

                                                              Nae1
                     SpAcc                                 NgoM4 |
                         |                                     | |
      TAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGA
4601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
      ATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCT

  BsrB1
      |
      GCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTT
4701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
      CGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAA
```

```
                                                                       BciV1
                                                                    BspH1  |
                                      polyA                       BsrB1 |  |
                                          |                           | |  |
      TTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATA
4801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
      AAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTAT

                                           Eci1
    Ssp1  Ear1        Bsu36              Pvu2 |                                      BseY1
       |     |            |                 | |                                          |
      ATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTA
4901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
      TATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCAT

               Nsi1                                                                    Nsi1
             Sph1 |                                                                  Sph1 |
            BfrB1 |                                                                 BfrB1 |
         BstAP  | |            SexA1                     BseY1                   BstAP  | |
             |  | |                |                         |                       |  | |
      TGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGC
5001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
      ACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCG

                                             Eci1
              Eci1                 Eci1     Bmr1|       Eci1            Nco1                   polyA
                 |                    |        ||          |               |                       |
      AACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCA
5101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
      TTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAAATAAATACGT

                                                                 Avr2
                  Sfi1                                          Stu1|
                  Bgl1                    SpDon             BseR1  ||              Cla1
                     |                        |                 |  ||                 |
      GAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGA
5201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
      CTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCTACT
```

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                             BspM1
 BsaB1                       BfuA1          Eag1                                       Bmr1
     |                           |                  |                                          |
      GGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCG
5301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5400
      CCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGC

                                           Nar1
                                          Kas1|                       Drd1
                                             ||                          |
      GCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGA
5401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5500
      CGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCT

                                                 Pvu2
                         Msc1                Fsp1   |       PflF1                       Eco57
                            |                   |   |           |                           |
      GGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAA
5501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5600
      CCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTT

                               SpDon                         BciV1         BsrD1
                                   |                             |             |
      GTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTA
5601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5700
      CACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGAT

             BtgZ1
          BspM1  |                                                                     Sap1
          BfuA1  |                                                                     Ear1
              |  |                                                                        |
      CCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCA
5701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5800
      GGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGT

                  BpuE1                         Sph1                       Nco1               BtgZ1
                      |                            |                          |                   |
      GGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATC
5801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5900
      CCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAG
```

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                                              BseY1
                                             Nae1 |                                              Sap1
                                          NgoM4 | |        Rsr2         Eci1                     Ear1
                                              | | |           |            |                        |
      ATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTG
5901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6000
      TACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAACGAC

                                                         BtgZ1
                    Eco57         BssS1                BsrB1 |
                        |             |                    | |
      AAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTT
6001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6100
      TTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAA

                                                            BssS1
                                                            BspM1
         BsrB1          BstB1                               BfuA1                      SpAcc
             |              |                                   |                          |
      CTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGG
6101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6200
      GAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACC

                            Nae1                                                   Bpm1
                         NgoM4 |                                               SpAcc  |
                          Bpm1 |                                                Avr2  |
                             | |                                                   |  |
      GCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAAC
6201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6300
      CGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTG

                                           polyA        polyA
                                               |            |
      ACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTT
6301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6400
      TGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAA
```

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                                Bsa1
                                   |
      CGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGG
6401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6500
      GCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCC

                                           BstAP
 SpDon                                     AlwN1      Bsu36                            Dra1
     |                                         |          |                               |
      GTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTA
6501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6600
      CACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAAT

      Dra1                              BspH1
         |                                  |
      ATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAG
6601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6700
      TAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTC

                                    BpuE1
                                        |
      ATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAG
6701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6800
      TAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTC

                  Eco57                                               SpAcc
                      |                                                   |
      AGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAA
6801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6900
      TCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTT

                                                   AlwN1                BpuE1
                                                       |                         |
      CTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGA
6901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7000
      GAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCT
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                                              ApaL1     BseY1
                                                  |         |
      TAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGC
7001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7100
      ATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCG

                                                              BciV1
      SpAcc                                                Eci1   |                    BssS1
          |                                                   |   |                        |
      GTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCC
7101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7200
      CACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGG

                            SpAcc                          Drd1            BpuE1               SpAcc
                                |                             |                |                   |
      AGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGG
7201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7300
      TCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCCGCCTCGGATACC

                                                             SpDon
     Eci1                                                   BspLU|
        |                                                       ||
      AAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTT
7301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||| 7368
      TTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAA
```

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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
   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    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
    EcoK   EcoRV   ScFRT    Fse1   FspA1   I_Ceu    loxP    Mlu1    Nru1    Pac1    Pme1    Pvu1    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
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