pFusionRed-vinculin vector restriction map

The data has not been verified by restriction digestion with each enzyme listed and does not take into account possible methylation sites.

Enzymes that recognize unambiguous sequences less than 6 base pairs long are not included – for the more complete enzyme list please refer to the Table of restriction sites.

Unique sites are shown in bold blue. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site).

FusionRed amino acids are shown in red, Vinculin 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
```

```
                                                          Aat2                                             Eci1
                                                             |                                                |
               TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
          401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 500
               ATCGCCAAACTGAGTGCCCCTAAAGGTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT


                                                                                                      Nhe1
                                                                                                         |
               ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCACCG
          501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
               TGTTGAGGCGGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGTGGC


                                                                          Bpm1       Dra3
                                          Pvu1                          Bgl2 |  SexA1   |     BssS1
                                             |                             | |      |   |         |
               CCACCATGCCAGTGTTTCATACGCGCACGATCGAGAGCATCCTGGAGCCGGTGGCACAGCAGATCTCCCACCTGGTGATAATGCACGAGGAGGGCGAGGT
          601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
               GGTGGTACGGTCACAAAGTATGCGCGTGCTAGCTCTCGTAGGACCTCGGCCACCGTGTCGTCTAGAGGGTGGACCACTATTACGTGCTCCTCCCGCTCCA
Vinculin     >      M  P  V  F  H  T  R  T  I  E  S  I  L  E  P  V  A  Q  Q  I  S  H  L  V  I  M  H  E  E  G  E  V

                                                              Eag1
            BseR1                                     Bgl1   |          Bsg1
                |                                            |   |             |
               GGACGGCAAAGCCATTCCTGACCTCACCGCGCCCGTGGCCGCCGTGCAGGCGGCCGTCAGCAACCTCGTCCGGGTTGGAAAAGAGACTGTTCAAACCACT
          701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
               CCTGCCGTTTCGGTAAGGACTGGAGTGGCGCGGGCACCGGCGGCACGTCCGCCGGCAGTCGTTGGAGCAGGCCCAACCTTTTCTCTGACAAGTTTGGTGA
Vinculin     >  D  G  K  A  I  P  D  L  T  A  P  V  A  A  V  Q  A  A  V  S  N  L  V  R  V  G  K  E  T  V  Q  T  T


                     Ear1             _Chi          polyA           Bsm1  Hind3    Eco57
                        |                |              |              |      |        |
               GAGGATCAGATTTTGAAGAGAGATATGCCACCAGCATTTATTAAGGTTGAGAATGCTTGCACCAAGCTTGTCCAGGCAGCTCAGATGCTTCAGTCAGACC
          801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
               CTCCTAGTCTAAAACTTCTCTCTATACGGTGGTCGTAAATAATTCCAACTCTTACGAACGTGGTTCGAACAGGTCCGTCGAGTCTACGAAGTCAGTCTGG
Vinculin     > E  D  Q  I  L  K  R  D  M  P  P  A  F  I  K  V  E  N  A  C  T  K  L  V  Q  A  A  Q  M  L  Q  S  D  P
```

```
                           Xho1                                                          SpDon       Bpu10
                      AlwN1   |                                                       BspM1  |       BbvC1
                          |   |                                                           |  |           |
               CTTACTCAGTGCCTGCTCGAGATTATCTAATTGATGGGTCAAGGGGCATCCTCTCTGGAACATCAGACCTGCTCCTTACCTTCGATGAGGCTGAGGTCCG
          901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
               GAATGAGTCACGGACGAGCTCTAATAGATTAACTACCCAGTTCCCCGTAGGAGAGACCTTGTAGTCTGGACGAGGAATGGAAGCTACTCCGACTCCAGGC
Vinculin     >   Y  S  V  P  A  R  D  Y  L  I  D  G  S  R  G  I  L  S  G  T  S  D  L  L  L  T  F  D  E  A  E  V  R

                                                                        SpAcc
                                                                            |
               TAAAATTATTAGAGTTTGCAAAGGAATTTTGGAATATCTTACAGTGGCAGAGGTGGTGGAGACTATGGAAGATTTGGTCACTTACACAAAGAATCTTGGG
         1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
               ATTTTAATAATCTCAAACGTTTCCTTAAAACCTTATAGAATGTCACCGTCTCCACCACCTCTGATACCTTCTAAACCAGTGAATGTGTTTCTTAGAACCC
Vinculin     >  K  I  I  R  V  C  K  G  I  L  E  Y  L  T  V  A  E  V  V  E  T  M  E  D  L  V  T  Y  T  K  N  L  G

                                                             Sac1
                              Msc1                         Ecl2 |  SpDon        Dra3
                                 |                            | |      |           |
               CCAGGAATGACTAAGATGGCCAAGATGATTGACGAGAGACAGCAGGAGCTCACTCACCAGGAGCACCGAGTGATGTTGGTGAACTCGATGAACACCGTGA
         1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
               GGTCCTTACTGATTCTACCGGTTCTACTAACTGCTCTCTGTCGTCCTCGAGTGAGTGGTCCTCGTGGCTCACTACAACCACTTGAGCTACTTGTGGCACT
Vinculin     > P  G  M  T  K  M  A  K  M  I  D  E  R  Q  Q  E  L  T  H  Q  E  H  R  V  M  L  V  N  S  M  N  T  V  K

                                     SpAcc                                               Hind3  Dra1
                                         |                                                   |     |
               AAGAGTTGCTGCCAGTTCTCATTTCAGCTATGAAGATTTTTGTAACAACTAAAAACTCAAAAAACCAAGGCATAGAGGAAGCTTTAAAAAATCGCAATTT
         1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
               TTCTCAACGACGGTCAAGAGTAAAGTCGATACTTCTAAAAACATTGTTGATTTTTGAGTTTTTTGGTTCCGTATCTCCTTCGAAATTTTTTAGCGTTAAA
Vinculin     >   E  L  L  P  V  L  I  S  A  M  K  I  F  V  T  T  K  N  S  K  N  Q  G  I  E  E  A  L  K  N  R  N  F

               Xba1
              SpAcc                   Ase1                         SpDon                                    Ear1
                  |                      |                             |                                        |
               TACTCTAGAAAAAATGAGTGCTGAAATTAATGAGATAATTCGTGTGTTACAACTCACCTCTTGGGATGAAGATGCCTGGGCCAGCAAGGACACTGAAGCC
         1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
               ATGAGATCTTTTTTACTCACGACTTTAATTACTCTATTAAGCACACAATGTTGAGTGGAGAACCCTACTTCTACGGACCCGGTCGTTCCTGTGACTTCGG
Vinculin     >  T  L  E  K  M  S  A  E  I  N  E  I  I  R  V  L  Q  L  T  S  W  D  E  D  A  W  A  S  K  D  T  E  A
```

```
                        Eco57      SpAcc                    PflM1                        SpAcc    SpDon
                            |          |                        |                            |        |
               ATGAAGAGAGCATTGGCCTCCATAGACTCCAAACTGAACCAGGCCAAAGGTTGGCTCCGTGACCCTAGTGCCTCCCCAGGGGATGCTGGTGAGCAGGCCA
         1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
               TACTTCTCTCGTAACCGGAGGTATCTGAGGTTTGACTTGGTCCGGTTTCCAACCGAGGCACTGGGATCACGGAGGGGTCCCCTACGACCACTCGTCCGGT
Vinculin     > M  K  R  A  L  A  S  I  D  S  K  L  N  Q  A  K  G  W  L  R  D  P  S  A  S  P  G  D  A  G  E  Q  A  I

                  Bgl2         SpAcc                                       Bsg1
                     |             |                                          |
               TCAGACAGATCTTAGATGAAGCTGGAAAAGTTGGTGAACTCTGTGCAGGCAAAGAACGCAGGGAGATTCTGGGAACTTGCAAAATGCTAGGGCAGATGAC
         1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
               AGTCTGTCTAGAATCTACTTCGACCTTTTCAACCACTTGAGACACGTCCGTTTCTTGCGTCCCTCTAAGACCCTTGAACGTTTTACGATCCCGTCTACTG
Vinculin     >   R  Q  I  L  D  E  A  G  K  V  G  E  L  C  A  G  K  E  R  R  E  I  L  G  T  C  K  M  L  G  Q  M  T

                                                     SgrA1
            Bcl1                             BamH1    Age1   Msc1   BspM1 Blp1              AlwN1
               |                                 |       |      |       |    |                  |
               TGATCAAGTGGCTGACCTCCGTGCCAGAGGACAAGGATCCTCACCGGTGGCCATGCAGAAAGCTCAGCAGGTATCTCAGGGTCTGGATGTGCTCACAGCA
         1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
               ACTAGTTCACCGACTGGAGGCACGGTCTCCTGTTCCTAGGAGTGGCCACCGGTACGTCTTTCGAGTCGTCCATAGAGTCCCAGACCTACACGAGTGTCGT
Vinculin     >  D  Q  V  A  D  L  R  A  R  G  Q  G  S  S  P  V  A  M  Q  K  A  Q  Q  V  S  Q  G  L  D  V  L  T  A

                                                               BsrD1           Cla1
                                                                   |              |
               AAAGTGGAAAATGCAGCTCGCAAGCTGGAAGCCATGACCAACTCAAAGCAGAGCATTGCAAAGAAGATCGATGCTGCTCAGAACTGGCTTGCAGATCCAA
         1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
               TTTCACCTTTTACGTCGAGCGTTCGACCTTCGGTACTGGTTGAGTTTCGTCTCGTAACGTTTCTTCTAGCTACGACGAGTCTTGACCGAACGTCTAGGTT
Vinculin     > K  V  E  N  A  A  R  K  L  E  A  M  T  N  S  K  Q  S  I  A  K  K  I  D  A  A  Q  N  W  L  A  D  P  N

                        Sap1
             PflM1      Ear1                                              Eco57         SpAcc
                 |         |                                                  |             |
               ATGGTGGACCGGAAGGAGAAGAGCAGATTCGAGGTGCTTTGGCTGAAGCTCGGAAAATAGCAGAATTATGTGATGATCCTAAAGAAAGAGATGACATTCT
         1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
               TACCACCTGGCCTTCCTCTTCTCGTCTAAGCTCCACGAAACCGACTTCGAGCCTTTTATCGTCTTAATACACTACTAGGATTTCTTTCTCTACTGTAAGA
Vinculin     >   G  G  P  E  G  E  E  Q  I  R  G  A  L  A  E  A  R  K  I  A  E  L  C  D  D  P  K  E  R  D  D  I  L
```

```
                                                        SpAcc        Bbs1
                                                      Bgl2  |       Bpm1|                   Xho1       Msc1
                                                         |  |          ||                      |          |
               ACGTTCCCTTGGGGAAATATCTGCTCTGACTTCTAAATTAGCAGATCTACGAAGACAGGGGAAAGGAGATTCTCCAGAGGCTCGAGCCTTGGCCAAACAG
         1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
               TGCAAGGGAACCCCTTTATAGACGAGACTGAAGATTTAATCGTCTAGATGCTTCTGTCCCCTTTCCTCTAAGAGGTCTCCGAGCTCGGAACCGGTTTGTC
Vinculin     >  R  S  L  G  E  I  S  A  L  T  S  K  L  A  D  L  R  R  Q  G  K  G  D  S  P  E  A  R  A  L  A  K  Q

                               BstAP
               Msc1            AlwN1   BspM1                                         BsrG1
          BstX1   |         Pst1   | Pst1  |         Xcm1   Msc1                    Pvu2 |
              |   |            |   |    |  |            |      |                       | |
               GTGGCCACGGCCCTGCAGAACCTGCAGACCAAAACCAACCGGGCTGTGGCCAACAGCAGACCGGCCAAAGCAGCTGTACACCTTGAGGGCAAGATTGAGC
         2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
               CACCGGTGCCGGGACGTCTTGGACGTCTGGTTTTGGTTGGCCCGACACCGGTTGTCGTCTGGCCGGTTTCGTCGACATGTGGAACTCCCGTTCTAACTCG
Vinculin     > V  A  T  A  L  Q  N  L  Q  T  K  T  N  R  A  V  A  N  S  R  P  A  K  A  A  V  H  L  E  G  K  I  E  Q

             BpuE1 Ale1                              Drd1
                 |    |                                 |
               AAGCACAGCGGTGGATTGATAATCCCACAGTGGATGACCGTGGAGTCGGTCAGGCTGCCATCCGGGGGCTTGTGGCCGAAGGGCATCGTCTGGCTAATGT
         2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
               TTCGTGTCGCCACCTAACTATTAGGGTGTCACCTACTGGCACCTCAGCCAGTCCGACGGTAGGCCCCCGAACACCGGCTTCCCGTAGCAGACCGATTACA
Vinculin     >   A  Q  R  W  I  D  N  P  T  V  D  D  R  G  V  G  Q  A  A  I  R  G  L  V  A  E  G  H  R  L  A  N  V

                                                                               Bgl1
                                                                              Pvu2|
                           Bgl1  Bgl2                             Pvu2   BseY1   ||
                              |     |                                |       |   ||
               TATGATGGGGCCTTATCGGCAAGATCTTCTCGCCAAGTGTGACCGAGTGGACCAGCTGACAGCCCAGCTGGCTGACCTGGCTGCCAGAGGGGAAGGGGAG
         2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
               ATACTACCCCGGAATAGCCGTTCTAGAAGAGCGGTTCACACTGGCTCACCTGGTCGACTGTCGGGTCGACCGACTGGACCGACGGTCTCCCCTTCCCCTC
Vinculin     >  M  M  G  P  Y  R  Q  D  L  L  A  K  C  D  R  V  D  Q  L  T  A  Q  L  A  D  L  A  A  R  G  E  G  E

               Bsu36 BssS1                                                                                   BsaXb
                   |     |                                                                                       |
               AGTCCTCAGGCACGAGCACTTGCATCTCAGCTCCAAGACTCCTTAAAGGATCTAAAAGCTCGGATGCAGGAGGCCATGACTCAGGAAGTGTCAGATGTTT
         2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
               TCAGGAGTCCGTGCTCGTGAACGTAGAGTCGAGGTTCTGAGGAATTTCCTAGATTTTCGAGCCTACGTCCTCCGGTACTGAGTCCTTCACAGTCTACAAA
Vinculin     > S  P  Q  A  R  A  L  A  S  Q  L  Q  D  S  L  K  D  L  K  A  R  M  Q  E  A  M  T  Q  E  V  S  D  V  F
```

```
                                       BsaXa               Nar1               Ear1
                                     Xcm1  | BsaXb Bts1   Kas1|            BsaXa |
                                        |  |     |    |     ||                | |
               TCAGCGATACCACAACTCCCATCAAGCTGTTGGCAGTGGCAGCCACGGCGCCTCCTGATGCGCCTAACAGGGAAGAGGTATTTGATGAGAGGGCAGCTAA
         2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
               AGTCGCTATGGTGTTGAGGGTAGTTCGACAACCGTCACCGTCGGTGCCGCGGAGGACTACGCGGATTGTCCCTTCTCCATAAACTACTCTCCCGTCGATT
Vinculin     >   S  D  T  T  T  P  I  K  L  L  A  V  A  A  T  A  P  P  D  A  P  N  R  E  E  V  F  D  E  R  A  A  N

                                                                                               Xmn1
                              Hind3         Eag1    Bgl1                  polyA                Bsm1    Stu1
                                  |            |       |                      |                   |       |
               CTTTGAAAACCATTCAGGAAAGCTTGGTGCTACGGCCGAGAAGGCGGCTGCGGTTGGTACTGCTAATAAATCAACAGTGGAAGGCATTCAGGCCTCAGTG
         2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
               GAAACTTTTGGTAAGTCCTTTCGAACCACGATGCCGGCTCTTCCGCCGACGCCAACCATGACGATTATTTAGTTGTCACCTTCCGTAAGTCCGGAGTCAC
Vinculin     >  F  E  N  H  S  G  K  L  G  A  T  A  E  K  A  A  A  V  G  T  A  N  K  S  T  V  E  G  I  Q  A  S  V

                  Bbs1                         Bsa1                                             Bsa1
                     |                            |                                                |
               AAGACGGCCCGAGAACTCACACCCCAGGTGGTCTCGGCTGCTCGTATCTTACTTAGGAACCCTGGAAATCAAGCTGCTTATGAACATTTTGAGACCATGA
         2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
               TTCTGCCGGGCTCTTGAGTGTGGGGTCCACCAGAGCCGACGAGCATAGAATGAATCCTTGGGACCTTTAGTTCGACGAATACTTGTAAAACTCTGGTACT
Vinculin     > K  T  A  R  E  L  T  P  Q  V  V  S  A  A  R  I  L  L  R  N  P  G  N  Q  A  A  Y  E  H  F  E  T  M  K

                                                                               Xcm1
                        Cla1                            _Chi              Eco57   |
                           |                               |                  |   |
               AGAACCAGTGGATCGATAATGTTGAAAAAATGACAGGGCTGGTGGACGAAGCCATTGATACCAAATCTCTGTTGGATGCTTCAGAAGAAGCAATTAAAAA
         2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
               TCTTGGTCACCTAGCTATTACAACTTTTTTACTGTCCCGACCACCTGCTTCGGTAACTATGGTTTAGAGACAACCTACGAAGTCTTCTTCGTTAATTTTT
Vinculin     >   N  Q  W  I  D  N  V  E  K  M  T  G  L  V  D  E  A  I  D  T  K  S  L  L  D  A  S  E  E  A  I  K  K

                                        Msc1               AlwN1  BseY1                             BamH1
                                           |                   |      |                                 |
               AGACCTGGACAAGTGCAAGGTAGCTATGGCCAACATTCAGCCTCAGATGCTGGTTGCTGGGGCAACCAGTATTGCTCGTCGGGCCAACCGGATCCTGCTG
         2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
               TCTGGACCTGTTCACGTTCCATCGATACCGGTTGTAAGTCGGAGTCTACGACCAACGACCCCGTTGGTCATAACGAGCAGCCCGGTTGGCCTAGGACGAC
Vinculin     >  D  L  D  K  C  K  V  A  M  A  N  I  Q  P  Q  M  L  V  A  G  A  T  S  I  A  R  R  A  N  R  I  L  L
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              SpAcc
               _Chi                     BamH1              SpAcc                                     Xcm1
                  |                         |                  |                                        |
               GTGGCTAAGAGGGAGGTGGAAAATTCCGAGGATCCCAAGTTCCGTGAGGCTGTGAAAGCTGCCTCTGATGAATTGAGCAAAACCATCTCCCCGATGGTGA
         2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
               CACCGATTCTCCCTCCACCTTTTAAGGCTCCTAGGGTTCAAGGCACTCCGACACTTTCGACGGAGACTACTTAACTCGTTTTGGTAGAGGGGCTACCACT
Vinculin     > V  A  K  R  E  V  E  N  S  E  D  P  K  F  R  E  A  V  K  A  A  S  D  E  L  S  K  T  I  S  P  M  V  M

                                                                                   BamH1
                                     Xmn1          SpAcc                       EcoRV   |             Msc1
                                        |              |                           |   |                |
               TGGATGCAAAAGCTGTGGCTGGAAACATTTCCGACCCTGGACTGCAAAAGAGCTTCCTGGACTCAGGATATCGGATCCTGGGAGCTGTGGCCAAGGTCAG
         3001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
               ACCTACGTTTTCGACACCGACCTTTGTAAAGGCTGGGACCTGACGTTTTCTCGAAGGACCTGAGTCCTATAGCCTAGGACCCTCGACACCGGTTCCAGTC
Vinculin     >   D  A  K  A  V  A  G  N  I  S  D  P  G  L  Q  K  S  F  L  D  S  G  Y  R  I  L  G  A  V  A  K  V  R

                                                                                    T7Ter
                         Bsu36                                                    BseR1 |
                             |                                                        | |
               AGAAGCCTTCCAACCTCAGGAGCCTGACTTCCCGCCGCCTCCACCAGACCTTGAACAACTCCGACTAACAGATGAGCTTGCTCCTCCCAAACCACCTCTG
         3101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
               TCTTCGGAAGGTTGGAGTCCTCGGACTGAAGGGCGGCGGAGGTGGTCTGGAACTTGTTGAGGCTGATTGTCTACTCGAACGAGGAGGGTTTGGTGGAGAC
Vinculin     >  E  A  F  Q  P  Q  E  P  D  F  P  P  P  P  P  D  L  E  Q  L  R  L  T  D  E  L  A  P  P  K  P  P  L

                                      Stu1
                                 Eco57   |
                 SpDon           Avr2|   |                Ear1          Bpu10
                     |              ||   |                   |              |
               CCTGAAGGTGAGGTCCCTCCACCTAGGCCTCCACCACCAGAGGAAAAGGATGAAGAGTTCCCTGAGCAGAAGGCCGGGGAGGTGATTAACCAGCCAATGA
         3201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
               GGACTTCCACTCCAGGGAGGTGGATCCGGAGGTGGTGGTCTCCTTTTCCTACTTCTCAAGGGACTCGTCTTCCGGCCCCTCCACTAATTGGTCGGTTACT
Vinculin     > P  E  G  E  V  P  P  P  R  P  P  P  P  E  E  K  D  E  E  F  P  E  Q  K  A  G  E  V  I  N  Q  P  M  M

                                                                       BsrD1
                                                                     BsrD1 |              BstX1
                                                                         | |                  |
               TGATGGCTGCCAGACAGCTCCATGATGAAGCTCGCAAATGGTCCAGCAAGGGCAATGACATCATTGCAGCAGCCAAGCGCATGGCTCTGCTGATGGCTGA
         3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
               ACTACCGACGGTCTGTCGAGGTACTACTTCGAGCGTTTACCAGGTCGTTCCCGTTACTGTAGTAACGTCGTCGGTTCGCGTACCGAGACGACTACCGACT
Vinculin     >   M  A  A  R  Q  L  H  D  E  A  R  K  W  S  S  K  G  N  D  I  I  A  A  A  K  R  M  A  L  L  M  A  E
```

```
                                            Kpn1
                                          Bts1 |
                       SpDon           Acc65 | |           BtgZ1                     Stu1                    Msc1
                           |               | | |               |                        |                       |
               GATGTCTCGGCTGGTAAGAGGGGGCAGTGGTACCAAGCGGGCACTCATTCAGTGTGCCAAGGACATCGCCAAGGCCTCAGATGAGGTGACTCGGTTGGCC
         3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
               CTACAGAGCCGACCATTCTCCCCCGTCACCATGGTTCGCCCGTGAGTAAGTCACACGGTTCCTGTAGCGGTTCCGGAGTCTACTCCACTGAGCCAACCGG
Vinculin     >  M  S  R  L  V  R  G  G  S  G  T  K  R  A  L  I  Q  C  A  K  D  I  A  K  A  S  D  E  V  T  R  L  A


                                 Bts1
                            ApaL1   |                      EcoN1SpAcc                        BseY1
                                |   |                          |    |                            |
               AAGGAGGTTGCCAAGCAGTGCACAGATAAACGGATTAGAACCAACCTCTTACAGGTATGTGAGCGAATCCCAACCATAAGCACCCAGCTCAAAATCCTGT
         3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
               TTCCTCCAACGGTTCGTCACGTGTCTATTTGCCTAATCTTGGTTGGAGAATGTCCATACACTCGCTTAGGGTTGGTATTCGTGGGTCGAGTTTTAGGACA
Vinculin     > K  E  V  A  K  Q  C  T  D  K  R  I  R  T  N  L  L  Q  V  C  E  R  I  P  T  I  S  T  Q  L  K  I  L  S


                              BstX1
                              BseY1                                   BseR1    Xcm1       SpDon
                                  |                                       |       |           |
               CCACAGTGAAGGCCACCATGCTGGGCCGGACCAACATCAGTGATGAGGAGTCTGAGCAGGCCACAGAGATGCTGGTTCACAATGCCCAGAACCTCATGCA
         3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
               GGTGTCACTTCCGGTGGTACGACCCGGCCTGGTTGTAGTCACTACTCCTCAGACTCGTCCGGTGTCTCTACGACCAAGTGTTACGGGTCTTGGAGTACGT
Vinculin     >   T  V  K  A  T  M  L  G  R  T  N  I  S  D  E  E  S  E  Q  A  T  E  M  L  V  H  N  A  Q  N  L  M  Q


                                                           BstB1     T7Ter
            SpAcc                                         Eco57|     AlwN1     Bts1  BseY1                Acc65
                |                                             ||         |        |      |                    |
               GTCTGTGAAGGAGACTGTGCGGGAAGCTGAAGCTGCTTCAATCAAAATTCGAACAGATGCTGGATTTACACTGCGCTGGGTTAGAAAGACTCCCTGGTAC
         3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
               CAGACACTTCCTCTGACACGCCCTTCGACTTCGACGAAGTTAGTTTTAAGCTTGTCTACGACCTAAATGTGACGCGACCCAATCTTTCTGAGGGACCATG
Vinculin     >  S  V  K  E  T  V  R  E  A  E  A  A  S  I  K  I  R  T  D  A  G  F  T  L  R  W  V  R  K  T  P  W  Y
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```
                                                          BamH1
                                                         Sma1 |
                                                        Apa1| |
                                                   PspOM   || |
                                                   Sac2|   || |                SpDon
                                      Sal1      Kpn1  ||   || |               Ale1 |
           Kpn1  BstX1     EcoR1     Pst1| Acc65   |  ||   || |  Age1       Nco1 | |
              |      |         |        ||     |   |  ||   || |     |          | | |
               CAGTCCGGTGGCAGCGGAATTCTGCAGTCGACGGTACCGCGGGCCCGGGATCCACCGGTCGCCACCATGGTGAGCGAGCTGATTAAGGAGAACATGCCCA
         3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
               GTCAGGCCACCGTCGCCTTAAGACGTCAGCTGCCATGGCGCCCGGGCCCTAGGTGGCCAGCGGTGGTACCACTCGCTCGACTAATTCCTCTTGTACGGGT
Vinculin/    > Q  S  G  G  S  G  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  P  M
FusionRed

                 BsrG1                                ApaL1                     SpAcc
                     |                                    |                         |
               TGAAGCTGTACATGGAGGGCACCGTGAACAACCACCACTTCAAGTGCACATCCGAGGGCGAAGGCAAGCCCTACGAGGGCACCCAGACCATGAGAATCAA
         3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
               ACTTCGACATGTACCTCCCGTGGCACTTGTTGGTGGTGAAGTTCACGTGTAGGCTCCCGCTTCCGTTCGGGATGCTCCCGTGGGTCTGGTACTCTTAGTT
FusionRed    >   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  K

               GGTCGTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGCTACCAGCTTCATGTACGGCAGCAGAACCTTCATCAAGCACCCTCCGGGCATCCCC
         4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
               CCAGCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTCGAAGTACATGCCGTCGTCTTGGAAGTAGTTCGTGGGAGGCCCGTAGGGG
FusionRed    >  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  K  H  P  P  G  I  P

                                 Bsu36       SpDon                          Bbs1             Bpm1
                                     |           |                             |                |
               GACTTCTTTAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACATACGAAGACGGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCC
         4101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
               CTGAAGAAATTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGGTGTATGCTTCTGCCCCCGCACGACTGGCGATGGGTCCTGTGGTCGGAGG
FusionRed    > 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  Q

                                                                                                          BsmB1
                                                         BseY1                                 BseY1    Stu1  |
                                                             |                                     |       |  |
               AGGACGGCTGCCTCATCTACAACGTCAAGGTTAGAGGGGTGAACTTCCCAGCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCTCCAC
         4201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
               TCCTGCCGACGGAGTAGATGTTGCAGTTCCAATCTCCCCACTTGAAGGGTCGGTTGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCTCCGGAGGTG
FusionRed    >   D  G  C  L  I  Y  N  V  K  V  R  G  V  N  F  P  A  N  G  P  V  M  Q  K  K  T  L  G  W  E  A  S  T
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                                            Bgl1                     BssS1          Eco57        Bsa1
                                               |                         |              |           |
               CGAGACGATGTACCCCGCTGACGGCGGCCTGGAAGGCGCATGTGACATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACCTTGAGACCACA
         4301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
               GCTCTGCTACATGGGGCGACTGCCGCCGGACCTTCCGCGTACACTGTACCGGGACTTCGAGCACCCGCCCCCGGTGGACTAGACGTTGGAACTCTGGTGT
FusionRed    >  E  T  M  Y  P  A  D  G  G  L  E  G  A  C  D  M  A  L  K  L  V  G  G  G  H  L  I  C  N  L  E  T  T

                       BpuE1                                             SpAcc
                    BpuE1  |                                             PflM1                  Bsa1       PshA1
                        |  |                                                 |                     |           |
               TACAGATCCAAGAAACCCGCTACGAACCTCAAGATGCCCGGCGTCTACAACGTGGACCACAGACTGGAAAGAATCAAGGAGGCCGACGATGAGACCTACG
         4401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
               ATGTCTAGGTTCTTTGGGCGATGCTTGGAGTTCTACGGGCCGCAGATGTTGCACCTGGTGTCTGACCTTTCTTAGTTCCTCCGGCTGCTACTCTGGATGC
FusionRed    > Y  R  S  K  K  P  A  T  N  L  K  M  P  G  V  Y  N  V  D  H  R  L  E  R  I  K  E  A  D  D  E  T  Y  V

                                                                              Not1
                                                                              Eag1
                   BssS1 Dra3      Msc1                            SpDon    BsrB1|      Xba1   BsaB1
                       |    |         |                                |        ||         |       |
               TCGAGCAGCACGAGGTGGCTGTGGCCAGATACTCTACTGGTGGCGCTGGTGATGGAGGTAAATGAGCGGCCGCGACTCTAGATCATAATCAGCCATACCA
         4501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
               AGCTCGTCGTGCTCCACCGACACCGGTCTATGAGATGACCACCGCGACCACTACCTCCATTTACTCGCCGGCGCTGAGATCTAGTATTAGTCGGTATGGT
FusionRed    >   E  Q  H  E  V  A  V  A  R  Y  S  T  G  G  A  G  D  G  G  K  *

                                                                                     Bsm1
                            SpDon   Dra1                                            Mfe1|        Hpa1       polyA
                                |      |                                               ||           |           |
               CATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGC
         4601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
               GTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACG

                 Psi1      polyA                        polyA            Bts1 Bsm1
                    |          |                            |               |    |
               AGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAAT
         4701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
               TCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTA
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       Afl2         SpDon        Ssp1
          |             |           |
      GTATCTTAAGGCGTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGC
4801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
      CATAGAATTCCGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCG

             Psi1                                                         BsaXb                 Drd1
                |                                                             |                    |
      AAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCA
4901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
      TTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGT

                                         BtgZ1
    BsaXa                                Dra3|
        |                                   ||
      AAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAA
5001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
      TTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTT

                                            Nae1
   SpAcc                                 NgoM4 |                                    BsrB1
       |                                     | |                                        |
      CCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTG
5101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
      GGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGAC


      GCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCG
5201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
      CGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGC

                                                     BciV1
                                                  BspH1  |
                    polyA                       BsrB1 |  |                            Ssp1  Ear1
                        |                           | |  |                               |     |
      GAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAG
5301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5400
      CTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTC
```

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                                                                                                 Nsi1
                                                                                               Sph1 |
                         Eci1                                                                 BfrB1 |
    Bsu36              Pvu2 |                                      BseY1                   BstAP  | |
        |                 | |                                          |                       |  | |
      TCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCA
5401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5500
      AGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGT

                                                                     Nsi1
                                                                   Sph1 |
                                                                  BfrB1 |
             SexA1                     BseY1                   BstAP  | |                       Eci1
                 |                         |                       |  | |                          |
      ATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCT
5501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5600
      TAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGA

                           Eci1                                                                     Sfi1
                 Eci1     Bmr1|       Eci1            Nco1                   polyA                  Bgl1
                    |        ||          |               |                       |                     |
      AACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCG
5601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5700
      TTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGC

                                               Avr2
                                              Stu1|
                        SpDon             BseR1  ||              Cla1              BsaB1
                            |                 |  ||                 |                  |
      GCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATT
5701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5800
      CGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAA

           BspM1               Eag1                                       Bmr1
               |                  |                                          |
      GAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCG
5801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5900
      CTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGC
```

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                         Nar1
                        Kas1|                       Drd1
                           ||                          |
      TGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTG
5901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6000
      ACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCAC

                               Pvu2
       Msc1                Fsp1   |       PflF1                       Eco57
          |                   |   |           |                           |
      GCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTC
6001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6100
      CGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAG

                                                                                               BtgZ1
             SpDon                         BciV1         BsrD1                              BspM1  |
                 |                             |             |                                  |  |
      CTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACC
6101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6200
      GACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGG

                                                                     Sap1
                                                                     Ear1                           BpuE1
                                                                        |                               |
      AAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGA
6201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6300
      TTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCT

                              Sph1                       Nco1               BtgZ1
                                 |                          |                   |
      ACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGC
6301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6400
      TGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCG
```

```
                            BseY1
                           Nae1 |                                              Sap1
                        NgoM4 | |        Rsr2         Eci1                     Ear1
                            | | |           |            |                        |
      TTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAAT
6401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6500
      AAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTA

                                       BtgZ1
  Eco57         BssS1                BsrB1 |                                               BsrB1
      |             |                    | |                                                   |
      GGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTG
6501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6600
      CCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGAC

                                          BssS1
      BstB1                               BspM1                      SpAcc
          |                                   |                          |
      GGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCC
6601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6700
      CCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGG

          Nae1                                                   Bpm1
       NgoM4 |                                               SpAcc  |
        Bpm1 |                                                Avr2  |
           | |                                                   |  |
      GGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACC
6701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6800
      CCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGG

                         polyA        polyA
                             |            |
      GGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGCAC
6801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6900
      CCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTG
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              Bsa1
                 |
      TCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCG
6901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7000
      AGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGC

                         BstAP
                         AlwN1      Bsu36                            Dra1               Dra1
                             |          |                               |                  |
      CAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGT
7001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7100
      GTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCA


                      BspH1
                          |
      GAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGA
7101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7200
      CTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACT


                  BpuE1                                                                             Eco57
                      |                                                                                 |
      GATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTC
7201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7300
      CTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAG


                                                    SpAcc
                                                        |
      CGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTAC
7301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7400
      GCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATG


                                 AlwN1                     BpuE1
                                     |                         |
      ATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCG
7401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7500
      TATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGC
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                            ApaL1     BseY1                                             SpAcc
                                |         |                                                 |
      CAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCG
7501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7600
      GTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGC


                                            BciV1
                                         Eci1   |                    BssS1
                                            |   |                        |
      CCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTA
7601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7700
      GGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCAT


          SpAcc                          Drd1            BpuE1               SpAcc     Eci1
              |                             |                |                   |        |
      TCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCG
7701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7800
      AGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGC


                                           SpDon                                                    Nsi1
                                          BspLU|                                                 BfrB1 |
                                              ||                                                     | |
      GCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
7801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*||||||||| 7899
      CGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

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Found:

    Aat2   Acc65    Afl2    Age1    Ale1   AlwN1    Apa1   ApaL1    Ase1    Avr2   BamH1    Bbs1   BbvC1   BciV1
    Bcl1   BfrB1    Bgl1    Bgl2    Blp1    Bmr1    Bpm1   Bpu10   BpuE1    Bsa1   BsaB1   BsaXa   BsaXb   BseR1
   BseY1    Bsg1    Bsm1   BsmB1   BspH1   BspLU   BspM1   BsrB1   BsrD1   BsrG1   BssS1   BstAP   BstB1   BstX1
   Bsu36   BtgZ1    Bts1    _Chi    Cla1    Dra1    Dra3    Drd1    Eag1    Ear1    Eci1    Ecl2   Eco57   EcoN1
   EcoR1   EcoRV    Fsp1   Hind3    Hpa1    Kas1    Kpn1    Mfe1    Msc1    Nae1    Nar1    Nco1    Nde1   NgoM4
    Nhe1    Not1    Nsi1   PflF1   PflM1   polyA   PshA1    Psi1   PspOM    Pst1    Pvu1    Pvu2    Rsr2    Sac1
    Sac2    Sal1    Sap1   SexA1    Sfi1   SgrA1    Sma1   SnaB1   SpAcc   SpDon    Sph1    Ssp1    Stu1   T7Ter
    Xba1    Xcm1    Xho1    Xmn1

Unique:

    Afl2    Apa1   BbvC1    Bcl1    Blp1   BsmB1   BspLU    Ecl2   EcoN1   EcoR1   EcoRV    Fsp1    Hpa1    Mfe1
    Nde1    Nhe1    Not1   PflF1   PshA1   PspOM    Pvu1    Rsr2    Sac1    Sac2    Sal1    Sfi1   SgrA1    Sma1
   SnaB1

Not found:

    Aar1    Acl1    Afe1    Ahd1    Asc1   AsiS1   Bae1a   Bae1b   Bcg1a   Bcg1b   BmgB1   BsiW1   BspE1   BssH2
   BstE2   BstZ1   BxatB   BxatL   BxatR   BxatP    EcoK   FCatB   FCatL   FCatR   FCatP   ScFRT    Fse1   FspA1
   I_Ceu    loxP    Mlu1    Nru1    Pac1    Pme1    Pml1   R4atB   R4atL   R4atP   R4atR   SanD1    Sbf1    Sca1
    Sgf1    Spe1    Srf1    Swa1   T3RNA   T7RNA   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
```