pTagRFP-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). TagRFP 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
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                                                  Aat2                                                  Eci1
                                                    |                                                     |
     TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 500
     ATCGCCAAACTGAGTGCCCCTAAAGGTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT

                                                                                                Nhe1 Afe1
                                                                                                  |    |
     ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCGCTA
501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
     TGTTGAGGCGGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT

                Ale1      Sap1
 Age1        Nco1 |      Ear1                                BsrG1                                ApaL1
    |           | |         |                                    |                                    |
     CCGGTCGCCACCATGGTGTCTAAGGGCGAAGAGCTGATTAAGGAGAACATGCACATGAAGCTGTACATGGAGGGCACCGTGAACAACCACCACTTCAAGT
601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
     GGCCAGCGGTGGTACCACAGATTCCCGCTTCTCGACTAATTCCTCTTGTACGTGTACTTCGACATGTACCTCCCGTGGCACTTGTTGGTGGTGAAGTTCA
TagRFP     >            M  V  S  K  G  E  E  L  I  K  E  N  M  H  M  K  L  Y  M  E  G  T  V  N  N  H  H  F  K  C

                          SpAcc
                             |
     GCACATCCGAGGGCGAAGGCAAGCCCTACGAGGGCACCCAGACCATGAGAATCAAGGTGGTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGC
701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
     CGTGTAGGCTCCCGCTTCCGTTCGGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCCACCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCG
TagRFP     >  T  S  E  G  E  G  K  P  Y  E  G  T  Q  T  M  R  I  K  V  V  E  G  G  P  L  P  F  A  F  D  I  L  A

                                                                                Bsu36       SpDon
                                                                                  |           |
     TACCAGCTTCATGTACGGCAGCAGAACCTTCATCAACCACACCCAGGGCATCCCCGACTTCTTTAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGA
801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
     ATGGTCGAAGTACATGCCGTCGTCTTGGAAGTAGTTGGTGTGGGTCCCGTAGGGGCTGAAGAAATTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCT
TagRFP     >  T  S  F  M  Y  G  S  R  T  F  I  N  H  T  Q  G  I  P  D  F  F  K  Q  S  F  P  E  G  F  T  W  E  R

                         Bbs1            Bpm1
                           |                |
     GTCACCACATACGAAGACGGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACT
901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
     CAGTGGTGTATGCTTCTGCCCCCGCACGACTGGCGATGGGTCCTGTGGTCGGAGGTCCTGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCCACTTGA
TagRFP     > V  T  T  Y  E  D  G  G  V  L  T  A  T  Q  D  T  S  L  Q  D  G  C  L  I  Y  N  V  K  I  R  G  V  N  F
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                                                BseY1                                                Bgl1
                                                  |                                                    |
            TCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCAACACCGAGATGCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAAGCGA
      1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
            AGGGTAGGTTGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCTCCGGTTGTGGCTCTACGACATGGGGCGACTGCCGCCGGACCTTCCGTCTTCGCT
TagRFP        >   P  S  N  G  P  V  M  Q  K  K  T  L  G  W  E  A  N  T  E  M  L  Y  P  A  D  G  G  L  E  G  R  S  D

                      BssS1          Eco57                                  BpuE1
                        |              |                                      |
            CATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACTTCAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGCGTC
      1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
            GTACCGGGACTTCGAGCACCCGCCCCCGGTGGACTAGACGTTGAAGTTCTGGTGTATGTCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCGCAG
TagRFP        >  M  A  L  K  L  V  G  G  G  H  L  I  C  N  F  K  T  T  Y  R  S  K  K  P  A  K  N  L  K  M  P  G  V

                        SpAcc
                        PflM1                   Bsa1       PshA1       BssS1 Dra3      Msc1  AlwN1
                          |                       |           |           |    |         |      |
            TACTATGTGGACCACAGACTGGAAAGAATCAAGGAGGCCGACAAAGAGACCTACGTCGAGCAGCACGAGGTGGCTGTGGCCAGATACTGCGACCTCCCTA
      1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
            ATGATACACCTGGTGTCTGACCTTTCTTAGTTCCTCCGGCTGTTTCTCTGGATGCAGCTCGTCGTGCTCCACCGACACCGGTCTATGACGCTGGAGGGAT
TagRFP        > Y  Y  V  D  H  R  L  E  R  I  K  E  A  D  K  E  T  Y  V  E  Q  H  E  V  A  V  A  R  Y  C  D  L  P  S

                                  BpuE1     Xho1    Hind3  EcoR1
          SpAcc          Bmr1    BspE1   | Bgl2   |   Sac1 |BstB1 |        Xho1     Hind3       Eag1     Sph1
            |              |        |    |    |    |      | |    | |           |         |           |        |
            GCAAACTGGGGCACAAACTTAATTCCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCGGGAAACTCGAGAACAAAGCTTGAAAACGGCCGCATGCCAGT
      1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
            CGTTTGACCCCGTGTTTGAATTAAGGCCTGAGTCTAGAGCTCGAGTTCGAAGCTTAAGCCCTTTGAGCTCTTGTTTCGAACTTTTGCCGGCGTACGGTCA
TagRFP/Vinculin  K  L  G  H  K  L  N  S  G  L  R  S  R  A  Q  A  S  N  S  G  N  S  R  T  K  L  E  N  G  R  M  P  V

                                                      Bpm1       Dra3
                          Pvu1                      Bgl2 |  SexA1   |     BssS1             BseR1
                            |                         | |      |    |         |                |
            GTTTCATACGCGCACGATCGAGAGCATCCTGGAGCCGGTGGCACAGCAGATCTCCCACCTGGTGATAATGCACGAGGAGGGCGAGGTGGACGGCAAAGCC
      1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
            CAAAGTATGCGCGTGCTAGCTCTCGTAGGACCTCGGCCACCGTGTCGTCTAGAGGGTGGACCACTATTACGTGCTCCTCCCGCTCCACCTGCCGTTTCGG
Vinculin      >  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  D  G  K  A
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                                        Eag1
                                   Bgl1   |          Bsg1                                        Ear1
                                      |   |             |                                          |
            ATTCCTGACCTCACCGCGCCCGTGGCCGCCGTGCAGGCGGCCGTCAGCAACCTCGTCCGGGTTGGAAAAGAGACTGTTCAAACCACTGAGGATCAGATTT
      1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
            TAAGGACTGGAGTGGCGCGGGCACCGGCGGCACGTCCGCCGGCAGTCGTTGGAGCAGGCCCAACCTTTTCTCTGACAAGTTTGGTGACTCCTAGTCTAAA
Vinculin    > 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  E  D  Q  I  L

                      _Chi          polyA           Bsm1  Hind3    Eco57                                AlwN1
                         |              |              |      |        |                                     |
            TGAAGAGAGATATGCCACCAGCATTTATTAAGGTTGAGAATGCTTGCACCAAGCTTGTCCAGGCAGCTCAGATGCTTCAGTCAGACCCTTACTCAGTGCC
      1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
            ACTTCTCTCTATACGGTGGTCGTAAATAATTCCAACTCTTACGAACGTGGTTCGAACAGGTCCGTCGAGTCTACGAAGTCAGTCTGGGAATGAGTCACGG
Vinculin    >   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  Y  S  V  P

                                                                   SpDon
                                                              BspM1  |       Bpu10
             Xho1                                             BfuA1  |       BbvC1
                |                                                |  |           |
            TGCTCGAGATTATCTAATTGATGGGTCAAGGGGCATCCTCTCTGGAACATCAGACCTGCTCCTTACCTTCGATGAGGCTGAGGTCCGTAAAATTATTAGA
      1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
            ACGAGCTCTAATAGATTAACTACCCAGTTCCCCGTAGGAGAGACCTTGTAGTCTGGACGAGGAATGGAAGCTACTCCGACTCCAGGCATTTTAATAATCT
Vinculin    >  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  K  I  I  R

                                                 SpAcc
                                                    |
            GTTTGCAAAGGAATTTTGGAATATCTTACAGTGGCAGAGGTGGTGGAGACTATGGAAGATTTGGTCACTTACACAAAGAATCTTGGGCCAGGAATGACTA
      1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
            CAAACGTTTCCTTAAAACCTTATAGAATGTCACCGTCTCCACCACCTCTGATACCTTCTAAACCAGTGAATGTGTTTCTTAGAACCCGGTCCTTACTGAT
Vinculin    > 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  P  G  M  T  K

                Msc1                            Sac1  SpDon        Dra3
                   |                               |      |           |
            AGATGGCCAAGATGATTGACGAGAGACAGCAGGAGCTCACTCACCAGGAGCACCGAGTGATGTTGGTGAACTCGATGAACACCGTGAAAGAGTTGCTGCC
      1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
            TCTACCGGTTCTACTAACTGCTCTCTGTCGTCCTCGAGTGAGTGGTCCTCGTGGCTCACTACAACCACTTGAGCTACTTGTGGCACTTTCTCAACGACGG
Vinculin    >   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  E  L  L  P
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                                                                                                  Xba1
                        SpAcc                                                Hind3  Dra1          SpAcc
                          |                                                    |     |              |
             AGTTCTCATTTCAGCTATGAAGATTTTTGTAACAACTAAAAACTCAAAAAACCAAGGCATAGAGGAAGCTTTAAAAAATCGCAATTTTACTCTAGAAAAA
        2001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
             TCAAGAGTAAAGTCGATACTTCTAAAAACATTGTTGATTTTTGAGTTTTTTGGTTCCGTATCTCCTTCGAAATTTTTTAGCGTTAAAATGAGATCTTTTT
Vinculin     >  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  T  L  E  K

                         Ase1                          SpDon                                    Ear1
                           |                             |                                        |
             ATGAGTGCTGAAATTAATGAGATAATTCGTGTGTTACAACTCACCTCTTGGGATGAAGATGCCTGGGCCAGCAAGGACACTGAAGCCATGAAGAGAGCAT
        2101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
             TACTCACGACTTTAATTACTCTATTAAGCACACAATGTTGAGTGGAGAACCCTACTTCTACGGACCCGGTCGTTCCTGTGACTTCGGTACTTCTCTCGTA
Vinculin     > 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  M  K  R  A  L

          Eco57      SpAcc                    PflM1                        SpAcc    SpDon               Bgl2
             |          |                       |                            |        |                  |
             TGGCCTCCATAGACTCCAAACTGAACCAGGCCAAAGGTTGGCTCCGTGACCCTAGTGCCTCCCCAGGGGATGCTGGTGAGCAGGCCATCAGACAGATCTT
        2201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
             ACCGGAGGTATCTGAGGTTTGACTTGGTCCGGTTTCCAACCGAGGCACTGGGATCACGGAGGGGTCCCCTACGACCACTCGTCCGGTAGTCTGTCTAGAA
Vinculin     >   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  R  Q  I  L

                SpAcc                                      Bsg1                                  Bcl1
                   |                                         |                                     |
             AGATGAAGCTGGAAAAGTTGGTGAACTCTGTGCAGGCAAAGAACGCAGGGAGATTCTGGGAACTTGCAAAATGCTAGGGCAGATGACTGATCAAGTGGCT
        2301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
             TCTACTTCGACCTTTTCAACCACTTGAGACACGTCCGTTTCTTGCGTCCCTCTAAGACCCTTGAACGTTTTACGATCCCGTCTACTGACTAGTTCACCGA
Vinculin     >  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  D  Q  V  A

                                   SgrA1          BspM1
                          BamH1    Age1    Msc1   BfuA1 Blp1              AlwN1
                             |       |       |       |    |                  |
             GACCTCCGTGCCAGAGGACAAGGATCCTCACCGGTGGCCATGCAGAAAGCTCAGCAGGTATCTCAGGGTCTGGATGTGCTCACAGCAAAAGTGGAAAATG
        2401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
             CTGGAGGCACGGTCTCCTGTTCCTAGGAGTGGCCACCGGTACGTCTTTCGAGTCGTCCATAGAGTCCCAGACCTACACGAGTGTCGTTTTCACCTTTTAC
Vinculin     > 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  K  V  E  N  A
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                                          BsrD1          Cla1                              PflM1
                                            |              |                                  |
            CAGCTCGCAAGCTGGAAGCCATGACCAACTCAAAGCAGAGCATTGCAAAGAAGATCGATGCTGCTCAGAACTGGCTTGCAGATCCAAATGGTGGACCGGA
      2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
            GTCGAGCGTTCGACCTTCGGTACTGGTTGAGTTTCGTCTCGTAACGTTTCTTCTAGCTACGACGAGTCTTGACCGAACGTCTAGGTTTACCACCTGGCCT
Vinculin     >  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  G  G  P  E

          Sap1
          Ear1                                              Eco57         SpAcc
             |                                                |             |
            AGGAGAAGAGCAGATTCGAGGTGCTTTGGCTGAAGCTCGGAAAATAGCAGAATTATGTGATGATCCTAAAGAAAGAGATGACATTCTACGTTCCCTTGGG
      2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
            TCCTCTTCTCGTCTAAGCTCCACGAAACCGACTTCGAGCCTTTTATCGTCTTAATACACTACTAGGATTTCTTTCTCTACTGTAAGATGCAAGGGAACCC
Vinculin     >  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  R  S  L  G

                                         SpAcc        Bbs1                                        Msc1
                                       Bgl2  |       Bpm1|                   Xho1       Msc1   BstX1   |
                                          |  |          ||                     |          |       |   |
            GAAATATCTGCTCTGACTTCTAAATTAGCAGATCTACGAAGACAGGGGAAAGGAGATTCTCCAGAGGCTCGAGCCTTGGCCAAACAGGTGGCCACGGCCC
      2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
            CTTTATAGACGAGACTGAAGATTTAATCGTCTAGATGCTTCTGTCCCCTTTCCTCTAAGAGGTCTCCGAGCTCGGAACCGGTTTGTCCACCGGTGCCGGG
Vinculin     > 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  V  A  T  A  L

                BstAP   BspM1
                AlwN1   BfuA1                                        BsrG1
            Pst1   | Pst1  |         Xcm1   Msc1                   Pvu2 |                       BpuE1 Ale1
               |   |    |  |            |      |                     | |                          |    |
            TGCAGAACCTGCAGACCAAAACCAACCGGGCTGTGGCCAACAGCAGACCGGCCAAAGCAGCTGTACACCTTGAGGGCAAGATTGAGCAAGCACAGCGGTG
      2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
            ACGTCTTGGACGTCTGGTTTTGGTTGGCCCGACACCGGTTGTCGTCTGGCCGGTTTCGTCGACATGTGGAACTCCCGTTCTAACTCGTTCGTGTCGCCAC
Vinculin     >  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  A  Q  R  W

                                         Drd1
                                           |
            GATTGATAATCCCACAGTGGATGACCGTGGAGTCGGTCAGGCTGCCATCCGGGGGCTTGTGGCCGAAGGGCATCGTCTGGCTAATGTTATGATGGGGCCT
      2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
            CTAACTATTAGGGTGTCACCTACTGGCACCTCAGCCAGTCCGACGGTAGGCCCCCGAACACCGGCTTCCCGTAGCAGACCGATTACAATACTACCCCGGA
Vinculin     >  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  M  M  G  P
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                                                        Bgl1
                                                       Pvu2|
             Bgl1  Bgl2                          Pvu2   BseY1   ||                                Bsu36 BssS1
                |     |                             |       |   ||                                    |     |
             TATCGGCAAGATCTTCTCGCCAAGTGTGACCGAGTGGACCAGCTGACAGCCCAGCTGGCTGACCTGGCTGCCAGAGGGGAAGGGGAGAGTCCTCAGGCAC
        3001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
             ATAGCCGTTCTAGAAGAGCGGTTCACACTGGCTCACCTGGTCGACTGTCGGGTCGACCGACTGGACCGACGGTCTCCCCTTCCCCTCTCAGGAGTCCGTG
Vinculin     > 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  S  P  Q  A  R

                                                                                                BsaXb
                                                                                                   |
             GAGCACTTGCATCTCAGCTCCAAGACTCCTTAAAGGATCTAAAAGCTCGGATGCAGGAGGCCATGACTCAGGAAGTGTCAGATGTTTTCAGCGATACCAC
        3101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
             CTCGTGAACGTAGAGTCGAGGTTCTGAGGAATTTCCTAGATTTTCGAGCCTACGTCCTCCGGTACTGAGTCCTTCACAGTCTACAAAAGTCGCTATGGTG
Vinculin     >   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  S  D  T  T

                       BsaXa                Nar1                Ear1
                     Xcm1  | BsaXb Bts1   Kas1|             BsaXa |
                        |  |     |    |      ||                | |
             AACTCCCATCAAGCTGTTGGCAGTGGCAGCCACGGCGCCTCCTGATGCGCCTAACAGGGAAGAGGTATTTGATGAGAGGGCAGCTAACTTTGAAAACCAT
        3201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
             TTGAGGGTAGTTCGACAACCGTCACCGTCGGTGCCGCGGAGGACTACGCGGATTGTCCCTTCTCCATAAACTACTCTCCCGTCGATTGAAACTTTTGGTA
Vinculin     >  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  F  E  N  H

                                                                                   Xmn1
               Hind3         Eag1    Bgl1                  polyA                   Bsm1    Stu1           Bbs1
                    |            |       |                     |                      |       |              |
             TCAGGAAAGCTTGGTGCTACGGCCGAGAAGGCGGCTGCGGTTGGTACTGCTAATAAATCAACAGTGGAAGGCATTCAGGCCTCAGTGAAGACGGCCCGAG
        3301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
             AGTCCTTTCGAACCACGATGCCGGCTCTTCCGCCGACGCCAACCATGACGATTATTTAGTTGTCACCTTCCGTAAGTCCGGAGTCACTTCTGCCGGGCTC
Vinculin     > 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  K  T  A  R  E

                                 Bsa1                                                  Bsa1
                                    |                                                     |
             AACTCACACCCCAGGTGGTCTCGGCTGCTCGTATCTTACTTAGGAACCCTGGAAATCAAGCTGCTTATGAACATTTTGAGACCATGAAGAACCAGTGGAT
        3401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
             TTGAGTGTGGGGTCCACCAGAGCCGACGAGCATAGAATGAATCCTTGGGACCTTTAGTTCGACGAATACTTGTAAAACTCTGGTACTTCTTGGTCACCTA
Vinculin     >   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  N  Q  W  I
```

```
                                                        Xcm1
          Cla1                          _Chi          Eco57   |
             |                            |                |   |
             CGATAATGTTGAAAAAATGACAGGGCTGGTGGACGAAGCCATTGATACCAAATCTCTGTTGGATGCTTCAGAAGAAGCAATTAAAAAAGACCTGGACAAG
        3501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
             GCTATTACAACTTTTTTACTGTCCCGACCACCTGCTTCGGTAACTATGGTTTAGAGACAACCTACGAAGTCTTCTTCGTTAATTTTTTCTGGACCTGTTC
Vinculin     >  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  D  L  D  K

                                                                                                   SpAcc
                           Msc1                AlwN1  BseY1                             BamH1          _Chi
                              |                    |      |                                |             |
             TGCAAGGTAGCTATGGCCAACATTCAGCCTCAGATGCTGGTTGCTGGGGCAACCAGTATTGCTCGTCGGGCCAACCGGATCCTGCTGGTGGCTAAGAGGG
        3601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
             ACGTTCCATCGATACCGGTTGTAAGTCGGAGTCTACGACCAACGACCCCGTTGGTCATAACGAGCAGCCCGGTTGGCCTAGGACGACCACCGATTCTCCC
Vinculin     > 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  V  A  K  R  E

                           BamH1              SpAcc                                     Xcm1
                              |                  |                                        |
             AGGTGGAAAATTCCGAGGATCCCAAGTTCCGTGAGGCTGTGAAAGCTGCCTCTGATGAATTGAGCAAAACCATCTCCCCGATGGTGATGGATGCAAAAGC
        3701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
             TCCACCTTTTAAGGCTCCTAGGGTTCAAGGCACTCCGACACTTTCGACGGAGACTACTTAACTCGTTTTGGTAGAGGGGCTACCACTACCTACGTTTTCG
Vinculin     >   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  D  A  K  A

                                                                  BamH1
                      Xmn1          SpAcc                      EcoRV   |             Msc1
                        |              |                            |   |               |
             TGTGGCTGGAAACATTTCCGACCCTGGACTGCAAAAGAGCTTCCTGGACTCAGGATATCGGATCCTGGGAGCTGTGGCCAAGGTCAGAGAAGCCTTCCAA
        3801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
             ACACCGACCTTTGTAAAGGCTGGGACCTGACGTTTTCTCGAAGGACCTGAGTCCTATAGCCTAGGACCCTCGACACCGGTTCCAGTCTCTTCGGAAGGTT
Vinculin     >  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  E  A  F  Q

                                                                T7Ter
           Bsu36                                              BseR1 |                            SpDon
              |                                                  | |                               |
             CCTCAGGAGCCTGACTTCCCGCCGCCTCCACCAGACCTTGAACAACTCCGACTAACAGATGAGCTTGCTCCTCCCAAACCACCTCTGCCTGAAGGTGAGG
        3901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
             GGAGTCCTCGGACTGAAGGGCGGCGGAGGTGGTCTGGAACTTGTTGAGGCTGATTGTCTACTCGAACGAGGAGGGTTTGGTGGAGACGGACTTCCACTCC
Vinculin     > 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  P  E  G  E  V
```

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                     Stu1
                Eco57   |
                Avr2|   |                Ear1          Bpu10
                   ||   |                   |             |
            TCCCTCCACCTAGGCCTCCACCACCAGAGGAAAAGGATGAAGAGTTCCCTGAGCAGAAGGCCGGGGAGGTGATTAACCAGCCAATGATGATGGCTGCCAG
      4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
            AGGGAGGTGGATCCGGAGGTGGTGGTCTCCTTTTCCTACTTCTCAAGGGACTCGTCTTCCGGCCCCTCCACTAATTGGTCGGTTACTACTACCGACGGTC
Vinculin     >  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  M  A  A  R

                                                  BsrD1
                                                BsrD1 |              BstX1
                                                   | |                 |
            ACAGCTCCATGATGAAGCTCGCAAATGGTCCAGCAAGGGCAATGACATCATTGCAGCAGCCAAGCGCATGGCTCTGCTGATGGCTGAGATGTCTCGGCTG
      4101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
            TGTCGAGGTACTACTTCGAGCGTTTACCAGGTCGTTCCCGTTACTGTAGTAACGTCGTCGGTTCGCGTACCGAGACGACTACCGACTCTACAGAGCCGAC
Vinculin     > 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  M  S  R  L

                          Kpn1
                        Bts1 |
         SpDon           Acc65 | |           BtgZ1                     Stu1                     Msc1
             |               | | |               |                       |                        |
            GTAAGAGGGGGCAGTGGTACCAAGCGGGCACTCATTCAGTGTGCCAAGGACATCGCCAAGGCCTCAGATGAGGTGACTCGGTTGGCCAAGGAGGTTGCCA
      4201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
            CATTCTCCCCCGTCACCATGGTTCGCCCGTGAGTAAGTCACACGGTTCCTGTAGCGGTTCCGGAGTCTACTCCACTGAGCCAACCGGTTCCTCCAACGGT
Vinculin     > 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  K  E  V  A  K

                Bts1
            ApaL1   |                      EcoN1SpAcc                        BseY1
                |   |                         |    |                            |
            AGCAGTGCACAGATAAACGGATTAGAACCAACCTCTTACAGGTATGTGAGCGAATCCCAACCATAAGCACCCAGCTCAAAATCCTGTCCACAGTGAAGGC
      4301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
            TCGTCACGTGTCTATTTGCCTAATCTTGGTTGGAGAATGTCCATACACTCGCTTAGGGTTGGTATTCGTGGGTCGAGTTTTAGGACAGGTGTCACTTCCG
Vinculin     >  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  T  V  K  A
```

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                BstX1
                BseY1                                   BseR1    Xcm1       SpDon                 SpAcc
                    |                                       |       |           |                     |
           CACCATGCTGGGCCGGACCAACATCAGTGATGAGGAGTCTGAGCAGGCCACAGAGATGCTGGTTCACAATGCCCAGAACCTCATGCAGTCTGTGAAGGAG
      4401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
           GTGGTACGACCCGGCCTGGTTGTAGTCACTACTCCTCAGACTCGTCCGGTGTCTCTACGACCAAGTGTTACGGGTCTTGGAGTACGTCAGACACTTCCTC
Vinculin     >  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  S  V  K  E

                                        BstB1     T7Ter                                   Kpn1    Not1
                                       Eco57|     AlwN1     Bts1  BseY1                Acc65   |    Eag1
                                           ||         |        |      |                   |   |       |
           ACTGTGCGGGAAGCTGAAGCTGCTTCAATCAAAATTCGAACAGATGCTGGATTTACACTGCGCTGGGTTAGAAAGACTCCCTGGTACCAGTAGGCGGCCG
      4501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
           TGACACGCCCTTCGACTTCGACGAAGTTAGTTTTAAGCTTGTCTACGACCTAAATGTGACGCGACCCAATCTTTCTGAGGGACCATGGTCATCCGCCGGC
Vinculin     > 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  Q  *

                Xba1   BsaB1                            SpDon   Dra1
                   |       |                               |      |
           CGACTCTAGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATG
      4601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
           GCTGAGATCTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTAC

              Bsm1
             Mfe1|        Hpa1       polyA    Psi1      polyA                         polyA            Bts1 Bsm1
           ||           |           |       |          |                           |               |    |
           CAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTC
      4701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
           GTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGACGTAAG

                                          Mlu1     SpDon        Ssp1
                                             |         |           |
           TAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAACGCGTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTC
      4801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
           ATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTGCGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAG

                                            Psi1
                                              |
           ATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCA
      4901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
           TAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGT
```

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                                                                  BtgZ1
  BsaXb                 Drd1    BsaXa                             Dra3|
      |                    |        |                                ||
      CTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGT
5001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
      GATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCCA

                                                                     Nae1
                              SpAcc                               NgoM4 |
                                  |                                  | |
      CGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAA
5101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
      GCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTT

            BsrB1
                |
      AGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCA
5201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
      TCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGT

                                                                        BciV1
                                                                     BspH1  |
                                                polyA                BsrB1 |  |
                                                    |                    | |  |
      GGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAA
5301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5400
      CCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTT

                                                  Eci1
                Ssp1  Ear1        Bsu36            Pvu2 |                                      BseY1
                   |     |            |                | |                                         |
      TGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCA
5401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5500
      ACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTCGT
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                        Nsi1                                                                    Nsi1
                      Sph1 |                                                                  Sph1 |
                     BfrB1 |                                                                 BfrB1 |
                  BstAP  | |            SexA1                      BseY1                   BstAP  | |
                      |  | |                |                        |                       |  | |
      GGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCA
5501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5600
      CCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGT

                                                   Eci1
                      Eci1                 Eci1     Bmr1|       Eci1            Nco1
                         |                    |        ||          |               |
      ATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTT
5601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5700
      TAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAA

                                                                          Avr2
                          Sfi1                                           Stu1|
     polyA                Bgl1                     SpDon             BseR1  ||              Cla1
        |                    |                        |                 |  ||                |
      TATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGA
5701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5800
      ATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCT

                                   BspM1
           BsaB1                   BfuA1               Eag1
              |                       |                  |
      GACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAA
5801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5900
      CTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTT

                                                 Nar1
  Bmr1                                          Kas1|                        Drd1
     |                                             ||                          |
      CAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAC
5901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6000
      GTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTG
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                                                   Pvu2
                                Msc1               Fsp1   |       PflF1                        Eco57
                                   |                   |   |           |                           |
     TGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCT
6001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6100
     ACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGA

                                      SpDon                        BciV1         BsrD1
                                          |                            |             |
     ATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTT
6101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6200
     TAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAA

                        BtgZ1
                    BspM1  |                                                                  Sap1
                    BfuA1  |                                                                  Ear1
                       |   |                                                                     |
     GATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACG
6201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6300
     CTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGC

                           BpuE1                        Sph1                       Nco1
                              |                            |                          |
     AAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTT
6301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6400
     TTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAA

                                                 BseY1
                                                Nae1 |
    BtgZ1                                     NgoM4 | |        Rsr2         Eci1
       |                                          | | |           |            |
     GCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGT
6401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6500
     CGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCA
```

```
       Sap1                                                  BtgZ1
       Ear1                  Eco57         BssS1                BsrB1 |
          |                      |             |                    | |
     GATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTC
6501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6600
     CTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAG

                                                                BssS1
                                                                BspM1
                 BsrB1          BstB1                           BfuA1                      SpAcc
                    |              |                               |                          |
     TTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTAT
6601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6700
     AACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATA

                                   Nae1                                                   Bpm1
                                NgoM4 |                                              SpAcc  |
                                 Bpm1 |                                               Avr2  |
                                    | |                                                  |  |
     GAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGC
6701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6800
     CTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCG

                                                  polyA        polyA
                                                     |            |
     TAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAA
6801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 6900
     ATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAAACAAGTATT

                                          Bsa1
                                            |
     ACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCC
6901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7000
     TGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGG
```

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                                                BstAP
                                                AlwN1      Bsu36                           Dra1
                                                    |          |                               |
     CCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAAC
7001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7100
     GGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTG

               Dra1                              BspH1
                  |                                 |
     TTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCC
7101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7200
     AAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGG

                                            BpuE1
                                                |
     CGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTG
7201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7300
     GCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAAC

                          Eco57                                                 SpAcc
                              |                                                     |
     CCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACC
7301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7400
     GGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGG

                                                          AlwN1                     BpuE1
                                                              |                         |
     ACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGA
7401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7500
     TGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCT

                                                                ApaL1     BseY1
                                                                    |         |
     CTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGA
7501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7600
     GAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCT
```

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                                                                  BciV1
                SpAcc                                           Eci1   |                    BssS1
                    |                                              |   |                       |
     TACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGA
7601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7700
     ATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCT

                                   SpAcc                        Drd1           BpuE1
                                       |                           |               |
     GGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCG
7701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7800
     CCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCCGC

                                                                 SpDon
    SpAcc     Eci1                                              BspLU|
        |        |                                                  ||
     GAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCT
7801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 7900
     CTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGA

                          Nsi1
                       BfrB1 |
                           | |
     GTGGATAACCGTATTACCGCCATGCAT
7901 |||||||||*|||||||||*||||||| 7927
     CACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aat2	Acc65	**Afe1**	Age1	Ale1	AlwN1	ApaL1	Ase1	Avr2	BamH1	Bbs1	**BbvC1**	BciV1	**Bcl1**
BfrB1	BfuA1	Bgl1	Bgl2	**Blp1**	Bmr1	Bpm1	Bpu10	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**
EcoRV	**Fsp1**	Hind3	**Hpa1**	Kas1	Kpn1	**Mfe1**	**Mlu1**	Msc1	Nae1	Nar1	Nco1	**Nde1**	NgoM4
Nhe1	**Not1**	Nsi1	**PflF1**	PflM1	polyA	**PshA1**	Psi1	Pst1	**Pvu1**	Pvu2	**Rsr2**	Sac1	Sap1
SexA1	**Sfi1**	**SgrA1**	**SnaB1**	SpAcc	SpDon	Sph1	Ssp1	Stu1	T7Ter	Xba1	Xcm1	Xho1	Xmn1

Unique:

Afe1	**BbvC1**	**Bcl1**	**Blp1**	**BspE1**	**BspLU**	**EcoN1**	**EcoR1**	**EcoRV**	**Fsp1**	**Hpa1**	**Mfe1**	**Mlu1**	**Nde1**
Nhe1	**Not1**	**PflF1**	**PshA1**	**Pvu1**	**Rsr2**	**Sfi1**	**SgrA1**	**SnaB1**					

Not found:

Aar1	Acl1	Afl2	Ahd1	Apa1	Asc1	AsiS1	Bae1a	Bae1b	Bcg1a	Bcg1b	BmgB1	BsiW1	BsmB1
BssH2	BstE2	BstZ1	EcoK	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	I_Ceu	loxP	Nru1
Pac1	Pme1	Pml1	PspOM	R4atB	R4atL	R4atP	R4atR	Sac2	Sal1	SanD1	Sbf1	Sca1	Sgf1
Sma1	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													