pFusionRed-f-mem vector restriction map

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

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

FusionRed amino acids are shown in red, farnesylation signal (FS) amino acids are shown in green, linker amino acids are shown in black.

```
        Ase1                                                                               Bgl1
           |                                                                                  |
     TAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCG
  1  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 100
     ATCAATAATTATCATTAGTTAATGCCCCAGTAATCAAGTATCGGGTATATACCTCAAGGCGCAATGTATTGAATGCCATTTACCGGGCGGACCGACTGGC

                          Aat2                   SpAcc                         Aat2
                             |                       |                            |
     CCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGT
101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 200
     GGGTTGCTGGGGGCGGGTAACTGCAGTTATTACTGCATACAAGGGTATCATTGCGGTTATCCCTGAAAGGTAACTGCAGTTACCCACCTCATAAATGCCA

             Bgl1                  Nde1                       Aat2                  Bgl1  Bmr1
                |                     |                          |                     |     |
     AAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTA
201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 300
     TTTGACGGGTGAACCGTCATGTAGTTCACATAGTATACGGTTCATGCGGGGGATAACTGCAGTTACTGCCATTTACCGGGCGGACCGTAATACGGGTCAT

                                  BtgZ1 SnaB1                Nco1
                                      |     |                   |
     CATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGA
301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 400
     GTACTGGAATACCCTGAAAGGATGAACCGTCATGTAGATGCATAATCAGTAGCGATAATGGTACCACTACGCCAAAACCGTCATGTAGTTACCCGCACCT
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                                                                Aat2                                             Eci1
                                                                   |                                                |
                     TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
                401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 500
                     ATCGCCAAACTGAGTGCCCCTAAAGGTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT


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


                               SpDon
                              Ale1 |
                 Age1       Nco1 | |                                 BsrG1                                ApaL1
                    |          | | |                                     |                                    |
                     CCGGTCGCCACCATGGTGAGCGAGCTGATTAAGGAGAACATGCCCATGAAGCTGTACATGGAGGGCACCGTGAACAACCACCACTTCAAGTGCACATCCG
                601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
                     GGCCAGCGGTGGTACCACTCGCTCGACTAATTCCTCTTGTACGGGTACTTCGACATGTACCTCCCGTGGCACTTGTTGGTGGTGAAGTTCACGTGTAGGC
      FusionRed    >             M  V  S  E  L  I  K  E  N  M  P  M  K  L  Y  M  E  G  T  V  N  N  H  H  F  K  C  T  S  E


                                SpAcc
                                    |
                     AGGGCGAAGGCAAGCCCTACGAGGGCACCCAGACCATGAGAATCAAGGTCGTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGCTACCAGCTT
                701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
                     TCCCGCTTCCGTTCGGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCCAGCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTCGAA
      FusionRed    >   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  T  S  F


                                                                                     Bsu36       SpDon
                                                                                         |           |
                     CATGTACGGCAGCAGAACCTTCATCAAGCACCCTCCGGGCATCCCCGACTTCTTTAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACA
                801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
                     GTACATGCCGTCGTCTTGGAAGTAGTTCGTGGGAGGCCCGTAGGGGCTGAAGAAATTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGGTGT
      FusionRed    >  M  Y  G  S  R  T  F  I  K  H  P  P  G  I  P  D  F  F  K  Q  S  F  P  E  G  F  T  W  E  R  V  T  T
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                      Bbs1             Bpm1                                                            BseY1
                         |                |                                                                |
               TACGAAGACGGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGGTTAGAGGGGTGAACTTCCCAGCCA
          901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
               ATGCTTCTGCCCCCGCACGACTGGCGATGGGTCCTGTGGTCGGAGGTCCTGCCGACGGAGTAGATGTTGCAGTTCCAATCTCCCCACTTGAAGGGTCGGT
FusionRed    > 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  V  R  G  V  N  F  P  A  N

                                                    BsmB1
                                         BseY1    Stu1  |                                 Bgl1
                                             |       |  |                                    |
               ACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCTCCACCGAGACGATGTACCCCGCTGACGGCGGCCTGGAAGGCGCATGTGACATGGCCCT
         1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
               TGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCTCCGGAGGTGGCTCTGCTACATGGGGCGACTGCCGCCGGACCTTCCGCGTACACTGTACCGGGA
FusionRed    >   G  P  V  M  Q  K  K  T  L  G  W  E  A  S  T  E  T  M  Y  P  A  D  G  G  L  E  G  A  C  D  M  A  L

                                                                     BpuE1
               BssS1          Eco57        Bsa1                   BpuE1  |
                   |              |           |                       |  |
               GAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACCTTGAGACCACATACAGATCCAAGAAACCCGCTACGAACCTCAAGATGCCCGGCGTCTACAACGTG
         1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
               CTTCGAGCACCCGCCCCCGGTGGACTAGACGTTGGAACTCTGGTGTATGTCTAGGTTCTTTGGGCGATGCTTGGAGTTCTACGGGCCGCAGATGTTGCAC
FusionRed    >  K  L  V  G  G  G  H  L  I  C  N  L  E  T  T  Y  R  S  K  K  P  A  T  N  L  K  M  P  G  V  Y  N  V

                   SpAcc
                   PflM1                  Bsa1       PshA1       BssS1 Dra3      Msc1
                       |                     |           |           |    |         |
               GACCACAGACTGGAAAGAATCAAGGAGGCCGACGATGAGACCTACGTCGAGCAGCACGAGGTGGCTGTGGCCAGATACTCTACTGGTGGCGCTGGTGATG
         1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
               CTGGTGTCTGACCTTTCTTAGTTCCTCCGGCTGCTACTCTGGATGCAGCTCGTCGTGCTCCACCGACACCGGTCTATGAGATGACCACCGCGACCACTAC
FusionRed    > D  H  R  L  E  R  I  K  E  A  D  D  E  T  Y  V  E  Q  H  E  V  A  V  A  R  Y  S  T  G  G  A  G  D  G

                                         Bgl2
             SpDon             BspE1  BseR1 |                                         BstAP                  EcoR1
                 |                 |      | |                                             |                      |
               GAGGTAAAGGTGGAGGAGGTTCCGGACTCAGATCTAAGCTGAACCCTCCTGATGAGAGTGGCCCCGGCTGCATGAGCTGCAAGTGTGTGCTCTCCTGAGA
         1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
               CTCCATTTCCACCTCCTCCAAGGCCTGAGTCTAGATTCGACTTGGGAGGACTACTCTCACCGGGGCCGACGTACTCGACGTTCACACACGAGAGGACTCT
FusionRed/FS >   G  K  G  G  G  G  S  G  L  R  S  K  L  N  P  P  D  E  S  G  P  G  C  M  S  C  K  C  V  L  S  *
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                               BamH1
                              Sma1 |
                             Apa1| |
                        PspOM   || |
                        Sac2|   || |
           Sal1      Kpn1  ||   || |
          Pst1| Acc65   |  ||   || |        Xba1      Bcl1BsaB1                            SpDon   Dra1
             ||     |   |  ||   || |           |         |    |                                |      |
      ATTCTGCAGTCGACGGTACCGCGGGCCCGGGATCCACCGGATCTAGATAACTGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAA
1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
      TAAGACGTCAGCTGCCATGGCGCCCGGGCCCTAGGTGGCCTAGATCTATTGACTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTT

                                                Bsm1
                                               Mfe1|        Hpa1       polyA    Psi1      polyA
                                                  ||           |           |       |          |
      AAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAAT
1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
      TTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTA

                   polyA            Bts1 Bsm1                                      Mlu1     SpDon
                       |               |    |                                         |         |
      AGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAACGCGTAAATTGTAAGCGTT
1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
      TCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTGCGCATTTAACATTCGCAA

     Ssp1                                                                            Psi1
        |                                                                               |
      AATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGA
1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
      TTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCT

                                              BsaXb                 Drd1    BsaXa
                                                  |                    |        |
      CCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGA
1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
      GGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCT
```

```
             BtgZ1
             Dra3|                                                         SpAcc
                ||                                                             |
      TGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCT
1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
      ACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGA

                Nae1
             NgoM4 |                                    BsrB1
                 | |                                        |
      TGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAA
2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
      ACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATT

                                                                                            polyA
                                                                                                |
      CCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAAT
2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
      GGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTA

                         BciV1
                      BspH1  |                                                                   Eci1
                    BsrB1 |  |                            Ssp1  Ear1        Bsu36              Pvu2 |
                        | |  |                               |     |            |                 | |
      ACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGA
2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
      TGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCT

                                                                     Nsi1
                                                                   Sph1 |
                                                                  BfrB1 |
                                       BseY1                   BstAP  | |            SexA1
                                           |                       |  | |                |
      ATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTC
2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
      TACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAG
```

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                                         Nsi1
                                       Sph1 |
                                      BfrB1 |                                                      Eci1
           BseY1                   BstAP  | |                       Eci1                 Eci1     Bmr1|
               |                       |  | |                          |                    |        ||
      CCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCG
2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
      GGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGC

                                                                        Sfi1
          Eci1            Nco1                   polyA                  Bgl1                    SpDon
             |               |                       |                     |                        |
      CCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAG
2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
      GGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTC

                   Avr2
                  Stu1|
              BseR1  ||              Cla1              BsaB1                       BspM1
                  |  ||                 |                  |                           |
      GAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTC
2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
      CTCCGAAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAG

                                                                                                 Nar1
   Eag1                                       Bmr1                                              Kas1|
      |                                          |                                                 ||
      CGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCC
2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
      GCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGG

                        Drd1                                                   Msc1                Fsp1
                           |                                                      |                   |
      GGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCA
2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
      CCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGT
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   Pvu2       PflF1                       Eco57                                      SpDon
      |           |                           |                                          |
      GCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGA
2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
      CGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCT

                                                                   BtgZ1
               BciV1         BsrD1                              BspM1  |
                   |             |                                  |  |
      AAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACG
3001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
      TTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGC

                                         Sap1
                                         Ear1                           BpuE1
                                            |                               |
      TACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATG
3101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
      ATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTAC

                                                                                                    BseY1
                                                                                                   Nae1 |
  Sph1                       Nco1               BtgZ1                                           NgoM4 | |
     |                          |                   |                                               | | |
      CCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGC
3201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
      GGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCG

                                                   Sap1
             Rsr2         Eci1                     Ear1                   Eco57        BssS1
                |            |                        |                       |            |
      TGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGG
3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
      ACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCC
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           BtgZ1
         BsrB1 |                                               BsrB1          BstB1
             | |                                                   |              |
      TATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGC
3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
      ATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCG


                                                                                  Nae1
              BssS1                                                            NgoM4 |
              BspM1                      SpAcc                                  Bpm1 |
                  |                          |                                     | |
      CCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCG
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      GGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGC


                                     Bpm1
                                 SpAcc  |
                                  Avr2  |                                                        polyA
                                     |  |                                                            |
      CGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATA
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      GCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTAT


          polyA                                                                       Bsa1
              |                                                                          |
      AAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATT
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      TTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAA


                                                                                                 BstAP
                                                                                                 AlwN1
                                                                                                     |
      GGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGC
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      CCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACG
```

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        Bsu36                            Dra1               Dra1                              BspH1
            |                               |                  |                                  |
      CATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACC
3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
      GTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGG


                                                                                          BpuE1
                                                                                              |
      AAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCT
4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
      TTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGA


                                                                        Eco57
                                                                            |
      GCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCA
4101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
      CGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGT


                        SpAcc
                            |
      GATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCA
4201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
      CTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGT


     AlwN1                     BpuE1                                                                ApaL1
         |                         |                                                                    |
      GTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGT
4301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
      CACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCA


          BseY1                                             SpAcc
              |                                                 |
      GCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGA
4401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
      CGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCT
```

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                BciV1
             Eci1   |                    BssS1                                    SpAcc
                |   |                        |                                        |
      CAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCAC
4501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
      GTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTG


             Drd1            BpuE1               SpAcc     Eci1
                |                |                   |        |
      CTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCT
4601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
      GAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGA


               SpDon                                                    Nsi1
              BspLU|                                                 BfrB1 |
                  ||                                                     | |
      GGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
4701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*| 4771
      CCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

```
Found:

    Aat2   Acc65    Afe1    Age1    Ale1   AlwN1    Apa1   ApaL1    Ase1    Avr2   BamH1    Bbs1   BciV1    Bcl1
   BfrB1    Bgl1    Bgl2    Bmr1    Bpm1   BpuE1    Bsa1   BsaB1   BsaXa   BsaXb   BseR1   BseY1    Bsm1   BsmB1
   BspE1   BspH1   BspLU   BspM1   BsrB1   BsrD1   BsrG1   BssS1   BstAP   BstB1   Bsu36   BtgZ1    Bts1    Cla1
    Dra1    Dra3    Drd1    Eag1    Ear1    Eci1   Eco57   EcoR1    Fsp1    Hpa1    Kas1    Kpn1    Mfe1    Mlu1
    Msc1    Nae1    Nar1    Nco1    Nde1   NgoM4    Nhe1    Nsi1   PflF1   PflM1   polyA   PshA1    Psi1   PspOM
    Pst1    Pvu2    Rsr2    Sac2    Sal1    Sap1   SexA1    Sfi1    Sma1   SnaB1   SpAcc   SpDon    Sph1    Ssp1
    Stu1    Xba1


Unique:

   Acc65    Afe1    Age1    Ale1    Apa1    Ase1   BamH1    Bbs1    Bcl1    Bgl2   BsaXa   BsaXb   BsmB1   BspE1
   BspLU   BsrD1   BsrG1   BstB1    Bts1    Cla1    Eag1   EcoR1    Fsp1    Hpa1    Kas1    Kpn1    Mfe1    Mlu1
    Nar1    Nde1    Nhe1   PflF1   PflM1   PshA1   PspOM    Pst1    Rsr2    Sac2    Sal1   SexA1    Sfi1    Sma1
   SnaB1    Xba1



Not found:

    Aar1    Acl1    Afl2    Ahd1    Asc1   AsiS1   Bae1a   Bae1b   BbvC1   Bcg1a   Bcg1b    Blp1   BmgB1   Bpu10
    Bsg1   BsiW1   BssH2   BstE2   BstX1   BstZ1   BxatB   BxatL   BxatR   BxatP    _Chi    Ecl2    EcoK   EcoN1
   EcoRV   FCatB   FCatL   FCatR   FCatP   ScFRT    Fse1   FspA1   Hind3   I_Ceu    loxP    Not1    Nru1    Pac1
    Pme1    Pml1    Pvu1   R4atB   R4atL   R4atP   R4atR    Sac1   SanD1    Sbf1    Sca1    Sgf1   SgrA1    Spe1
    Srf1    Swa1   T3RNA   T7RNA   T7Ter   PISce    Xcm1    Xho1    Xmn1

Excluded by site complexity:

    Acc1    Aci1    Afl3    Alu1    Alw1    Apo1    Ava1    Ava2    Ban1    Ban2    Bbv1   BceA1    Bfa1   Bme15
   BsaA1   BsaH1   BsaJ1   BsaW1   BseM2   BsiE1   BsiH1    Bsl1   BsmA1   BsmF1   Bsp12   BspCa   BspCb    Bsr1
   BsrF1   BssK1   BstF5   BstN1   BstU1   BstY1    Btg1    Cac8   CviJ1    Dde1    Eae1   EcoO1    Fau1   Fnu4H
    Fok1    Hae2    Hae3    Hga1    Hha1   Hinc2   Hinf1   HinP1    Hpa2    Hph1   Hpy99    Hpy1    Hpy3   HpyC3
   HpyC4   HpyC5    Mae3    Mbo2    Mnl1    Mse1    Msl1   MspA1    Mwo1    Nci1    Nla3    Nla4    Nsp1    Ple1
   PpuM1    Rsa1   Sau3A   Sau96   SfaN1    Sfc1    Sml1    Sty1    Taq1    Tat1    Tfi1    Tse1   Tsp45   Tsp50
   TspR1
```