pFusionRed-annexin 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, annexin 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
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                                             Xho1
                                         Bgl2   |
                                      BseR1 |   |    Hind3
                                   BpuE1  | |   |   Sac1 |  EcoR1       Nco1
             SpDon             BspE1   |  | |   | Ecl2 | |BstB1 |      Msc1| BsaXa       Eco57             BsaXb
                 |                 |   |  | |   |    | | |    | |         ||     |           |                 |
               GAGGTAAAGGTGGAGGAGGTTCCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCTATGGCCATGGCAACCAAAGGAGGTACTGTCAAAGCTGCTTCAGG
         1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
               CTCCATTTCCACCTCCTCCAAGGCCTGAGTCTAGAGCTCGAGTTCGAAGCTTAAGATACCGGTACCGTTGGTTTCCTCCATGACAGTTTCGACGAAGTCC
FusionRed/   >   G  K  G  G  G  G  S  G  L  R  S  R  A  Q  A  S  N  S  M  A  M  A  T  K  G  G  T  V  K  A  A  S  G
      Annexin

                                          EcoN1
                                       Bsu36  |
                                      SpAcc|  |
                    Nco1              AlwN1|  |                                 Bbs1
                       |                  ||  |                                    |
               ATTCAATGCCATGGAAGATGCCCAGACCCTGAGGAAGGCCATGAAAGGGCTCGGCACCGATGAAGACGCCATTATTAGCGTCCTTGCCTACCGCAACACC
         1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
               TAAGTTACGGTACCTTCTACGGGTCTGGGACTCCTTCCGGTACTTTCCCGAGCCGTGGCTACTTCTGCGGTAATAATCGCAGGAACGGATGGCGTTGTGG
Annexin      >  F  N  A  M  E  D  A  Q  T  L  R  K  A  M  K  G  L  G  T  D  E  D  A  I  I  S  V  L  A  Y  R  N  T

                                                                                               Eco57
                                                                                              BspM1|
            BseY1                   SpAcc                                    Ahd1              Aar1|
                |                       |                                       |                 ||
               GCCCAGCGCCAGGAGATCAGGACAGCCTACAAGAGCACCATCGGCAGGGACTTGATAGACGACCTGAAGTCAGAACTGAGTGGCAACTTCGAGCAGGTGA
         1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
               CGGGTCGCGGTCCTCTAGTCCTGTCGGATGTTCTCGTGGTAGCCGTCCCTGAACTATCTGCTGGACTTCAGTCTTGACTCACCGTTGAAGCTCGTCCACT
Annexin      > A  Q  R  Q  E  I  R  T  A  Y  K  S  T  I  G  R  D  L  I  D  D  L  K  S  E  L  S  G  N  F  E  Q  V  I

                                                      SpAcc                    Nae1
                                             BmgB1    BstAP                 NgoM4 |
                                                 |        |                     | |
               TTGTGGGGATGATGACGCCCACGGTGCTGTATGACGTGCAAGAGCTGCGAAGGGCCATGAAGGGAGCCGGCACTGATGAGGGCTGCCTAATTGAGATCCT
         1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
               AACACCCCTACTACTGCGGGTGCCACGACATACTGCACGTTCTCGACGCTTCCCGGTACTTCCCTCGGCCGTGACTACTCCCGACGGATTAACTCTAGGA
Annexin      >   V  G  M  M  T  P  T  V  L  Y  D  V  Q  E  L  R  R  A  M  K  G  A  G  T  D  E  G  C  L  I  E  I  L
```

```
                         Bsu36
                        SpAcc|            BseR1                 Xcm1
                            ||                |                    |
               GGCCTCCCGGACCCCTGAGGAGATCCGGCGCATAAGCCAAACCTACCAGCAGCAATATGGACGGAGCCTTGAAGATGACATTCGCTCTGACACATCGTTC
         1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
               CCGGAGGGCCTGGGGACTCCTCTAGGCCGCGTATTCGGTTTGGATGGTCGTCGTTATACCTGCCTCGGAACTTCTACTGTAAGCGAGACTGTGTAGCAAG
Annexin      >  A  S  R  T  P  E  E  I  R  R  I  S  Q  T  Y  Q  Q  Q  Y  G  R  S  L  E  D  D  I  R  S  D  T  S  F

                                                                                                           EcoN1
                                          Pvu2   _Chi                           BssS1                  AlwN1   |
                                             |      |                               |                      |   |
               ATGTTCCAGCGAGTGCTGGTGTCTCTGTCAGCTGGTGGGAGGGATGAAGGAAATTATCTGGACGATGCTCTCGTGAGACAGGATGCCCAGGACCTGTATG
         1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
               TACAAGGTCGCTCACGACCACAGAGACAGTCGACCACCCTCCCTACTTCCTTTAATAGACCTGCTACGAGAGCACTCTGTCCTACGGGTCCTGGACATAC
Annexin      > M  F  Q  R  V  L  V  S  L  S  A  G  G  R  D  E  G  N  Y  L  D  D  A  L  V  R  Q  D  A  Q  D  L  Y  E

             SpAcc                  Bpm1  SpDon
                 |                     |      |
               AGGCTGGAGAGAAGAAATGGGGGACAGATGAGGTGAAATTTCTAACTGTTCTCTGTTCCCGGAACCGAAATCACCTGTTGCATGTGTTTGATGAATACAA
         1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
               TCCGACCTCTCTTCTTTACCCCCTGTCTACTCCACTTTAAAGATTGACAAGAGACAAGGGCCTTGGCTTTAGTGGACAACGTACACAAACTACTTATGTT
Annexin      >   A  G  E  K  K  W  G  T  D  E  V  K  F  L  T  V  L  C  S  R  N  R  N  H  L  L  H  V  F  D  E  Y  K

                EcoRV                                                                    SpDon
                    |                                                                        |
               AAGGATATCACAGAAGGATATTGAACAGAGTATTAAATCTGAAACATCTGGTAGCTTTGAAGATGCTCTGCTGGCTATAGTAAAGTGCATGAGGAACAAA
         2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
               TTCCTATAGTGTCTTCCTATAACTTGTCTCATAATTTAGACTTTGTAGACCATCGAAACTTCTACGAGACGACCGATATCATTTCACGTACTCCTTGTTT
Annexin      >  R  I  S  Q  K  D  I  E  Q  S  I  K  S  E  T  S  G  S  F  E  D  A  L  L  A  I  V  K  C  M  R  N  K

                    BstAP                 Cla1                                            Xho1          BspLU
                        |                    |                                               |              |
               TCTGCATATTTTGCTGAAAAGCTCTATAAATCGATGAAGGGCTTGGGCACCGATGATAACACCCTCATCAGAGTGATGGTTTCTCGAGCAGAAATTGACA
         2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
               AGACGTATAAAACGACTTTTCGAGATATTTAGCTACTTCCCGAACCCGTGGCTACTATTGTGGGAGTAGTCTCACTACCAAAGAGCTCGTCTTTAACTGT
Annexin      > S  A  Y  F  A  E  K  L  Y  K  S  M  K  G  L  G  T  D  D  N  T  L  I  R  V  M  V  S  R  A  E  I  D  M
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                                                                                                         Bpm1
                  EcoRV                  SpAcc                                           SpAcc        Sca1  |
                      |                      |                                               |           |  |
               TGTTGGATATCCGGGCACACTTCAAGAGACTCTATGGAAAGTCTCTGTACTCGTTCATCAAGGGTGACACATCTGGAGACTACAGGAAAGTACTGCTTGT
         2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
               ACAACCTATAGGCCCGTGTGAAGTTCTCTGAGATACCTTTCAGAGACATGAGCAAGTAGTTCCCACTGTGTAGACCTCTGATGTCCTTTCATGACGAACA
Annexin      >   L  D  I  R  A  H  F  K  R  L  Y  G  K  S  L  Y  S  F  I  K  G  D  T  S  G  D  Y  R  K  V  L  L  V

                                  BseR1
             SpAcc               BamH1|       Xba1      Bcl1BsaB1                            SpDon   Dra1
                 |                   ||          |         |    |                                |      |
               TCTCTGTGGAGGAGATGATTAAGGATCCACCGGATCTAGATAACTGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTC
         2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
               AGAGACACCTCCTCTACTAATTCCTAGGTGGCCTAGATCTATTGACTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAG
Annexin      >  L  C  G  G  D  D  *

                                                  Bsm1
                                                 Mfe1|        Hpa1       polyA    Psi1      polyA
                                                    ||           |           |       |          |
               CCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCA
         2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
               GGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGT

                     polyA            Bts1 Bsm1                                      Mlu1     SpDon        Ssp1
                         |               |    |                                         |         |           |
               CAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAACGCGTAAATTGTAAGCGTTAATATTT
         2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
               GTTTAAAGTGTTTATTTCGTAAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTGCGCATTTAACATTCGCAATTATAAA

                                                                                       Psi1
                                                                                          |
               TGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGAT
         2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
               ACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTA

                                                BsaXb                Drd1    BsaXa
                                                    |                    |       |
               AGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCA
         2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
               TCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGT
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      BtgZ1
      Dra3|                                                         SpAcc
         ||                                                             |
      CTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGG
2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
      GATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCC


         Nae1
      NgoM4 |                                    BsrB1
          | |                                        |
      GAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCAC
2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
      CTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTG


                                                                                     polyA
                                                                                         |
      ACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCA
3001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
      TGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGT


                  BciV1
               BspH1  |                                                                   Eci1
             BsrB1 |  |                            Ssp1  Ear1        Bsu36              Pvu2 |
                 | |  |                               |     |            |                 | |
      AATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTG
3101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
      TTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACAC


                                                              Nsi1
                                                            Sph1 |
                                                           BfrB1 |
                                BseY1                   BstAP  | |            SexA1
                                    |                       |  | |                |
      TCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGC
3201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
      AGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCG
```

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                                  Nsi1
                                Sph1 |
                               BfrB1 |                                                      Eci1
    BseY1              BstAP  | |                       Eci1                 Eci1     Bmr1|
        |                       |  | |                          |                    |        ||
      TCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTT
3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
      AGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAA

                                                                 Sfi1
   Eci1            Nco1                   polyA                  Bgl1                    SpDon
      |               |                       |                     |                        |
      CCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTT
3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
      GGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAA

            Avr2
           Stu1|
       BseR1  ||              Cla1              BsaB1                       BspM1               Eag1
           |  ||                 |                  |                           |                  |
      TTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGC
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      AAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCG

                                                                                          Nar1
                                       Bmr1                                              Kas1|
                                          |                                                 ||
      TTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTT
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      AACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAA

                                                                                                Pvu2
                 Drd1                                                   Msc1                Fsp1   |
                    |                                                      |                   |   |
      TTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGC
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      AAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACG
```

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       PflF1                       Eco57                                      SpDon
           |                           |                                          |
      TCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATC
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      AGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAG

                                                            BtgZ1
        BciV1         BsrD1                              BspM1  |
            |             |                                  |  |
      CATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGG
3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
      GTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCC

                                  Sap1
                                  Ear1                           BpuE1                         Sph1
                                     |                               |                            |
      ATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACG
4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
      TACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGC

                                                                                             BseY1
                                                                                            Nae1 |
                      Nco1               BtgZ1                                           NgoM4 | |
                         |                   |                                               | | |
      GCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGT
4101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
      CGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACA

                                            Sap1
      Rsr2         Eci1                     Ear1                   Eco57         BssS1
         |            |                        |                       |             |
      GGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCC
4201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
      CCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGG
```

```
    BtgZ1
  BsrB1 |                                               BsrB1          BstB1
      | |                                                   |              |
      GCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCT
4301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
      CGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGA


                                                                           Nae1
       BssS1                                                            NgoM4 |
       BspM1                      SpAcc                                  Bpm1 |
           |                          |                                     | |
      GCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGAT
4401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
      CGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTA


                              Bpm1
                          SpAcc  |
                           Avr2  |                                                        polyA
                              |  |                                                            |
      CTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGAC
4501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
      GAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTG


   polyA                                                                       Bsa1
       |                                                                          |
      AGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCA
4601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
      TCTTATTTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGT


                                                                                          BstAP
                                                                                          AlwN1
                                                                                              |
      ATACGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCC
4701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
      TATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGG
```

```
 Bsu36                            Dra1               Dra1                              BspH1
     |                               |                  |                                  |
      TCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCC
4801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
      AGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGG


                                                                                   BpuE1
                                                                                       |
      CTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCA
4901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
      GAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGT


                                                                 Eco57
                                                                     |
      AACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCA
5001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
      TTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGT


                 SpAcc                                                                            AlwN1
                     |                                                                                |
      AATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTG
5101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
      TTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGAC


                        BpuE1                                                               ApaL1
                            |                                                                   |
      CTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACA
5201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
      GACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGT


   BseY1                                             SpAcc
       |                                                 |
      GCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTAT
5301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5400
      CGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATA
```

```
         BciV1
      Eci1   |                    BssS1                                    SpAcc
         |   |                        |                                        |
      CCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGAC
5401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5500
      GGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTG


      Drd1            BpuE1               SpAcc     Eci1
         |                |                   |        |
      TTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTT
5501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5600
      AACTCGCAGCTAAAAACACTACGAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAA


        SpDon                                                    Nsi1
       BspLU|                                                 BfrB1 |
           ||                                                     | |
      TGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
5601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||| 5664
      ACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aar1 Aat2 **Afe1** **Age1** **Ahd1** **Ale1** AlwN1 ApaL1 **Ase1** Avr2 **BamH1** Bbs1 BciV1 **Bcl1**
BfrB1 Bgl1 **Bgl2** **BmgB1** Bmr1 Bpm1 BpuE1 Bsa1 BsaB1 BsaXa BsaXb BseR1 BseY1 Bsm1
BsmB1 **BspE1** BspH1 BspLU BspM1 BsrB1 **BsrD1** **BsrG1** BssS1 BstAP BstB1 Bsu36 BtgZ1 **Bts1**
_Chi Cla1 Dra1 Dra3 Drd1 **Eag1** Ear1 Eci1 **Ecl2** Eco57 EcoN1 **EcoR1** EcoRV **Fsp1**
Hind3 **Hpa1** **Kas1** **Mfe1** **Mlu1** Msc1 Nae1 **Nar1** Nco1 **Nde1** NgoM4 **Nhe1** Nsi1 **PflF1**
PflM1 polyA **PshA1** Psi1 Pvu2 **Rsr2** **Sac1** Sap1 **Sca1** **SexA1** **Sfi1** **SnaB1** SpAcc SpDon
Sph1 Ssp1 Stu1 **Xba1** **Xcm1** Xho1

Unique:

Aar1 **Afe1** **Age1** **Ahd1** **Ale1** **Ase1** **BamH1** **Bcl1** **Bgl2** **BmgB1** **BsmB1** **BspE1** **BsrD1** **BsrG1**
Bts1 **_Chi** **Eag1** **Ecl2** **EcoR1** **Fsp1** **Hind3** **Hpa1** **Kas1** **Mfe1** **Mlu1** **Nar1** **Nde1** **Nhe1**
PflF1 **PflM1** **PshA1** **Rsr2** **Sac1** **Sca1** **SexA1** **Sfi1** **SnaB1** **Xba1** **Xcm1**

Not found:

Acc65 Acl1 Afl2 Apa1 Asc1 AsiS1 Bae1a Bae1b BbvC1 Bcg1a Bcg1b Blp1 Bpu10 Bsg1
BsiW1 BssH2 BstE2 BstX1 BstZ1 BxatB BxatL BxatR BxatP EcoK FCatB FCatL FCatR FCatP
ScFRT Fse1 FspA1 I_Ceu Kpn1 loxP Not1 Nru1 Pac1 Pme1 Pml1 PspOM Pst1 Pvu1
R4atB R4atL R4atP R4atR Sac2 Sal1 SanD1 Sbf1 Sgf1 SgrA1 Sma1 Spe1 Srf1 Swa1
T3RNA T7RNA T7Ter PISce 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