peTurboGFP-PRL-dest1 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 shown in bold blue. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site).

MCS sequence shown in frame, amino acids coded by MCS and MODC amino acids are shown in bold black.

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                                                                                        BamH1
                                                                                       Sma1 |
                                                                                      Apa1| |
                                                                                 PspOM   || |
                                                  Hind3                          Sac2|   || |
                                          Xho1   Sac1 |  EcoR1      Sal1      Kpn1  ||   || |
                         Afe1   BpuE1 Bgl2   | Ecl2 | |BstB1 |     Pst1| Acc65   |  ||   || |  Age1       Nco1
                            |       |    |   |    | | |    | |        ||     |   |  ||   || |     |          |
               TAGTTATTACTAGCGCTACCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCTGCAGTCGACGGTACCGCGGGCCCGGGATCCACCGGTCGCCACCATGG
            1  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 100
               ATCAATAATGATCGCGATGGCCTGAGTCTAGAGCTCGAGTTCGAAGCTTAAGACGTCAGCTGCCATGGCGCCCGGGCCCTAGGTGGCCAGCGGTGGTACC
MCS/TurboGFP >    L  L  L  A  L  P  D  S  D  L  E  L  K  L  R  I  L  Q  S  T  V  P  R  A  R  D  P  P  V  A  T  M  E


                                    Nco1
                       BsrB1   BsaXa   |                     BsaXb                             _Chi
                           |       |   |                         |                                |
               AGAGCGACGAGAGCGGCCTGCCCGCCATGGAGATCGAGTGCCGCATCACCGGCACCCTGAACGGCGTGGAGTTCGAGCTGGTGGGCGGCGGAGAGGGCAC
          101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 200
               TCTCGCTGCTCTCGCCGGACGGGCGGTACCTCTAGCTCACGGCGTAGTGGCCGTGGGACTTGCCGCACCTCAAGCTCGACCACCCGCCGCCTCTCCCGTG
TurboGFP     >   S  D  E  S  G  L  P  A  M  E  I  E  C  R  I  T  G  T  L  N  G  V  E  F  E  L  V  G  G  G  E  G  T
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                                                                                            PflM1
                                                        Nar1                              Pml1  |
                                     Sap1              Kas1|                         BspM1   |  |
              Eci1                   Ear1         Eco57   ||                      Blp1   |   |  |
                 |                      |             |   ||                         |   |   |  |
               CCCCGAGCAGGGCCGCATGACCAACAAGATGAAGAGCACCAAAGGCGCCCTGACCTTCAGCCCCTACCTGCTGAGCCACGTGATGGGCTACGGCTTCTAC
          201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 300
               GGGGCTCGTCCCGGCGTACTGGTTGTTCTACTTCTCGTGGTTTCCGCGGGACTGGAAGTCGGGGATGGACGACTCGGTGCACTACCCGATGCCGAAGATG
TurboGFP     >  P  E  Q  G  R  M  T  N  K  M  K  S  T  K  G  A  L  T  F  S  P  Y  L  L  S  H  V  M  G  Y  G  F  Y

                                    Bsg1
                          BseY1  SpAcc |     Xmn1                                                     Bsg1
                              |      | |        |                                                        |
               CACTTCGGCACCTACCCCAGCGGCTACGAGAACCCCTTCCTGCACGCCATCAACAACGGCGGCTACACCAACACCCGCATCGAGAAGTACGAGGACGGCG
          301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 400
               GTGAAGCCGTGGATGGGGTCGCCGATGCTCTTGGGGAAGGACGTGCGGTAGTTGTTGCCGCCGATGTGGTTGTGGGCGTAGCTCTTCATGCTCCTGCCGC
TurboGFP     > H  F  G  T  Y  P  S  G  Y  E  N  P  F  L  H  A  I  N  N  G  G  Y  T  N  T  R  I  E  K  Y  E  D  G  G

                                                   Fse1
                                                 Nae1 |
                                                 Eag1 |
            Eco57     Pml1                    NgoM4 | |
                |        |                        | | |
               GCGTGCTGCACGTGAGCTTCAGCTACCGCTACGAGGCCGGCCGCGTGATCGGCGACTTCAAGGTGATGGGCACCGGCTTCCCCGAGGACAGCGTGATCTT
          401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 500
               CGCACGACGTGCACTCGAAGTCGATGGCGATGCTCCGGCCGGCGCACTAGCCGCTGAAGTTCCACTACCCGTGGCCGAAGGGGCTCCTGTCGCACTAGAA
TurboGFP     >   V  L  H  V  S  F  S  Y  R  Y  E  A  G  R  V  I  G  D  F  K  V  M  G  T  G  F  P  E  D  S  V  I  F

                                                           Nco1
                                                          BspM1
                                     Bsg1                  Aar1       BsaB1        Eco57
                                        |                     |           |            |
               CACCGACAAGATCATCCGCAGCAACGCCACCGTGGAGCACCTGCACCCCATGGGCGATAACGATCTGGATGGCAGCTTCACCCGCACCTTCAGCCTGCGC
          501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
               GTGGCTGTTCTAGTAGGCGTCGTTGCGGTGGCACCTCGTGGACGTGGGGTACCCGCTATTGCTAGACCTACCGTCGAAGTGGGCGTGGAAGTCGGACGCG
TurboGFP     >  T  D  K  I  I  R  S  N  A  T  V  E  H  L  H  P  M  G  D  N  D  L  D  G  S  F  T  R  T  F  S  L  R
```

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                                                                                                    Eci1
                                                                                               Apa1    |
            BsaXb                         BsaXa                         BseY1         Pst1  PspOM   |  |
                |                             |                             |            |      |   |  |
                GACGGCGGCTACTACAGCTCCGTGGTGGACAGCCACATGCACTTCAAGAGCGCCATCCACCCCAGCATCCTGCAGAACGGGGGCCCCATGTTCGCCTTCC
           601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
                CTGCCGCCGATGATGTCGAGGCACCACCTGTCGGTGTACGTGAAGTTCTCGCGGTAGGTGGGGTCGTAGGACGTCTTGCCCCCGGGGTACAAGCGGAAGG
TurboGFP      > D  G  G  Y  Y  S  S  V  V  D  S  H  M  H  F  K  S  A  I  H  P  S  I  L  Q  N  G  G  P  M  F  A  F  R

                                                                                                             Xho1
                                   BseR1   BseY1                                                         Bgl2   |
                                       |       |                                                            |   |
                GCCGCGTGGAGGAGGATCACAGCAACACCGAGCTGGGCATCGTGGAGTACCAGCACGCCTTCAAGACCCCGGATGCAGATGCCGGTGAAGAAAGATCTCG
           701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
                CGGCGCACCTCCTCCTAGTGTCGTTGTGGCTCGACCCGTAGCACCTCATGGTCGTGCGGAAGTTCTGGGGCCTACGTCTACGGCCACTTCTTTCTAGAGC
TurboGFP      >   R  V  E  E  D  H  S  N  T  E  L  G  I  V  E  Y  Q  H  A  F  K  T  P  D  A  D  A  G  E  E  R  S  R

                                    Nae1
                                 SgrA1 |
               EcoRV  Nco1       NgoM4 |                                                 BsrB1
                   |     |           | |                                                     |
                AGATATCAGCCATGGCTTCCCGCCGGCGGTGGCGGCGCAGGATGATGGCACGCTGCCCATGTCTTGTGCCCAGGAGAGCGGGATGGACCGTCACCCTGCA
           801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
                TCTATAGTCGGTACCGAAGGGCGGCCGCCACCGCCGCGTCCTACTACCGTGCGACGGGTACAGAACACGGGTCCTCTCGCCCTACCTGGCAGTGGGACGT
MODC          >  D  I  S  H  G  F  P  P  A  V  A  A  Q  D  D  G  T  L  P  M  S  C  A  Q  E  S  G  M  D  R  H  P  A

                                            Not1                  BamH1
               BstAP                        Eag1            Pml1  |
            Pst1   |                        Bsg1           Eco57  |                         SanD1
               |   |                           |                   |  |                             |
                GCCTGTGCTTCTGCTAGGATCAATGTGTAGGCGGCCGCGTGACAAGCTGCACGTGGATCCTGAGAACTTCAGGGTGAGTCTATGGGACCCTTGATGTTTT
           901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
                CGGACACGAAGACGATCCTAGTTACACATCCGCCGGCGCACTGTTCGACGTGCACCTAGGACTCTTGAAGTCCCACTCAGATACCCTGGGAACTACAAAA
MODC          > A  C  A  S  A  R  I  N  V  *

                CTTTCCCCTTCTTTTCTATGGTTAAGTTCATGTCATAGGAAGGGGATAAGTAACAGGGTACAGTTTAGAATGGGAAACAGACGAATGATTGCATCAGTGT
          1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
                GAAAGGGGAAGAAAAGATACCAATTCAAGTACAGTATCCTTCCCCTATTCATTGTCCCATGTCAAATCTTACCCTTTGTCTGCTTACTAACGTAGTCACA
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                                  polyA         Mfe1
                                      |            |
      GGAAGTCTCAGGATCGTTTTAGTTTCTTTTATTTGCTGTTCATAACAATTGTTTTCTTTTGTTTAATTCTTGCTTTCTTTTTTTTTCTTCTCCGCAATTT
1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
      CCTTCAGAGTCCTAGCAAAATCAAAGAAAATAAACGACAAGTATTGTTAACAAAAGAAAACAAATTAAGAACGAAAGAAAAAAAAAGAAGAGGCGTTAAA

     SpDon
         |
      TTACTATTATACTTAATGCCTTAACATTGTGTATAACAAAAGGAAATATCTCTGAGATACATTAAGTAACTTAAAAAAAAACTTTACACAGTCTGCCTAG
1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
      AATGATAATATGAATTACGGAATTGTAACACATATTGTTTTCCTTTATAGAGACTCTATGTAATTCATTGAATTTTTTTTTGAAATGTGTCAGACGGATC

                                                              polyA     polyA
                                                                  |         |
      TACATTACTATTTGGAATATATGTGTGCTTATTTGCATATTCATAATCTCCCTACTTTATTTTCTTTTATTTTTAATTGATACATAATCATTATACATAT
1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
      ATGTAATGATAAACCTTATATACACACGAATAAACGTATAAGTATTAGAGGGATGAAATAAAAGAAAATAAAAATTAACTATGTATTAGTAATATGTATA

                                BsrG1                                         Dra1
                                    |                                            |
      TTATGGGTTAAAGTGTAATGTTTTAATATGTGTACACATATTGACCAAATCAGGGTAATTTTGCATTTGTAATTTTAAAAAATGCTTTCTTCTTTTAATA
1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
      AATACCCAATTTCACATTACAAAATTATACACATGTGTATAACTGGTTTAGTCCCATTAAAACGTAAACATTAAAATTTTTTACGAAAGAAGAAAATTAT

                                                     SpAcc
                                                         |
      TACTTTTTTGTTTATCTTATTTCTAATACTTTCCCTAATCTCTTTCTTTCAGGGCAATAATGATACAATGTATCATGCCTCTTTGCACCATTCTAAAGAA
1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
      ATGAAAAAACAAATAGAATAAAGATTATGAAAGGGATTAGAGAAAGAAAGTCCCGTTATTACTATGTTACATAGTACGGAGAAACGTGGTAAGATTTCTT

                                      Ssp1            Ssp1                     SpDon
                                         |               |                         |
      TAACAGTGATAATTTCTGGGTTAAGGCAATAGCAATATTTCTGCATATAAATATTTCTGCATATAAATTGTAACTGATGTAAGAGGTTTCATATTGCTAA
1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
      ATTGTCACTATTAAAGACCCAATTCCGTTATCGTTATAAAGACGTATATTTATAAAGACGTATATTTAACATTGACTACATTCTCCAAAGTATAACGATT
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                                      polyA
                                          |
       TAGCAGCTACAATCCAGCTACCATTCTGCTTTTATTTTATGGTTGGGATAAGGCTGGATTATTCTGAGTCCAAGCTAGGCCCTTTTGCTAATCATGTTCA
1701   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
       ATCGTCGATGTTAGGTCGATGGTAAGACGAAAATAAAATACCAACCCTATTCCGACCTAATAAGACTCAGGTTCGATCCGGGAAAACGATTAGTACAAGT

                            AlwN1
                         SpAcc  |                                BstX1    EcoR1
                             |  |                                    |        |
       TACTTCTTATCTTCCTCCCACAGCTCCTGGGCAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCACCCCACCAGTGCAGGCTGCCTA
1801   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
       ATGAAGAATAGAAGGAGGGTGTCGAGGACCCGTTGCACGACCAGACACACGACCGGGTAGTGAAACCGTTTCTTAAGTGGGGTGGTCACGTCCGACGGAT

           Bsg1
              |
       TCAGAAAGTGGTGGCTGGTGTGGCTAATGCCCTGGCCCACAAGTATCACTAAGCTCGCTTTCTTGCTGTCCAATTTCTATTAAAGGTTCCTTTGTTCCCT
1901   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
       AGTCTTTCACCACCGACCACACCGATTACGGGACCGGGTGTTCATAGTGATTCGAGCGAAAGAACGACAGGTTAAAGATAATTTCCAAGGAAACAAGGGA

                                                             BpuE1
                             Bmr1                            Xba1|  BsaB1                            SpDon
                                |                               ||      |                                |
       AAGTCCAACTACTAAACTGGGGGATATTATGAAGGGCCTTGAGCATTGGATTCTGCCTCTAGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACT
2001   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
       TTCAGGTTGATGATTTGACCCCCTATAATACTTCCCGGAACTCGTAACCTAAGACGGAGATCTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGA

                                                          Bsm1
         Dra1                                            Mfe1|        Hpa1       polyA    Psi1      polyA
            |                                               ||           |           |       |          |
       TGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAA
2101   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
       ACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTT

                             polyA            Bts1 Bsm1                                  Afl2
                                 |               |    |                                     |
       TAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATT
2201   |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
       ATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTCCGCATTTAA
```

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 SpDon        Ssp1                                                                            Psi1
     |           |                                                                               |
      GTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAA
2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
      CATTCGCAATTATAAAACAATTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTT

                                                       BsaXb                 Drd1    BsaXa
                                                           |                    |        |
      AAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTA
2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
      TTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGAT

                      BtgZ1
                      Dra3|                                                         SpAcc
                         ||                                                             |
      TCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGA
2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
      AGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCT

                         Nae1
                      NgoM4 |                                    BsrB1
                          | |                                        |
      TTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGC
2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
      AAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCG


      TGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATT
2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
      ACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAA

                                  BciV1
                               BspH1  |
 polyA                       BsrB1 |  |                            Ssp1  Ear1        Bsu36
     |                           | |  |                               |     |            |
      TTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACC
2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
      AAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGG
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                                                                              Nsi1
                                                                            Sph1 |
      Eci1                                                                 BfrB1 |
    Pvu2 |                                      BseY1                   BstAP  | |            SexA1
       | |                                          |                       |  | |                |
      AGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTG
2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
      TCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCAC

                                                  Nsi1
                                                Sph1 |
                                               BfrB1 |
                    BseY1                   BstAP  | |                       Eci1                 Eci1
                        |                       |  | |                          |                    |
      TGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCC
3001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
      ACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGG

        Eci1                                                                     Sfi1
       Bmr1|       Eci1            Nco1                   polyA                  Bgl1
          ||          |               |                       |                     |
      CTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGA
3101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
      GATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCT

                            Avr2
                           Stu1|
     SpDon             BseR1  ||              Cla1              BsaB1                       BspM1
         |                 |  ||                 |                  |                           |
      AGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACG
3201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
      TCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGC

            Eag1                                       Bmr1
               |                                          |
      CAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCA
3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
      GTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGT
```

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      Nar1
     Kas1|                       Drd1                                                   Msc1
        ||                          |                                                      |
      GGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTT
3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
      CCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAA

            Pvu2
        Fsp1   |       PflF1                       Eco57                                      SpDon
           |   |           |                           |                                          |
      CCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTC
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      GGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAG

                                                                            BtgZ1
                        BciV1         BsrD1                              BspM1  |
                            |             |                                  |  |
      CTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGA
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      GACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCT

                                                  Sap1
                                                  Ear1                           BpuE1
                                                     |                               |
      GCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAG
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      CGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTC

           Sph1                       Nco1               BtgZ1
              |                          |                   |
      GCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACT
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      CGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGA
```

```
         BseY1
        Nae1 |                                              Sap1
     NgoM4 | |        Rsr2         Eci1                     Ear1                   Eco57         BssS1
         | | |           |            |                        |                       |             |
      GTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGT
3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
      CACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCA

                    BtgZ1
                  BsrB1 |                                               BsrB1          BstB1
                      | |                                                   |              |
      GCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACC
4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
      CGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGG

                                                                                           Nae1
                       BssS1                                                            NgoM4 |
                       BspM1                      SpAcc                                  Bpm1 |
                           |                          |                                     | |
      AAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGAT
4101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
      TTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTA

                                              Bpm1
                                          SpAcc  |
                                           Avr2  |
                                              |  |
      CCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATG
4201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
      GGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATAC

      polyA        polyA                                                                       Bsa1
          |            |                                                                          |
      ACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGA
4301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
      TGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCT
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      GACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGC
4401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
      CTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCG

      BstAP
      AlwN1      Bsu36                            Dra1                 Dra1
          |          |                              |                  |
      AGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAAT
4501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
      TCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTA

   BspH1                                                                                     BpuE1
       |                                                                                         |
      CTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCG
4601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
      GAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGC

                                                                                 Eco57
                                                                                     |
      TAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAG
4701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
      ATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTC

                                 SpAcc
                                     |
      CAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATC
4801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
      GTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAG

              AlwN1                     BpuE1
                  |                         |
      CTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGG
4901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
      GACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCC
```

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         ApaL1     BseY1                                             SpAcc
             |         |                                                 |
      GGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAG
5001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
      CCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTC


                         BciV1
                      Eci1   |                    BssS1                                    SpAcc
                         |   |                        |                                        |
      AAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGG
5101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
      TTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCC


                      Drd1            BpuE1               SpAcc     Eci1
                         |                |                   |        |
      TTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGG
5201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
      AAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACC


                        SpDon                                                    Nsi1
                       BspLU|                                                 BfrB1 |
                           ||                                                     | |
      CCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
5301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5380
      GGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aar1 **Acc65** **Afe1** **Afl2** **Age1** AlwN1 Apa1 **ApaL1** Avr2 BamH1 BciV1 BfrB1 **Bgl1** Bgl2
Blp1 Bmr1 Bpm1 BpuE1 **Bsa1** BsaB1 BsaXa BsaXb BseR1 BseY1 Bsg1 Bsm1 BspH1 **BspLU**
BspM1 BsrB1 **BsrD1** **BsrG1** BssS1 BstAP BstB1 **BstX1** Bsu36 BtgZ1 **Bts1** **_Chi** **Cla1** Dra1
Dra3 Drd1 Eag1 Ear1 Eci1 **Ecl2** Eco57 EcoR1 **EcoRV** **Fse1** **Fsp1** **Hind3** **Hpa1** Kas1
Kpn1 Mfe1 **Msc1** Nae1 Nar1 Nco1 NgoM4 **Not1** Nsi1 **PflF1** **PflM1** Pml1 polyA Psi1
PspOM Pst1 Pvu2 **Rsr2** **Sac1** **Sac2** **Sal1** **SanD1** Sap1 **SexA1** **Sfi1** **SgrA1** **Sma1** SpAcc
SpDon Sph1 Ssp1 **Stu1** **Xba1** Xho1 **Xmn1**

Unique:

Aar1 **Acc65** **Afe1** **Afl2** **Age1** **ApaL1** **Bgl1** **Blp1** **Bsa1** **BspLU** **BsrD1** **BsrG1** **BstX1** **Bts1**
_Chi **Cla1** **Dra3** **Ecl2** **EcoRV** **Fse1** **Fsp1** **Hind3** **Hpa1** **Kpn1** **Msc1** **Not1** **PflF1** **PflM1**
Rsr2 **Sac1** **Sac2** **Sal1** **SanD1** **SexA1** **Sfi1** **SgrA1** **Sma1** **Stu1** **Xba1** **Xmn1**

Not found:

Aat2 Acl1 Ahd1 Ale1 Asc1 Ase1 AsiS1 Baela Baelb Bbs1 BbvC1 Bcgla Bcglb Bcl1
BmgB1 Bpu10 BsiW1 BsmB1 BspE1 BssH2 BstE2 BstZ1 BxatB BxatL BxatR BxatP EcoK EcoN1
FCatB FCatL FCatR FCatP ScFRT FspA1 I_Ceu loxP Mlu1 Nde1 Nhe1 Nru1 Pac1 Pme1
PshA1 Pvu1 R4atB R4atL R4atP R4atR Sbf1 Sca1 Sgf1 SnaB1 Spe1 Srf1 Swa1 T3RNA
T7RNA T7Ter PISce Xcm1

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